RESEARCH CENTER

FIELD

Activity Report 2015

Section Software

Edition: 2016-03-21

ABS Project-Team

5. New Software and Platforms

5.1. The Structural Bioinformatics Library

5.1.1. Web site:

http://sbl.inria.fr

5.1.2. The SBL : Overview

The `SBL` is a generic C++/python library providing algorithms and applications to solve complex problems in computational structural biology (CSB).

For Biologists, the key advantages are:

- comprehensive in silico environment providing applications,
- answering complex bio-physical problems,
- in a robust, fast and reproducible way.

For Developers, the striking facts are:

- broad C++/python toolbox,
- with modular design and careful specifications,
- fostering the development of complex applications.

5.1.3. The SBL : Rationale and Design

Software development generally faces a dichotomy, with on the one hand generic libraries providing methods of ubiquitous interest, and on the other hand application driven libraries targeting specific application areas. Libraries in the former category typically provide state-of-the art low level algorithms carefully specified, at the detriment of high level applications. Libraries in the latter category are generally high level and user-friendly, but the lack of formalism often makes it difficult to couple them to low level algorithms with formal specifications. The `SBL` ambitions to reconcile both software development philosophies, based on an advanced design suited for all classes of users and developers.

In terms of high-level operations, the `SBL` provides various applications revolving around the problem of understanding the relationship between the structure and the function of macro-molecules and their complexes (see below). In terms of low-level operations, the design of the `SBL` is meant to accommodate both the variety of models coding the physical and chemical properties of macro-molecular systems (models based on unions of balls such as van der Walls models or solvent accessible models, or models based on conformations and conformational ensembles), as well as the variety of operations (geometric, topological, and combinatorial) undertaken on these models.

More precisely, the `SBL` consists of the following software components, detailed below:

- `SBL-APPLICATIONS`: high level applications solving specific applied problems.
- `SBL-CORE`: low-level generic C++ classes templated by traits classes specifying C++ concepts [0].
- `SBL-MODELS`: C++ models matching the C++ concepts required to instantiate classes from `SBL-CORE`.
- `SBL-MODULES`: C++ classes instantiating classes from the `SBL-CORE` with specific biophysical models from `SBL-MODELS`. A module may be seen as a black box transforming an input into an output. With modules, an application workflow consists of interconnected modules.

---

[0] The design has been guided by that used in the Computational Geometry Algorithm Library (CGAL), see http://www.cgal.org. In a nutshell, concepts are a type system for types, and models are specific classes following this system.

5.1.4. The SBL for End-users: SBL-APPLICATIONS

End users will find in the `SBL` portable applications running on all platforms (Linux, MacOS, Windows). These applications split into the following categories:

- **Space Filling Models:** applications dealing with molecular models defined by unions of balls.
- **Conformational Analysis:** applications dealing with molecular flexibility.
- **Large assemblies:** applications dealing with macro-molecular assemblies involving from tens to hundreds of macro-molecules.
- **Data Analysis:** applications providing novel data analysis - statistical analysis tools.
- **Data Management:** applications to handle input data and results, using standard tools revolving around the XML file format (in particular the XPath query language). These tools allow automating data storage, parsing and retrieval, so that upon running calculations with applications, statistical analysis and plots are a handful of python lines away.

5.1.5. The SBL for Developers: SBL-CORE, SBL-MODELS and SBL-MODULES

The `SBL` makes it easy to develop novel high-level applications, by providing high level ready to use C++ classes instantiating various biophysical models.

In particular, modules allow the development of applications without the burden of instantiating low level classes. In fact, once modules are available, designing an application merely consists of connecting modules.

5.1.6. SBL-CORE: the SBL for Low-level Developers and Contributors

Low level developments may use classes from / contribute classes to `SBL-CORE` and `SBL-MODELS`. In fact, such developments are equivalent to those based upon C++ libraries such as CGAL (http://www.cgal.org/) or boost C++ libraries (http://www.boost.org/). It should be noticed that the `SBL` heavily relies on these libraries. The `SBL-CORE` is organized into into four sub-sections:

- CADS : Combinatorial Algorithms and Data Structures.
- GT : Computational Geometry and Computational Topology.
- CSB : Computational Structural Biology.
- IO : Input / Output.

It should also be stressed that these packages implement algorithms not available elsewhere, or available in a non-generic guise. Due to the modular structure of the library, should valuable implementations be made available outside the `SBL` (e.g. in CGAL or boost), a substitution may occur.

5.1.7. Interoperability

The `SBL` is interoperable with existing molecular modeling systems, at several levels:

- At the library level, our state-of-the-art algorithms (e.g. the computation of molecular surfaces and volumes) can be integrated within existing software (e.g. molecular dynamics software), by instantiating the required classes from `SBL-CORE`, or using the adequate modules.
- At the application level, our applications can easily be integrated within processing pipelines, since the format used for input and output are standard ones. (For input, the PDB format can always be used. For output, our applications generate XML files.)
- Finally, for visualization purposes, our applications generate outputs for the two reference molecular modeling environments, namely Visual Molecular Dynamics (http://www.ks.uiuc.edu/Research/vmd/) and Pymol (http://www.pymol.org/).

5.1.8. Releases, Distribution, and License

The `SBL` is released under a proprietary open source license, see http://sbl.inria.fr/license/.

The source code is distributed from http://sbl.inria.fr, using tarballs and a git repository. Bugzilla is used to handle user's feedback and bug tracking.

ACUMES Team

5. New Software and Platforms

5.1. BuildingSmart

BuildingSmart interactive visualization
KEYWORDS: Physical simulation - 3D rendering - 3D interaction

- Contact: Abderrahmane Habbal

The aim of the BuildingSmart project is to develop a software environment for the simulation and interactive vizualisation for the design of buildings (structural safety, thermal confort). The software is to be integrated in an immersive space (https://www.youtube.com/watch?v=wAm7faixBak) The project is hosted by the ACUMES team(https://team.inria.fr/acumes) in collaboration with the SED service (Service d'Expérimentation et de Développement) and Experts from ArcelorMittal Construction. The project is financed by an Inria ADT which recruited an experienced engineer (starting in december 2015), whose main task is to study and develop solutions dedicated to interactive vizualisation of building performances (heat, structural) in relation to the Building Information Modeling BIM framework.

5.2. Interoperability between Num3sis and Axel Platforms

Num3sis (http://num3sis.inria.fr) is a modular platform devoted to scientific computing and numerical simulation developed at Inria Sophia Antipolis Mediterranee Center. It is not restricted to a particular application field, but is designed to host complex multidisciplinary simulations. Main application fields are currently Computational Fluid Dynamics and pedestrian traffic simulation (by Acumes team), Computational Electro-Magnetics (by Nachos project-team). Some components of the platform are also used by Tosca project-team for CO2 market simulation and wind simulation (in collaboration with Ciric Inria-Chile), and by Inria Project-Lab C2S@EXA for high-performance computing applications. Finally, Lemon team will initiate developments for costal environment simulation in a near future.

To facilitate the coupling between simulation and CAD (Computer-Aided Design), a refactoring of the grid management has been achieved (supported by ADT Simon). This allows interoperability between num3sis and Axel platform, which is developed by Galaad team and is devoted to algebraic geometry. From a practical point of view, grids generated by Axel can now be used by Num3sis for simulation, while PDE solvers in Num3sis libraries can by used interactively by Axel to simulate physical problems.

AIRSEA Team

6. New Software and Platforms

6.1. AGRIF

Adaptive Grid Refinement In Fortran
FUNCTIONAL DESCRIPTION

AGRIF is a Fortran 90 package for the integration of full adaptive mesh refinement (AMR) features within a multidimensional finite difference model written in Fortran. Its main objective is to simplify the integration of AMR potentialities within an existing model with minimal changes. Capabilities of this package include the management of an arbitrary number of grids, horizontal and/or vertical refinements, dynamic regridding, parallelization of the grids interactions on distributed memory computers. AGRIF requires the model to be discretized on a structured grid, like it is typically done in ocean or atmosphere modelling.

- Participants: Laurent Debreu, Marc Honnorat
- Contact: Laurent Debreu
- URL: http://www-ljk.imag.fr/MOISE/AGRIF

6.2. BALAISE

Bilbliothèque d'Assimilation Lagrangienne Adaptée aux Images Séquencées en Environnement
KEYWORDS: Multi-scale analysis - Data assimilation - Optimal control
FUNCTIONAL DESCRIPTION

BALAISE (Bilbliothèque d'Assimilation Lagrangienne Adaptée aux Images Séquencées en Environnement) is a test bed for image data assimilation. It includes a shallow water model, a multi-scale decomposition library and an assimilation suite.

- Contact: Arthur Vidard

6.3. NEMOVAR

Variational data assimilation for NEMO
KEYWORDS: Oceanography - Data assimilation - Adjoint method - Optimal control
FUNCTIONAL DESCRIPTION

NEMOVAR is a state-of-the-art multi-incremental variational data assimilation system with both 3D and 4D capabilities, and which is designed to work with NEMO on the native ORCA grids. The background error covariance matrix is modelled using balance operators for the multivariate component and a diffusion operator for the univariate component. It can also be formulated as a linear combination of covariance models to take into account multiple correlation length scales associated with ocean variability on different scales. NEMOVAR has recently been enhanced with the addition of ensemble data assimilation and multi-grid assimilation capabilities. It is used operationnaly in both ECMWF and the Met Office (UK)

- Partners: CERFACS - ECMWF - Met Office
- Contact: Arthur Vidard

6.4. Sensitivity

FUNCTIONAL DESCRIPTION

This package is useful for conducting sensitivity analysis of complex computer codes.

- Contact: Laurent Gilquin
- URL: https://cran.r-project.org/web/packages/sensitivity/index.html

ALF Project-Team

6. New Software and Platforms

6.1. ATC

Address Trace Compression
KEYWORDS: Compressing - Decompressing - Address traces
FUNCTIONAL DESCRIPTION

ATC is a utility and a C library for compressing/decompressing address traces. It implements a new lossless transformation, Bytesort, that exploits spatial locality in address traces. ATC leverages existing general-purpose compressors such as gzip and bzip2. ATC also provides a lossy compression mode that yields higher compression ratios while preserving certain important characteristics of the original trace.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/alf/software/atc/

6.2. ATMI

Modeling microprocessor temperature.

SCIENTIFIC DESCRIPTION

Research on temperature-aware computer architecture requires a chip temperature model. General purpose models based on classical numerical methods like finite differences or finite elements are not appropriate for such research, because they are generally too slow for modeling the time-varying thermal behavior of a processing chip.

We have developed an ad hoc temperature model, ATMI (Analytical model of Temperature in MIcroprocessors), for studying thermal behaviors over a time scale ranging from microseconds to several minutes. ATMI is based on an explicit solution to the heat equation and on the principle of superposition. ATMI can model any power density map that can be described as a superposition of rectangle sources, which is appropriate for modeling the microarchitectural units of a microprocessor.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/alf/software/atmi/

6.3. Barra

Modelisation of a GPU architecture
KEYWORDS: Simulator - GPU - Computer architecture
SCIENTIFIC DESCRIPTION

Research on throughput-oriented architectures demands accurate and representative models of GPU architectures in order to be able to evaluate new architectural ideas, explore design spaces and characterize applications. The Barra project is a simulator of the NVIDIA Tesla GPU architecture.

Barra builds upon knowledge acquired through micro-benchmarking, in order to provide a baseline model representative of industry practice. The simulator provides detailed statistics to identify optimization opportunities and is fully customizable to experiment ideas of architectural modifications. Barra incorporates both a functional model and a cycle-level performance model.
FUNCTIONAL DESCRIPTION

Barra simulates CUDA programs at the assembly language level (Tesla ISA). Its ultimate goal is to provide a 100 % bit-accurate simulation, offering bug-for-bug compatibility with NVIDIA G80-based GPUs. It works directly with CUDA executables, neither source modification nor recompilation is required.

Barra is primarily intended as a tool for research in computer architecture, although it can also be used to debug, profile and optimize CUDA programs at the lowest level.

- Participants: Sylvain Collange, David Defour, Alexandre Kouyoumdjian and Fabrice Mouhartem
- Contact: Sylvain Collange
- URL: http://barra.gforge.inria.fr/

6.4. HEPTANE

Static analyser of Worst-Case Execution Time
KEYWORD: WCET
FUNCTIONAL DESCRIPTION

The aim of Heptane is to produce upper bounds of the execution times of applications. It is targeted at applications with hard real-time requirements (automotive, railway, aerospace domains). Heptane computes WCETs using static analysis at the binary code level. It includes static analyses of microarchitectural elements such as caches and cache hierarchies.
Status: Registered with APP (Agence de Protection des Programmes). Available under GNU General Public License v3, with number IDDN.FR.001.510039.000.S.P.2003.000.10600.

- Participants: Isabelle Puaut, Damien Hardy, Benjamin Lesage, Thomas Piquet and François Joulaud
- Partner: Université de Rennes 1
- Contact: Isabelle Puaut or Damien Hardy
- URL: https://team.inria.fr/alf/software/heptane/

6.5. If-memo

KEYWORD: Performance, function memoization, dynamic optimization
Status: Ongoing development, early prototype. Registered with APP (Agence de Protection des Programmes) under number IDDN.FR.001.250013.000.S.P.2015.000.10800.

SCIENTIFIC DESCRIPTION

Memoization is the technique of saving result of executions so that future executions can be omitted when the inputs repeat. Memoization has been proposed in previous literature at the instruction level, basic block level and function level using hardware as well as pure software level approaches including changes to programming language.

We proposed software memoization of pure functions for procedural languages. We rely on the operating system loader, taking advantage of the LD_PRELOAD feature of UNIX systems. By setting this variable to the path of a shared library, we instruct the loader to first look to missing symbols in that library. Our library redefines the functions we wish to intercept. The interception code is very straightforward: it receives the same parameter as the target function and checks in a table (a software cache) if this value is readily available. In the favorable case, the result value is immediately returned. Otherwise, we invoke the original function, and store the result in the cache before returning it.

Our technique does not require the availability of source code and thus can be applied even to commercial applications as well as applications with legacy codes. As far as users are concerned, enabling memoization is as simple as setting an environment variable. We validated If-memo with x86-64 platform using both GCC and icc compiler tool-chains, and ARM cortex-A9 platform using GCC.

- Participants: Erven Rohou and Arjun Suresh
- Contact: Erven Rohou

6.6. Padrone

KEYWORDS: Legacy code - Optimization - Performance analysis - Dynamic Optimization
Status: Registered with APP (Agence de Protection des Programmes) under number IDDN.FR.001.250013.000.S.P.2015.000.1080

FUNCTIONAL DESCRIPTION

Padrone is new platform for dynamic binary analysis and optimization. It provides an API to help clients design and develop analysis and optimization tools for binary executables. Padrone attaches to running applications, only needing the executable binary in memory. No source code or debug information is needed. No application restart is needed either. This is especially interesting for legacy or commercial applications, but also in the context of cloud deployment, where actual hardware is unknown, and other applications competing for hardware resources can vary. The profiling overhead is minimum.

- Participants: Erven Rohou and Emmanuel Riou
- Contact: Erven Rohou
- https://team.inria.fr/alf/software/Padrone/

6.7. STiMuL

Steady temperature in Multi-Layers components
FUNCTIONAL DESCRIPTION

STiMuL is a C library for modeling steady-state heat conduction in microprocessors. It can be used to obtain temperature from power density or power density from temperature. It can also be used to model stacked dies. STiMuL does not model time-varying temperature. For time-varying temperature, other models must be used, such as ATMI.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/alf/software/stimul/

6.8. TPCalc

Throughput calculator
KEYWORDS: Architecture - Performance analysis
FUNCTIONAL DESCRIPTION

TPCalc is a throughput calculator for microarchitecture studies concerned with multi-program workloads consisting of sequential programs. Because microarchitecture simulators are slow, it is difficult to simulate throughput experiments where a multicore executes many jobs that enter and leave the system. The usual practice of measuring instantaneous throughput on independent coschedules chosen more or less randomly is not a rigorous practice because it assumes that all the coschedules are equally important, which is not always true. TPCalc can compute the average throughput of a throughput experiment without actually doing the throughput experiment. The user first defines the workload heterogeneity (number of different job types), the multicore configuration (number of cores and symmetries). TPCalc provides a list of base coschedules. The user then simulates these coschedules, using some benchmarks of his choice, and feeds back to TPCalc the measured execution rates (e.g., instructions per cycle or instructions per second).TPCalc eventually outputs the average throughput.

- Participant: Pierre Michaud
- Partner: Ghent University
- Contact: Pierre Michaud
- URL: http://www.irisa.fr/alf/downloads/michaud/tpcalc.html

6.9. tiptop

KEYWORDS: Performance, hardware counters, analysis tool.
SCIENTIFIC DESCRIPTION

Status: Registered with APP (Agence de Protection des Programmes). Available under GNU General Public License v2, with number IDDN.FR.001.450006.000.S.P.2011.000.10800. Current version is 2.3, released June 2015.

Tiptop is a new simple and flexible user-level tool that collects hardware counter data on Linux platforms (version 2.6.31+). Tiptop has been integrated in major Linux distributions, such as Fedora, Debian, Ubuntu. FUNCTIONAL DESCRIPTION The goal is to make the collection of performance and bottleneck data as simple as possible, including simple installation and usage. In particular, we stress the following points.

- Installation is only a matter of compiling the source code. No patching of the Linux kernel is needed, and no special-purpose module needs to be loaded.
- No privilege is required, any user can run *tiptop* — non-privileged users can only watch processes they own, ability to monitor anybody's process opens the door to side-channel attacks.
- The usage is similar to *top*. There is no need for the source code of the applications of interest, making it possible to monitor proprietary applications or libraries. And since there is no probe to insert in the application, understanding of the structure and implementation of complex algorithms and code bases is not required.
- Applications do not need to be restarted, and monitoring can start at any time (obviously, only events that occur after the start of *tiptop* are observed).
- Events can be counted per thread, or per process.
- Any expression can be computed, using the basic arithmetic operators, constants, and counter values.
- A configuration file lets users define their prefered setup, as well as custom expressions.
- Participant: Erven Rohou
- Contact: Erven Rohou
- URL: http://tiptop.gforge.inria.fr

6.10. Parasuite

Participants: Sylvain Collange, Thibault Person, Erven Rohou, André Seznec.

Parasuite: parallel benchmarks for multi-core CPUs, clusters and accelerators

Despite the ubiquity of parallel architectures in all computing segments, the research community often lacks benchmarks representative of parallel applications. The Inria Parallel Benchmark Suite (Parasuite) seeks to address this need by providing a set of representative parallel benchmarks for the architecture, compiler and system research communities. Parasuite targets the main contemporary parallel programming technologies: shared-memory multi-thread parallelism for multi-core, message-passing parallelism for clusters and fine-grained data-level parallelism for GPU architectures and SIMD extensions.

All benchmarks come with input datasets of various sizes, to accommodate use cases ranging from microarchitecture simulation to large-scale performance evaluation. Correctness checks on the computed results enable automated regression testing. In order to support computer arithmetic optimization and approximate computing research scenarios, the correctness checks favor accuracy metrics evaluating domain-specific relevance rather than bit-exact comparisons against an arbitrary reference output.

Visit http://parasuite.inria.fr/

ALICE Project-Team

6. New Software and Platforms

6.1. Vorpaline

Participants: Dobrina Boltcheva, Bruno Lévy.

Vorpaline is a commercial software / programming library. The Vorpaline software takes a new approach to 3D mesh generation, based on the theory of numerical optimization. The optimal mesh generation algorithm, developed as part of the European Research Council GOODSHAPE project, globally and automatically optimizes the mesh elements with respect to geometric constraints. It is the subject of two patents. The mathematical foundations of this algorithm, *i.e.*, the minimization of a smooth energy function, result in practice in a faster algorithm, and–more importantly–in a higher flexibility. For instance, it will allow automatic generation of the aforementioned "hex-dominant" meshes. Vorpaline is based on Geogram (see below). It adds some specialized components targeted to specific industrial usage, such as 3D gridding for the oil and gas industry. It includes our latest research results in automatic meshing. Vorpaline is licensed under a proprietary license.

6.2. IceSL

Participants: Jérémie Dumas, Jean Hergel, Sylvain Lefebvre, Frédéric Claux, Jonas Martínez Bayona, Samuel Hornus.

IceSL exploits parallel algorithms running on the GPU to afford for interactive modeling of objects described by a Constructive Solid Geometry [0] scripting language. This also enables direct slicing for additive manufacturing by considering the printer bed as a screen onto which each object slice has to be drawn as quickly as possible. During display and slicing the CSG model is converted on the fly into an intermediate representation enabling fast processing on the GPU. Slices can be quickly extracted, and the tool path is prepared through image erosion. The interactive preview of the final geometry uses the exact same code path as the slicer, providing an immediate, accurate visual feedback.

IceSL allows practitioners to design and combine complex objects with unprecedented ease. Our latest version can combine meshes as well as analytical primitives (*i.e.*, shapes described by an equation), and outputs printer instructions for filament printers as well as stereolithography printers and laser cutters.

We also augmented IceSL with a modern UI that allows users to immediately visualize changes made to the script, as well as expose a set of parameters to non-expert users who are interested in customizing a model created with IceSL. https://youtu.be/I2y_yZ4VEgk.

IceSL is the recipient software for our ERC research project "ShapeForge", led by Sylvain Lefebvre and includes several research results from the project.

6.3. Graphite

Participants: Dobrina Boltcheva, Samuel Hornus, Bruno Lévy, Nicolas Ray.

Graphite is an experimental 3D modeler, built in top of the Geogram programming library. It has data structures and efficient OpenGL visualization for pointsets, surfacic meshes (triangles and polygons), volumetric meshes (tetrahedra and hybrid meshes). It has state-of-the-art mesh repair, remeshing, reconstruction algorithms. It also has an interface to the Tetgen tetrahedral mesh generator (by Hang Si). This year, Graphite3 was released. It is a major rewrite, based on Geogram, with increased software quality standards (zero warnings on all platforms, systematic documentation of all classes / all functions / all parameters, dramatically improved performances). It embeds Geogram (and optionally Vorpaline) with an easy-to-use Graphic User Interface. Graphite is licensed under the GPLv3.

---

[0] Boolean operations between solids: difference, union, intersection.

6.4. GraphiteLifeExplorer

Participant: Samuel Hornus.

GLE is a 3D modeler, developed as a plugin of Graphite, dedicated to molecular biology. It is developed in cooperation with the Fourmentin Guilbert foundation and has recently been renamed "GraphiteLifeExplorer". Biologists need simple spatial modeling tools to help in understanding the role of the relative position of objects in the functioning of the cell. In this context, we develop a tool for easy DNA modeling. The tool generates DNA along any user-given curve, open or closed, allows fine-tuning of atomic positions and, most importantly, exports to PDB (Protein Daba Bank) file format.

The development of GLE is currently on hold, but it is still downloaded (freely) regularly. We plan to add some functionalities in 2016.

6.5. OpenNL - Open Numerical Library

Participants: Bruno Lévy, Nicolas Ray, Rhaleb Zayer.

OpenNL is a standalone library for numerical optimization, especially well-suited to mesh processing. The API is inspired by the graphics API OpenGL, this makes the learning curve easy for computer graphics practitioners. The included demo program implements our LSCM [36] mesh unwrapping method. It was integrated in Blender by Brecht Van Lommel and others to create automatic texture mapping methods. OpenNL is extended with two specialized modules :

- CGAL parameterization package: this software library, developed in cooperation with Pierre Alliez and Laurent Saboret, is a CGAL package for mesh parameterization.
- Concurrent Number Cruncher: this software library extends OpenNL with parallel computing on the GPU, implemented using the CUDA API.

6.6. Geogram

Participant: Bruno Lévy.

Stemming from project GOODSHAPE (ERC Starting Grant) and project VORPALINE (ERC Proof of Concept) Geogram is a programming library of geometric algorithms. It includes a simple yet efficient mesh data structure (for surface and volumetric meshes), exact computer arithmetics (a-la Shewchuck, implemented in GEO::expansion), a predicate code generator (PCK: Predicate Construction Kit), standard geometric predicates (orient/insphere), Delaunay triangulation, Voronoi diagram, spatial search data structures, spatial sorting, and less standard ones (more general geometric predicates, intersection between a Voronoi diagram and a triangular or tetrahedral mesh embedded in n dimensions). The latter is used by FWD/WarpDrive, the first algorithm that computes semi-discrete optimal transport in 3D that scales up to 1 million Dirac masses (see compute_OTM in the example programs). Geogram is licensed under the three-clauses BSD license.

Geogram Pluggable Software Modules: Some users are interested in small subsets of Geogram. Following the principle that Geogram should be as easy to use/compile as possible, some subsets of functionalities are alternatively available as a standalone pair of (header,implementation) files, automatically extracted/assembled from Geogram sourcetree. This makes the functionality usable with 0 dependency: client code that uses a PSM just need to insert the header and the implementation file into the project (rather than linking with the entire Geogram library). The Pluggable Software Modules are licensed under the three-clause BSD license. These Pluggable Software Modules include:

- OpenNL: a library of easy-to-use numerical solvers for sparse matrices,
- MultiPrecision: a number-type that can be used for computations in arbitrary precision, based on Shewchuk's arithmetic expansion [43]. It is shipped with wrapper classes to use it as a number type for CGAL,
- Predicates: implementation of exact and symbolically perturbed predicates with arithmetic filters (based on a combination of Meyer and Pion's arithmetic filter generator [38] and our MultiPrecision library).

6.7. LibSL

Participant: Sylvain Lefebvre.

LibSL is a Simple library for graphics. Sylvain Lefebvre continued development of the LibSL graphics library (under CeCill-C licence, filed at the APP). LibSL is a toolbox for rapid prototyping of computer graphics algorithms, under both OpenGL, DirectX 9/10, Windows and Linux. The library is actively used in both the REVES / Inria Sophia-Antipolis Méditerrannée and the ALICE / Inria Nancy - Grand Est teams.

ALPAGE Project-Team

6. New Software and Platforms

6.1. Alexina

Atelier pour les LEXiques INformatiques et leur Acquisition
FUNCTIONAL DESCRIPTION

Alexina is Alpage's Alexina framework for the acquisition and modeling of morphological and syntactic lexical information. The first and most advanced lexical resource developed in this framework is the Lefff, a morphological and syntactic lexicon for French.

- Participants: Benoît Sagot and Laurence Danlos
- Contact: Benoît Sagot
- URL: http://gforge.inria.fr/projects/alexina/

6.2. Bonsai

FUNCTIONAL DESCRIPTION

Alpage has developed a statistical parser for French, named Bonsai, trained on the French Treebank. This parser provides both a phrase structure and a projective dependency structure specified in [66] as output. This parser operates sequentially: (1) it first outputs a phrase structure analysis of sentences reusing the Berkeley implementation of a PCFG-LA trained on French by Alpage (2) it applies on the resulting phrase structure trees a process of conversion to dependency parses using a combination of heuristics and classifiers trained on the French treebank. The parser currently outputs several well known formats such as Penn treebank phrase structure trees, Xerox like triples and CONLL-like format for dependencies. The parsers also comes with basic preprocessing facilities allowing to perform elementary sentence segmentation and word tokenisation, allowing in theory to process unrestricted text. However it is believed to perform better on newspaper-like text.

- Participants: Marie-Hélène Candito, Djamé Seddah and Benoit Crabbé
- Contact: Marie-Hélène Candito
- URL: http://alpage.inria.fr/statgram/frdep/fr_stat_dep_parsing.html

6.3. Crapbank

French Social Media Bank
FUNCTIONAL DESCRIPTION

The French Social Media Bank is a treebank of French sentences coming from various social media sources (Twitter(c), Facebook(c)) and web forums (JeuxVidéos.com(c), Doctissimo.fr(c)). It contains different kind of linguistic annotations: - part-of-speech tags - surface syntactic representations (phrase-based representations) as well as normalized form whenever necessary.

- Contact: Djamé Seddah

6.4. DyALog

FUNCTIONAL DESCRIPTION

DyALog provides an environment to compile and execute grammars and logic programs. It is essentially based on the notion of tabulation, i.e. of sharing computations by tabulating traces of them. DyALog is mainly used to build parsers for Natural Language Processing (NLP). It may nevertheless be used as a replacement for traditional PROLOG systems in the context of highly ambiguous applications where sub-computations can be shared.

- Participant: Éric Villemonte de La Clergerie
- Contact: Éric Villemonte de La Clergerie
- URL: http://dyalog.gforge.inria.fr/

6.5. FDTB1

- Contact: Laurence Danlos

6.6. FQB

French QuestionBank

FUNCTIONAL DESCRIPTION

The French QuestionBanks is a corpus of around 2000 questions coming from various domains (TREC data set, French governmental organisation, NGOs, etc..) it contains different kind of annotations - morpho-syntactic ones (POS, lemmas) - surface syntaxe (phrase based and dependency structures) with long-distance dependency annotations.

The TREC part is aligned with the English QuestionBank (Judge et al, 2006).

- Contact: Djamé Seddah

6.7. FRMG

- Participant: Éric Villemonte de La Clergerie
- Contact: Éric de La Clergerie
- URL: http://mgkit.gforge.inria.fr/

6.8. French Question Bank

- Contact: Djamé Seddah

6.9. LexConn

- Contact: Laurence Danlos

6.10. LexViz

FUNCTIONAL DESCRIPTION

In the context of the industrial collaboration of ALPAGE with the company Lingua et Machina, we have extended their WEB plateform Libellex with a new component used to visualize and collaboratively validate lexical resources. In particular, this extension is used to manage terminological lists and lexical networks. The implemented graph-based representation has proved to be intuitive and quite useful for navigating in such large lexical resources (on the order to 10K to 100K entries).

- Participants: Éric Villemonte de La Clergerie and Mickael Morardo
- Contact: Éric Villemonte de La Clergerie

6.11. MElt

Maximum-Entropy lexicon-aware tagger

KEYWORD: Part-of-speech tagger
FUNCTIONAL DESCRIPTION

MElt is a freely available (LGPL) state-of-the-art sequence labeller that is meant to be trained on both an annotated corpus and an external lexicon. It was developed by Pascal Denis and Benoît Sagot within the Alpage team, a joint Inria and Université Paris-Diderot team in Paris, France. MElt allows for using multiclass Maximum-Entropy Markov models (MEMMs) or multiclass perceptrons (multitrons) as underlying statistical devices. Its output is in the Brown format (one sentence per line, each sentence being a space-separated sequence of annotated words in the word/tag format).

MElt has been trained on various annotated corpora, using Alexina lexicons as source of lexical information. As a result, models for French, English, Spanish and Italian are included in the MElt package.

MElt also includes a normalization wrapper aimed at helping processing noisy text, such as user-generated data retrieved on the web. This wrapper is only available for French and English. It was used for parsing web data for both English and French, respectively during the SANCL shared task (Google Web Bank) and for developing the French Social Media Bank (Facebook, twitter and blog data).

- Contact: Benoît Sagot
- URL: https://www.rocq.inria.fr/alpage-wiki/tiki-index.php?page=MElt

6.12. Mgwiki

FUNCTIONAL DESCRIPTION

Mgwiki is a linguistic wiki that may used to discuss linguistic phenomena with the possibility to add annotated illustrative sentences. The work is essentially devoted to the construction of an instance for documenting and discussing FRMG, with the annotations of the sentences automatically provided by parsing them with FRMG. This instance also offers the possibility to parse small corpora with FRMG and an interface of visualization of the results. Large parsed corpora (like French Wikipedia or Wikisource) are also available. The parsed corpora can also be queried through the use of the DPath language.

- Participants: Éric Villemonte de La Clergerie and Paul Bui–quang
- Contact: Éric Villemonte de La Clergerie
- URL: http://alpage.inria.fr/frmgwiki/

6.13. OGRE

Optimized Graph Rewriting Engine
FUNCTIONAL DESCRIPTION

OGRE is a graph rewriting system specifically designed for manipulating linguistic trees and graphs, It relies on a rule specification language for expressing graph rewriting patterns. The transformation is performed in two steps:

First, the system performs simple transformations following the rewriting patterns,

Second, constraints can be applied on edges, which applies transformations depending on their environment that are propagated while all constraints are satisfied.

The system has been designd for the analysis and manipulation of attributed oriented and multi-relational graphs.

- Participants: Corentin Ribeyre, Djamé Seddah, Éric Villemonte de La Clergerie and Marie-Hélène Candito
- Contact: Corentin Ribeyre
- URL: http://www.corentinribeyre.fr/projects/view/OGRE

6.14. SYNTAX

FUNCTIONAL DESCRIPTION

Syntax system includes various deterministic and non-deterministic CFG parser generators. It includes in particular an efficient implementation of the Earley algorithm, with many original optimizations, that is used in several of Alpage's NLP tools, including the pre-processing chain Sx Pipe and the LFG deep parser SxLfg . This implementation of the Earley algorithm has been recently extended to handle probabilistic CFG (PCFG), by taking into account probabilities both during parsing (beam) and after parsing (n-best computation).

- Participants: Pierre Boullier, Philippe Deschamps and Benoît Sagot
- Contact: Pierre Boullier
- URL: http://syntax.gforge.inria.fr/

6.15. Sequoia corpus

FUNCTIONAL DESCRIPTION

The Sequoia corpus contains French sentences, annotated with various linguistic information: - parts-of-speech - surface syntactic representations (both constituency trees and dependency trees) - deep syntactic representations (which are deep syntactic dependency graphs)

- Contact: Djamé Seddah

6.16. SxPipe

SCIENTIFIC DESCRIPTION

Developed for French and for other languages, Sx Pipe includes, among others, various named entities recognition modules in raw text, a sentence segmenter and tokenizer, a spelling corrector and compound words recognizer, and an original context-free patterns recognizer, used by several specialized grammars (numbers, impersonal constructions, quotations...). It can now be augmented with modules developed during the former ANR EDyLex project for analysing unknown words, this involves in particular (i) new tools for the automatic pre-classification of unknown words (acronyms, loan words...) (ii) new morphological analysis tools, most notably automatic tools for constructional morphology (both derivational and compositional), following the results of dedicated corpus-based studies. New local grammars for detecting new types of entities and improvement of existing ones, developed in the context of the PACTE project, will soon be integrated within the standard configuration.

FUNCTIONAL DESCRIPTION

SxPipe is a modular and customizable chain aimed to apply to raw corpora a cascade of surface processing steps. It is used as a preliminary step before Alpage's parsers (e.g., FRMG) and for surface processing (named entities recognition, text normalization, unknown word extraction and processing...).

- Participants: Pierre Boullier, Benoît Sagot, Kata Gábor, Marion Baranes, Pierre Magistry, Éric Villemonte de La Clergerie and Djamé Seddah
- Contact: Benoît Sagot
- URL: http://lingwb.gforge.inria.fr/

6.17. VerbeNet

- Contact: Laurence Danlos

6.18. hyparse

Alpage Hybrid Parser
KEYWORDS: Parsing - NLP
FUNCTIONAL DESCRIPTION

Multilingual Phrase Structure Parser

- Contact: Benoit Crabbé
- URL: http://hyparse.gforge.inria.fr

6.19. DyALog-sr

DYALOG-sr
KEYWORDS: Parsing - NLP
FUNCTIONAL DESCRIPTION

DyALog-SR is a transition-based dependency parser, built on top of DyALog system. Parsing relies on dynamic programming techniques to handle beams. Supervised learning exploit a perceptron and aggressive early updates. DyALog-SR can handle word lattice and produce dependency graphs (instead of basic trees). It was tested during several shared tasks (SPMRL'2013 and SEMEVAL'2014). It achieves very good accuracy on French TreeBank, alone or by coupling with FRMG parser.

- Contact: Éric de La Clergerie

ALPINES Project-Team

6. New Software and Platforms

6.1. FreeFem++

FeeFrem++
SCIENTIFIC DESCRIPTION

FreeFem++ is a partial differential equation solver. It has its own language. FreeFem++ scripts can solve multiphysics non linear systems in 2D and 3D.

Problems involving PDE (2d, 3d) from several branches of physics such as fluid-structure interactions require interpolations of data on several meshes and their manipulation within one program. FreeFem++ includes a fast 2d-tree-based interpolation algorithm and a language for the manipulation of data on multiple meshes (as a follow up of bamg (now a part of FreeFem++).

FreeFem++ is written in C++ and the FreeFem++ language is a C++ idiom. It runs on Macs, Windows, Unix machines. FreeFem++ replaces the older freefem and freefem+.
FUNCTIONAL DESCRIPTION

FreeFem++ is a PDE (partial differential equation) solver based on a flexible language that allows a large number of problems to be expressed (elasticity, fluids, etc) with different finite element approximations on different meshes.

- Partner: UPMC
- Contact: Frederic Hecht
- URL: http://www.freefem.org/ff++/

6.2. HPDDM

SCIENTIFIC DESCRIPTION

HPDDM is an efficient implementation of various domain decomposition methods (DDM) such as one- and two-level Restricted Additive Schwarz methods, the Finite Element Tearing and Interconnecting (FETI) method, and the Balancing Domain Decomposition (BDD) method. This code has been proven to be efficient for solving various elliptic problems such as scalar diffusion equations, the system of linear elasticity, but also frequency domain problems like the Helmholtz equation. A comparison with modern multigrid methods can be found in the thesis of Pierre Jolivet.
FUNCTIONAL DESCRIPTION

HPDDM is an efficient implementation of various domain decomposition methods (DDM) such as one- and two-level Restricted Additive Schwarz methods, the Finite Element Tearing and Interconnecting (FETI) method, and the Balancing Domain Decomposition (BDD) method.

- Participants: Pierre Jolivet and Frédéric Nataf
- Contact: Pierre Jolivet and Frédéric Nataf
- URL: https://github.com/hpddm

6.3. DPREPack

KEYWORD: Large scale
FUNCTIONAL DESCRIPTION

This library solves linear systems on parallel computers from PCs based on multicore processors to large scale computers. It implements recent parallel algorithms issued from domain decomposition methods and parallel approximate factorizations.

- Partners: CNRS - UPMC
- Contact: Laura Grigori
- URL: https://team.inria.fr/alpines/

Submodules:

- Sparse Toolbox
  KEYWORDS: Preconditioner - Interactive method - Linear system
  - Participants: Laura Grigori and Rémi Lacroix
  - Contact: Laura Grigori
  - not yet publicly available
- Block Filtering Decomposition preconditioner
  KEYWORDS: Preconditioner - Linear system
  FUNCTIONAL DESCRIPTION

  Iterative methods are used in many industrial and academic applications to solve large sparse linear systems of equations, and preconditioning these methods is often necessary to accelerate their convergence. Several highly used preconditioners as incomplete LU factorizations are known to have scalability problems, often due to the presence of several low frequency modes that hinder the convergence of the iterative method. To address this problem, we work on filtering preconditioners. A judicious choice of the filtering vector allows to alleviate the effect of low frequency modes, and can accelerate significantly the convergence of the iterative method.
  - Participants: Laura Grigori, Rémi Lacroix and Frédéric Nataf
  - Partners: CNRS - UPMC
  - Contact: Laura Grigori
  - not yet publicly available
- LORASC preconditioner
  KEYWORD: Preconditioner
  - Participants: Laura Grigori and Rémi Lacroix
  - Contact: Laura Grigori
  - URL: not yet publicly available
- NFF Nested Filtering Factorization
  KEYWORDS: Preconditioner - Interactive method - Linear system
  - Participants: Laura Grigori, Frédéric Nataf and Long Qu
  - Partners: UPMC - Université Paris-Sud
  - Contact: Laura Grigori
  - not yet publicly available

AMIB Project-Team

5. New Software and Platforms

5.1. VARNA

KEYWORDS: Bioinformatics - Structural Biology
FUNCTIONAL DESCRIPTION

A lightweight Java Applet dedicated to the quick drawing of an RNA secondary structure. VARNA is open-source and distributed under the terms of the GNU GPL license. Automatically scales up and down to make the most out of a limited space. Can draw multiple structures simultaneously. Accepts a wide range of documented and illustrated options, and offers editing interactions. Exports the final diagrams in various file formats (svg,eps,jpeg,png,xfig)

- Participants: Yann Ponty
- Contact: Yann Ponty
- URL: http://varna.lri.fr/

5.2. KGS

KEYWORDS: Bioinformatics - Structural Biology -protein kinematics -RNA kinematics
FUNCTIONAL DESCRIPTION

The Kino-Geometric Sampling (KGS) software suite uses advanced, robotics-inspired algorithms to rapidly explore the conformational landscape of folded proteins, RNA, and their complexes. Combined with powerful statistical techniques, it structurally characterizes collective motions and excited substates from sparse, spatiotemporally averaged data.

- Participants: Amélie Héliou.
- Contact: Amélie Héliou
- URL: https://simtk.org/home/kgs/

5.3. SV-BAY

KEYWORDS: Bioinformatics - NGS- Cancer
FUNCTIONAL DESCRIPTION

SV-BAY is a software to detect structural variants in cancer genomes. It relies on a Bayesian approach and a correction for GC-content and read mappability is provided. SV-BAY is written in Python with small insertions in C++ code.

- Participants: Daria Iakovishina and M. Régnier
- Contact: M. Régnier
- URL: https://github.com/InstitutCurie/SV-Bay

5.4. DeClone

KEYWORDS: Bioinformatics - Comparative Genomics - Genome rearrangements
FUNCTIONAL DESCRIPTION

DECLONE is a software to predict ancestral adjacencies from reconciled gene trees. It offers multiple indicators to assess the robustness of predictions, including individual supports, the (stochastic) generation of (co/sub)-optimal solutions, and the domain of validity of a given prediction in the parameter space.

- Participants: Y. Ponty
- Contact: Y. Ponty
- URL: https://github.com/yannponty/DeClone

ANGE Project-Team

6. New Software and Platforms

6.1. Freshkiss3D (FREe Surface Hydrodynamics using KInetic SchemeS)

FUNCTIONAL DESCRIPTION

Freshkiss3D is a numerical code solving the 3D hydrostatic and incompressible Navier-Stokes equations with variable density.

- Participants: Jacques Sainte-Marie, Emmanuel Audusse, Marie-Odile Bristeau, Raouf Hamouda, David Froger and Anne-Céline Boulanger
- Partners: UPMC - CEREMA
- Contact: Jacques Sainte-Marie

For a list of recent developments, refer to §7.5.1 .

6.2. TSUNAMATHS

FUNCTIONAL DESCRIPTION

Tsunamaths is an educational platform aiming at simulating historical tsunamis. Real data and mathematical explanations are provided to enable people to better understand the overall process of tsunamis.

- Participants: Jacques Sainte-Marie, Emmanuel Audusse and Raouf Hamouda
- Contact: Jacques Sainte-Marie
- URL: http://ange.raoufhamouda.com/tsunami/en_motivation.htm

ANTIQUE Project-Team

5. New Software and Platforms

5.1. APRON

SCIENTIFIC DESCRIPTION

The APRON library is intended to be a common interface to various underlying libraries/abstract domains and to provide additional services that can be implemented independently from the underlying library/abstract domain, as shown by the poster on the right (presented at the SAS 2007 conference. You may also look at:

FUNCTIONAL DESCRIPTION

The Apron library is dedicated to the static analysis of the numerical variables of a program by abstract interpretation. Its goal is threefold: provide ready-to-use numerical abstractions under a common API for analysis implementers, encourage the research in numerical abstract domains by providing a platform for integration and comparison of domains, and provide a teaching and demonstration tool to disseminate knowledge on abstract interpretation.

- Participants: Antoine Miné and Bertrand Jeannet
- Contact: Antoine Miné
- URL: http://apron.cri.ensmp.fr/library/

5.2. Astrée

SCIENTIFIC DESCRIPTION

Astrée analyzes structured C programs, with complex memory usages, but without dynamic memory allocation nor recursion. This encompasses many embedded programs as found in earth transportation, nuclear energy, medical instrumentation, and aerospace applications, in particular synchronous control/command. The whole analysis process is entirely automatic.

Astrée discovers all runtime errors including:

- undefined behaviors in the terms of the ANSI C99 norm of the C language (such as division by 0 or out of bounds array indexing),
- any violation of the implementation-specific behavior as defined in the relevant Application Binary Interface (such as the size of integers and arithmetic overflows),
- any potentially harmful or incorrect use of C violating optional user-defined programming guidelines (such as no modular arithmetic for integers, even though this might be the hardware choice),
- failure of user-defined assertions.

FUNCTIONAL DESCRIPTION

Astrée is a static analyzer for sequential programs based on abstract interpretation. The Astrée static analyzer aims at proving the absence of runtime errors in programs written in the C programming language.

- Participants: Patrick Cousot, Jérôme Feret, Laurent Mauborgne, Antoine Miné and Xavier Rival
- Partner: CNRS
- Contact: Patrick Cousot
- URL: http://www.astree.ens.fr/

5.3. AstréeA

The AstréeA Static Analyzer of Asynchronous Software

SCIENTIFIC DESCRIPTION

AstréeA analyzes C programs composed of a fixed set of threads that communicate through a shared memory and synchronization primitives (mutexes, FIFOs, blackboards, etc.), but without recursion nor dynamic creation of memory, threads nor synchronization objects. AstréeA assumes a real-time scheduler, where thread scheduling strictly obeys the fixed priority of threads. Our model follows the ARINC 653 OS specification used in embedded industrial aeronautic software. Additionally, AstréeA employs a weakly-consistent memory semantics to model memory accesses not protected by a mutex, in order to take into account soundly hardware and compiler-level program transformations (such as optimizations). AstréeA checks for the same run-time errors as Astrée , with the addition of data-races.

FUNCTIONAL DESCRIPTION

AstréeA is a static analyzer prototype for parallel software based on abstract interpretation. The AstréeA prototype is a fork of the Astrée static analyzer that adds support for analyzing parallel embedded C software.

- Participants: Patrick Cousot, Radhia Cousot, Jérôme Feret, Antoine Miné and Xavier Rival est toujours membre de Inria. logiciels Inria): https://bil.inria.fr/
- Contact: Patrick Cousot
- URL: http://www.astreea.ens.fr/

5.4. ClangML

FUNCTIONAL DESCRIPTION

ClangML is an OCaml binding with the Clang front-end of the LLVM compiler suite. Its goal is to provide an easy to use solution to parse a wide range of C programs, that can be called from static analysis tools implemented in OCaml, which allows to test them on existing programs written in C (or in other idioms derived from C) without having to redesign a front-end from scratch. ClangML features an interface to a large set of internal AST nodes of Clang , with an easy to use API. Currently, ClangML supports all C language AST nodes, as well as a large part of the C nodes related to C++ and Objective-C.

- Participants: François Berenger, Pippijn Van Steenhoven and Devin Mccoughlin toujours membre de Inria. Inria): https://bil.inria.fr/
- Contact: François Berenger
- URL: https://github.com/Antique-team/clangml/tree/master/clang

5.5. FuncTion

SCIENTIFIC DESCRIPTION

FuncTion is based on an extension to liveness properties of the framework to analyze termination by abstract interpretation proposed by Patrick Cousot and Radhia Cousot. FuncTion infers ranking functions using piecewise-defined abstract domains. Several domains are available to partition the ranking function, including intervals, octagons, and polyhedra. Two domains are also available to represent the value of ranking functions: a domain of affine ranking functions, and a domain of ordinal-valued ranking functions (which allows handling programs with unbounded non-determinism).

FUNCTIONAL DESCRIPTION

FuncTion is a research prototype static analyzer to analyze the termination and functional liveness properties of programs. It accepts programs in a small non-deterministic imperative language. It is also parameterized by a property: either termination, or a recurrence or a guarantee property (according to the classification by Manna and Pnueli of program properties). It then performs a backward static analysis that automatically infers sufficient conditions at the beginning of the program so that all executions satisfying the conditions also satisfy the property.

- Participants: Caterina Urban and Antoine Miné
- Contact: Caterina Urban
- URL: http://www.di.ens.fr/~urban/FuncTion.html

5.6. HOO

Heap Abstraction for Open Objects
FUNCTIONAL DESCRIPTION

JSAna with HOO is a static analyzer for JavaScript programs. The primary component, HOO, which is designed to be reusable by itself, is an abstract domain for a dynamic language heap. A dynamic language heap consists of open, extensible objects linked together by pointers. Uniquely, HOO abstracts these extensible objects, where attribute/field names of objects may be unknown. Additionally, it contains features to keeping precise track of attribute name/value relationships as well as calling unknown functions through desynchronized separation.

As a library, HOO is useful for any dynamic language static analysis. It is designed to allow abstractions for values to be easily swapped out for different abstractions, allowing it to be used for a wide-range of dynamic languages outside of JavaScript.

- Participant: Arlen Cox
- Contact: Arlen Cox

5.7. MemCAD

The MemCAD static analyzer
FUNCTIONAL DESCRIPTION

MemCAD is a static analyzer that focuses on memory abstraction. It takes as input C programs, and computes invariants on the data structures manipulated by the programs. It can also verify memory safety. It comprises several memory abstract domains, including a flat representation, and two graph abstractions with summaries based on inductive definitions of data-structures, such as lists and trees and several combination operators for memory abstract domains (hierarchical abstraction, reduced product). The purpose of this construction is to offer a great flexibility in the memory abstraction, so as to either make very efficient static analyses of relatively simple programs, or still quite efficient static analyses of very involved pieces of code. The implementation consists of over 30 000 lines of ML code, and relies on the ClangML front-end. The current implementation comes with over 350 small size test cases that are used as regression tests.

- Participants: Antoine Toubhans, Huisong Li, François Berenger and Xavier Rival
- Contact: Xavier Rival
- URL: http://www.di.ens.fr/~rival/memcad.html

5.8. OPENKAPPA

La platte-forme de modélisation OpenKappa
KEYWORDS: Systems Biology - Modeling - Static analysis - Simulation - Model reduction
SCIENTIFIC DESCRIPTION

OpenKappa is a collection of tools to build, debug and run models of biological pathways. It contains a compiler for the Kappa Language, a static analyzer (for debugging models), a simulator, a compression tool for causal traces, and a model reduction tool.

- Participants: Pierre Boutillier, Vincent Danos, Jérôme Feret, Walter Fontana, Russ Harmer, Jean Krivine and Kim Quyen Ly
- Partners: ENS Lyon - Université Paris-Diderot - Harvard Medical School
- Contact: Jérôme Feret
- URL: http://www.kappalanguage.org/

5.9. QUICr

FUNCTIONAL DESCRIPTION

QUICr is an OCaml library that implements a parametric abstract domain for sets. It is constructed as a functor that accepts any numeric abstract domain that can be adapted to the interface and produces an abstract domain for sets of numbers combined with numbers. It is relational, flexible, and tunable. It serves as a basis for future exploration of set abstraction.

- Participant: Arlen Cox
- Contact: Arlen Cox

5.10. Translation Validation

SCIENTIFIC DESCRIPTION

The compilation certification process is performed automatically, thanks to a prover designed specifically. The automatic proof is done at a level of abstraction which has been defined so that the result of the proof of equivalence is strong enough for the goals mentioned above and so that the proof obligations can be solved by efficient algorithms.

FUNCTIONAL DESCRIPTION

Abstract interpretation, Certified compilation, Static analysis, Translation validation, Verifier. The main goal of this software project is to make it possible to certify automatically the compilation of large safety critical software, by proving that the compiled code is correct with respect to the source code: When the proof succeeds, this guara Furthermore, this approach should allow to meet some domain specific software qualification criteria (such as those in DO-178 regulations for avionics software), since it allows proving that successive development levels are correct with respect to each other i.e., that they implement the same specification. Last, this technique also justifies the use of source level static analyses, even when an assembly level certification would be required, since it establishes separately that the source and the compiled code are equivalent.ntees that no compiler bug did cause incorrect code to be generated.

- Participant: Xavier Rival
- Contact: Xavier Rival

5.11. Zarith

FUNCTIONAL DESCRIPTION

Zarith is a small (10K lines) OCaml library that implements arithmetic and logical operations over arbitrary-precision integers. It is based on the GNU MP library to efficiently implement arithmetic over big integers. Special care has been taken to ensure the efficiency of the library also for small integers: small integers are represented as Caml unboxed integers and use a specific C code path. Moreover, optimized assembly versions of small integer operations are provided for a few common architectures.

Zarith is currently used in the Astrée analyzer to enable the sound analysis of programs featuring 64-bit (or larger) integers. It is also used in the Frama-C analyzer platform developed at CEA LIST and Inria Saclay.

- Participants: Antoine Miné, Xavier Leroy and Pascal Cuoq
- Contact: Antoine Miné
- URL: http://forge.ocamlcore.org/projects/zarith

5.12. CELIA

The MemCAD static analyzer

FUNCTIONAL DESCRIPTION

CELIA is a tool for the static analysis and verification of C programs manipulating dynamic lists. The static analyzer computes for each control point of a C program the assertions which are true (i.e., invariant) at this control point. The specification language is a combination of Separation Logic with a first order logic over sequences of integers. The inferred properties describe the shape of the lists, their size, the relations between the data (or the sum, or the multiset of data) in list cells. The analysis is inter-procedural, i.e., the assertions computed relate the procedure local heap on entry to the corresponding local heap on exit of the procedure. The results of the analysis can provide insights about equivalence of procedures on lists or null pointer dereferencing. The analysis is currently extended to programs manipulating concurrent data structures.

- Participants: Ahmed Bouajjani, Cezara Drăgoi, Constantin Enea, Mihaela Sighireanu
- Contact: Cezara Drăgoi
- URL: http://www.liafa.jussieu.fr/celia/

AOSTE Project-Team

6. New Software and Platforms

6.1. SynDEx

KEYWORDS: Embedded systems - Real time - Optimization - Distributed - Scheduling analyses
SCIENTIFIC DESCRIPTION

SynDEx is a system level CAD software implementing the AAA methodology for rapid prototyping and for optimizing distributed real-time embedded applications. It is developed in OCaML.

Architectures are represented as graphical block diagrams composed of programmable (processors) and non-programmable (ASIC, FPGA) computing components, interconnected by communication media (shared memories, links and busses for message passing). In order to deal with heterogeneous architectures it may feature several components of the same kind but with different characteristics.

Two types of non-functional properties can be specified for each task of the algorithm graph. First, a period that does not depend on the hardware architecture. Second, real-time features that depend on the different types of hardware components, ranging amongst execution and data transfer time, memory, etc.. Requirements are generally constraints on deadline equal to period, latency between any pair of tasks in the algorithm graph, dependence between tasks, etc.

Exploration of alternative allocations of the algorithm onto the architecture may be performed manually and/or automatically. The latter is achieved by performing real-time multiprocessor schedulability analyses and optimization heuristics based on the minimization of temporal or resource criteria. For example while satisfying deadline and latency constraints they can minimize the total execution time (makespan) of the application onto the given architecture, as well as the amount of memory. The results of each exploration is visualized as timing diagrams simulating the distributed real-time implementation.

Finally, real-time distributed embedded code can be automatically generated for dedicated distributed real-time executives, possibly calling services of resident real-time operating systems such as Linux/RTAI or Osek for instance. These executives are deadlock-free, based on off-line scheduling policies. Dedicated executives induce minimal overhead, and are built from processor-dependent executive kernels. To this date, executives kernels are provided for: TMS320C40, PIC18F2680, i80386, MC68332, MPC555, i80C196 and Unix/Linux workstations. Executive kernels for other processors can be achieved at reasonable cost following these examples as patterns.
FUNCTIONAL DESCRIPTION

Software for optimising the implementation of embedded distributed real-time applications and generating efficient and correct by construction code

- Participants: Yves Sorel
- Contact: Yves Sorel
- URL: http://www.syndex.org

6.2. TimeSquare

KEYWORDS: Profil MARTE - Embedded systems - UML - IDM
SCIENTIFIC DESCRIPTION TimeSquare offers six main functionalities:

* graphical and/or textual interactive specification of logical clocks and relative constraints between them,

* definition and handling of user-defined clock constraint libraries,

* automated simulation of concurrent behavior traces respecting such constraints, using a Boolean solver for consistent trace extraction,

* call-back mechanisms for the traceability of results (animation of models, display and interaction with waveform representations, generation of sequence diagrams...).

* compilation to pure java code to enable embedding in non eclipse applications or to be integrated as a time and concurrency solver within an existing tool.

* a generation of the whole state space of a specification (if finite of course) in order to enable model checking of temporal properties on it

FUNCTIONAL DESCRIPTION

TimeSquare is a software environment for the modeling and analysis of timing constraints in embedded systems. It relies specifically on the Time Model of the Marte UML profile, and more accurately on the associated Clock Constraint Specification Language (CCSL) for the expression of timing constraints.

- Participants: Frédéric Mallet, and Julien Deantoni
- Contact: Frédéric Mallet
- URL: http://timesquare.inria.fr

6.3. Lopht

KEYWORDS: Real-time scheduling, compilation, ARINC 653, TTEthernet, Many-core, Network-on-chip

SCIENTIFIC DESCRIPTION

Lopht is an acronym for Logical to Physical Time Compiler. Lopht has been designed as an implementation of the AAA methodology. Like SynDEx, Lopht relies on off-line allocation and scheduling techniques to allow real-time implementation of dataflow synchronous specifications (e.g. Scade/Heptagon) onto multiprocessor systems. The main originality is that Lopht takes a compilation-like approach based on:

- Precise modeling of its implementation platforms. For this reason, Lopht targets novel, more complex architectures such as many-core chips and time-triggered embedded systems based on standards such as ARINC 653 and TTEthernet.
- Taking into account complex non-functional specifications covering real-time (release dates and deadlines possibly different from period, major time frame, end-to-end flow constraints), ARINC 653 partitioning, the possibility to preempt or not each task, and finally SynDEx-like allocation
- Tight integration of program analysis, scheduling, and optimization approaches coming from 3 research fields (real-time scheduling, compilation, and synchronous languages) to improve the efficiency of resulting implementations while ensuring functional correctness, the respect of non-functional requirements, and scalability.

FUNCTIONAL DESCRIPTION Lopht is a software tool similar in functioning to a compiler. It takes as input one file defining the functional and non-functional specification of a system (including a model of the execution platform and non-functional requirements). It automatically produces all files needed to build a running implementation (the C code for each processor cores and the configuration files).

- Participants: Dumitru Potop-Butucaru, Keryan Didier
- Contact: Dumitru Potop-Butucaru (dumitru.potop@inria.fr)

6.4. EVT Kopernic

KEYWORD: Embedded systems

EVT Kopernic provides a probabilistic worst case execution time estimation for a program on a processor. The tool takes a set of measurements (execution times of the program on the processor) as input and it provides a probability distribution. The first version released in 2015 is restricted to independent data and a second version has been obtained for dependent data during the last part of the year. A third version provides rules for obtaining the measurements is to be released in the first part of 2016.

- Participants: Liliana Cucu and Adriana Gogonel
- Contact: Liliana Cucu
- URL: Currently restricted distribution

6.5. SAS

Simulation and Analysis of Scheduling

SCIENTIFIC DESCRIPTION

The SAS (Simulation and Analysis of Scheduling) software allows the user to perform the schedulability analysis of periodic task systems in the monoprocessor case.

The main contribution of SAS, when compared to other commercial and academic softwares of the same kind, is that it takes into account the exact preemption cost between tasks during the schedulability analysis. Beside usual real-time constraints (precedence, strict periodicity, latency, etc.) and fixed-priority scheduling policies (Rate Monotonic, Deadline Monotonic, Audsley++, User priorities), SAS additionaly allows to select dynamic scheduling policy algorithms such as Earliest Deadline First (EDF). The resulting schedule is displayed as a typical Gantt chart with a transient and a permanent phase, or as a disk shape called "dameid", which clearly highlights the idle slots of the processor in the permanent phase.

FUNCTIONAL DESCRIPTION

The SAS software allows the user to perform the schedulability analysis of periodic task systems in the monoprocessor case.

- Participants: Daniel De Rauglaudre and Yves Sorel
- Contact: Yves Sorel
- URL: http://pauillac.inria.fr/~ddr/sas-dameid/

APICS Project-Team

5. New Software and Platforms

5.1. Dedale-HF

Recent developments allow to use Dedale-HF in combination with Presto-HF and in replacement of the former software RGC. A circuit optimizer has also been added to handle specific coupling topologies, the admissible set of which is not known in terms of a simple polynomial description.

5.2. FindSources3D

A new (Matlab) version of the software that automatically performs the estimation of the quantity of sources is being built (see Section 3.4.2). It uses an alignment criterion in addition to other clustering tests for the selection. Also, the team benefit from an “Action de Développement Technologique” (ADT Inria) BOLIS, 2014-2016, and of the young engineer N. Schnitzler at half-part of the time. The aim is to get from FindSources3D a modular, ergonomic, accessible and interactive platform, providing a convenient graphical interface and a tool that can be easily distributed and used, for medical imaging (EEG, MEG, EIT) or other applications (like inverse source problems in planetary sciences, see Section 6.1.3). Modularity is now granted, though still in progress (using the tools dtk, Qt, still with compiled Matlab libraries; translation in C++ will be continued). The related version of the software now offers a detailed and nice visualization of the data and tuning parameters, of the processing steps and of the computed results (using VTK).

ARAMIS Project-Team

6. New Software and Platforms

6.1. Brain Networks Toolbox

KEYWORDS: Neuroimaging - Medical imaging
FUNCTIONAL DESCRIPTION

Brain Networks Toolbox is a collection of Matlab routines developed to quantify topological metrics of complex brain networks.

- Participants: Mario Chavez and Fabrizio De Vico Fallani
- Contact: Mario Chavez
- URL: https://sites.google.com/site/fr2eborn/download

6.2. Deformetrica

KEYWORDS: 3D modeling - C++ - Automatic Learning - Mesh - Anatomy - Image analysis
SCIENTIFIC DESCRIPTION

Deformetrica is a software for the statistical analysis of 2D and 3D shape data. It essentially computes deformations of the 2D or 3D ambient space, which, in turn, warp any object embedded in this space, whether this object is a curve, a surface, a structured or unstructured set of points, or any combination of them.

Deformetrica comes with two applications:

registration, which computes the best possible deformation between two sets of objects, atlas construction, which computes an average object configuration from a collection of object sets, and the deformations from this average to each sample in the collection.

Deformetrica has very little requirements about the data it can deal with. In particular, it does not require point correspondence between objects!
FUNCTIONAL DESCRIPTION

Deformetrica is a software for the statistical analysis of 2D and 3D shape data. It essentially computes deformations of the 2D or 3D ambient space, which, in turn, warp any object embedded in this space, whether this object is a curve, a surface, a structured or unstructured set of points, or any combination of them.

Deformetrica comes with two applications:

- Registration, which computes the optimal deformation between two sets of objects,

- Atlas construction, which computes an average object configuration from a collection of object sets, and the deformations from this average to each sample in the collection.

Deformetrica has very little requirements about the data it can deal with. In particular, it does not require point correspondence between objects!

- Participants: Stanley Durrleman, Alexandre Routier, Pietro Gori, Marcel Prastawa, Ana Fouquier, Joan Alexis Glaunès, Benjamin Charlier, Cédric Doucet and Mauricio Diaz-Melo
- Partners: University of Utah - Université de Montpellier 2 - Université Paris-Descartes
- Contact: Stanley Durrleman
- URL: http://www.deformetrica.org/

6.3. SACHA

Segmentation Automatisée Compétitive de l'Hippocampe et de l'Amygdale

KEYWORDS: Neuroimaging - 3D - Hippocampus - Amygdala - Brain scan - Medical imaging

SCIENTIFIC DESCRIPTION

The current stable version is fully automatic and focused on cross-sectional segmentation. The software can be used both as a command-line program or through a graphical user interface (GUI). The core of the program is coded in C++. It has a dependency to the AIMS library and preprocessing steps rely on processes in Matlab from SPM. The GUI is coded in Python and is based on BrainVISA.

FUNCTIONAL DESCRIPTION

SACHA is a software for the fully automatic segmentation of the hippocampus and the amygdala from MRI 3D T1 brain scans. It has been validated in various populations including healthy controls and patients with Alzheimer's disease, epilepsy and depression. It has been successfully applied to over 3,000 subjects, both controls, from adolescents to elderly subjects, and patients with different types of pathologies.

- Participants: Marie Chupin and Ludovic Fillon
- Contact: Marie Chupin
- URL: http://www.brainvisa.info

6.4. WHASA

White matter Hyperintensity Automatic Segmentation Algorithm

KEYWORDS: Health - Neuroimaging - Biomedical imaging

SCIENTIFIC DESCRIPTION

The current stable version is fully automatic and focused on cross-sectional segmentation. The software can be used both as a Matlab command-line or through a graphical user interface (GUI). The core of the program is coded in Matlab. It has a dependency to the SPM environment. The GUI is coded in Python and is based on BrainVISA.

FUNCTIONAL DESCRIPTION

WHASA ("White matter Hyperintensity Automatic Segmentation Algorithm") is a software for the fully automatic segmentation of age-related white matter hyperintensities from MRI FLAIR and 3D T1 brain scans. It has been validated on a population showing a wide range of lesion load, and is being further evaluated on elderly subjects with few clinical abnormalisties and with different acquisition characteristics.

- Participants: Marie Chupin, Ludovic Fillon and Thomas Samaille
- Contact: Marie Chupin
- URL: http://www.brainvisa.info/

6.5. qualiCATI

KEYWORDS: Health - Neuroimaging - Medical imaging

SCIENTIFIC DESCRIPTION

QualiCATI requires training for the visual parts, and is closely linked with a team of clinical research assistants. It has been used to analyse about 5000 subjects from about 15 multi centre research projects initiated before or after the CATI started. Other modules will be added in the future to embed new aspects of the MRI protocol proposed by the CATI. The Aramis team is in charge of the second and third modules and jointly in charge of the first module. The software is centered on a graphical user interface (GUI). The whole program is coded in Python within the pyPTK environment. It has dependencies to SPM and brainVISA environments as well as specific tools for DICOM management.

FUNCTIONAL DESCRIPTION

qualiCATI is a software designed for comprehensive quality control of multimodal MRI data acquisition in large multicentre clinical studies. The software is built as a platform receiving several modules, developped by several CATI engineers. The first module is dedicated to acquisition requirement checking and conversion to nifti format. The second module aims at making 3DT1 acquisition quality check more systematic, and relies both on visual inspection and quantitative indices. The third module allows a simultaneous evaluation of the clinical part of the CATI acquisition protocol. The fourth module embeds automatic indices to evaluate resting state fMRI acquisition. The fifth module is dedicated to first preprocessings and quality indices for dMRI. The sixth module is dedicated to qMRI, with visual and automated quality control together with preprocessings. The last module is dedicated to data and project management.

- Participants: Marie Chupin and Hugo Dary
- Contact: Marie Chupin
- URL: http://www.fil.ion.ucl.ac.uk/spm/

ARIC Project-Team

6. New Software and Platforms

6.1. FPLLL: a lattice reduction library

fplll contains several algorithms on lattices that rely on floating-point computations. This includes implementations of the floating-point LLL reduction algorithm, offering different speed/guarantees ratios. It contains a “wrapper” choosing the estimated best sequence of variants in order to provide a guaranteed output as fast as possible. In the case of the wrapper, the succession of variants is oblivious to the user. It also includes a rigorous floating-point implementation of the Kannan-Fincke-Pohst algorithm that finds a shortest non-zero lattice vector, and the BKZ reduction algorithm.

The fplll library is distributed under the LGPL license. It has been used in or ported to several mathematical computation systems such as Magma, Sage, and PariGP. It is also used for cryptanalytic purposes, to test the resistance of cryptographic primitives.

- Participants: Shi Bai, Damien Stehlé
- Contact: Damien Stehlé
- URL: https://github.com/dstehle/fplll

6.2. GNU MPFR: a library for arbitrary precision floating-point arithmetic

KEYWORDS: Multiple-Precision - Floating-point - Correct Rounding
GNU MPFR is an efficient multiple-precision floating-point library written in C with well-defined semantics (copying the good ideas from the IEEE-754 standard), in particular correct rounding in 5 rounding modes. GNU MPFR provides about 80 mathematical functions, in addition to utility functions (assignments, conversions...). Special data (*Not a Number*, infinities, signed zeros) are handled like in the IEEE-754 standard. It is distributed under the LGPL license.

The development of MPFR started in Loria (Nancy). When Vincent Lefèvre moved from Nancy to Lyon, it became a joint project between the project-team Caramel (Nancy) and AriC. Many systems use MPFR, several of them being listed on its web page. MPFR 3.1.3 was released on 19 June 2015.

New developments in the trunk: Full rewrite of `mpfr_sum` completed, with new tests [38]. Generic tests improved. Bug fixes and various improvements, in particular concerning the flags.

- Participants: Vincent Lefèvre, Guillaume Hanrot and Paul Zimmermann
- Contact: Vincent Lefèvre
- URL: http://www.mpfr.org/

6.3. Gfun: a Maple package for solutions of linear differential or recurrence equations

Gfun is a Maple package that provides tools for: guessing a sequence or a series from its first terms; manipulating rigorously solutions of linear differential or recurrence equations, using the equation as a data-structure.

Its development moved to AriC with Bruno Salvy in 2012, while a submodule NumGfun dedicated to symbolic-numeric computations with linear ODEs has been developed by Marc Mezzarobba during his post-doc at AriC. An old version of gfun is distributed with the Maple library. Newer versions are available on the web page of gfun, which also lists a number of articles by scientists who cited it.

- Contact: Bruno Salvy
- URL: http://perso.ens-lyon.fr/bruno.salvy/software/the-gfun-package/

6.4. Sipe: a library for very low precision computations with correct rounding

KEYWORDS: Floating-point - Correct Rounding

Sipe is a mini-library in the form of a C header file, to perform radix-2 floating-point computations in very low precisions with correct rounding, either to nearest or toward zero. The goal of such a tool is to do proofs of algorithms/properties or computations of tight error bounds in these precisions by exhaustive tests, in order to try to generalize them to higher precisions. It is distributed under the LGPL license and mostly used internally.

- Participant: Vincent Lefèvre
- Contact: Vincent Lefèvre
- URL: https://www.vinc17.net/research/sipe/

6.5. LinBox: a C++ library for exact, high-performance linear algebra computation

LinBox is a C++ template library for exact, high-performance linear algebra computation with dense, sparse, and structured matrices over the integers and over finite fields. LinBox is distributed under the LGPL license. The library is developed by a consortium of researchers in Canada, USA, and France. Clément Pernet is a main contributor, especially with a focus on parallel aspects during the period covered by this report.

- Participant:
- Contact: Clément Pernet
- URL: http://www.linalg.org

6.6. Exhaustive Tests for the Correct Rounding of Mathematical Functions

Participant: Vincent Lefèvre.

The search for the worst cases for the correct rounding (hardest-to-round cases) of mathematical functions ($\exp$, $\log$, $\sin$, $\cos$, etc.) in a fixed precision (mainly double precision) using Lefèvre's algorithm is implemented by a set of utilities written in Perl, with calls to Maple/intpakX for computations on intervals and with C code generation for fast computations. It also includes a client-server system for the distribution of intervals to be tested and for tracking the status of intervals (fully tested, being tested, aborted).

The support for the $\tanh$ function has been added, and this function has been tested on the full domain (together with its inverse function). Results are available from: https://www.vinc17.net/research/testlibm/

- Participant: Vincent Lefèvre
- Contact: Vincent Lefèvre

6.7. Multiplication by Integer Constants

Participant: Vincent Lefèvre.

A Perl implementation of algorithms for the multiplication by integer constants has been updated to get more results based on exhaustive tests: threading has been implemented in this part of the script.

- Participant: Vincent Lefèvre
- Contact: Vincent Lefèvre
- URL: https://www.vinc17.net/research/mulbyconst/#patterns

ASAP Project-Team

5. New Software and Platforms

5.1. Brow2Brow

Browser-to-browser serverless toolboxes
FUNCTIONAL DESCRIPTION

Brow2Brow is an “Action de Development Technologique”, i.e. a collaborative development project that aims at providing a middleware and software library for browser-to-browser applications. Brow2Brow involves the ASAP team as well as the DICE Team from Inria Grenoble (Antenne de Lyon). The project seeks to provide an alternative to the current model followed by Web2.0 applications by exploiting the recently introduced WebRTC standard. Existing Web 2.0 applications collect data on browsers and send it to servers that store and process it. The goal of Brow2Brow is to provide an alternative approach where browsers can themselves proceed to collaborative data processing. This will make it possible avoid data concentration at a single server. The project has resulted so far in the development of WebGC, a library for gossip-based applications on browsers.

- Participants: Anne-Marie Kermarrec, Davide Frey and Raziel Carvajal Gomez
- Contact: Davide Frey

5.2. Dashboard

MediEgo Dashboard: A personalized news dashboard
KEYWORDS: Recommender system - Personalized stream of news - Dashboard
FUNCTIONAL DESCRIPTION

This work has led to the development of MEDIEGO Dashboard, a personalized news recommendation system. In MEDIEGO Dashboard, users benefit from a personalized stream of news matching their interests. Additionally, users can use explicit subscriptions as well as post content and navigate through tags. MEDIEGO Dashboard is available through a web interface and a mobile-based Android application. To provide personalization, MEDIEGO Dashboard exploits the users’ opinions regarding their received news to identify users with similar interests. MEDIEGO Dashboard is centralized and it allows us to test and evaluate different recommendation schemes. In collaboration with EIT/ICT Lab, an experiment has been conducted with a set of users at Trento (Italie). This experiment allowed us to collect traces and to perform a user survey to assess and improve our solution. This solution will soon be interconnected to AllYours-P2P.

- Participants: Anne-Marie Kermarrec, Antoine Boutet, Yuri Barssi and Jean-Francois Verdonck
- Contact: Anne-Marie Kermarrec
- URL: http://www.mediego.com

5.3. GossipLib

KEYWORDS: Nat traversal - Epidemic protocols - Gossip protocols - Overlay maintenance - Peer-to-peer - Dissemination
FUNCTIONAL DESCRIPTION

GossipLib is a library consisting of a set of Java classes aimed to facilitate the development of gossip-based application in a large-scale setting. It provides developers with a set of support classes that constitute a solid starting point for building any gossip-based application. GossipLib is designed to facilitate code reuse and testing of distributed application and as thus also provides the implementation of a number of standard gossip protocols that may be used out of the box or extended to build more complex protocols and applications. These include for example the peer-sampling protocols for overlay management.

GossipLib also provides facility for the configuration and deployment of applications as final-product but also as research prototype in environments like PlanetLab, clusters, network emulators, and even as event-based simulation. The code developed with GossipLib can be run both as a real application and in simulation simply by changing one line in a configuration file.

- Participants: Davide Frey, Ribeiro Heverson, Anne Marie Kermarrec, Imane Al Ifdal, and Ilham Ikbal
- Contact: Davide Frey
- URL: http://gossiplib.gforge.inria.fr/

5.4. MediEgo

KEYWORDS: Widget web - Social network - Recommendation
FUNCTIONAL DESCRIPTION

MediEgo is a solution for content recommendation based on the users navigation history. The solution 1) collects the usages of the Web users and store them in a profile, 2) uses this profile to associate to each user her most similar users, 3) leverages this implicit network of close users in order to infer their preferences and recommend advertisements and recommendations. MediEgo achieves scalability using a sampling method, which provides very good results at a drastically reduced cost.

- Participants: Antoine Boutet, Jacques Falcou, Jean-Francois Verdonck, Anne Marie Kermarrec, Sébastien Campion, Rachid Guerraoui, Davide Frey and Arnaud Jegou
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Sébastien Campion
- URL: http://www.mediego.com

5.5. WebGC

Web-based Gossip Communication
SCIENTIFIC DESCRIPTION

The library currently includes the implementation of two peer sampling protocols, Cyclon and the generic peer-sampling protocol from, as well as a clustering protocol. All protocols implement a common GossipProtocol “interface”
FUNCTIONAL DESCRIPTION

WebGC is a library for gossip-based communication between web-browsers. It has been developed in collaboration with Mathieu Simonin in the context of the Brow2Brow ADT project. WebGC builds on the recent WebRTC standard as well as on PeerJS, an open-source project that provides primitives for data transfer on top of WebRTC.

- Participants: Raziel Carvajal Gomez, Davide Frey and Anne-Marie Kermarrec
- Contact: Davide Frey

5.6. WhatsUp

KEYWORD: Recommender system
FUNCTIONAL DESCRIPTION

WhatsUp is a distributed recommendation system aimed to distribute instant news in a large scale dynamic system. WhatsUp has two parts, an embedded application server in order to exchange with others peers in the system and a fully dynamic web interface for displaying news and collecting opinions about what the user reads. Underlying this web-based application lies Beep, a biased epidemic dissemination protocol that delivers news to interested users in a fast manner while limiting spam. Beep is parametrized on the fly to manage the orientation and the amplification of news dissemination. Every user forwards the news of interest to a randomly selected set of users with a preference towards those that have similar interests (orientation). The notion of interest does not rely on any explicit social network or subscription scheme, but rather on an implicit and dynamic overlay capturing the commonalities between users with respect to they are interested in. The size of the set of users to which a news is forwarded depends on the interest of the news (amplification). A centralized version of WhatsUp is already up and running and the decentralized one is still in beta version.

- Participants: Davide Frey, Ribeiro Heverson, Antoine Boutet, Anne Marie Kermarrec, Arnaud Jegou, Rachid Guerraoui and Jean-Francois Verdonck
- Contact: Davide Frey

5.7. YALPS

KEYWORDS: Traffic-shaping - Nat traversal - Experimentation - Peer-to-peer - Simulator - Deployment

FUNCTIONAL DESCRIPTION

YALPS is an open-source Java library designed to facilitate the development, deployment, and testing of distributed applications. Applications written using YALPS can be run both in simulation and in real-world mode without changing a line of code or even recompiling the sources. A simple change in a configuration file will load the application in the proper environment. A number of features make YALPS useful both for the design and evaluation of research prototypes and for the development of applications to be released to the public. Specifically, YALPS makes it possible to run the same application as a simulation or in a real deployment. Applications communicate by means of application-defined messages which are then routed either through UDP/TCP or through YALPS's simulation infrastructure. In both cases, YALPS's communication layer offers features for testing and evaluating distributed protocols and applications. Communication channels can be tuned to incorporate message losses or to constrain their outgoing bandwidth. Finally, YALPS includes facilities to support operation in the presence of NATs and firewalls using relaying and NAT-traversal techniques. The implementation of YALPS includes approximately 16K lines of code, and is used in several projects by ASAP, including HEAP, AllYours-P2P, and Behave.

This year's new work consisted in adding support for Non-Blocking I/O. It was carried out during the internship of Nominoe Kervadec.

- Participants: Davide Frey, Maxime Monod, Heverson Borba Ribeiro, Anne Marie Kermarrec and Arnaud Jegou, and Nominoe Kervadec
- Contact: Davide Frey
- URL: http://yalps.gforge.inria.fr/

5.8. p2p-allyours

Peer-to-Peer AllYours

FUNCTIONAL DESCRIPTION

P2P AllYours is customization of WhatsUp developed in the context of the EIT/ICT-Labs AllYours project. In addition to WhatsUp (the distributed recommender engine), p2p-AllYours comprises the following features: - a new web interface, which users can access through a local web-server integrated in P2PAllYours, - a set of automatic nodes (BOTs) that can extract news items from RSS feeds and insert them into the recommender system - a content-bootstrap that solves the issues related to bootstrapping the recommender system when a user connects for the first time. - An experiment management server that allows users to register for the application in the context of the testing program.

- Participants: Davide Frey, Heverson Borba Ribeiro, Raziel Carvajal Gomez, Arnaud Jegou and Anne-Marie Kermarrec
- Contact: Davide Frey

ASCLEPIOS Project-Team

5. New Software and Platforms

5.1. MedInria

KEYWORDS: Segmentation - Health - DWI - Visualization - Medical Imaging
FUNCTIONAL DESCRIPTION:
MedInria is a medical imaging software platform developed by the Asclepios research project in collaboration with the Athena, Parietal and Visages Inria research projects. It aims at providing clinicians with state of the art algorithms dedicated to medical image processing and visualization. Efforts have been made to simplify the user interface, while keeping high-level algorithms.

The core of medInria is Open Source with a BSD license; additional plug-ins can have any license.

The latest release of medInria, 2.2.3, was made in September 2015.

- Participants: Théodore Papadopoulo, Olivier Commowick, René-Paul Debroize, Florian Vichot, Loic Cadour, Michael Buckingham, Maxime Sermesant and Hakim Fadil
- Partners: HARVARD Medical School - IHU - LIRYC - IHU - Strasbourg - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

5.2. MUSIC

KEYWORDS: Health - Cardiac - Computer-Assisted Surgery - Cardiac Electrophysiology - Medical Imaging
FUNCTIONAL DESCRIPTION:
MUSIC (Multi-modality Platform for Specific Imaging in Cardiology) is developed by the Asclepios research project in close collaboration with the IHU LIRYC in order to propose functionalities dedicated to cardiac interventional planning and guidance. This includes specific tools (algorithms of segmentation, registration, etc.) as well as pipelines. The software is based on the MedInria platform.
For more information, see the web page or this video on the MUSIC software application.

- Participants: Loic Cadour, Maxime Sermesant, Hakim Fadil, Florent Collot and Mathilde Merle (Software Engineer at IHU LIRYC)
- Contact: Maxime Sermesant
- URL: https://team.inria.fr/asclepios/software/music/

5.3. SOFA

KEYWORDS: Simulation of the Human Body - Physical Simulation - Health - Biomechanics - GPU - Computer-Assisted Surgery
FUNCTIONAL DESCRIPTION:
SOFA (Simulation Open Framework Architecture) is an Open Source framework primarily targeted at real-time simulation, with an emphasis on medical simulation. It is mostly intended for the research community to help develop new algorithms, but it can also be used as a prototyping tool. Based on an advanced software architecture, it allows the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of a simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods.

It is developed mainly by the Inria team projects Shacra, Evasion and Asclepios and it is available under the LGPL licence.

- Participants: Chloé Audigier, Sophie Giffard-Roisin, Roch-Philippe Molléro and Hervé Delingette
- Contact: Hervé Delingette
- URL: http://www.sofa-framework.org

5.4. VP2HF

KEYWORDS: Health - Cardiac - Medical Image Processing - Medical Imaging
FUNCTIONAL DESCRIPTION:
The proprietary VP2HF software is developed by the Asclepios team and brings together all the research produced by the VP2HF's partners. It contains MedInria plugins implemented by teams such as UPF Barcelona and KCL, and specific tools provided by Philips (algorithms of segmentation, scar segmentation, etc.). It aims at integrating, in a single clinical workflow, tools to improve the therapy selection and treatment optimisation for patients suffering from heart failure.

- Participants: Maxime Sermesant, Hakim Fadil and Loic Cadour
- Contact: Maxime Sermesant
- URL: http://www.vp2hf.eu

5.5. LSVF

KEYWORDS: Health - Brain - Medical Image Processing - Medical Imaging
FUNCTIONAL DESCRIPTION:

The Longitudinal Stationary Velocity Fields Framework is a set of tools based on the SVF parameterization of diffeomorphic deformations that allows a new type of longitudinal deformation-based morphometric analyses. The framework comprises tools to compute the deformation encoded by the exponential of an SVF, the log-demons registration software and the Pole ladder, an algorithm to parallel transport deformation trajectories. These tools can be organized in a Longitudinal Log-Demons Pipeline (LLDP), to estimate the longitudinal brain deformations from image data series, transport them in a common space and perform statistical groupwise analyses.
Sources are available under custom licence.

- Participants: Mehdi Hadj-Hamou, Marco Lorenzi and Xavier Pennec
- Contact: Xavier Pennec
- URL: http://team.inria.fr/asclepios/software/stationary-velocity-field-tools/
- URL: http://team.inria.fr/asclepios/software/lcclogdemons/

ASCOLA Project-Team

5. New Software and Platforms

5.1. CSLA

Cloud Service Level Agreement language
KEYWORDS: Cloud computing - Service-level agreement - Elasticity
FUNCTIONAL DESCRIPTION

CSLA, the Cloud Service Level Agreement language, allows the definition of SLA properties for arbitrary Cloud services (XaaS). CSLA addresses QoS uncertainty in unpredictable and dynamic environment and provides a cost model of Cloud computing. Besides the standard formal definition of contracts – comprising validity, parties, services definition and guarantees/violations – CSLA is enriched with features, such as QoS degradation and an advanced penalty model, thus introducing fine-grained language support for Cloud elasticity management.

- Participants: Thomas Ledoux and Md Sabbir Hasan
- Contact: Thomas Ledoux
- URL: http://www.emn.fr/z-info/csla/

5.2. JEScala

FUNCTIONAL DESCRIPTION

JEScala is a Scala library which implements a seamless programming model combining object-oriented, aspect-oriented, event-based and concurrent programming. Events are object members. They can be explicitly triggered as in standard event-based programming but also implicitly triggered, as join points in aspect-oriented programming. Event expressions make it possible to compose events, filter them, and alter their content. Event handlers can be registered, and unregistered, dynamically.

Concurrency can be handled without any explicit thread manipulation. By default, primitive events are synchronous but they can also be declared as asynchronous. This creates concurrency between the source of the event and its handlers. This concurrency can then be handled by composing events with the join operator and creating disjunctions of the resulting events.

- Participants: Jurgen Van Ham, Guido Salvaneschi, Mira Mezini and Jacques Noyé
- Partners: *Technische Universität Darmstadt*
- Contact: Jacques Noyé
- URL: http://www.stg.tu-darmstadt.de/research/jescala_menu/index.en.jsp

5.3. SimGrid

KEYWORDS: Large-scale Emulators - Grid Computing - Distributed Applications
FUNCTIONAL DESCRIPTION

Scientific Instrument for the study of Large-Scale Distributed Systems. SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments.

The contributions by the ASCOLA team are related to the virtualization abstractions in particular the different models to simulate VM manipulations (*e.g.*, the live migration model).

- Participants: Jonathan Rouzaud-Cornabas, Frédéric Suter, Martin Quinson, Arnaud Legrand, Adrien Lebre, Jonathan Pastor, Mario Südholt, Luka Stanisic, Augustin Degomme, Jean-Marc Vincent and Florence Perronnin
- Partners: CNRS - Université de Nancy - University of Hawaii - Université de Reims Champagne-Ardenne - Femto-st
- Contact: Arnaud Legrand
- URL: http://simgrid.gforge.inria.fr/

5.4. VMPlaces

FUNCTIONAL DESCRIPTION

VMPlaces is a dedicated framework to evaluate and compare VM placement algorithms. This framework is composed of two major components: the injector and the VM placement algorithm. The injector is the generic part of the framework (i.e. the one you can directly use) while the VM placement algorithm is the part you want to study (or compare with available algorithms). Currently, the VMPlaceS is released with three algorithms:

Entropy, a centralized approach using a constraint programming approach to solve the placement/reconfiguration VM problem

Snooze, a hierarchical approach where each manager of a group invokes Entropy to solve the placement/reconfiguration VM problem. Note that in the original implementation of Snooze, it is using a specific heuristic to solve the placement/reconfiguration VM problem. As the sake of simplicity, we have simply reused the entropy scheduling code.

DVMS, a distributed approach that dynamically partitions the system and invokes Entropy on each partition.

- Participants: Adrien Lebre, Jonathan Pastor, and Mario Südholt
- Contact: Adrien Lebre
- URL: http://beyondtheclouds.github.io/VMPlaceS/

5.5. btrCloud

KEYWORDS: Cloud computing - Virtualization - Grid - Energy - Orchestration - Autonomic system - Placement - Cluster - Data center - Scheduler

FUNCTIONAL DESCRIPTION

Orchestration, virtualization, energy, autonomic system, placement, cloud computing, cluster, data center, scheduler, grid

btrCloud is a virtual machine manager for clusters and provides a complete solution for the management and optimization of virtualized data centers. btrCloud (acronym of better cloud) is composed of three parts.

The analysis function enables operatives and people in charge to monitor and analyze how a data-center works - be it on a daily basis, on the long run, or in order to predict future trends. This feature includes boards for performance evaluation and analysis as well as trends estimation.

btrCloud, by the integration of btrScript, provides (semi-)automated VM lifecycle management, including provisioning, resource pool management, VM tracking, cost accounting, and scheduled deprovisioning. Key features include a thin client interface, template-based provisioning, approval workflows, and policy-based VM placement.

Finally, several kinds of optimizations are currently available, such as energy and load balancing. The former can help save up to around 20% of the data-center energy consumption. The latter provides optimized quality of service properties for applications that are hosted in the virtualized datacenters.

- Participants: Guillaume Le Louët, Frédéric Dumont and Jean-Marc Menaud
- Contact: Guillaume Le Louët
- URL: http://www.btrcloud.org/btrCloud/index_EN.html

ASPI Project-Team (section vide)

ATEAMS Project-Team

5. New Software and Platforms

5.1. MicroMachinations

FUNCTIONAL DESCRIPTION

Objective: To create an integrated, live environment for modelling and evolving game economies. This will allow game designers to experiment with different strategies to realise game mechanics. The environment integrates with the SPIN model checker to prove properties (reachability, liveness). A runtime system for executing game economies allows MicroMachinations models to be embedded in actual games.

Impact: One of the important problems in game software development is the distance between game design and implementation in software. MicroMachinations has the potential to bridge this gap by providing live design tools that directly modify or create the desired software behaviours.

- Participants: Paul Klint and Riemer Van Rozen
- Contact: Riemer Van Rozen
- URL: https://github.com/vrozen/MM-Lib

5.2. OSSMETER

KEYWORDS: Software Quality, Metrics, Open-source SCIENTIFIC DESCRIPTION: OSSMETER meets the challenge of software project quality assessment via fact-based business intelligence. The goal of the project was to design and evaluate a platform for incremental analysis of long lasting open-source projects to support decision making on the corporate level. FUNCTIONAL DESCRIPTION: OSSMETER is a platform which integrates metrics of open-source projects: their source code quality, the contents of their social interactions and their activity in issue tracking systems. It includes a fully programmable user-defined quality model utility and configurable dash-board user-interface. The basic metrics of the platform and their aggregation to the project level are carefully considered and rationalised.

- Participants: Paul Klint, Jurgen Vinju, Tijs Van Der Storm, Ashim Shahi, Bas Basten.
- Contact: Jurgen Vinju
- URL: http://www.ossmeter.org/

5.3. Rascal

KEYWORDS: Metaprogramming - Language
SCIENTIFIC DESCRIPTION

Rascal primitives include immutable data, context-free grammars and algebraic data-types, relations, relational calculus operators, advanced patterns matching, generic type-safe traversal, comprehensions, concrete syntax for objects, lexically scoped backtracking, and string templates for code generation. It has libraries for integrating language front-ends, for reusing analysis algorithms, for getting typed meta-data out of version management systems, for interactive visualization, etc.

FUNCTIONAL DESCRIPTION

Rascal is a programming language, such that meta programs can be created by, understood by, and debugged by programmers.

You want to use the best tool for the job when analyzing, transforming or generating source code, so normally you will end up with many different tools, possibly even written in different languages. Now the problem is to integrate these tools again. Rascal solves this problem by integrating source code analysis, transformation, and generation primitives on the language level. Use it for any kind of metaprogramming task: to construct parsers for programming languages, to analyze and transform source code, or to define new DSLs with full IDE support.

- Participants: Paul Klint, Jurgen Vinju, Tijs Van Der Storm, Davy Landman, Bert Lisser, Atze Van Der Ploeg, Vadim Zaytsev, Anastasia Izmaylova, Michael Steindorfer, Jouke Stoel, Ali Afroozeh and Ashim Shahi
- Contact: Paul Klint
- URL: http://www.rascal-mpl.org/

5.4. Meerkat

FUNCTIONAL DESCRIPTION

Objective: To enable fully context-free general parsing using a parser combinator library (including allowing left recursion and arbitrary context-sensitive disambiguation).

Impact: Meerkat explores algorithmic advances in context-free general parsing (based on the GLL parsing algorithm and memoized continuations) in the context of a scala parsing combinator library. This library uniquely combines the worst-case execution time guarantees of GLL with the flexibility of parsing combinators. [47]

- Participants: Anastasia Izmaylova, Ali Afroozeh and Tijs van der Storm.
- Contact: Anastasia Izmaylova, Ali Afroozeh
- URL: http://meerkat-parser.github.io/

5.5. Iguana

FUNCTIONAL DESCRIPTION

Objective: To provide a data-dependent context-free general parsing infra-structure for parsing programming languages and other formal data, program and modeling notations.

Impact: Iguana is a fast implementation of data-dependent grammars based on the GLL context-free parsing algorithm with data-dependent non-terminals and constraints on top. It comes with a number of high-level disambiguation constructs which are translated to the intermediate layer of data-dependent (E)BNF before being loaded into an object-oriented implementation of GLL based on abstract transition network. Using Iguana parsers for languages which are considered to be hard to parse (such as Haskell and OCAML) are within reach of being generated from simple declarative specifications [25].

- Participants: Anastasia Izmaylova, Ali Afroozeh.
- Contact: Anastasia Izmaylova, Ali Afroozeh
- URL: http://iguana-parser.github.io/

5.6. Capsule

FUNCTIONAL DESCRIPTION

Objective: A generic and highly optimised product-family of immutable collection data-structures.

Impact: Capsule is a library for immutable sets, maps and tables. The code is generated using high-level descriptions of the requirements and internal trade-offs of hash-trie map based implementations. We are using this code generator to experiment with the fastest and leanest representations of these persistent data-types to satisfy the requirements of Rascal meta-programming applications in static analysis, empirical research in software engineering and software analytics [37].

- Participants: Michael Steindorfer, Jurgen Vinju
- Contact: Michael Steindorfer
- URL: http://usethesource.io/projects/capsule/

ATHENA Project-Team

5. New Software and Platforms

5.1. High Performance Diffusion MRI

KEYWORDS: Health - Neuroimaging - Medical imaging
FUNCTIONAL DESCRIPTION

We have been closely involved in pushing the frontiers of the diffusion MRI (dMRI) in the recent years, especially in the mathematical modelling and processing of the dMRI signal and have developed state-of-the-art software implementations in the form of a C++ library that can be effectively used to infer the complex microstructure of the cerebral white matter. These algorithms and software fall into four categories: (i) local tissue modelling, which includes both popular 2nd order models and advanced higher than 2nd order models such as DTI, higher order Cartesian tensors (HOTs), ODF, FOD, EAP, maxima extraction, regularization and segmentation, (ii) generation of scalar indices (or biomarkers), which include DTI biomarkers, Diffusion Kurtosis Imaging (DKI) and invariants of 4th order tensors, (iii) global structure estimation, which includes deterministic and probabilistic tractography, and (iv) data visualisation for scalar indices, local models and global structures. This library has been transfered to the company Olea Medical where it is currently under test and validation, thanks to the contributions of Aurobrata Ghosh.

- Participants: Demian Wassermann, Théodore Papadopoulo and Rachid Deriche
- Contact: Demian Wassermann
- URL: https://gforge.inria.fr/projects/athenadmri2013

5.2. DIPY

Diffusion Imaging in Python
KEYWORDS: MRI - Medical imaging
FUNCTIONAL DESCRIPTION

Dipy is a free and open source software project focusing mainly on diffusion magnetic resonance imaging (dMRI) analysis. Nonetheless, as we solve problems in dMRI some of the solutions are applicable to the greater medical imaging and image processing communities. See for example our registration and denoising tutorials.

- Participants: Demian Wassermann and Rutger Fick
- Contact: Demian Wassermann
- URL: http://nipy.org/dipy/

5.3. The White Matter Query Language

KEYWORDS: Health - Neuroimaging - Medical imaging
FUNCTIONAL DESCRIPTION
The White Matter Query Language (WMQL) is a technique to formally describe white matter tracts and to automatically extract them from diffusion MRI volumes. This query language allows us to construct a dictionary of anatomical definitions describing white matter tracts. The definitions include adjacent gray and white matter regions, and rules for spatial relations. This enables the encoding of anatomical knowledge of the human brain white matter as well as the automated coherent labeling of white matter anatomy across subjects.

- Participant: Demian Wassermann
- Contact: Demian Wassermann
- URL: http://tract-querier.readthedocs.org/en/latest/

5.4. MedInria

KEYWORDS: Segmentation - Health - DWI - Visualization - Medical imaging
SCIENTIFIC DESCRIPTION

It aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010 and renewed in 2012. The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.
FUNCTIONAL DESCRIPTION

MedInria is a free software platform dedicated to medical data visualization and processing.

- Participants: Jaime Garcia Guevara, Théodore Papadopoulo, Olivier Commowick, René-Paul Debroize, Guillaume Pasquier, Laurence Catanese, Alexandre Abadie, Benoît Bleuzé, Clément Philipot, Fatih Arslan, Florian Vichot, John Stark, Julien Wintz, Loic Cadour, Maxime Sermesant, Michael Knopke, Nicolas Toussaint, Olivier Clatz, Pierre Fillard, Sergio Medina, Stephan Schmitt, Nicolas Schnitzler and Hakim Fadil
- Partners: HARVARD Medical School - IHU - LIRYC - IHU - Strasbourg - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

5.5. Coadapt P300 Stimulator

KEYWORDS: Health - Brain-Computer Interface
FUNCTIONAL DESCRIPTION

In the domain of Brain Computer Interfaces, extracting relevant features requires a precise timing of all events occurring in the system. In particular, when dealing with evoked responses as in the P300 speller, the timing of the visual stimulations must be well controlled. To alleviate some timing issues with the P300 speller initially provided with OpenViBE, we have implemented an external visual stimulator that allows to flash the visual targets, in a time-robust manner.

- Participants: Dieter Devlaminck, Loïc Mahé, Maureen Clerc, Théodore Papadopoulo, Emmanuel Maby and Jérémie Mattout
- Partner: INSERM
- Contact: Maureen Clerc

5.6. FindSources3D

KEYWORDS: Health - Neuroimaging - Visualization - Medical - Image - Processing
FUNCTIONAL DESCRIPTION

FindSources3D is a Matlab software program dedicated to the resolution of inverse source problems in electroencephalography (EEG). From pointwise measurements of the electric potential, numerically obtained or taken by electrodes on the scalp, FindSources3D estimates pointwise dipolar current sources within the brain.

- Participants: Juliette Leblond, Maureen Clerc, Théodore Papadopoulo and Jean-Paul Marmorat
- Contact: Juliette Leblond
- URL: http://www-sop.inria.fr/apics/FindSources3D/en/index.html

5.7. OpenMEEG

KEYWORDS: Health - Neuroimaging - Medical imaging

FUNCTIONAL DESCRIPTION

OpenMEEG provides state-of-the art tools for processing EEG and MEG data. It incorporates a newly proposed, symmetric BEM for the forward problem, and a distributed source inverse problem, with three different types of regularizations, two of which are original, based on norms of the surface gradient of the source distribution. OpenMEEG is a free, open software written in C++, and can be accessed either through a command line interface or through a user-friendly interface.

- Participants: Théodore Papadopoulo, Maureen Clerc, Alexandre Gramfort, Geoffroy Adde, Perrine Landreau, Renaud Keriven and Jan Kybic
- Contact: Théodore Papadopoulo
- URL: http://openmeeg.github.io/

5.8. OpenVIBE

KEYWORDS: Neurosciences - Interaction - Virtual reality - Health - Real time - Neurofeedback - Brain-Computer Interface - EEG - 3D interaction

FUNCTIONAL DESCRIPTION

OpenViBE is a software platform for real-time neurosciences (that is, for real-time processing of brain signals). It can be used to acquire, filter, process, classify and visualize brain signals in real time from various signal sources. OpenViBE is free and open source software. It works on Windows and Linux operating systems.

- Participants: Yann Renard, Anatole Lécuyer, Fabien Lotte, Bruno Renier, Vincent Delannoy, Laurent Bonnet, Baptiste Payan, Jozef Legény, Jussi Tapio Lindgren, Alison Cellard, Loïc Mahé, Guillaume Serriere and Marsel Mano
- Partners: INSERM - CEA-List - GIPSA-Lab
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

ATLANMODELS Team

6. New Software and Platforms

6.1. AM3

AtlanMod MegaModel Management
KEYWORDS: Modeling artifact - MDA - MDE - Megamodeling
FUNCTIONAL DESCRIPTION

AM3 (AtlanMod MegaModel Management) is a generic and extensible tool/framework dedicated to global model management, i.e., the management of different modeling artifacts as well as their interrelationships.

- Participant: Hugo Brunelière
- Partner: Ecole des Mines de Nantes
- Contact: Hugo Brunelière
- URL: http://wiki.eclipse.org/AM3

6.2. AMW

Atlas Model Weaver
KEYWORDS: MDA - MDE - Weaving - Link - Model element
FUNCTIONAL DESCRIPTION

AMW is a generic and extensible tool dedicated to the creation and handling of weavings between models, these weavings representing sets of links existing between elements potentially coming from different models. Language

- Participant: Frédéric Jouault
- Contact: Hugo Brunelière
- URL: http://wiki.eclipse.org/AMW

6.3. ATL

Atlanmod Transformation Language
KEYWORDS: MDA - MDE - ATL - QVT - Model - Transformation
FUNCTIONAL DESCRIPTION

ATL is a tool dedicated to model transformation, complete, integrated into Eclipse and including its own development and execution environment, concrete examples as well as the corresponding associated documentation.

- Participants: Jean Bézivin, Frédéric Jouault and Patrick Valduriez
- Partner: Ecole des Mines de Nantes
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/m2m/atl/

6.4. ATL-MR

ATL-MapReduce
KEYWORDS: Transformation - Distributed
SCIENTIFIC DESCRIPTION

ATL-MapReduce

ATL-MapReduce (ATL-MR) is a prototype tool for running complex ATL transformation in the cloud using Hadoop MapReduce. ATL-MapReduce is implemented on top of an extended ATL VM that can be found on (https://github.com/atlanmod/org.eclipse.atl.atlMR/tree/master). Coupling ATL-MR with the [the extended VM](https://github.com/atlanmod/org.eclipse.atl.atlMR/tree/master) has proved a good performance, especially in terms of execution time. [In our experiments](http://www.emn.fr/z-info/atlanmod/index.php/Image:Atlmr-experiments-raw-data.zip), ATL-MR runs up to 6x faster compared to the regular VM while distributing it over 8 machines.

- Participants: Amine Benelallam, Abel Gomez Llana and Massimo Tisi
- Contact: Amine Benelallam
- URL: https://github.com/atlanmod/ATL_MR

6.5. ATLAS model weaver

ATLAS Model Weaver
KEYWORDS: Model - Metamodel - Weaving model
SCIENTIFIC DESCRIPTION

AMW is a component-based platform for model weaving that can be used to establish and manage abstract correspondences between models. The platform is generic and based on the Eclipse contribution mechanism: components are defined in separate plugins. The plugins are further interconnected to create the model weaver workbench. Components for user interface, matching algorithms and serialization of models may be plugged as necessary. We extended the Eclipse EMF architecture for model manipulation to coordinate the weaving actions. We use the EMF reflective API to obtain a standard weaving editor which adapts its interface according to metamodels modifications. The ATL transformation engine is plugged as the standard transformation platform.

FUNCTIONAL DESCRIPTION

The AMW is a tool for establishing relationships (i.e., links) between models. The links are stored in a model, called weaving model. It is created conforming to a weaving metamodel.

- Participants: Jean Bézivin, Erwan Breton, Marcos Didonet Del Fabro, Guillaume Gueltas, Frédéric Jouault and Patrick Valduriez
- Contact: Frédéric Jouault
- URL: http://www.eclipse.org/gmt/amw/

6.6. AmmA

Atlas Model Management Architecture
FUNCTIONAL DESCRIPTION

The AMMA platform is a model management platform. It is composed of several elements. Three of them: AM3, AMW, and MoDisco are available as GMT components. ATL is a component of M2M project.

- Participants: Mikaël Barbero and Frédéric Jouault
- Contact: Frédéric Jouault
- URL: https://wiki.eclipse.org/AMMA

6.7. Collaboro

SCIENTIFIC DESCRIPTION

Collaboro is an approach to make language development processes more participative, meaning that both developers and users of the language can collaborate together to create and evolve it. Collaboro supports both the collaborative definition of the abstract (i.e., metamodel) and concrete (i.e., notation) syntaxes for your DSL by providing a collaborative enviroment enabling the discussion.

Anyone has the chance to request changes, propose solutions and give an opinion (and vote) about those from others. This discussion enrichs the language definition signicantly and ensures that the end result satisfies as much as possible the expectations of the end-users.

- Participants: Jordi Cabot, Robin Boncorps and Javier Canovas Izquierdo
- Contact: Hugo Brunelière
- URL: http://atlanmod.github.io/collaboro/#/

6.8. EMF Facet

KEYWORDS: MDE - Model - Metamodel - Extension - Dynamicity - Querying
FUNCTIONAL DESCRIPTION

EMF Facet is a tool/framework dedicated to the non-intrusive and dynamic extension of metamodels (adding of new types, attributes, references, etc), based on a model query generic mechanism

- Partners: Ecole des Mines de Nantes - Mia-Software
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/modeling/emft/facet/

6.9. EMF Views

Eclipse Modeling Framework Views
FUNCTIONAL DESCRIPTION

Some users only need to see some parts of a model, others have to get the full model extended with data from another model, and others simply access to a combination of information coming from different models. Based on the unquestionable success/usefulness of database views to solve similar problems in databases, EMF Views aims to bring the same concept to the modeling world.

- Contact: Hugo Brunelière
- URL: https://github.com/atlanmod/emfviews

6.10. EMF-REST

Eclipse Modeling Framework Rest
FUNCTIONAL DESCRIPTION

EMF is the modeling framework of the Eclipse community. While EMF is able to automatically generate Java APIs from Ecore models, it is still missing support to deal with Web APIs such as RESTful ones that could boost the use of modeling techniques in the Web. However, the creation of RESTful APIs requires from developers not only an investment in implementation but also a good understanding of the REST Principles to apply them correctly. We therefore created EMF-REST, a tool that empowers EMF to get Truly RESTFul APIs from Ecore models, thus allowing web developers to generate JSON-based Web APIs for their applications. It generates both a JavaScript API to work with models as Javascript Objects in the client-side (without any EMF dependency) and REST services in the server-side based on the Java JAX-RS specification.

- Contact: Gerson Sunyé
- URL: http://emf-rest.com/

6.11. EMFtoCSP

SCIENTIFIC DESCRIPTION

Essentially, the EMFtoCSP is a sophisticated bounded model finder that yields instances of the model that conform not only to the structural definition of the model (e.g. the multiplicity constraints), but also to the OCL constraints. Based on this core, several correctness properties can be verified:

Satisfiability – is the model able to express our domain? For this check, the minimal number of instances and links can be specified to ensure non-trivial instances.

Unsatisfiability – is the model unable to express undesirable states? To verify this, we add further constraints to the model that state undesired conditions. Then we can check if is it impossible to instantiate the amended model.

Constraint subsumption – is one constraint already implied by others (and could therefore be removed)?

Constraint redundancy – do different constraints express the same fact (and could therefore be removed)?

FUNCTIONAL DESCRIPTION

EMFtoCSP is a tool for the verification of precisely defined conceptual models and metamodels. For these models, the definition of the general model structure (using UML or EMF) is supplemented by OCL constraints. The Eclipse Modeling Development Tools (MDT) provides mature tool support for such OCL-annotated models with respect to model definition, transformation, and validation.

- Contact: Hugo Brunelière
- URL: https://github.com/SOM-Research/EMFtoCSP

6.12. GiLA

GitHub Label Analyzer

FUNCTIONAL DESCRIPTION

Reporting bugs, asking for new features and in general giving any kind of feedback is the easiest way to contribute to an Open-Source Software (OSS) project. In GitHub, the largest code hosting service for OSS, this feedback is typically expressed as new issues for the project managed by an issue-tracking system available in each new project repository. Among other features, the issue tracker allows creating and assigning labels to issues with the goal of helping the project community to better classify and manage those issues (e.g., facilitating the identification of issues for top priority components or candidate developers that could solve them). Nevertheless, as the project grows a manual browsing of the project issues is no longer feasible.

- Contact: Gerson Sunyé

6.13. JSON Discoverer

FUNCTIONAL DESCRIPTION

The JSON discoverer allows you to discover the implicit schema of your JSON documents. Any JSON document includes both metadata (i.e., the schema) and data (i.e., the objects/values conforming to the schema). Given a (set of) JSON documents our discoverer analyzes the JSON definitions and generates for you a class diagram showing graphically the implicit JSON schema of your documents plus an object diagram representing their data.

- Participants: Jordi Cabot and Javier Canovas Izquierdo
- Contact: Hugo Brunelière
- URL: http://atlanmod.github.io/json-discoverer/#/

6.14. MODISCO

analyser, refactorer et comprendre le legacy

KEYWORDS: MDA - MDE - Model - Modernisation - Discoverer

SCIENTIFIC DESCRIPTION

MoDisco is an open source Eclipse project that provides a generic and extensible framework dedicated to the elaboration of Model Driven Reverse Engineering (MDRE) solutions. Gathering contributions from both academics and industrials, the goal of the project is to federate common efforts in the model-based transformation of legacy software systems implemented using different technologies (e.g. Java, COBOL, C). The first principle is to discover models out of legacy artifacts, representing appropriately all the relevant information, to be then used as part of reverse engineering processes for software understanding, evolution or modernization. Targeted scenarios include software (technical or architectural) migration of large legacy systems, but also retro-documentation, refactoring, quality assurance, etc. Within this context, MoDisco has collaborations with the OMG Architecture Driven Modernization (ADM) Task Force, for which the project provides several reference implementations of its standards: Knowledge Discovery Metamodel (KDM), Software Measurement Metamodel (SMM) and Abstract Syntax Tree Metamodel (ASTM).

The MoDisco framework is composed of a set of Eclipse plugins, and relies on the de-facto standard Eclipse Modeling Framework (EMF) for model handling. Thanks to its modular architecture, it allows completely covering the three steps of a standard MDRE approach: 1) Discovery (i.e. extracting a complete model of the source code), 2) Understanding (i.e. browsing and providing views on this model for a given purpose) and 3) Transformation (evolving the model towards a new technology, architecture, etc). More specifically, as part of its Infrastructure layer, MoDisco offers the set of generic (i.e., legacy technology-independent) reusable components really useful to build the core of MDRE solutions: Discovery Manager and Workflow for MDRE task orchestration, Model Browser for advanced navigation in complex models, model extension and customization capabilities for understanding (e.g. views definition), etc. As part of its Technologies layer, it provides an advanced support for the Java, JEE and XML technologies, including complete metamodels, corresponding model discoverers, transformations, code generators, customizations, query libraries, etc.

MoDisco (or some of its components) is being used by different partners including other academics, industrials (e.g. Sodifrance on several of their real modernization projects for their customers) or Eclipse projects (e.g. Eclipse-MDT Papyrus as developed by CEA). Moreover, the Eclipse-EMFT EMF Facet project has been initiated as a MoDisco spin-off, in order to externalize some features which are not actually specific to reverse engineering problems and thus may be reused in many different contexts (cf. corresponding EMF Facet section).

The initiative continues to be developed within the context of the European FP7-ICT project named ARTIST (http://www.artist-project.eu/), and also to a lower extent within the context of the French FUI 13 project named TEAP.

FUNCTIONAL DESCRIPTION

MoDisco is an Eclipse generic and extensible tool/framework providing to developers a set of reusable base components and dedicated to the elaboration of model driven reverse engineering (MDRE) solutions.

- Participant: Hugo Brunelière
- Partners: Ecole des Mines de Nantes - Mia-Software
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/MoDisco/

6.15. NeoEMF

FUNCTIONAL DESCRIPTION

NeoEMF is an open source software distributed under the terms of the Eclipse Public License that provides a backend-agnostic persistence solution for big, complex and highly interconnected EMF models. NeoEMF is a model repository and persistence framework allowing on-demand loading, storage, and unloading of large-scale EMF models.

- Partner: Mia-Software
- Contact: Gerson Sunyé
- URL: http://www.neoemf.com/

6.16. Reactive-ATL

KEYWORDS: Transformation - Reactive

SCIENTIFIC DESCRIPTION

Reactive engine for the ATL transformation language. In a model-driven application environment it works by activating only the strictly needed computation in response to updates or requests of model elements. Computation is updated when necessary, in an autonomous and optimized way by using incrementality and lazy evaluation.

- Participants: Salvador Martinez Perez and Massimo Tisi
- Contact: Salvador Martinez Perez
- URL: http://atlanmod.github.io/org.eclipse.atl.reactive

AVALON Project-Team

6. New Software and Platforms

6.1. Active Data

Participants: Gilles Fedak [correspondant], Anthony Simonet.

FUNCTIONAL DESCRIPTION

Active Data is a free software system that tracks the life cycle of data distributed across heterogeneous software and infrastructures.

As the volume of data grows exponentially, the management of these data becomes more complex in proportion. A key point is to handle the complexity of the Data Life Cycle, i.e. the various operations performed on data: transfer, archiving, replication, deletion, etc. Indeed, data-intensive applications span over a large variety of devices and e-infrastructures which implies that many systems are involved in data management and processing. Active Data is a new approach to automate and improve the expressiveness of data management applications. Active Data consists of a formal model that captures the essential data life cycle stages and properties : creation, deletion, replication, derivation, transient unavailability, uniform naming, and many more. Active Data provides a programming model that simplify the development of data life cycle management applications. Active Data allows code execution at each stage of the data life cycle: routines provided by programmers are executed when a set of events (creation, replication, transfer, deletion) happen to any data.

- URL: http://active-data.gforge.inria.fr

6.2. BitDew

Participants: Gilles Fedak [correspondant], Anthony Simonet.

FUNCTIONAL DESCRIPTION

The BitDew framework is a programmable environment for management and distribution of data for Grid, Desktop Grid and Cloud Systems.BitDew offers programmers a simple API for creating, accessing, storing and moving data with ease, even on highly dynamic and volatile environments.The BitDew programming model relies on 5 abstractions to manage the data : i) replication indicates how many occurrences of a data should be available at the same time on the network, ii) fault-tolerance controls the policy in presence of machine crash, iii) lifetime is an attribute absolute or relative to the existence of other data, which decides the life cycle of a data in the system, iv) affinity drives movement of data according to dependency rules, v) protocol gives the runtime environment hints about the protocol to distribute the data (http, ftp or bittorrent). Programmers define for every data these simple criteria, and let the BitDew runtime environment manage operations of data creation, deletion, movement, replication, and fault-tolerance operation.

- URL: http://www.bitdew.net

6.3. DIET

Participants: Daniel Balouek Thomert, Eddy Caron [correspondant], Maurice Faye, Arnaud Lefray.

FUNCTIONAL DESCRIPTION

Middleware for grids and clouds. Toolbox for the use and porting of intensive computing applications on heterogeneous architectures.

In 2015 we have published a new release of DIET. A short list of the major improvements over the version 2.9 of DIET:

Security: SSL communications are now available.

Cloud: some improvements

More information are provided to the user

OAR binding improvement

QuickStart documentation is provided

- Partners: CNRS - ENS Lyon - UCBL Lyon 1
- URL: http://graal.ens-lyon.fr/diet/

6.4. Kwapi

Participants: Laurent Lefèvre [correspondant], Jean-Patrick Gelas, Laurent Pouilloux.

FUNCTIONAL DESCRIPTION

Kwapi is a software framework dealing with energy monitoring of large scale infrastructures through heterogeneous energy sensors. Kwapi has been designed inside the FSN XLCloud project for Openstack infrastructures. Through the support of Hemera Inria project, kwapi has been extended and deployed in production mode to support easy and large scale energy profiling of the Grid'5000 resources.

- URL: https://launchpad.net/kwapi

6.5. DirectL2C

Participants: Vincent Lanore, Christian Perez [correspondant].

KEYWORDS: HPC, Software Components, Reconfiguration

FUNCTIONAL DESCRIPTION

L2C (http://hlcm.gforge.inria.fr/l2c:start) is a Low Level Component model implementation targeting at use-cases where overhead matters such as High-Performance Computing. L2C does not offer network transparency neither language transparency. Instead, L2C lets the user choose between various kinds of interactions between components, some with ultra low overhead and others that support network transport. L2C is extensible as additional interaction kinds can be added quite easily. L2C currently supports C++, FORTRAN 2013, MPI and CORBA interactions.

In 2015, we have prototyped DirectL2C on top of L2C. DirectL2C enables efficient and consistent reconfiguration of large scale L2C based assemblies. It provides an assembly model enhanced with domains, tranformations, and transformation adapters.

- URL: http://hlcm.gforge.inria.fr/l2c:start

6.6. Sam4C

Participants: Eddy Caron [correspondant], Arnaud Lefray.

SCIENTIFIC DESCRIPTION

This editor is generated in Java from an EMF -Eclipse Modeling Framework- metamodel to simplify any modifications or extensions. The application model and the associated security policy are compiled in a single XML file which serves as input for an external Cloud security-aware scheduler. Alongside with this editor, Cloud architecture models and provisioning algorithms are provided for simulation (in the current version) or real deployments (in future versions).

FUNCTIONAL DESCRIPTION

Sam4C (Security-Aware Models for Clouds) is a graphical and textual editor to model Cloud applications (as virtual machines, processes, files and communications) and describe its security policy. Sam4C is suitable to represent any static application without deadline or execution time such as n-tiers or parallel applications.

- URL: https://gforge.inria.fr/projects/sam4c/

6.7. SimGrid

Participant: Frédéric Suter [correspondant].

KEYWORDS: Large-scale Emulators - Grid Computing - Distributed Applications
FUNCTIONAL DESCRIPTION

Scientific Instrument for the study of Large-Scale Distributed Systems. SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments. In 2015, we published a new release, SimGrid 3.12.

- Partners: CNRS - Ecole Normale Supérieure de Rennes - University of Hawaii - Université de Reims Champagne-Ardenne - Femto-st
- URL: http://simgrid.gforge.inria.fr/

6.8. execo

Participants: Matthieu Imbert [correspondant], Laurent Pouilloux.

FUNCTIONAL DESCRIPTION

Execo offers a Python API for asynchronous control of local or remote, standalone or parallel, unix processes. It is especially well suited for quickly and easily scripting workflows of parallel/distributed operations on local or remote hosts: automate a scientific workflow, conduct computer science experiments, perform automated tests, etc. The core python package is execo. The execo_g5k package provides a set of tools and extensions for the Grid'5000 testbed. The execo_engine package provides tools to ease the development of computer sciences experiments.

- URL: http://execo.gforge.inria.fr

6.9. Grid'5000 Experimental Platform

Participants: Laurent Lefèvre [correspondant], Simon Delamare, David Loup, Christian Perez, Marc Pinhède, Laurent Pouilloux.

FUNCTIONAL DESCRIPTION

The Grid'5000 experimental platform is a scientific instrument to support computer science research related to distributed systems, including parallel processing, high performance computing, cloud computing, operating systems, peer-to-peer systems and networks. It is distributed on 10 sites in France and Luxembourg, including Lyon. Grid'5000 is a unique platform as it offers to researchers many and varied hardware resources and a complete software stack to conduct complex experiments, ensure reproducibility and ease understanding of results.

- URL: https://www.grid5000.fr/mediawiki/index.php/Grid5000:Home

AVIZ Project-Team

6. New Software and Platforms

6.1. Bertifier

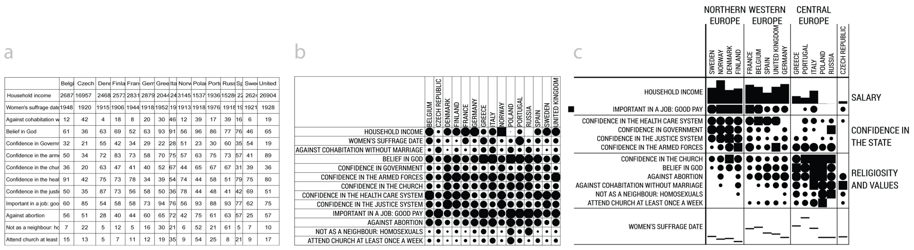


Figure 3. Image of Bertifier, a web application for creating tabular visualizations from spreadsheets.

FUNCTIONAL DESCRIPTION

Bertifier is a web application for rapidly creating tabular visualizations from spreadsheets (see Figure 3). Bertifier draws from Jacques Bertin's matrix analysis method, whose goal was to "simplify without destroying" by encoding cell values visually and grouping similar rows and columns. Although there were several attempts to bring this method to computers, no implementation exists today that is both exhaustive and accessible to a large audience. Bertifier remains faithful to Bertin's method while leveraging the power of today's interactive computers. Tables are formatted and manipulated through crossets, a new interaction technique for rapidly applying operations on rows and columns. Bertifier also introduces visual reordering, a semi-interactive reordering approach that lets users apply and tune automatic reordering algorithms in a WYSIWYG manner. We showed in an evaluation that Bertifier has the potential to bring Bertin's method to a wider audience of both technical and non-technical users, and empower them with data analysis and communication tools that were so far only accessible to a handful of specialists.

- Participants: Jean-Daniel Fekete, Charles Perin and Pierre Dragicevic
- Partner: Université Paris-Sud
- Contact: Jean-Daniel Fekete
- URL: http://www.bertifier.com

6.2. CENDARI Note-Taking-Environment

SCIENTIFIC DESCRIPTION

CENDARI (http://www.aviz.fr/Research/CENDARI) Is a European Infrastructure project funded by the EU for 4 years: 2012-2016. Aviz is in charge of the Human-Computer Interface for the project, and develops a tool to allow historians and archivists to take notes, enter them online, manage their images in relations with the notes and documents, and visualize the entities they find in the documents and notes. This system is an extension of the original EditorsNotes project, integrating several innovative components asked by the historians: visualizations, relations with the Semantic Web, and a management of access rights respecting the researchers' desire of privacy for their notes, as well as desire of sharing entities and relations gathered throught the notes and documents.

FUNCTIONAL DESCRIPTION

The Note-Taking-Environment [24] is an open-source, web-based tool for recording, organizing, preserving, and opening access to research notes, built with the needs of documentary editing projects, archives, and library special collections in mind.

- Participants: Evanthia Dimara, Nadia Boukhelifa Sari Ali, Emmanouil Giannisakis, and Jean-Daniel Fekete
- Contact: Jean-Daniel Fekete
- URL: https://github.com/CENDARI/editorsnotes

6.3. GraphCoiffure

SCIENTIFIC DESCRIPTION

Node-link infographics are visually very rich and can communicate messages effectively, but can be very difficult to create, often involving a painstaking and artisanal process. We have investigated node-link visualizations for communication, and have explored how to better support their creation. We have developed a set of techniques aimed at improving their creation workflow by bringing more flexibility and power to users, letting them manipulate all aspects of a node-link diagram (layout, visual attributes, etc.) while taking into account the context in which it will appear. We then implemented these techniques in a proof-of-concept prototype called GraphCoiffure, which we designed as an intermediary step between graph drawing/editing software and image authoring applications.

FUNCTIONAL DESCRIPTION

GraphCoiffure [21] is a proof-of-concept prototype designed to bridge the gap between graph editors and image authoring software by supporting graph beautification, i. e., the touching up of a node-link diagram to enhance its communicative power, or to make it conform to a desired aesthetics. GraphCoiffure is not meant to replace graph editors and graph drawing software, but rather to extend them by letting users import and beautify diagrams that have been created in these programs. GraphCoiffure does not itself enhance these diagrams, but it empowers users to do so. Its features include tools for interactive graph manipulation, a CSS-like stylesheet system, and a possibility of using page layout schemas to tailor a diagram for a specific context of use. Unlike graphics editors, it preserves visual mappings and makes it easier for users to make modifications based on the semantics of the graphs and their context of use.

- Participants: Andre Suslik Spritzer, Jeremy Boy, Pierre Dragicevic, Jean-Daniel Fekete, and Carla Maria dal Sasso Freitas
- Contact: Andre Suslik Spritzer

6.4. Hybrid Image Visualisation

Hybrid-image visualizations blend two different visual representations into a single static view, such that each representation can be perceived at a different viewing distance. Our work is motivated by data analysis scenarios that incorporate one or more displays with sufficiently large size and resolution to be comfortably viewed by different people from various distances. Hybrid-image visualizations can be used, in particular, to enhance overview tasks from a distance and detail-in-context tasks when standing close to the display. By taking advantage of humans' perceptual capabilities, hybrid-image visualizations do not require tracking of viewers in front of a display. Moreover, because hybrid-images use a perception-based blending approach, visualizations intended for different distances can each utilize the entire display. We contribute a design space, discuss the perceptual rationale for our work, provide examples and a set of techniques for hybrid-image visualizations, and describe tools for designing hybrid-image visualizations. An example can be found in Figure 4 .

KEYWORDS: Wall-Sized Displays, Perception, Hybrid Images

FUNCTIONAL DESCRIPTION

- Participants: Jean-Daniel Fekete, Petra Isenberg, Pierre Dragicevic, Wesley Willett, Romain Primet.
- Contact: Petra Isenberg
- URL: http://aviz.fr/Research/HybridImageVisualizations

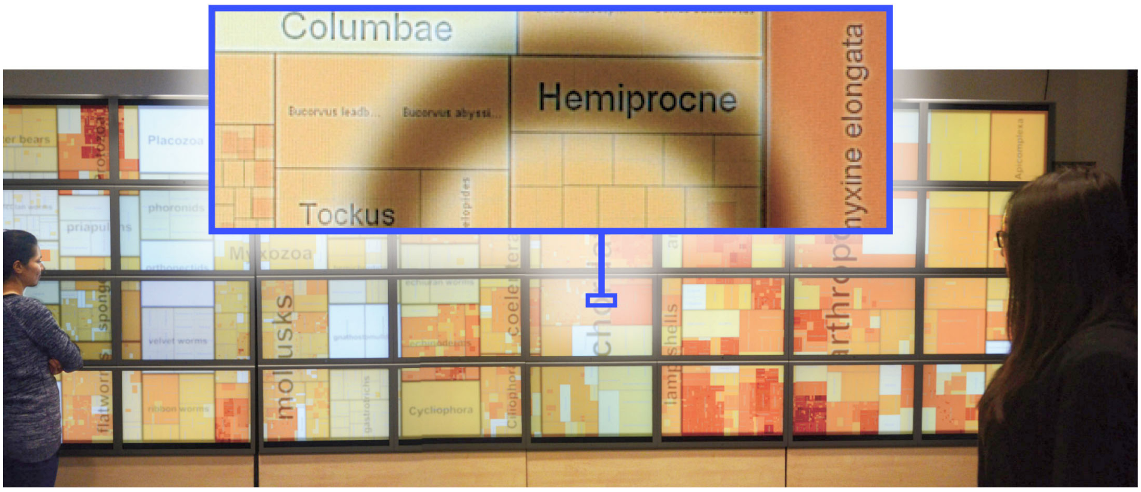


Figure 4. Hybrid image visualization software for the creation of visualizations for distant and close viewing on large displays.

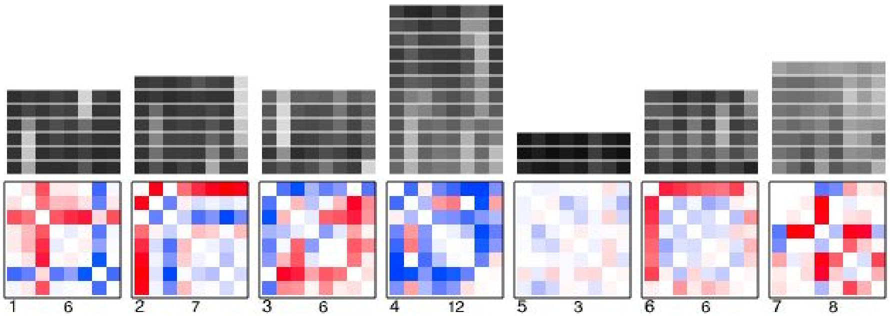


Figure 5. Small Multipiles is software for visualizing temporal networks such as for brain connectivity analysis.

6.5. Small Multipiles

SCIENTIFIC DESCRIPTION

MultiPiles [11] is a visualization to explore time-series of dense, weighted networks (see Figure 5). The interface is based on the physical analogy of piling adjacency matrices, each one representing a single temporal snapshot. Common interfaces for visualizing dynamic networks use techniques such as: flipping/animation; small multiples; or summary views in isolation. Our proposed ‘piling’ metaphor presents a hybrid of these techniques, leveraging each one’s advantages, as well as offering the ability to scale to networks with hundreds of temporal snapshots. While MultiPiles is applicable to many domains, our prototype was initially designed to help neuroscientists investigate changes in brain connectivity networks over several hundred snapshots. The piling metaphor and associated interaction and visual encodings allowed neuroscientists to explore their data, prior to a statistical analysis. They detected high-level temporal patterns in individual networks and this helped them to formulate and reject several hypotheses.

FUNCTIONAL DESCRIPTION

MultiPiles is a visualization interface for the exploration of dense dynamic networks with changing edge weights. Dynamic networks are networks which change topology over time and/or edge weights change over time.

- Participants: Benjamin Bach, Nathalie Henry-Riche, Tim Dwyer, Tara Madhyastha, Jean-Daniel Fekete, Thomas Grabowski
- Contact: Benjamin Bach
- URL: http://visualizingbrainconnectivity.org/multipiles

6.6. Network Cube

SCIENTIFIC DESCRIPTION

Network visualizations support research in a range of scientific domains from biology to humanities. We created a platform to bridge the gap between domain scientists and visualisation researchers; NetworkCube [42] aims in being a fast way to deploy experimental visualizations from research to domain experts analyzing dynamic networks. In turn, InfoVis researchers benefit from studying how their visualizations are used in the wild.

FUNCTIONAL DESCRIPTION

NetworkCube is implemented in Java and JavaScript and will be available shortly online.

- Participants: Benjamin Bach, Nathalie Henry Riche, Roland Fernandez, Emmanoulis Giannisakis, Bongshin Lee, Jean-Daniel Fekete
- Contact: Benjamin Bach

6.7. Time Curves

SCIENTIFIC DESCRIPTION

Time curves [12], as seen in Figure 6 , are a general approach for visualizing patterns of evolution in temporal data. Examples of such patterns include slow and regular progressions, large sudden changes, and reversals to previous states. These patterns can be of interest in a range of domains, such as collaborative document editing, dynamic network analysis, and video analysis. Time curves employ the metaphor of folding a timeline visualization into itself so as to bring similar time points close to each other. This metaphor can be applied to any dataset where a similarity metric between temporal snapshots can be defined, thus it is largely datatype-agnostic. We illustrate how time curves can visually reveal informative patterns in a range of different datasets.

FUNCTIONAL DESCRIPTION

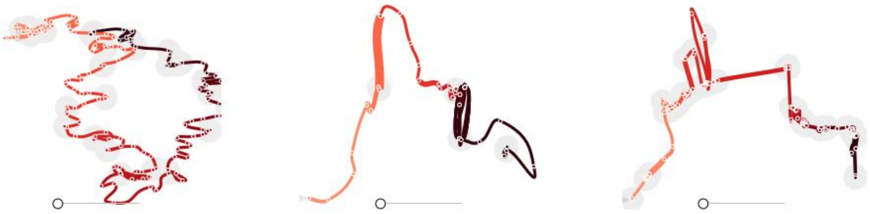


Figure 6. Time Curves is software for visualizing the evolution of patterns in temporal data.

Time Curves are implemented in Java and JavaScript.

- Participants: Benjamin Bach, Conglei Shi, Nicolas Heulot, Tara Madhyastha, Tom Grabowski, Pierre Dragicevic
- Contact: Benjamin Bach
- URL: http://www.aviz.fr/~bbach/timecurves/

6.8. SmartTokens

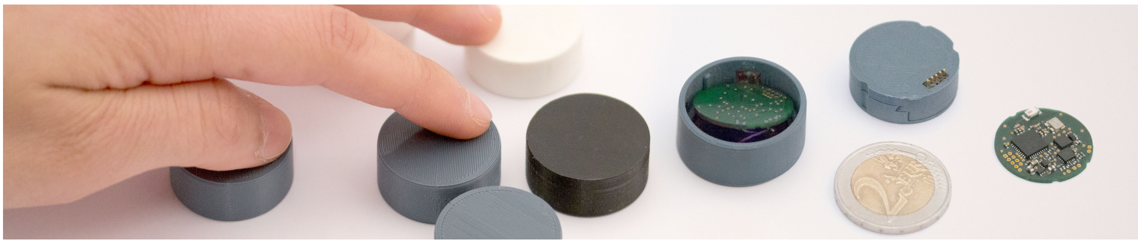


Figure 7. SmartTokens are small-sized tokens supporting touch and motion sensing, and wireless communication with a coordinator.

SCIENTIFIC DESCRIPTION

SmartTokens are small-sized tangible tokens that can sense multiple types of motion, multiple types of touch/grip, and send input events wirelessly as state-machine transitions. By providing an open platform for embedding basic sensing capabilities within small form-factors, SmartTokens extend the design space of tangible user interfaces. We describe the design and implementation of SmartTokens and illustrate how they can be used in practice by introducing a novel TUI design for event notification and personal task management.

FUNCTIONAL DESCRIPTION

SmartTokens are simple and cost-effective, but smart enough to be used as handles for digital information. SmartTokens allow to make generic, scalable and affordable user interfaces. They embed custom electronics, including touch and motion sensors as well as wireless communication functionalities.

- Participants: Mathieu Le Goc, Pierre Dragicevic, Samuel Huron, Jeremy Boy, Jean-Daniel Fekete
- Contact: Mathieu Le Goc
- URL: http://www.aviz.fr/smarttokens

6.9. Sparklificator

FUNCTIONAL DESCRIPTION

Sparklificator is a general open-source jQuery library that eases the process of integrating word-scale visualizations into HTML documents. It provides a range of options for adjusting the position (on top, to the right, as an overlay), size, and spacing of visualizations within the text. The library includes default visualizations, including small line and bar charts, and can also be used to integrate custom word-scale visualizations created using web-based visualization toolkits such as D3.

- Participants: Pascal Goffin, Wesley Willett and Petra Isenberg
- Contact: Jean-Daniel Fekete
- URL: http://inria.github.io/sparklificator/

AYIN Team

6. New Software and Platforms

6.1. SAAD

- Participants: Zhao Liu and Josiane Zerubia
- Contact: Josiane Zerubia

The code SAAD (Semi-Automatic Acne Detection) V1.0, related to a new acne detection approach using a Markov random field model and chromophore descriptors extracted by bilateral decomposition, developed by Zhao Liu and Josiane Zerubia and deposited at APP (Agence de Protection des Programmes) in December 2013, has been transferred to L'OREAL company for research tests in February 2015.

6.2. ED

- Participants: Paula Craciun and Josiane Zerubia
- Contact: Josiane Zerubia

The code ED (Ellipses Detection) V1.0, related to a new elliptic object detection approach using Marked Point Process (MPP), developed by Paula Craciun and Josiane Zerubia, has been deposited to APP in December.

6.3. ET

- Participants: Paula Craciun and Josiane Zerubia
- Contact: Josiane Zerubia

The code ET (Ellipses Tracking) V1.0, related to a new elliptic object tracking approach using MPP, developed by Paula Craciun and Josiane Zerubia, has been deposited to APP in December. This code is available in a sequential or in a parallel (multi-core) version and can be applied to image sequences in biology or remote sensing (between 2 and 30 frames/second)

6.4. ETK

- Participants: Paula Craciun and Josiane Zerubia
- Contact: Josiane Zerubia

The code ETK (Ellipses Tracking Kalman) V1.0, which is a variant of of the ET V1.0 code (without the parallel implementation) using a Kalman filter, developed by Paula Craciun and Josiane Zerubia, has been deposited to BNF (Bibliothèque Nationale de France) in December.

6.5. CLESTO

- Participants: Seong-Gyun Jeong, Yuliya Taralka and Josiane Zerubia
- Contact: Josiane Zerubia

The code CLESTO (CurviLinear structure Extraction with STOchastic process) V1.0, related to a new method for the extraction of curvilinear structures based on MPP, developed by Seong-Gyun Jeong, Yuliya Taralka and Josiane Zerubia, has been deposited to BNF in December.

6.6. CLERANK

- Participants: Seong-Gyun Jeong, Yuliya Taralka and Josiane Zerubia
- Contact: Josiane Zerubia

The code CLERANK (CurviLinear structure Extraction with RANKing) V1.0, related to a new method for the extraction of curvilinear structures using ranking, developed by Seong-Gyun Jeong, Yuliya Taralka and Josiane Zerubia, has been deposited to BNF in December.

6.7. Consulting for Industry

Josiane Zerubia is a scientific consultant for the Galderma company [http://www.galderma.com/About-Galderma/Worldwide-presence/R-D-Locations]

BEAGLE Project-Team

6. New Software and Platforms

6.1. DeCo

Detection of Co-evolution
KEYWORDS: Bioinformatics - Evolution
SCIENTIFIC DESCRIPTION

The software DeCo computes adjacencies (or any type of relation, like regulation, interaction, functional relationships) between ancestral genes from gene phylogenies reconciled with a species phylogeny according to duplications and losses. It takes as input (1) a species tree (2) a set of extant genes (3) a set of exant adjacencies (relations) between extant genes and (4) gene trees which leaves are the extant genes. It outputs ancestral species, genes, and adjacencies. It also highlights the duplications involving several genes.

FUNCTIONAL DESCRIPTION

DeCo for Detection of Co-evolution, reconstructs neighborhood relationships between genes of ancient genomes, in the presence of gene duplications, transfer and losses.

- Participant: Eric Tannier
- Contact: Eric Tannier
- URL: http://pbil.univ-lyon1.fr/software/DeCo/

6.2. DeCoLT

Detection of Co-evolution with Lateral gene Transfer
KEYWORDS: Bioinformatics - Evolution
SCIENTIFIC DESCRIPTION

The software DeCoLT computes adjacencies (or any type of relation, like regulation, interaction, functional relationships) between ancestral genes from gene phylogenies reconciled with a species phylogeny according to duplications, losses and lateral gene transfer. It takes as input a species tree a set of extant genes a set of exant adjacencies (relations) between extant genes and reconciled gene trees which leaves are the extant genes. It outputs ancestral species, genes, and adjacencies. It also highlights the duplications or transfers involving several genes.

FUNCTIONAL DESCRIPTION

The software DeCoLT computes adjacencies (or any type of relation, like regulation, interaction, functional relationships) between ancestral genes from gene phylogenies reconciled with a species phylogeny according to duplications, losses and lateral gene transfer.

- Participant: Eric Tannier
- Contact: Eric Tannier
- URL: http://pbil.univ-lyon1.fr/software/DeCoLT/

6.3. aevol

Artificial Evolution
FUNCTIONAL DESCRIPTION

Aevol is a digital genetics model: populations of digital organisms are subjected to a process of selection and variation, which creates a Darwinian dynamics. By modifying the characteristics of selection (e.g. population size, type of environment, environmental variations) or variation (e.g. mutation rates, chromosomal rearrangement rates, types of rearrangements, horizontal transfer), one can study experimentally the impact of these parameters on the structure of the evolved organisms. In particular, since Aevol integrates a precise and realistic model of the genome, it allows for the study of structural variations of the genome (e.g. number of genes, synteny, proportion of coding sequences).

The simulation platform comes along with a set of tools for analysing phylogenies and measuring many characteristics of the organisms and populations along evolution.

An extension of the model (R-Aevol), integrates an explicit model of the regulation of gene expression, thus allowing for the study of the evolution of gene regulation networks.

- Participants: Carole Knibbe, Guillaume Beslon, Jonathan Rouzaud-Cornabas, Priscila Do Nascimento Biller, Yoram Vadee Le Brun, David Parsons and Vincent Liard
- Partners: UCBL Lyon 1 - INSERM - Universite Paris-Descartes - Insa de Lyon
- Contact: Carole Knibbe
- URL: http://www.aevol.fr/

6.4. EvoEvo

In silico experimental evolution
KEYWORDS: Bioinformatics - Biology - Evolution
FUNCTIONAL DESCRIPTION

In the context of the EvoEvo european project we are developing an integrated model of microorganisms evolution. This model will extend the current evolutionary models developped in the team (Aevol and R-Aevol) by adding a metabolic level and an ecosystem level. In 2014, a first version has been developed and released that includes the genomic, genetic and metabolic levels.

- Participants: Guillaume Beslon, Charles Rocabert and Carole Knibbe
- Contact: Guillaume Beslon
- URL: http://www.evoevo.eu/

6.5. FluoBacTracker

KEYWORDS: Bioinformatics - Biology - Biomedical imaging
FUNCTIONAL DESCRIPTION FluoBacTracker is an ImageJ () plugin designed to segment and track growing E. Coli cells from microscopy images and movies. FluoBacTracker is a software tool to : i) Select regions of interest in each image (detect the colony), (ii) Denoise and renormalize the images, (iii) Identify each cells in each image (segmentation), (iv) Follow cells through the whole movie (tracking) and (v) Detect divisions and construct cell lineage in the population

- Participants: Magali Vangkeosay, David Parsons and Hugues Berry
- Partner: Universite Descartes
- Contact: Hugues Berry
- URL: http://fluobactracker.inrialpes.fr/

BIGS Project-Team

6. New Software and Platforms

6.1. SesIndexCreatoR: An R Package for Socioeconomic Indices Computation and Visualization

KEYWORDS: socioeconomic status, multidimensional index, principal component analysis, hierarchical classification, R

SCIENTIFIC DESCRIPTION

In order to study social inequalities, indices can be used to summarize the multiple dimensions of the socioeconomic status. As a part of the Equit'Area Project, a public health program focused on social and environmental health inequalities, a statistical procedure to create (neighborhood) socioeconomic indices was developed. This procedure uses successive principal components analyses to select variables and create the index. In order to simplify the application of the procedure for non-specialists, the R package SesIndexCreatoR was created. It allows the creation of the index with all the possible options of the procedure, the classification of the resulting index in categories using several classical methods, the visualization of the results, and the generation of automatic reports. [8]

FUNCTIONAL DESCRIPTION

This package allows computing and visualizing socioeconomic indices and categories distributions from datasets of socioeconomic variables (These tools were developed as part of the EquitArea Project, a public health program).

- Participants: Benoît Lalloué, Severine Deguen, Jean-Marie Monnez and Nolwenn Le Meur
- Contact: Benoît Lalloué
- URL: http://www.equitarea.org/documents/packages_1.0-0/

6.2. Angio-Analytics

KEYWORDS: Health - Cancer - Biomedical imaging

SCIENTIFIC DESCRIPTION

Angio Analytics at l'APP under identification N° FR001.280027.000.R.P.2015.000.10000 - Software for image analysis and statistical analysis of parameters issued from these images

Angiogenesis is the phenomenon by which new blood vessels are created from preexisting ones. But this natural process is also involved, in a chaotic way, in tumor development. Many molecules have shown particular efficiency in inhibiting this phenomenon, hopefully leading to either: (i) a reorganization of the neovessels allowing a better tumor uptake of cytotoxic molecules (as chemotherapy) or (ii) a deprivation of the tumor vascular network with the view to starve it. However, characterizing the anti-angiogenic effects of a molecule remains difficult, mainly because the proposed physical modeling approaches have barely been confronted to in vivo data, which are not directly available. We have developed an original approach to characterize and analyze the anti-angiogenic responses in cancerology that allows biologists to account for spatial and dynamical dimensions of the problem. The proposed solution relies on the association of a specific biological in vivo protocol using skinfold chambers, image processing and dynamic system identification. An empirical model structure of the anti-angiogenic effect of a tested molecule is selected according to experimental data. Finally the model is identified and its parameters are used to characterize and compare responses of the tested molecule. The solution has been implemented in a software developed in The Matlab environment.

FUNCTIONAL DESCRIPTION

Angio-Analytics allows the pharmacodynamic characterization of anti-vascular effects in anti-cancer treatments.

- Participant: Thierry Bastogne
- Contact: Thierry Bastogne

6.3. In silico design of nanoparticles for the treatment of cancers by enhanced radiotherapy

KEYWORDS: Bioinformatics - Cancer - Drug development

FUNCTIONAL DESCRIPTION

To speed up the preclinical development of medical engineered nanomaterials, we have designed an integrated computing platform dedicated to the virtual screening of nanostructured materials activated by X-ray making it possible to select nano-objects presenting interesting medical properties faster. The main advantage of this in silico design approach is to virtually screen a lot of possible formulations and to rapidly select the most promising ones. The platform can currently handle the accelerated design of radiation therapy enhancing nanoparticles and medical imaging nano-sized contrast agents as well as the comparison between nano-objects and the optimization of existing materials.

- Participant: Thierry Bastogne
- Contact: Thierry Bastogne

BIOCORE Project-Team

6. New Software and Platforms

6.1. In@lgae

KEYWORDS: Simulation - Microalgae system - Productivity
SCIENTIFIC DESCRIPTION The in@lgae simulation plateform is dedicated to the simulation of microalgae growth at different locations and for different periods of the year. The platform runs different submodels to account for the actual climate and compute biomass productivity together with the consumption of water, nitrogen, phosphorus, ... The platform runs models which describe mechanisms from fast time scale (dynamics of photosystems) down to slow time scales (growth photoacclimation). The models also include a description of the temperature evolution in the culturing systems. The simulation can also be coupled with a model of hydrodynamics as represented by the Freshkiss software developed by the Ange EPI.

FUNCTIONAL DESCRIPTION

In@lgae simulates the productivity of a microalgae production system, taking into account both the process type and its location and time of the year. The process is mainly defined by its thermal dynamics and by its associated hydrodynamics. For a given microalgal strain, a set of biological parameters describe the response to nitrogen limitation, temperature and light. As a result, the biomass production, CO_2 and nitrognen fluxes, lipid and sugar accumulation are predicted.

- Participants: Étienne Delclaux, Francis Mairet, Quentin Béchet and Olivier Bernard
- Contact: Olivier Bernard
- URL: https://gforge.inria.fr/projects/inalgae

6.2. Odin

KEYWORDS: Bioinformatics - Biotechnology
SCIENTIFIC DESCRIPTION

This C++ application is dedicated to deploy advanced control algorithms on real bioprocesses through the use of a Scilab interpreter. In Biocore we develop advanced algorithms for supervision and control, and ODIN is the media to apply them. ODIN is primarily developed in the C++ programming language and uses CORBA to define component interfaces and provide component isolation. ODIN is a distributed platform, enabling remote monitoring of the controlled processes as well as remote data acquisition. It also contains a Scilab-based process simulator which can be harnessed for experimentation and training purposes. It is very modular in order to adapt to any plant and to run most of the algorithms.

FUNCTIONAL DESCRIPTION

ODIN is a software framework for bioprocess control and supervision. ODIN is a distributed platform, where algorithms are described with a common structure easy to implement. Finally, ODIN can perform remote data acquisition and process these data to compute the signals to be applied to the actuators, together with estimates of state variables or process state. ODIN can handle the high level of uncertainties that characterises the biological processes through explicit management of confidence indexes.

- Participants: Melaine Gautier, Olivier Bernard and Francesco Novellis
- Contact: Olivier Bernard
- URL: https://team.inria.fr/biocore/software/odin/

BIPOP Project-Team

5. New Software and Platforms

5.1. ACEF

- Participants: Vincent Acary and Olivier Bonnefon

5.2. Approche

- Participants: Alexandre Derouet-Jourdan, Florence Bertails-Descoubes and Joëlle Thollot
- Contact: Florence Bertails-Descoubes
- URL: Approche

5.3. CloC

- Participants: Florence Bertails-Descoubes and Romain Casati
- Partner: UJF
- Contact: Florence Bertails-Descoubes
- URL: Cloc

5.4. MECHE-COSM

5.4.1. MECHE: Modeling Entangling within Contacting hair fibErs

Participants: Florence Bertails-Descoubes, Gilles Daviet, Alexandre Derouet-Jourdan, Romain Casati, Laurence Boissieux.

The software MECHE was essentially developed during the MECHE ADT (2009-2011, research engineer: Gilles Daviet), for simulating the dynamics of assemblies of thin rods (such as hair), subject to contact and friction. Currently, this software is extensively used by two PhD students (A. Derouet-Jourdan and R. Casati) and continues to be enriched with new rod models and inversion modules. This software combines a panel of well-accepted models for rods (ranging from reduced coordinates to maximal coordinates models, and including models recently developed by some members of the group) with classical as well as innovative schemes for solving the problem of frictional contact (incorporating the most recent results of the group, as well as the new contact solver we published in [11]). The aim of this software is twofold: first, to compare and analyze the performance of nonsmooth schemes for the frictional contact problem, in terms of realism (capture of dry friction, typically), robustness, and computational efficiency. A first study of this kind was conducted in 2010-2011 onto the different rod models that were available in the software. New studies are planned for evaluating further rod models. Second, we believe such a software will help us understand the behavior of a fibrous material (such as hair) through virtual experiments, thanks to which we hope to identify and understand some important emergent phenomena. A careful validation study against experiments started to be conducted in 2011 in collaboration with physicists from L'Oréal. Once this discrete elements model will be fully validated, our ultimate goal would be to build a continuous macroscopic model for the hair medium relying on nonsmooth laws (which we have started to build in Gilles Daviet's PhD thesis). The core of this software was transferred to L'Oréal in 2011, and to AGT Digital in early 2013, by Gilles Daviet and Florence Bertails-Descoubes. It was also used for generating a number of simulations supporting at least 4 of our research publications.

5.5. Platforms: SICONOS

5.5.1. Platform A : SICONOS

Participants: Vincent Acary, Maurice Brémond, Olivier Huber, Franck Pérignon.

In the framework of the FP5 European project Siconos (2002-2006), Bipop was the leader of the Work Package 2 (WP2), dedicated to the numerical methods and the software design for nonsmooth dynamical systems. This has given rise to the platform SICONOS which is the main software development task in the team. The aim of this work is to provide a common platform for the simulation, modeling, analysis and control of abstract nonsmooth dynamical systems. Besides usual quality attributes for scientific computing software, we want to provide a common framework for various scientific fields, to be able to rely on the existing developments (numerical algorithms, description and modeling software), to support exchanges and comparisons of methods, to disseminate the know-how to other fields of research and industry, and to take into account the diversity of users (end-users, algorithm developers, framework builders) in building expert interfaces in Python and end-user front-end through Scilab.

After the requirement elicitation phase, the Siconos Software project has been divided into 5 work packages which are identified to software products:

1. SICONOS/NUMERICS This library contains a set of numerical algorithms, already well identified, to solve non smooth dynamical systems. This library is written in low-level languages (C,F77) in order to ensure numerical efficiency and the use of standard libraries (Blas, Lapack, ...)
2. SICONOS/KERNEL This module is an object-oriented structure (C++) for the modeling and the simulation of abstract dynamical systems. It provides the users with a set of classes to describe their nonsmooth dynamical system (dynamical systems, intercations, nonsmooth laws, ...) and to perform a numerical time integration and solving.
3. SICONOS/FRONT-END. This module is mainly an auto-generated wrapper in Python which provides a user-friendly interface to the Siconos libraries. A scilab interface is also provided in the Front-End module.
4. SICONOS/CONTROL This part is devoted to the implementation of control strategies of non smooth dynamical systems.
5. SICONOS/MECHANICS. This part is dedicated to the modeling and the simulation of multi-body systems with 3D contacts, impacts and Coulomb's friction. It uses the Siconos/Kernel as simulation engine but relies on a industrial CAD library (OpenCascade and pythonOCC) to deal with complex body geometries and to compute the contact locations and distances between B-Rep description and on Bullet for contact detection between meshes.

Further informations may be found at http://siconos.gforge.inria.fr/

BONSAI Project-Team

6. New Software and Platforms

6.1. Iedera

Iedera : subset seed design tool
KEYWORDS: Computational biology - Sequence alignment - Spaced seeds
SCIENTIFIC DESCRIPTION

Iedera is a tool based on a weighted automata framework that enables to compute spaced seeds, associated probability distributions, scores/costs, counts, and even polynomials on a classical semi-ring framework. Seed design is computed by full enumeration or hill-climbing optimization.
FUNCTIONAL DESCRIPTION

Iedera is a tool to select and design subset seed and vectorized subset seed patterns. Spaced seeds and transition-constrained spaced seeds can be perfectly represented in the subset seed model.

- Participants: Laurent Noé, Grégory Kucherov and Mikhail Roytberg
- Partners: CNRS - Université de Nancy - Université de Lille
- Contact: Laurent Noé
- URL: http://bioinfo.lifl.fr/yass/iedera.php

6.2. NORINE

Nonribosomal peptides resource
KEYWORDS: Bioinformatics - Biotechnology - Biology - Genomics - Graph algorithmics - Chemistry - Knowledge database - Drug development - Computational biology
FUNCTIONAL DESCRIPTION

Norine is a public computational resource with a web interface and REST access to a knowledge-base of nonribosomal peptides. It also contains dedicated tools : 2D graph viewer and editor, comparison of NRPs, MyNorine, a tool allowing anybody to easly submit new nonribosomal peptides, Smiles2monomers (s2m), a tool that deciphers the monomeric structure of polymers from their chemical structure.

- Participants: Maude Pupin, Areski Flissi, Valerie Leclère, Laurent Noé, Yoann Dufresne, Juraj Michalik and Stéphane Janot
- Partners: CNRS - Université Lille 1 - Institut Charles Viollette
- Contact: Maude Pupin
- URL: http://bioinfo.lille.inria.fr/NRP

6.3. ProCARs

PROgressive Contiguous Ancestral RegionS
KEYWORDS: Bioinformatics - Evolution - Metagenomics
SCIENTIFIC DESCRIPTION

ProCars is a program used to reconstruct ancestral gene orders as CARs (Contiguous Ancestral Regions) with a progressive homology-based method. The method runs from a phylogeny tree (without branch lengths needed) with a marked ancestor and a block file. This homology-based method is based on iteratively detecting and assembling ancestral adjacencies, while allowing some micro-rearrangements of synteny blocks at the extremities of the progressively assembled CARs. The method starts with a set of blocks as initial set of CARs, and detects iteratively the potential ancestral adjacencies between extremities of CARs, while building up the CARs progressively by adding, at each step, new non-conflicting adjacencies that induce the less homoplasy phenomenon. The species tree is used, in some additional internal steps, to compute a score for the remaining conflicting adjacencies, and to detect other reliable adjacencies, in order to reach completely assembled ancestral genomes.

FUNCTIONAL DESCRIPTION

ProCARs is a program used to reconstruct ancestral gene orders as CARs (Contiguous Ancestral Regions) with a progressive homology-based method. The method runs from a phylogeny tree with a marked ancestor and a block file.

- Participants: Aïda Ouangraoua, Samuel Blanquart, Jean-Stéphane Varré and Amandine Perrin
- Partners: CNRS - Université de Lille
- Contact: Jean-Stéphane Varré
- URL: http://bioinfo.lifl.fr/procars

6.4. SortMeRNA

KEYWORDS: Bioinformatics - NGS - Genomic sequence

SCIENTIFIC DESCRIPTION

SortMeRNA is a biological sequence analysis tool for metatranscriptomic and metagenomic data filtering, mapping and OTU-picking. The main application of SortMeRNA is filtering and mapping ribosomal RNA from NGS reads.

FUNCTIONAL DESCRIPTION The core algorithm is based on approximate seeds as well as an optimized text index data structure. It allows for fast and sensitive analyses of nucleotide sequences.

SortMeRNA takes as input a file of reads (fasta or fastq format) and one or multiple rRNA database file(s), and sorts apart rRNA and rejected reads into two files specified by the user. Optionally, it can provide high quality local alignments of rRNA reads against the rRNA database. SortMeRNA works with Illumina, 454, Ion Torrent and PacBio data, and can produce SAM and BLAST-like alignments. It is implemented in C++.

- Participants: Hélène Touzet, Laurent Noé and Evguenia Kopylova
- Contact: Hélène Touzet
- URL: http://bioinfo.lille.inria.fr/RNA/sortmerna/

6.5. Vidjil

High-Throughput Analysis of V(D)J Immune Repertoire

KEYWORDS: Bioinformatics - NGS - Indexation - Cancer - Drug development

SCIENTIFIC DESCRIPTION

Vidjil is made of three components: an algorithm, a visualisation browser and a server that allow an analysis of lymphocyte populations containing V(D)J recombinations.

Vidjil high-throughput algorithm extracts V(D)J junctions and gather them into clones. This analysis is based on a spaced seed heuristics and is fast and scalable, as, in the first phase, no alignment is performed with database germline sequences. Each sequence is put in a cluster depending on its V(D)J junction. Then a representative sequence of each cluster is computed in time linear in the size of the cluster. Finally, we perform a full alignment using dynamic programming of that representative sequence againt the germline sequences.

Vidjil also contains a dynamic browser (with D3JS) for visualization and analysis of clones and their tracking along the time in a MRD setup or in a immunological study.

FUNCTIONAL DESCRIPTION

Vidjil is an open-source platform for the analysis of high-throughput sequencing data from lymphocytes. V(D)J recombinations in lymphocytes are essential for immunological diversity. They are also useful markers of pathologies, and in leukemia, are used to quantify the minimal residual disease during patient follow-up. High-throughput sequencing (NGS/HTS) now enables the deep sequencing of a lymphoid population with dedicated Rep-Seq methods and software.

- Participants: Mathieu Giraud, Mikaël Salson, Marc Duez, Ryan Herbert, Tatiana Rocher and Florian Thonier
- Partners: CNRS - Inria - Université de Lille
- Contact: Mathieu Giraud
- URL: http://www.vidjil.org

6.6. Yass

KEYWORDS: Bioinformatics - Genomic sequence - Computational biology - Sequence alignment

SCIENTIFIC DESCRIPTION

As most of the heuristic DNA local alignment softwares (BLAST, FASTA, PATTERNHUNTER, BLASTZ, LAST...) YASS uses seeds to detect potential similarity regions, and then tries to extend them to actual alignments.

This genomic search tool uses multiple transition-constrained spaced seeds (most of the design of these seeds is provided by the Iedera tool) to search for more fuzzy repeats, such as non-coding DNA/RNA.

Main features of YASS are: (i) multiple, possibly overlapping seeds and a new hit criterion to ensure a good sensitivity/selectivity trade-off (ii) transition-constrained spaced seeds to improve sensitivity (transition mutations are purine to purine [AG] or pyrimidine to pyrimidine [CT]) (iii) using different scoring schemes with bit-score and E-value evaluated according to the sequence background frequencies (iv) parameterizable output filter for low complexity repeats (v) reporting of various alignment statistical parameters (mutation bias along triplets, transition/transversion), and (vi) post-processing step to group gapped alignments.

FUNCTIONAL DESCRIPTION

YASS is a genomic similarity search tool, for nucleic (DNA/RNA) sequences in fasta or plain text format : it produces local pairwise alignments.

- Participants: Laurent Noé and Grégory Kucherov
- Partners: CNRS - Université de Nancy - Université de Lille
- Contact: Laurent Noé
- URL: http://bioinfo.lifl.fr/yass

6.7. miRkwood

KEYWORDS: Bioinformatics - Genomics

SCIENTIFIC DESCRIPTION

miRkwood is a bioinformatic pipeline that allows for the fast and easy identification of microRNAs in plant genomes. It is both available as a webserver and a stand-alone software. It offers an user-friendly interface to navigate in the data, as well as many export options to allow the user to conduct further analyses on a local computer.

FUNCTIONAL DESCRIPTION

The method takes as input a set of small reads, that have been previously trimmed and aligned onto the reference genome. It identifies novel microRNAs on the basis of the distributions of reads and the potential of flanking genomic sequence to fold into a stem-loop secondary structure. Then the result is refined through a variety of additional complementary features that bring new evidence to the prediction: duplex stability, thermodynamic stability, phylogenetic conservation, repeats, etc.

- Participants: Hélène Touzet, Mohcen Benmounah, Jean-Frédéric Berthelot, Isabelle Guigon and Sylvain Legrand
- Contact: Hélène Touzet
- URL: http://bioinfo.lille.inria.fr/mirkwood/

CAGIRE Team

6. New Software and Platforms

6.1. AeroSol

Participants: Simon Delmas [Cagire], Benjamin Lux [Cagire], Nikolaos Pattakos [Cardamom], Vincent Perrier [Cagire, correspondent], Mario Ricchiuto [Cardamom].

Developed since 2011 by V. Perrier in partnership with the Cardamom Inria team, the AeroSol library is a high order finite element library written in C++. The code design has been carried for being able to perform efficient computations, with continuous and discontinuous finite element methods on hybrid and possibly curvilinear meshes.

The work of the Cardamom team is focused on continuous finite element methods, while we focus on discontinuous Galerkin methods. However, everything is done for sharing the largest possible part of code. The distribution of the unknowns is made with the software PaMPA, first developed within the Inria teams Bacchus and Castor, and currently maintained in the Tadaam team.

The generic features of the library are

- **High order**. It can be theoretically any order of accuracy, but the finite element basis, and quadrature formula are implemented for having up to a fifth order of accuracy.
- **Hybrid and curvilinear meshes**. AeroSol can deal with up to fifth order conformal meshes composed of lines, triangles, quadrangles, tetrahedra, hexahedra, prism, and pyramids.
- **Continuous and discontinuous discretization**. AeroSol deals with both continuous and discontinuous finite element methods.

We would like to emphasize three assets of this library:

- **Its development environment** For allowing a good collaborative work and a functional library, a strong emphasis has been put on the use of modern collaborative tools for developing our software. This includes the active use of a repository, the use of CMake for the compilation, the constant development of unitary and functional tests for all the parts of the library (using CTest), and the use of the continuous integration tool Jenkins for testing the different configurations of AeroSol and its dependencies. Efficiency is regularly tested with direct interfacing with the PAPI library or with tools like scalasca.
- **Its genericity** A lot of classes are common to all the discretization, for example classes concerning I/O, finite element functions, quadrature, geometry, time integration, linear solver, models and interface with PaMPA. Adding simple features (e.g. models, numerical flux, finite element basis or quadrature formula) can be easily done by writing the class, and declaring its use in only one class of the code.
- **Its efficiency** This modularity is achieved by means of template abstraction for keeping good performances. Dedicated efficient implementation, based on the data locality of the discontinuous Galerkin method has been developed. As far as parallelism is concerned, we use point-to-point communications, the HDF5 library for parallel I/O. The behavior of the AeroSol library at medium scale (1000 to 2000 cores) was studied in [19].

The AeroSol project fits with the first axis of the Bordeaux Sud Ouest development strategy, which is to build a coherent software suite scalable and efficient on new architectures, as the AeroSol library relies on several tools developed in other Inria teams, especially for the management of the parallel aspects.

At the end of 2014, AeroSol had the following features:

- **Development environment** Use of CMake for compilation (gcc, icc and xlc), CTest for automatic tests and memory checking, lcov and gcov for code coverage reports. Development of a CDash server for collecting the unitary tests and the memory checking. Beginning of the development of an interface for functional tests. Optional linking with HDF5, PAPI, with dense small matrices libraries (BLAS, Eigen)
- **In/Out** Link with the XML library for handling with parameter files. Parallel reader for GMSH, with an embedded geometrical pre-partitioner. Writer on the VTK-ASCII legacy format (cell and point centered). Parallel output in vtu and pvtu (Paraview) for cell-centered visualization, and XDMF/HDF5 format for both cell and point centered visualization. Ability of saving the high order solution and restarting from it. Computation of volumic and probe statistics. Ability of saving averaged layer data in quad and hexa meshes. Ability of defining user defined output visualization variables.
- **Quadrature formula** up to 11th order for Lines, Quadrangles, Hexaedra, Pyramids, Prisms, up to 14th order for tetrahedron, up to 21st order for triangles. Gauss-Lobatto type quadrature formula for lines, triangles, quadrangles and hexaedra.
- **Finite elements** up to fourth degree for Lagrange finite elements and hierarchical orthogonal finite element basis (with Dubiner transform on simplices) on lines, triangles, quadrangles, tetrahedra, prisms, hexaedra and pyramids. Finite element basis that are interpolation basis on Gauss-Legendre points for lines, quadrangles, and hexaedra, and triangle (only 1st and 2nd order).
- **Geometry** Elementary geometrical functions for first order lines, triangles, quadrangles, prisms, tetrahedra, hexaedra and pyramids. Handling of high order meshes.
- **Time iteration** explicit Runge-Kutta up to fourth order, explicit Strong Stability Preserving schemes up to third order. Optimized CFL time schemes: SSP(2,3) and SSP(3,4). CFL time stepping. Implicit integration with BDF schemes from 2nd to 6th order Newton method for stationary problems. Implicit unstationary time iterator non consistent in time for stationary problems. Implementation of in house GMRES and conjugate gradient based on Jacobian free iterations.
- **Linear Solvers** Link with the external linear solver UMFPack, PETSc and MUMPS. Internal solver for diagonal and block-diagonal matrices.
- **Memory handling** discontinuous and continuous, sequential and parallel discretizations based on PaMPA for generic meshes, including hybrid meshes.
- **Models** Perfect gas Euler system, real gas Euler system (template based abstraction for a generic equation of state), scalar advection, Waves equation in first order formulation, generic interface for defining space-time models from space models. Diffusive models: isotropic and anisotropic diffusion, compressible Navier-Stokes. Scalar advection-diffusion model.
- **Numerical schemes** Continuous Galerkin method for the Laplace problem (up to fifth order) with non consistent time iteration or with direct matrix inversion. Explicit and implicit discontinuous Galerkin methods for hyperbolic systems, diffusive and advection-diffusion problems. Beginning of optimization by stocking the geometry for advection problems. SUPG and Residual disribution schemes. Optimization of DG schemes for advection-diffusion problems: stocking of the geometry and use of BLAS for all the linear phases of the scheme.
- **Numerical fluxes** Centered fluxes, exact Godunov' flux for linear hyperbolic systems, and Lax-Friedrich flux. Riemann solvers for Low Mach flows. Numerical flux accurate for steady and unsteady computations.
- **Boundary conditions** Periodic boundary conditions, time-dependent inlet and outlet boundary conditions. Adiabatic wall and isothermal wall. Steger-Warming based boundary condition.
- **Parallel computing** Mesh redistribution, computation of Overlap with PaMPA. Collective asynchronous communications (PaMPA based). Asynchronous point to point communications. Tests on the cluster Avakas from MCIA, and on Mésocentre de Marseille, and PlaFRIM. Tier-1 Turing (Blue-Gene).

- **C++/Fortran interface** Tests for binding fortran with C++.
- **Instrumentation** Aerosol can give some traces on memory consumption/problems with an interfacing with the PAPI library. Tests have also been performed with VTUNE and TAU. Tests with Maqao and Scalasca (VIHPS workshop).
- **Validation** Poiseuille, Taylor-Green vortex. Laplace equation on a ring and Poiseuille flow on a ring. Implementation of volumic forcing based on wall dissipation.

In 2015, N. Pattakos was hired in the team Cardamom, in order to improve the code architecture and for easing the installation of the library. The following features were added or improved:

- **Development environment** The use of CMake was strongly improved, which induced also easier test launching. Documentation, code cleaning and refactorization have also been led. The shared project of Plafrim was updated, and so was the joint Aerosol/Scotch/PaMPA project on the continuous integration platform. Integration of SPack for handling dependencies has begun. Interface with ESSL was fixed.
- **Multigrid** Development of p-multigrid methods. This includes also the possibility of beginning a computation iwth an order and to decrease or increase the order of approximation when restarting. For the p multigrid methods, V and W cycle have been developed, and restriction and prolongation opertors have also been developed. Implementation of h-multigrid has started, with the development of tests of the aggregation methods of PaMPA, and the definition of finite element basis on arbitrary cells.
- **Boundary conditions** Development of the Synthetic Eddy Method boundary condition.
- **Models** Linearized Euler equations, and Sutherland model for non isothermal diffusive flows. Shallow-water model.
- **Parallel computing** Weighted load balancing for hybrid meshes.
- **Validation** Turbulent channel flow.
- **Postprocessing** Development of high order projections over line postprocessing, possibility of stocking averaged data, such as the average flow and the Reynolds stresses.

CAIRN Project-Team

6. New Software and Platforms

6.1. Panorama

With the ever raising complexity of embedded applications and platforms, the need for efficient and customizable compilation flows is stronger than ever. This need of flexibility is even stronger when it comes to research compiler infrastructures that are necessary to gather quantitative evidence of the performance/energy or cost benefits obtained through the use of reconfigurable platforms. From a compiler point of view, the challenges exposed by these complex reconfigurable platforms are quite significant, since they require the compiler to extract and to expose an important amount of coarse and/or fine grain parallelism, to take complex resource constraints into consideration while providing efficient memory hierarchy and power management.

Because they are geared toward industrial use, production compiler infrastructures do not offer the level of flexibility and productivity that is required for compiler and CAD tool prototyping. To address this issue, we have designed an extensible source-to-source compiler infrastructure that takes advantage of leading edge model-driven object-oriented software engineering principles and technologies.

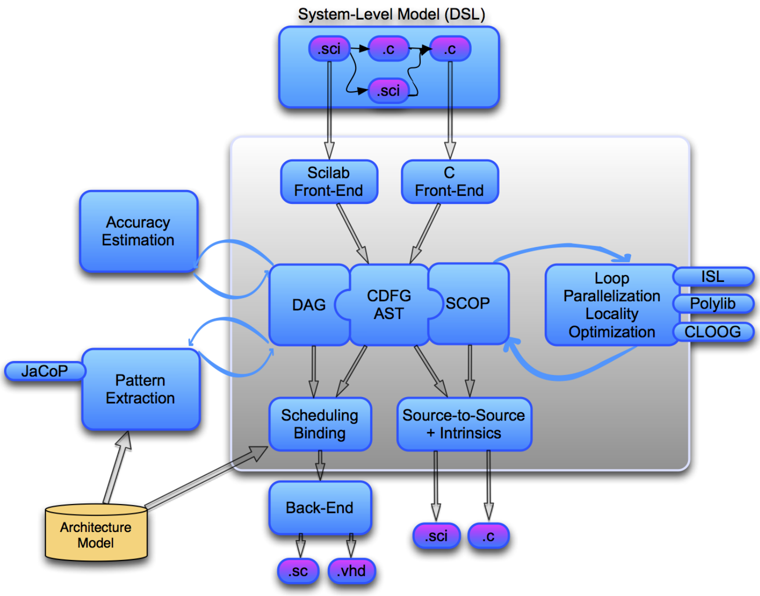


Figure 2. CAIRN's general software development framework.

Figure 2 shows the global framework that is being developed in the group. Our compiler flow mixes several types of intermediate representations. The baseline representation is a simple tree-based model enriched with control flow information. This model is mainly used to support our source-to-source flow, and serves as the backbone for the infrastructure. We use the extensibility of the framework to provide more advanced representations along with their corresponding optimizations and code generation plug-ins. For example, for our pattern selection and accuracy estimation tools, we use a data dependence graph model in all basic blocks instead of the tree model. Similarly, to enable polyhedral based program transformations and analysis, we introduced a specific representation for affine control loops that we use to derive a Polyhedral Reduced Dependence Graph (PRDG). Our current flow assumes that the application is specified as a hierarchy of communicating tasks, where each task is expressed using C or Matlab/Scilab, and where the system-level representation and the target platform model are often defined using Domain Specific Languages (DSL).

Gecos (Generic Compiler Suite) is the main backbone of CAIRN's flow. It is an open source Eclipse-based flexible compiler infrastructure developed for fast prototyping of complex compiler passes. Gecos is a 100% Java based implementation and is based on modern software engineering practices such as Eclipse plugin or model-driven software engineering with EMF (Eclipse Modeling Framework). As of today, our flow offers the following features:

- An automatic floating-point to fixed-point conversion flow (for HLS and embedded processors). **ID.Fix** is an infrastructure for the automatic transformation of software code aiming at the conversion of floating-point data types into a fixed-point representation. http://idfix.gforge.inria.fr.
- A polyhedral-based loop transformation and parallelization engine (mostly targeted at HLS). http://gecos.gforge.inria.fr.
- A custom instruction extraction flow (for ASIP and dynamically reconfigurable architectures). **Durase** and **UPaK** are developed for the compilation and the synthesis targeting reconfigurable platforms and the automatic synthesis of application specific processor extensions. They use advanced technologies, such as graph matching and graph merging together with constraint programming methods.
- Several back-ends to enable the generation of VHDL for specialized or reconfigurable IPs, and SystemC for simulation purposes (e.g., fixed-point simulations).

6.2. Gecos

Participants: Steven Derrien [corresponding author], Nicolas Simon, Nicolas Estibals, Ali Hassan El-Moussawi.

Keywords: source-to-source compiler, model-driven software engineering, retargetable compilation.

The Gecos (Generic Compiler Suite) project is a source-to-source compiler infrastructure developed in the Cairn group since 2004. It was designed to enable fast prototyping of program analysis and transformation for hardware synthesis and retargetable compilation domains.

Gecos is 100% Java based and takes advantage of modern model driven software engineering practices. It uses the Eclipse Modeling Framework (EMF) as an underlying infrastructure and takes benefits of its features to make it easily extensible. Gecos is open-source and is hosted on the Inria gforge at http://gecos.gforge.inria.fr.

The Gecos infrastructure is still under very active development, and serves as a backbone infrastructure to projects of the group. Part of the framework is jointly developed with Colorado State University and since 2012 it is used in the context of the ALMA European project. The Gecos infrastructure will also be used by the EMMTRIX start-up, a spin-off from tha ALMA project which aims at commercializing the results of the project.

Recent developments in Gecos have focused on polyhedral loop transformations and efficient SIMD code generation for fixed point arithmetic data-types as a part of the ALMA project. Significant efforts were also put to provide a coarse-grain parallelization engine targeting the data-flow actor model in the context of the COMPA ANR project.

6.3. ID.Fix: Infrastructure for the Design of Fixed-point Systems

Participants: Olivier Sentieys [corresponding author], Nicolas Simon.

Keywords: fixed-point arithmetic, source-to-source code transformation, accuracy optimization, dynamic range evaluation

The different techniques proposed by the team for fixed-point conversion are implemented on the ID.Fix infrastructure. The application is described with a C code using floating-point data types and different pragmas, used to specify parameters (dynamic, input/output word-length, delay operations) for the fixed-point conversion. This tool determines and optimizes the fixed-point specification and then, generates a C code using fixed-point data types (ac_fixed) from Mentor Graphics. The infrastructure is made-up of two main modules corresponding to the fixed-point conversion (ID.Fix-Conv) and the accuracy evaluation (ID.Fix-Eval). The last developments allowed to have a complete compatibility with GeCos and to avoid the use of Matlab for LTI and recursive systems. In the context of the ANR DEFIS project, the ID.Fix tool has been reorganized to be integrated in the DEFIS toolflow.

6.4. PowWow: Power Optimized Hardware and Software FrameWork for Wireless Motes

Participants: Olivier Sentieys [corresponding author], Arnaud Carer.

Keywords: Wireless Sensor Networks, Low Power, Preamble Sampling MAC Protocol, Hardware and Software Platform

PowWow is an open-source hardware and software platform designed to handle wireless sensor network (WSN) protocols and related applications. Based on an optimized preamble sampling medium access (MAC) protocol, geographical routing and `protothread` library, PowWow requires a lighter hardware system than Zigbee [72] to be processed (memory usage including application is less than 10kb). Therefore, network lifetime is increased and price per node is significantly decreased.

CAIRN's hardware platform (see Figure 3) is composed of:

- The motherboard, designed to reduce power consumption of sensor nodes, embeds an MSP430 microcontroller and all needed components to process PowWow protocol except radio chip. JTAG, RS232, and I2C interfaces are available on this board.
- The radio chip daughter board is currently based on a TI CC2420.
- The coprocessing daughter board includes a low-power FPGA which allows for hardware acceleration for some PowWow features and also includes dynamic voltage scaling features to increase power efficiency. The current version of PowWow integrates an Actel IGLOO AGL250 FPGA and a programmable DC-DC converter. We have shown that gains in energy of up to 700 can be obtained by using FPGA acceleration on functions like CRC-32 or error detection with regards to a software implementation on the MSP430.
- Finally, a last daughter board is dedicated to energy harvesting techniques. Based on the energy management component LTC3108 from Linear Technologies, the board can be configured with several types of stored energy (batteries, micro-batteries, super-capacitors) and several types of energy sources (a small solar panel to recover photovoltaic energy, a piezoelectric sensor for mechanical energy and a Peltier thermal energy sensor).

PowWow distribution also includes a generic software architecture using event-driven programming and organized into protocol layers. The software is based on Contiki [84], and more precisely on the `Protothread` library which provides a sequential control flow without complex state machines or full multi-threading.

To optimize the network regarding a particular application and to define a global strategy to reduce energy, PowWow offers the following extra tools: over-the-air reprogramming, analytical power estimation based on software profiling and power measurements, a dedicated network analyzer to probe and fix transmissions errors in the network. More information can be found at http://powwow.gforge.inria.fr.

6.5. Ziggie: a Platform for Wireless Body Sensor Networks

Participants: Olivier Sentieys [corresponding author], Arnaud Carer.

Figure 3. CAIRN*'s PowWow motherboard with radio and energy-harvesting boards connected*

Keywords: Wireless Body Sensor Networks, Low Power, Gesture Recognition, Localization, Hardware and Software Platform

The Zyggie sensor node has been developed in the team to create an autonomous Wireless Body Sensor Network (WBSN) with the capabilities of monitoring body movements. The Zyggie platform is part of the BoWI project funded by CominLabs. Zyggie is composed of: an ATMEGA128RFA1 microcontroller, an MPU9150 Inertial Measurement Unit (IMU), an RF AS193 switch with two antennas, an LSP331AP barometer, a DC/DC voltage regulator with a battery charge controller, a wireless inductive battery charge controller, and some switches and control LEDs.

Figure 4. CAIRN*'s Ziggie platform for WBSN*

The IMU is composed of a 3-axis accelerometer, a 3-axis gyrometer and a 3-axis magnetometer. The IMU is communicating its data to the embedded microcontroller via an I2C protocol. We also developed our own MAC protocol for synchronization and data exchanges between nodes.

CAMUS Team

6. New Software and Platforms

6.1. APOLLO

Automatic speculative POLyhedral Loop Optimizer
FUNCTIONAL DESCRIPTION

We are developing a framework called APOLLO (Automatic speculative POLyhedral Loop Optimizer), dedicated to automatic, dynamic and speculative parallelization of loop nests that cannot be handled efficiently at compile-time. It is composed of a static part consisting of specific passes in the LLVM compiler suite, plus a modified Clang frontend, and a dynamic part consisting of a runtime system. It has been extended in 2015 to apply on-the-fly any kind of polyhedral transformations, including tiling, and to handle nonlinear loops as while-loops referencing memory through pointers and indirections.

- Participants: Aravind Sukumaran-Rajam, Juan Manuel Martinez Caamaño, Luis Esteban Campostrini, Artiom Baloian, Willy Wolff and Philippe Clauss
- Contact: Juan Manuel Martinez Caamaño

6.2. CLooG

Code Generator in the Polyhedral Model
FUNCTIONAL DESCRIPTION

CLooG is a free software and library to generate code (or an abstract syntax tree of a code) for scanning Z-polyhedra. That is, it finds a code (e.g. in C, FORTRAN...) that reaches each integral point of one or more parameterized polyhedra. CLooG has been originally written to solve the code generation problem for optimizing compilers based on the polyhedral model. Nevertheless it is used now in various area e.g. to build control automata for high-level synthesis or to find the best polynomial approximation of a function. CLooG may help in any situation where scanning polyhedra matters. While the user has full control on generated code quality, CLooG is designed to avoid control overhead and to produce a very effective code. CLooG is widely used (including by GCC and LLVM compilers), disseminated (it is installed by default by the main Linux distributions) and considered as the state of the art in polyhedral code generation.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://www.cloog.org

6.3. Clan

A Polyhedral Representation Extraction Tool for C-Based High Level Languages
FUNCTIONAL DESCRIPTION

Clan is a free software and library which translates some particular parts of high level programs written in C, C++, C# or Java into a polyhedral representation called OpenScop. This representation may be manipulated by other tools to, e.g., achieve complex analyses or program restructurations (for optimization, parallelization or any other kind of manipulation). It has been created to avoid tedious and error-prone input file writing for polyhedral tools (such as CLooG, LeTSeE, Candl etc.). Using Clan, the user has to deal with source codes based on C grammar only (as C, C++, C# or Java). Clan is notably the frontend of the two major high-level compilers Pluto and PoCC.

- Participants: Cédric Bastoul and Imèn Fassi
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/clan/

6.4. Clay

Chunky Loop Alteration wizardrY

FUNCTIONAL DESCRIPTION

Clay is a free software and library devoted to semi-automatic optimization using the polyhedral model. It can input a high-level program or its polyhedral representation and transform it according to a transformation script. Classic loop transformations primitives are provided. Clay is able to check for the legality of the complete sequence of transformation and to suggest corrections to the user if the original semantics is not preserved.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/clay/

6.5. IBB

Iterate-But-Better

FUNCTIONAL DESCRIPTION

IBB is a source-to-source xfor compiler which automatically translates any C source code containing xfor-loops into an equivalent source code where xfor-loops have been transformed into equivalent for-loops.

- Participants: Imen Fassi, Philippe Clauss and Cédric Bastoul
- Contact: Philippe Clauss

6.6. XFOR-Wizard

XFOR-Wizard

FUNCTIONAL DESCRIPTION

Xfor-Wizard is a programming environment for XFOR programs, assisting users in writing XFOR codes and applying optimizing transformations. Automatic dependence analysis and comparisons against a referential code (XFOR-loops or classic for-loops) are achieved to order to help the user in ensuring semantic correctness of the written code.

- Participants: Imen Fassi, Philippe Clauss and Cédric Bastoul
- Contact: Philippe Clauss

6.7. XFORGEN

XFOR code generator

FUNCTIONAL DESCRIPTION

XFORGEN is a tool to automatically generate an XFOR code that is equivalent to for-loops that have been automatically transformed using a static polyhedral compiler. The generated XFOR code exhibits the parameters of the transformations that have been applied and thus can be modified for further optimizations.

- Participants: Imen Fassi, Philippe Clauss and Cédric Bastoul
- Contact: Philippe Clauss

6.8. OpenScop

A Specification and a Library for Data Exchange in Polyhedral Compilation Tools

FUNCTIONAL DESCRIPTION

OpenScop is an open specification that defines a file format and a set of data structures to represent a static control part (SCoP for short), i.e., a program part that can be represented in the polyhedral model. The goal of OpenScop is to provide a common interface to the different polyhedral compilation tools in order to simplify their interaction. To help the tool developers to adopt this specification, OpenScop comes with an example library (under 3-clause BSD license) that provides an implementation of the most important functionalities necessary to work with OpenScop.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/openscop/

6.9. ORWL and P99

ORWL is a reference implementation of the Ordered Read-Write Lock tools as described in [5]. The macro definitions and tools for programming in C99 that have been implemented for ORWL have been separated out into a toolbox called P99. ORWL is intended to become opensource, once it will be in a publishable state. P99 is available under a QPL at http://p99.gforge.inria.fr/.
Software classification: A-3-up, SO-4, SM-3, EM-3, SDL (P99: 4, ORWL: 2-up), DA-4, CD-4, MS-3, TPM-4

- Participants: Jens Gustedt, Mariem Saied, Daniel Salas
- Contact: Jens Gustedt
- http://p99.gforge.inria.fr/, http://orwl.gforge.inria.fr/

6.10. stdatomic and musl

We implement the libary side of the C11 atomic interface. It needs compiler support for the individual atomic operations and provides library supports for the cases where no low-level atomic instruction is available and a lock must be taken.

- This implementation builds entirely on the ABIs of the gcc compiler for atomics.
- It provide all function interfaces that the gcc ABIs and the C standard need.
- For compilers that don't offer the direct language support for atomics it provides a syntactically reduced but fully functional approach to atomic operations.
- At the core of the library is a new and very efficient futex-based lock algorithm that is implemented for the Linux operating system.

A description of the new lock algorithm has been given in [24]. A short version of it has been accepted for SAC'16.

The primary target of this library is an integration into musl to which we also contribute. It is a re-implementation of the C library as it is described by the C and POSIX standards. It is *lightweight*, *fast*, *simple*, *free*, and strives to be correct in the sense of standards-conformance and safety. Musl is production quality code that is mainly used in the area of embedded device. It gains more market share also in other area, *e.g.* there are now Linux distributions that are based on musl instead of Gnu LibC.

- Participant: Jens Gustedt
- Contact: Jens Gustedt
- http://stdatomic.gforge.inria.fr/, http://www.musl-libc.org/

6.11. PolyLib

The Polyhedral Library
FUNCTIONAL DESCRIPTION

PolyLib is a C library of polyhedral functions, that can manipulate unions of rational polyhedra of any dimension. It was the first to provide an implementation of the computation of parametric vertices of a parametric polyhedron, and the computation of an Ehrhart polynomial (expressing the number of integer points contained in a parametric polytope) based on an interpolation method. Vincent Loechner is the maintainer of this software.

- Participant: Vincent Loechner
- Contact: Vincent Loechner
- URL: http://icps.u-strasbg.fr/PolyLib/

CAPSID Project-Team

6. New Software and Platforms

6.1. Kpax

KEYWORDS: Protein Structure Alignment

SCIENTIFIC DESCRIPTION

Kpax is a program for flexibly aligning two or more protein structures and for searching databases of protein structures.

FUNCTIONAL DESCRIPTION

The Kpax program exploits the fact that each amino acid residue has a carbon atom with a highly predictable tetrahedral geometry. This allows the local environment of each residue to be transformed into a canonical orientation, thus allowing easy comparison between the canonical orientations of residues within pairs of proteins using a novel scoring function based on Gaussian overlaps. Kpax is now used by the KBDOCK web server [3] to find structural templates for docking which might be beyond the reach of sequence-based homology modeling approaches. In 2015, the Kpax program was extended to allow the flexible alignment and superposition of multiple protein structures, and a new multiple alignment quality measure has been developed. According to this quality measure, Kpax gives higher quality multiple structural alignments than all other published approaches. A journal article describing these new developments is under review.

- Contact: David Ritchie
- URL: http://kpax.loria.fr

6.2. KBDOCK

KEYWORDS: Protein Binding Sites

SCIENTIFIC DESCRIPTION

KBDOCK is a database of all known protein-protein interactions that have experimentally determined 3D structures. In 2015, we used the latest version of KBDOCK in several rounds of the community-wide “CAPRI” blind docking experiment [36]. A journal article has been accepted for publication in *Proteins*.

FUNCTIONAL DESCRIPTION

KBDOCK combines coordinate data from the PDB with the Pfam protein domain family classification [28] in order to describe and analyze all known protein-protein interactions for which the 3D structures are available.

- Contact: David Ritchie
- URL: http://kbdock.loria.fr

6.3. Hex

KEYWORDS: Protein Docking - 3D rendering - 3D interaction

SCIENTIFIC DESCRIPTION

Hex is an interactive protein docking and molecular superposition program. The underlying approach uses our polar Fourier correlation technique to accelerate the search for close-fitting orientations of the two protein molecules.

FUNCTIONAL DESCRIPTION

Hex understands protein and DNA structures in PDB format, and it can also read small-molecule SDF files. Hex will run on most Windows, Linux and Mac OS X computers. The recent versions include CUDA support for Nvidia GPUs. On a modern workstation, docking times range from a few minutes or less when the search is constrained to known binding sites, to about half an hour for a blind global search (or just a few seconds with CUDA). On multi-processor Linux systems, docking calculation times can be reduced in almost direct proportion to the number of CPUs and GPUs used. In 2015, the Hex code base was re-organised to separate the GUI and computational components into separate libraries. The computational library is now used in our Sam and Kpax software.

- Contact: David Ritchie
- URL: http://hex.loria.fr

6.4. Sam

KEYWORDS: Protein Symmetry Assembly - Protein Docking

SCIENTIFIC DESCRIPTION

Sam is a program for building models of protein complexes having arbitrary point group symmetry. The Sam program was developed in the frame of the ANR “PEPSI” project with The Nano-D team at Inria Grenoble – Rône Alpes. A journal article describing Sam has been accepted for publication in the Journal of Applied Crystallography [16].

FUNCTIONAL DESCRIPTION

The underlying approach makes use of multiple one-dimensional polar Fourier correlations (implemented in the Hex code-base) to search rapidly a symmetry-constrained rigid body protein docking search space. The approach may be used to build symmetrical multi-component protein complexes having a given cyclic (C_n), dihedral (D_n), tetrahedral (T), octahedral (O) or icosahedral (I) point group symmetry.

- Contact: David Ritchie
- URL: http://sam.loria.fr

6.5. EC-DomainMiner

KEYWORDS: Protein Domain Annotation

SCIENTIFIC DESCRIPTION

EC-DomainMiner is a recommender-based approach for associating EC (Enzyme Commission) numbers with Pfam domains.

FUNCTIONAL DESCRIPTION

EC-DomainMiner uses a statistical recommender-based approach to infer EC-Pfam relationships from EC-sequence relationships that have been annotated previously in the SIFTS and Uniprot databases.

- Contact: David Ritchie
- URL: http://ecdm.loria.fr

6.6. MD-Kmean

KEYWORDS: Molecular Dynamics Analysis

SCIENTIFIC DESCRIPTION

MD-Kmean is a fast program for the analysis of large numbers of Molecular Dynamics frames. The accurate comparison of different protein structures plays important roles in structural biology, structure prediction and functional annotation. The root-mean-square-deviation (RMSD) after optimal superposition is the predominant measure of similarity due to the ease and speed of computation. MD-Kmean was designed to perform both the RMSD and the clustering step necessary to compare large numbers of protein 3D structures stored in large datasets and was applied to a set of 2 microsecond MD simulations producing 2 million frames to be compared and clustered.

FUNCTIONAL DESCRIPTION

We have implemented a very fast version of RMSD for graphics processing units (GPUs) using a quaternion method for calculating the optimal superposition and RMSD that is designed for parallel applications. This acceleration in speed allows RMSD calculations to be used efficiently in computationally intensive applications such as the clustering of large number of molecular dynamics frames. MD-Kmean is 50 times faster on a Nvidia GPU, on average, than the original single-threaded CPU implementation on an Intel quad-core processor.

- Contact: Bernard Maigret

6.7. Protein-Marshmallow

KEYWORDS: Coarse-Grained Representation

SCIENTIFIC DESCRIPTION

A Protein-protein interaction may be considered in terms of physical interaction between two deformable objects. The description at the atomic level of such complex objects is beginning to be feasible by MD simulations, but this requires the use of petaflop machines which are out of reach of most laboratories.

FUNCTIONAL DESCRIPTION

The Protein-Marshmallow program represents the surface of a protein as “coarse grained” 3D triangle mesh. In this mesh, each triangle is colored according to some biological property. In this way, a large complex object may be represented by a much smaller number of samples in a 3D mesh. The Marshmallow program describes deformations of such meshes under the influence of an external force field to simulate the strains that one object may undergo over time due to the interaction with another one.

- Contact: Bernard Maigret

6.8. Platforms

6.8.1. The MBI Platform

The MBI (Modeling Biomolecular Interactions) platform (http://bioinfo.loria.fr) was established to support collaborations between Inria Nancy – Grand Est and other research teams associated with the University of Lorraine. The platform is a research node of the Institut Français de Bioinformatique (IFB), which is the French national network of bioinformatics platforms (http://www.france-bioinformatique.fr).

- Contact: Marie-Dominique Devignes

CARAMEL Project-Team

6. New Software and Platforms

6.1. Belenios

Belenios - Verifiable online voting system
KEYWORD: E-voting
FUNCTIONAL DESCRIPTION

In collaboration with the CASSIS team, we develop an open-source private and verifiable electronic voting protocol, named BELENIOS. Our system is an evolution of an existing system, Helios, developed by Ben Adida, and used e.g., by UCL and the IACR association in real elections. The main differences with Helios are the following ones:

- In Helios, the ballot box publishes the encrypted ballots together with their corresponding voters. This raises a privacy issue in the sense that whether someone voted or not shall not necessarily be publicized on the web. Publishing this information is in particular forbidden by CNIL's recommendation. BELENIOS no longer publishes voters' identities, still guaranteeing correctness of the tally.
- Helios is verifiable except that one has to trust that the ballot box will not add ballots. The addition of ballots is particularly hard to detect as soon as the list of voters is not public. We have therefore introduced an additional authority that provides credentials that the ballot box can verify but not forge [27].

This new version has been implemented by Stéphane Glondu [0]. The first public release has been done in January 2014. Belenios has been used in Sep 2015 for the election of the new leader of the GT-C2 (Groupe de Travail Codes et Cryptographie) which is part of the GdR-IM (Groupement de Recherche Informatique Mathématique). The GT calcul formel of the GdR-IM plans to use Belenios in 2016 for the election of its new leader.

An online platform [0] has been released in September 2015, so that setting up a new election can be done entirely from within a browser.

- Participants: Véronique Cortier, Pierrick Gaudry and Stéphane Glondu
- Contact: Stéphane Glondu
- URL: http://belenios.gforge.inria.fr/

6.2. CADO-NFS

Crible Algébrique: Distribution, Optimisation - Number Field Sieve
FUNCTIONAL DESCRIPTION

CADO-NFS is a complete implementation in C/C++ of the Number Field Sieve (NFS) algorithm for factoring integers and computing discrete logarithms in finite fields. It consists in various programs corresponding to all the phases of the algorithm, and a general script that runs them, possibly in parallel over a network of computers.

- Participants: Emmanuel Thomé, Pierrick Gaudry, Paul Zimmermann, Alexander Kruppa, François Morain, Cyril Bouvier.
- Contact: Emmanuel Thomé
- URL: http://cado-nfs.gforge.inria.fr/

---

[0] http://belenios.gforge.inria.fr/
[0] https://belenios.loria.fr/

In December 2015, a major new release of CADO-NFS, version 2.2.0, was published. It contains several bug fixes, efficiency improvements, and the computation of discrete logarithms is now almost “push-button”.

6.3. CMH

Computation of Igusa Class Polynomials
KEYWORDS: Mathematics - Cryptography - Number theory
FUNCTIONAL DESCRIPTION

Cmh computes Igusa class polynomials, parameterizing two-dimensional abelian varieties (or, equivalently, Jacobians of hyperelliptic curves of genus 2) with given complex multiplication.

- Participants: Emmanuel Thomé, Andreas Enge
- Contact: Emmanuel Thomé
- URL: http://cmh.gforge.inria.fr/

6.4. GF2X

FUNCTIONAL DESCRIPTION

GF2X is a software library for polynomial multiplication over the binary field, developed together with Richard Brent (Australian National University, Canberra, Australia). It holds state-of-the-art implementation of fast algorithms for this task, employing different algorithms in order to achieve efficiency from small to large operand sizes (Karatsuba and Toom-Cook variants, and eventually Schönhage’s or Cantor’s FFT-like algorithms). FG2X takes advantage of specific processor instructions (SSE, PCLMULQDQ).

- Participants: Pierrick Gaudry, Emmanuel Thomé and Paul Zimmermann
- Contact: Emmanuel Thomé
- URL: https://gforge.inria.fr/projects/gf2x/

6.5. GNU MPC

FUNCTIONAL DESCRIPTION

MPC is a C library for the arithmetic of complex numbers with arbitrarily high precision and correct rounding of the result. It is built upon and follows the same principles as MPFR. The library is written by Andreas Enge, Philippe Théveny and Paul Zimmermann.

- Participants: Andreas Enge, Paul Zimmermann, Philippe Théveny and Mickaël Gastineau
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/

6.6. GNU-MPFR

KEYWORDS: Multiple-Precision - Floating-point - Correct Rounding
FUNCTIONAL DESCRIPTION

GNU MPFR is an efficient multiple-precision floating-point library with well-defined semantics (copying the good ideas from the IEEE-754 standard), in particular correct rounding in 5 rounding modes. GNU MPFR provides about 80 mathematical functions, in addition to utility functions (assignments, conversions...). Special data (Not a Number, infinities, signed zeros) are handled like in the IEEE-754 standard.

- Participants: Vincent Lefèvre, Guillaume Hanrot, Philippe Théveny and Paul Zimmermann
- Contact: Vincent Lefèvre
- URL: http://www.mpfr.org/

6.7. MPFQ

FUNCTIONAL DESCRIPTION

MPFQ is (yet another) library for computing in finite fields, with automatic generation of code for fields known at compile-time. It consists of roughly 18,000 lines of Perl code, which generate most of the C code. MPFQ is used in CADO-NFS, in particular for the linear algebra step during discrete logarithm computations.

- Participants: Emmanuel Thomé, Pierrick Gaudry and Luc Sanselme
- Contact: Pierrick Gaudry
- URL: http://mpfq.gforge.inria.fr/

6.8. Tinygb

Tinygb is a small software tool written in C++. Its aim is to provide an interface between several existing libraries (finite field arithmetic, linear algebra) for Gröbner bases computations occurring in problems investigated by the CARAMEL group. The focus is not on the efficiency of the implementation, since this is already successfully achieved in other existing software such as *FGb* (developed by Jean-Charles Faugère) or in the CAS Magma (Gröbner bases algorithms are implemented by Alan Steel). The goal of Tinygb is to be a flexible research tool where variants of classical algorithms can be tested. Tinygb is still in development since it requires more testing and packaging before being released.

- Participants: Pierre-Jean Spaenlehauer

6.9. Platforms

6.9.1. CATREL cluster

Installed in 2013, the CATREL computer cluster now plays an essential role in providing the team with the necessary resources to achieve significant computations, which illustrate well the efficiency of the algorithms developed in our research, together with their implementations.

In 2015, the CATREL cluster was in particular used for the precomputations performed for the LOGJAM attack [15]. It was the main computing resource for a record discrete logarithm computation in finite fields of the form $\mathbb{F}_{p^3}$ of 512 bits, and a larger computation for this kind of fields is currently running. It was also used intensively to optimize the sieving parameters of CADO-NFS for factoring numbers from 60 to 155 digits, in the preparation of the release 2.2.0. It was used to factor 47 large integers from nine aliquot sequences starting from 276 to 204828, the largest one being a 190-digit composite number from sequence 660. The current largest element known from an aliquot sequence has 197 digits (sequence 19560), and we expect the 200-digit frontier will be reached in 2016. Several experiments were also made with variations of the polynomial selection algorithm from [10] on RSA-896 and RSA-1024.

CARDAMOM Team

6. New Software and Platforms

6.1. AeroSol

Developed in partnership with the Cagire Inria team, the AeroSol library is a high order finite element library written in C++. The code design has been carried for being able to perform efficient computations, with continuous and discontinuous finite element methods on hybrid and possibly curvilinear meshes.

The work of the Cardamom team is focused on continuous finite element methods, while we focus on discontinuous Galerkin methods. However, everything is done for sharing the largest possible part of code. The distribution of the unknowns is made with the software PaMPA, first developed within the Inria teams Bacchus and Castor, and currently maintained in the Tadaam team.

The generic features of the library are

- **High order**. It can be theoretically any order of accuracy, but the finite element basis, and quadrature formula are implemented for having up to a fifth order of accuracy.
- **Hybrid and curvilinear meshes**. AeroSol can deal with up to fifth order conformal meshes composed of lines, triangles, quadrangles, tetrahedra, hexahedra, prism, and pyramids.
- **Continuous and discontinuous discretization**. AeroSol deals with both continuous and discontinuous finite element methods.

We would like to emphasize three assets of this library:

- **Its development environment** For allowing a good collaborative work and a functional library, a strong emphasis has been put on the use of modern collaborative tools for developing our software. This includes the active use of a repository, the use of CMake for the compilation, the constant development of unitary and functional tests for all the parts of the library (using CTest), and the use of the continuous integration tool Jenkins for testing the different configurations of AeroSol and its dependencies. Efficiency is regularly tested with direct interfacing with the PAPI library or with tools like scalasca.
- **Its genericity** A lot of classes are common to all the discretization, for example classes concerning I/O, finite element functions, quadrature, geometry, time integration, linear solver, models and interface with PaMPA. Adding simple features (e.g. models, numerical flux, finite element basis or quadrature formula) can be easily done by writing the class, and declaring its use in only one class of the code.
- **Its efficiency** This modularity is achieved by means of template abstraction for keeping good performances. Dedicated efficient implementation, based on the data locality of the discontinuous Galerkin method has been developed. As far as parallelism is concerned, we use point-to-point communications, the HDF5 library for parallel I/O.

The AeroSol project fits with the first axis of the Bordeaux Sud Ouest development strategy, which is to build a coherent software suite scalable and efficient on new architectures, as the AeroSol library relies on several tools developed in other Inria teams, especially for the management of the parallel aspects.

At the end of 2014, AeroSol had the following features:

- **Development environment** Use of CMake for compilation (gcc, icc and xlc), CTest for automatic tests and memory checking, lcov and gcov for code coverage reports. Development of a CDash server for collecting the unitary tests and the memory checking. Beginning of the development of an interface for functional tests. Optional linking with HDF5, PAPI, with dense small matrices libraries (BLAS, Eigen)

- **In/Out** Link with the XML library for handling with parameter files. Parallel reader for GMSH, with an embedded geometrical pre-partitioner. Writer on the VTK-ASCII legacy format (cell and point centered). Parallel output in vtu and pvtu (Paraview) for cell-centered visualization, and XDMF/HDF5 format for both cell and point centered visualization. Ability of saving the high order solution and restarting from it. Computation of volumic and probe statistics. Ability of saving averaged layer data in quad and hexa meshes. Ability of defining user defined output visualization variables.
- **Quadrature formula** up to 11th or
- April-June 2015: A. Javadi (PhD student) from Chalmers University, Gothenburg, Sweden (3 months).der for Lines, Quadrangles, Hexaedra, Pyramids, Prisms, up to 14th order for tetrahedron, up to 21st order for triangles. Gauss-Lobatto type quadrature formula for lines, triangles, quadrangles and hexaedra.
- **Finite elements** up to fourth degree for Lagrange finite elements and hierarchical orthogonal finite element basis (with Dubiner transform on simplices) on lines, triangles, quadrangles, tetrahedra, prisms, hexaedra and pyramids. Finite element basis that are interpolation basis on Gauss-Legendre points for lines, quadrangles, and hexaedra, and triangle (only 1st and 2nd order)
- **Geometry** Elementary geometrical functions for first order lines, triangles, quadrangles, prisms, tetrahedra, hexaedra and pyramids. Handling of high order meshes.
- **Time iteration** explicit Runge-Kutta up to fourth order, explicit Strong Stability Preserving schemes up to third order. Optimized CFL time schemes: SSP(2,3) and SSP(3,4). CFL time stepping. Implicit integration with BDF schemes from 2nd to 6th order Newton method for stationary problems. Implicit unstationary time iterator non consistent in time for stationary problems. Implementation of in house GMRES and conjugate gradient based on Jacobian free iterations.
- **Linear Solvers** Link with the external linear solver UMFPack, PETSc and MUMPS. Internal solver for diagonal and block-diagonal matrices.
- **Memory handling** discontinuous and continuous, sequential and parallel discretizations based on PaMPA for generic meshes, including hybrid meshes.
- **Models** Perfect gas Euler system, real gas Euler system (template based abstraction for a generic equation of state), scalar advection, Waves equation in first order formulation, generic interface for defining space-time models from space models. Diffusive models: isotropic and anisotropic diffusion, compressible Navier-Stokes. Scalar advection-diffusion model.
- **Numerical schemes** Continuous Galerkin method for the Laplace problem (up to fifth order) with non consistent time iteration or with direct matrix inversion. Explicit and implicit discontinuous Galerkin methods for hyperbolic systems, diffusive and advection-diffusion problems. Beginning of optimization by stocking the geometry for advection problems. SUPG and Residual disribution schemes. Optimization of DG schemes for advection-diffusion problems: stocking of the geometry and use of BLAS for all the linear phases of the scheme.
- **Numerical fluxes** Centered fluxes, exact Godunov' flux for linear hyperbolic systems, and Lax-Friedrich flux. Riemann solvers for Low Mach flows. Numerical flux accurate for steady and unsteady computations.
- **Boundary conditions** Periodic boundary conditions, time-dependent inlet and outlet boundary conditions. Adiabatic wall and isothermal wall. Steger-Warming based boundary condition.
- **Parallel computing** Mesh redistribution, computation of Overlap with PaMPA. Collective asynchronous communications (PaMPA based). Asynchronous point to point communications. Tests on the cluster Avakas from MCIA, and on Mésocentre de Marseille, and PlaFRIM. Tier-1 Turing (Blue-Gene).
- **C++/Fortran interface** Tests for binding fortran with C++.

- **Instrumentation** Aerosol can give some traces on memory consumption/problems with an interfacing with the PAPI library. Tests have also been performed with VTUNE and TAU. Tests with Maqao and Scalasca (VIHPS workshop).
- **Validation** Poiseuille, Taylor-Green vortex. Laplace equation on a ring and Poiseuille flow on a ring. Implementation of volumic forcing based on wall dissipation.

In 2015, N. Pattakos was hired in the team Cardamom, in order to improve the code architecture and for easing the installation of the library. The following features were added or improved:

- **Development environment** The use of CMake was strongly improved, which induced also easier test launching. Documentation, code cleaning and refactorization have also been led. The shared project of Plafrim was updated, and so was the joint Aerosol/Scotch/PaMPA project on the continuous integration platform. Integration of SPack for handling dependencies has begun. Interface with ESSL was fixed.
- **Multigrid** Development of p-multigrid methods. This includes also the possibility of beginning a computation iwth an order and to decrease or increase the order of approximation when restarting. For the p multigrid methods, V and W cycle have been developed, and restriction and prolongation opertors have also been developed. Implementation of h-multigrid has started, with the development of tests of the aggregation methods of PaMPA, and the definition of finite element basis on arbitrary cells.
- **Boundary conditions** Development of the Synthetic Eddy Method boundary condition.
- **Models** Linearized Euler equations, and Sutherland model for non isothermal diffusive flows. Shallow-water model.
- **Parallel computing** Weighted load balancing for hybrid meshes.
- **Validation** Turbulent channel flow.
- **Postprocessing** Development of high order projections over line postprocessing, possibility of stocking averaged data, such as the average flow and the Reynolds stresses.

6.2. Cut-ANOVA

Participants: Pietro Marco Congedo, Kunkun Tang [Corresponding member].

An anchored analysis of variance (ANOVA) method is proposed to decompose the statistical moments. Compared to the standard ANOVA with mutually orthogonal component functions, the anchored ANOVA, with an arbitrary choice of the anchor point, loses the orthogonality if employing the same measure. However, an advantage of the anchored ANOVA consists in the considerably reduced number of deterministic solver's computations, which renders the uncertainty quantification of real engineering problems much easier. Different from existing methods, the covariance decomposition of the output variance is used in this work to take account of the interactions between non-orthogonal components, yielding an exact variance expansion and thus, with a suitable numerical integration method, provides a strategy that converges. This convergence is verified by studying academic tests. In particular, the sensitivity problem of existing methods to the choice of anchor point is analyzed via the Ishigami case, and we point out that covariance decomposition survives from this issue. Also, with a truncated anchored ANOVA expansion, numerical results prove that the proposed approach is less sensitive to the anchor point. The covariance-based sensitivity indices (SI) are also used, compared to the variance-based SI. Furthermore, we emphasize that the covariance decomposition can be generalized in a straightforward way to decompose higher-order moments. For academic problems, results show the method converges to exact solution regarding both the skewness and kurtosis. The proposed method can indeed be applied to a large number of engineering problems.

The Cut-ANOVA code (Fortran 90, MPI + OpenMP) is devoted to the stochastic analysis of numerical simulations. The method implemented is based on the spectral expansion of "anchored ANOVA", allowing the covariance-based sensitivity analysis. Compared to the conventional Sobol method, "Cut-ANOVA" provides three sensitivity indices instead of one, which allows a better analysis of the reliability of the numerical prediction. On the other hand, "Cut-ANOVA" is able to compute the higher order statistical moments such as the Skewness (3-rd order moment) and Kurtosis (4-th order moment). Several dimension reduction techniques have also been implemented to reduce the computational cost. Finally, thanks to the innovative method implemented into the Code Cut-ANOVA, one can obtain a similar accuracy for stochastic quantities by using a considerably less number of deterministic model evaluations, compared with the classical Monte Carlo method.

6.3. Sparse-PDD

Participants: Pietro Marco Congedo, Kunkun Tang [Corresponding member].

The polynomial dimensional decomposition (PDD) is employed in this code for the global sensitivity analysis and uncertainty quantification (UQ) of stochastic systems subject to a moderate to large number of input random variables. Due to the intimate structure between the PDD and the Analysis of Variance (ANOVA) approach, PDD is able to provide a simpler and more direct evaluation of the Sobol' sensitivity indices, when compared to the Polynomial Chaos expansion (PC). Unfortunately, the number of PDD terms grows exponentially with respect to the size of the input random vector, which makes the computational cost of standard methods unaffordable for real engineering applications. In order to address the problem of the curse of dimensionality, this code proposes essentially variance-based adaptive strategies aiming to build a cheap meta-model (i.e. surrogate model) by employing the sparse PDD approach with its coefficients computed by regression. Three levels of adaptivity are carried out in this code: 1) the truncated dimensionality for ANOVA component functions, 2) the active dimension technique especially for second- and higher-order parameter interactions, and 3) the stepwise regression approach designed to retain only the most influential polynomials in the PDD expansion. During this adaptive procedure featuring stepwise regressions, the surrogate model representation keeps containing few terms, so that the cost to resolve repeatedly the linear systems of the least-square regression problem is negligible. The size of the finally obtained sparse PDD representation is much smaller than the one of the full expansion, since only significant terms are eventually retained. Consequently, a much less number of calls to the deterministic model is required to compute the final PDD coefficients.

6.4. RobUQ

Participants: Pietro Marco Congedo [Corresponding member], Maria Giovanna Rodio, Kunkun Tang.

The `RobUQ` platform has been conceived to solve problems in uncertainty quantification and robust design. It includes the optimization code `ALGEN`, and the uncertainty quantification code `NISP`. It includes also some methods for the computation of high-order statistics, efficient strategies for robust optimization, the Simplex2 method. Some methods are developed in partnership with the Stanford University (in the framework of the associated team AQUARIUS). Other methods are developed in the context of ANR `UFO`.

6.5. ORComp

Participants: Pietro Marco Congedo [Corresponding member], Nassim Razaaly, Maria-Giovanna Rodio.

The ORComp platform is a simulation tool permitting to design an ORC cycle. Starting from the solar radiation, this plateform computes the cycle providing the best performance with optimal choices of the fluid and the operating conditions. It includes `RobUQ` , a simulation block of the ORC cycles, the fluidbox code for the simulation of the turbine and of the heat exchanger, the software `FluidProp` (developed at the University of Delft) for computing the fluid thermodynamic properties.

6.6. sDEM

Participants: Pietro Marco Congedo [Corresponding member], Maria-Giovanna Rodio.

The `sDEM` platform is a simulation tool permitting to simulate multiphase flows with transition modelling. In particular, the code relies on the formulation of a DEM method, the use of a complex thermodynamics, the possibility to model cavitating phenomena. Moreover, the method has been generalized in order to take into account directly uncertainty, thus proposing the so-called Stochastic DEM (sDEM) method. This is one of the first stochastic semi-intrusive scheme, permitting to consider uncertainties in multiphase flows including heat and mass transfer terms. This software is developed together with the University of Zurich.

6.7. SLOWS

Participants: Luca Arpaia, Andrea Filippini, Maria Kazolea, Mario Ricchiuto [Corresponding member].

SLOWS is a C-platform allowing the simulation of free surface shallow water flows with friction. It can be used to simulate near shore hydrodynamics, wave transformations processes, etc. Both hydrostatic (shallow water) and non-hydrostatic (Boussinesq-type) versions exist. The latter are currently based on the dispersive model of Madsen and Sorensen (1992). A fully nonlinear (Green-Naghdi) version is under development based on the one dimensional prototype discussed in [99]. Three different approaches are available, based on conditionally depth-positivity preserving implicit schemes, or on conditionally depth-positivity preserving genuinely explicit discretizations, or on an unconditionally depth-positivity preserving space-time approach. Newton and frozen Newton loops are used to solve the implicit nonlinear equations. The linear algebraic systems arising in the discretization are solved with the MUMPS library. This year implicit and explicit (extrapolated) multistep higher order time integration methods have been implemented, and a mesh adaptation technique based on mesh deformation (r-adaptation) has been also included. A node-centred high order MUSCL finite volume discretisation has also been added to benchmark the mesh adaptation strategies, and compare with the residual based method constituting the kernel of the code. To date, SLOWS is the only existing near shore code allowing to choose between a classical finite volume approximation, and the more recent non-linear residual distribution methods developed in CARDAMOM. It allows an accurate simulation of free surface flows on arbitrary topographies with both static and time dependent unstructured mesh adaptation, accounting for both hydrostatic and non-hydrostatic effects.

6.8. TUCWave

Participant: Maria Kazolea [Corresponding member].

TUCWave, developed within the PhD of M. Kazolea, is a high-order well-balanced unstructured finite volume (FV) solver for weakly nonlinear and weakly dispersive water waves over varying bathymetries, as described by the 2D depth-integrated extended Boussinesq equations of Nwogu (1993). The FV scheme numerically solves the conservative form of the equations following the median dual node-centered approach, for both the advective and dispersive part of the equations. The code uses an efficient edge based structure. For the advective fluxes Roe's approximate Riemann solver is used along with a well-balanced treatment of the topography source. Higher order accuracy i is achieved through a MUSCL-type reconstruction technique, and via a strong stability preserving explicit Runge-Kutta time stepping. The numerical techniques implemented in TUCWave are being imported in SLOWS.

6.9. Realfluids

Participants: Héloise Beaugendre [Corresponding member], Pietro Marco Congedo, Andrea Cortesi, Léo Nouveau, Quentin Viville.

`RealFluids` (developed in the `BACCHUS` team) solves compressible viscous turbulent flow equations, with real-gas effects and arbitrarily complex equations of state, with the most recent residual distribution schemes. It is currently used for simulating turbines in ORC optimization, and for the immersed boundary simulations for de-anti icing applications. It is being coupled to the Mutation library to be able to perform some CFD simulations of low-altitude re-entry flows.

6.10. FMG

Participants: Luca Arpaia, Cécile Dobrzynski [Corresponding member], Andrea Cortesi, Léo Nouveau, Mario Ricchiuto.

FMG is a library deforming an input/reference simplicial mesh w.r.t. a given smoothness error monitor (function gradient or Hessian), metric field, or given mesh size distribution. Displacements are computed by solving an elliptic Laplacian type equation with a continuous finite element method. The library returns an adapted mesh with a corresponding projected solution, obtained by either a second order projection, or by an ALE finite element remap. The addiction of a new mass conservative approach developed ad-hoc for shallow water flows is under way.

6.11. MMG platform

Participants: Cécile Dobrzynski [Corresponding member], Algiane Froehly.

MMG is an open source software for surface and volume remeshing. It provides three applications : 1) mmg2d: generation of a triangular mesh , adaptation and optimization of a triangular mesh 2) mmgs: adaptation and optimization of a surface triangulation representing a piecewise linear approximation of an underlying surface geometry 3) mmg3d: adaptation and optimization of a tetrahedral mesh and implicit domain meshing

URL : http://www.mmgtools.org

6.12. Nomesh

Participants: Cécile Dobrzynski [Corresponding member], Ghina El Jannoun.

`Nomesh` is a software allowing the generation of third order curved simplicial meshes. Starting from a "classical" mesh with straight elements composed by triangles and/or tetrahedra, we are able to curve the boundary mesh. Starting from a mesh with some curved elements, we can verify if the mesh is valid, that means there is no crossing elements and only positive Jacobian. If the curved mesh is non valid, we modify it using linear elasticity equations until having a valid curved mesh.

CARMEN Team

6. New Software and Platforms

6.1. CEPS: a Cardiac ElectroPhysiology Simulator

The Carmen team develops a software code to perform high performance numerical simulations in cardiac electrophysiology using unstructured three-dimensional grids. The software, called CEPS (*Cardiac Electrophysiology Simulation*) is developped as a common tool for researchers in the Carmen team and for our partners and colleagues in scientific computing and biomedical engineering. The goal of CEPS is to easily allow the development of new numerical methods and new physical models.

As compared to other existing softwares, CEPS aims at providing a more general framework of integration for new methods or models and a better efficiency in parallel. CEPS is designed to run on massively parallel architectures, and to make use of state-of-the-art and well known computing libraries to achieve realistic and complex heart simulations. CEPS also includes software engineering and and validation tools. We use the platform GForge (ceps) based on Git. This allows to keep a history of developments for developers and users.

Some of our collaborators actively participate to the testing and discussion for the development of CEPS, namely:

- C. Pierre, LMA University of Pau et des Pays de l'Adour;
- R. Turpault, IMB University of Bordeaux;

Several people work and make and an usefull code for researchers and users.

- Development of an external procedure to compile depandancies for CEPS. This allows a very simple way to install CEPS for partners or students.
- Improve continious integration test cases in order to have a best coverage of the code as possible.
- Overwrite C++ class for ionic models and adding new models in collaboration with A. Gérard.
- Integration of the partionneur PTSchotch in order to realise a partitionning on the nodes.
- Turorials for beginers on the code (linear algebra, installation, compilation...).
- New implementation of the bilayer model developped by L. Simon during his PhD thesis. The most important part will provide by M. Fuentes works. Difficulties are currently the specification of two layers in CEPS and how connect them.
- The strategy remains at this time is to have two meshes in entry (on global mesh for the auricles and an other *under-mesh* corresponding to the twolayers domain). This means, that we have to create a connectivity table between the global mesh and the *under-mesh*.
- Development of an interface for users in order to specify data in a text file for the code such physical values for ionic models or numerical values for numerical methods (especially in time) used.

6.2. IDAM

The goal of IDAM project is to defined a conceptual module in MUSIC in order to create realistic meshes for the CEPS code. Informations come from IRM done by doctors. Furthermore, objectives are the continuation of used methods in the team and the visualisation of numerical results obtained by CEPS (https://bil.inria.fr/fr/software/view/2630/tab.

This project started on 1st december 2015 for two years. M. Juhoor is in charge of this project in collaboration with the MedInria team and the IHU LIRYC.

CARTE Project-Team

6. New Software and Platforms

6.1. CoDisasm

FUNCTIONAL DESCRIPTION

Codisasm is a new disassembly program which supports self-modifying code and code overlapping. Up to our knowledge, it is the first which copes both aspects of program obfuscation. The tool is based on the notion of “wave” developed in the group.
It is written in C and contains about 3k lines of code.

- Contact: Fabrice Sabatier
- URL: http://www.lhs.loria.fr/wp/?p=289

6.2. DynamicTracer

FUNCTIONAL DESCRIPTION

DynamicTracer is a new tool with a public web interface which provides run traces of executable files. The trace is obtained by recording a dynamic execution in a safe environment. It contains instruction addresses, instruction opcodes and other optional information.
It is written in C++ and contains about 2.5k lines of code.

- Contact: Fabrice Sabatier
- URL: http://www.lhs.loria.fr

6.3. Gorille

FUNCTIONAL DESCRIPTION

Gorille (formerly MMDEX) is a virus detector based on morphological analysis. It is composed of our own disassembler tool, of a graph transformer and a specific tree-automaton implementation. The tool is used in the EU-Fiware project and by some other partners (e.g., DAVFI project).
It is written in C and contains about 100k lines of code.
APP License, IDDN.FR.001.300033.000.R.P.2009.000.10000, 2009.

- Contact: Philippe Antoine
- URL: http://www.lhs.loria.fr

CASCADE Project-Team (section vide)

CASSIS Project-Team

6. New Software and Platforms

6.1. Protocol Verification Tools

Participants: Véronique Cortier, Stéphane Glondu, Pierre-Cyrille Héam, Olga Kouchnarenko, Steve Kremer, Michaël Rusinowitch, Mathieu Turuani, Laurent Vigneron.

6.1.1. CL-AtSe

We develop *CL-AtSe*, a Constraint Logic based Attack Searcher for cryptographic protocols, initiated and continued by the European projects *AVISPA*, AVANTSSAR (for web-services) and Nessos respectively. The *CL-AtSe* approach to verification consists in a symbolic state exploration of the protocol execution for a bounded number of sessions, thus is both correct and complete. *CL-AtSe* includes a proper handling of sets, lists, choice points, specification of any attack states through a language for expressing e.g., secrecy, authentication, fairness, or non-abuse freeness, advanced protocol simplifications and optimizations to reduce the problem complexity, and protocol analysis modulo the algebraic properties of cryptographic operators such as XOR (exclusive or) and Exp (modular exponentiation).

CL-AtSe has been successfully used to analyse protocols from e.g., France Telecom R&D, Siemens AG, IETF, Gemalto, Electrum in funded projects. It is also employed by external users, e.g., from the AVISPA's community. Moreover, *CL-AtSe* achieves good analysis times, comparable and sometimes better than other state-of-the art tools.

CL-AtSe has been enhanced in various ways. It fully supports the Aslan semantics designed in the context of the AVANTSSAR project, including Horn clauses (for intruder-independent deductions, e.g., for credential management), and a large fragment of LTL-based security properties. A Bugzilla server collects bug reports, and online analysis and orchestration are available on our team server (https://cassis.loria.fr). Large models can be analysed on the TALC Cluster in Nancy with parallel processing. *CL-AtSe* also supports negative constraints on the intruder's knowledge, which reduces drastically the orchestrator's processing times and allows separation of duties and non-disclosure policies, as well as conditional security properties, like: i) an authentication to be verified iff some session key is safe; ii) relying on a leaking condition on some private data instead of an honesty predicate to trigger or block some agent's property. This was crucial for e.g., the Electrum's wallet where all clients can be dishonest but security guarantees must be preserved anyway.

6.1.2. Akiss

Akiss (Active Knowledge in Security Protocols) is a tool for verifying indistinguishability properties in cryptographic protocols, modelled as trace equivalence in a process calculus. Indistinguishability is used to model a variety of properties including anonymity properties, strong versions of confidentiality and resistance against offline guessing attacks, etc. *Akiss* implements a procedure to verify equivalence properties for a bounded number of sessions based on a fully abstract modelling of the traces of a bounded number of sessions of the protocols into first-order Horn clauses and a dedicated resolution procedure. The procedure can handle a large set of cryptographic primitives, namely those that can be modeled by an optimally reducing convergent rewrite system. The tool also include the possibility for checking everlasting indistinguishability properties [63].

The tool is still under active development, including optimisations to improve efficiency, but also the addition of new features, such as the possibility to model protocols using weak secrets, and the addition of support for exclusive or.

The *Akiss* tool is freely available at https://github.com/akiss/akiss.

6.1.3. Belenios

In collaboration with the Caramel project-team, we develop an open-source private and verifiable electronic voting protocol, named *Belenios*. Our system is an evolution and a new implementation of an existing system, Helios, developed by Ben Adida, and used e.g., by UCL and the IACR association in real elections. The main differences with Helios are a cryptographic protection against ballot stuffing and a practical threshold decryption system that allows to split the decryption key among several authorities, k out of n authorities being sufficient to decrypt. We will continue to add new cryptographic and protocol improvements to offer a secure, proved, and practical electronic voting system.

Belenios has been implemented (cf. http://belenios.gforge.inria.fr) by Stéphane Glondu and has been tested in December 2014 “in real conditions”, in a test election involving the members of Inria Nancy-Grand Est center and of the Loria lab (more than 500 potential voters) that had to elect the best pictures of the Loria. Since 2015, it is used by the CNRS for remote election among its councils. It has also been used to elect the leader of the C2 GdR-IM working group [0] (about 230 voters and 100 ballots cast). It has also been used in some smaller elections (eg to chose an invited speaker).

6.1.4. SAPIC

SAPIC is a tool that translates protocols from a high-level protocol description language akin to the applied pi-calculus into multiset rewrite rules, that can then be be analysed using the Tamarin Prover.

Its aim is the analysis of protocols that include states, for example Hardware Security Tokens communicating with a possibly malicious user, or protocols that rely on databases. It has been succesfully applied on several case studies including the Yubikey authentication protocol.

A recent extension, SAPIC* extends *SAPIC* by a Kleene star operator (*) which allows to iterate a process a finite but arbitrary number of times. This construction is useful to specify for instance stream authentication protocols. We used it to analyse a simple version of the TESLA protocol.

SAPIC is freely available at http://sapic.gforge.inria.fr/.

6.2. Testing Tools

Participants: Fabrice Bouquet, Frédéric Dadeau, Elizabeta Fourneret.

6.2.1. Hydra

Hydra is an Eclipse-like platform, based on Plug-ins architecture. Plug-ins can be of five kinds: *parser* is used to analyze source files and build an intermediate format representation of the source; *translator* is used to translate from a format to another or to a specific file; *service* denotes the application itself, i.e., the interface with the user; *library* denotes an internal service that can be used by a service, or by other libraries; *tool* encapsulates an external tool. The following services have been developed so far:

- BZPAnimator: performs the animation of a BZP model (a B-like intermediate format);
- Angluin: makes it possible to perform a machine learning algorithm (à la Angluin) in order to extract an abstraction of a system behavior;
- UML2SMT: aims at extracting first order logic formulas from the UML Diagrams and OCL code of a UML/OCL model to check them with a SMT solver.

These services involve various libraries (sometimes reusing each other), and rely on several *tool* plug-ins that are: SMTProver (encapsulating the Z3 solver), PrologTools (encapsulating the CLPS-B solver), Grappa (encapsulating a graph library). We are currently working on transferring the existing work on test generation from B abstract machines, JML, and statecharts using constraint solving techniques.

---

[0] https://crypto.di.ens.fr/c2:election

6.2.2. jMuHLPSL

jMuHLPSL [6] is a mutant generator tool that takes as input a verified HLPSL protocol, and computes mutants of this protocol by applying systematic mutation operators on its contents. The mutated protocol then has to be analyzed by a dedicated protocol analysis tool (here, the AVISPA tool-set). Three verdicts may then arise. The protocol can still be *safe*, after the mutation, this means that the protocol is not sensitive to the realistic "fault" represented by the considered mutation. This information can be used to inform the protocol designers of the robustness of the protocol w.r.t. potential implementation choices, etc. The protocol can also become *incoherent*, meaning that the mutation introduced a functional failure that prevents the protocol from being executed entirely (one of the participants remains blocked in a given non-final state). The protocol can finally become *unsafe* when the mutation introduces a security flaw that can be exploited by an attacker. In this case, the AVISPA tool-set is able to compute an attack-trace, that represents a test case for the implementation of the protocol. If the attack can be replayed entirely, then the protocol is not safe. If the attack can not be replayed then the implementation does not contain the error introduced in the original protocol.

The tool is written in Java, and it is freely available at: http://members.femto-st.fr/sites/femto-st.fr.frederic-dadeau/files/content/pub/jMuHLPSL.jar.

6.2.3. Praspel

Praspel is both a specification language, a test data generator and test execution driver for PHP programs. These latter are annotated to describe class (resp. method) contracts using invariants (resp. pre- and postconditions). Praspel contracts allow to describe data typing informations, by means of *realistic domains*. According to the contract-driven testing principles, the tool uses the contracts to both generate test data, using dedicated test generators (random for integer variables, grammar-based for strings, constraint-based for arrays), and establish the test verdict by checking the contract assertions at run-time.

The tool is open source and freely available at: http://hoa-project.net. It has been integrated into a PHP framework named Hoa, and coupled with the atoum tool (https://github.com/atoum/atoum) that can be used to execute the tests and report on their code coverage.

6.3. Other Tools

Several software tools described in previous sections are using tools that we have developed in the past. For instance BZ-TT uses the set constraints solver CLPS. Note that the development of the SMT prover haRVey has been stopped. The successor of haRVey is called veriT and is developed by David Déharbe (UFRN Natal, Brasil) and Pascal Fontaine (Veridis team). We have also developed, as a second back-end of *AVISPA*, TA4SP (Tree Automata based on Automatic Approximations for the Analysis of Security Protocols), an automata based tool dedicated to the validation of security protocols for an unbounded number of sessions.

We have also designed tools to manage collaborative works on shared documents using flexible access control models. These tools have been developed in order to validate and evaluate our approach on combining collaborative edition with optimistic access control.

CASTOR Project-Team

4. New Software and Platforms

4.1. CEDRES++

FUNCTIONAL DESCRIPTION

In Tokamaks, at the slow resistive diffusion time scale, the magnetic configuration can be described by the MHD equilibrium equations inside the plasma and the Maxwell equations outside. Moreover, the magnetic field is often supposed not to depend on the azimutal angle.

Under this assumption of axisymmetric configuration, the equilibrium in the whole space reduces to solving a 2D problem in which the magnetic field in the plasma is described by the well known Grad Shafranov equation. The unknown of this problem is the poloidal magnetic flux. The P1 finite element code CEDRES++ solves this free boundary equilibrium problem in direct, evolutive and inverse mode. The direct problem consists in the computation of the magnetic configuration and of the plasma boundary, given a plasma current density profile and the total current in each poloidal field coils (PF coils). In the evolutive mode, a time-dependent sequence of snapshots is obtained, being given a time evolution of the current density profiles in the plasmas and of the voltages in the power supplies of the poloidal field circuits. The aim of the inverse problem is to find currents in the PF coils in order to best fit a given plasma shape.

- Participants: Cédric Boulbe, Jacques Blum, Blaise Faugeras and Holger Heumann
- Partners: CNRS - CEA - Université de Nice Sophia Antipolis (UNS)
- Contact: Cédric Boulbe
- Reference: [16]

4.2. Equinox

FUNCTIONAL DESCRIPTION

EQUINOX is a code dedicated to the numerical reconstruction of the equilibrium of the plasma in a Tokamak. The problem solved consists in the identification of the plasma current density, a non-linear source in the 2D Grad-Shafranov equation which governs the axisymmetric equilibrium of a plasma in a Tokamak. The experimental measurements that enable this identification are the magnetics on the vacuum vessel, but also polarimetric and interferometric measures on several chords, as well as motional Stark effect measurements. The reconstruction can be obtained in real-time and the numerical method implemented involves a finite element method, a fixed-point algorithm and a least-square optimization procedure.

- Participants: Jacques Blum, Cédric Boulbe and Blaise Faugeras
- Contact: Blaise Faugeras
- Reference: [1]

4.3. FBGKI (Full Braginskii)

FUNCTIONAL DESCRIPTION The Full Braginskii solver considers the equations proposed by Braginskii (1965), in order to describe the plasma turbulent transport in the edge part of tokamaks. These equations rely on a two fluid (ion - electron) description of the plasma and on the electroneutrality and electrostatic assumptions. One has then a set of 10 coupled non-linear and strongly anisotropic PDEs. FBGKI makes use in space of high order methods: Fourier in the toroidal periodic direction and spectral elements in the poloidal plane. The spectral vanishing viscosity (SVV) technique is implemented for stabilization. Static condensation is used to reduce the computational cost. In its sequential version, a matrix free solver is used to compute the potential. The parallel version of FBGKI presents two layers of parallelization: The first one corresponds to the poloidal plane and the second one to the toroidal direction. In the poloidal plane, the domain decomposition is achieved using the software METIS. For the parallel linear algebra, one uses the software PETSC (Portable Extensible Toolkit for Scientific Computation). The time discretization makes use of a Strang splitting, that decouples the explicit treatment of the advection and Braginskii terms, from the implicit treatment of the Lorentz forces and the computation of the electric potential. Whereas the explicit part is easily parallelized, the implicit one requires solving a strongly anisotropic elliptic problem for the potential. In the parallel version of FBGKI the system matrix is assembled in sparse manner, in order to allow using the multigrid HYPRE preconditionner implemented in PETSC. Till now results have only been obtained for computations done on a few tens of processors. Both the weak and strong scalings look satisfactory. Numerical experiments are still required to go up to hundreds or thousands of processors.

- Participants: Sébastian Minjeaud and Richard Pasquetti
- Contact: Sebastian Minjeaud
- Reference: [25]

4.4. FEEQS.M

FUNCTIONAL DESCRIPTION

FEEQS.M (Finite Element Equilibrium Solver in Matlab) is a MATLAB implementation of the numerical methods in [16] to solve equilibrium problems for toroidal plasmas. Direct and inverse problems for both the static and transient formulations of plasma equilibrium can be solved. FEEQS.M exploits MATLAB‘s evolved sparse matrix methods and uses heavily the vectorization programming paradigm, which results in running times comparable to C/C++ implementations. FEEQS.M complements the production code CEDRES++ in being considered as fast prototyping test bed for computational methods for equilibrium problems. This includes aspects of numerics such as improved robustness of the Newton iterations or optimization algorithms for inverse problems. The latest developments aim at incorporating the resistive diffusion equation.

- Participant: Holger Heumann
- Contact: Holger Heumann
- URL: https://scm.gforge.inria.fr/svn/holgerheumann/Matlab/FEEQS.M

4.5. Fluidbox

FUNCTIONAL DESCRIPTION

FluidBox is a software dedicated to the simulation of inert or reactive flows. It is also able to simulate multiphase, multi-material and MDH flows. There exist 2D and 3D dimensional versions. The 2D version is used to test new ideas that are later implemented in 3D. Two classes of schemes are available : a classical finite volume scheme and the more recent residual distribution schemes. Several low Mach number preconditioning are also implemented. The code has been parallelized with and without domain overlapping.

- Participants: Rémi Abgrall, Boniface Nkonga, Michael Papin and Mario Ricchiuto
- Contact: Boniface Nkonga

4.6. Jorek-Django

FUNCTIONAL DESCRIPTION

Jorek-Django is a non-production version of the JOREK software, for MHD modeling of plasma dynamic in tokamak geometries. The numerical approximation is derived in the context of finite elements where 3D basic functions are tensor products of 2D basis functions in the poloidal plane by 1D basis functions in the toroidal direction. More specifically, Jorek uses curved bicubic isoparametric elements in 2D and a spectral decomposition (sine, cosine) in the toroidal axis. Continuity of derivatives and mesh alignment to equilibrium surface fluxes are enforced. Resulting linear systems are solved by the PASTIX software developed at Inria-Bordeaux.

- Participants: Boniface Nkonga, Hervé Guillard, Emmanuel Franck (EPI Tonus), Ayoub Iaagoubi and Ahmed Ratnani (IPP, Garching)
- Contact: Hervé Guillard
- URL: https://gforge.inria.fr/projects/jorek/

4.7. Plato

A platform for Tokamak simulation

FUNCTIONAL DESCRIPTION

PlaTo (A platform for Tokamak simulation) is a suite of data and software dedicated to the geometry and physics of Tokamaks. Plato offers interfaces for reading and handling distributed unstructured meshes, numerical templates for parallel discretizations, interfaces for distributed matrices and linear and non-linear equation solvers. Plato provides meshes and solutions corresponding to equilibrium solutions that can be used as initial data for more complex computations as well as tools for visualization using Visit or Paraview. Plato is no more developed and is in the process of being merged with Jorek-Django

- Participants: Boniface Nkonga, Hervé Guillard, Giorgio Giorgiani, Afeintou Sangam and Elise Estibals
- Contact: Hervé Guillard

4.8. VacTH

FUNCTIONAL DESCRIPTION

VacTH implements a method based on the use of toroidal harmonics and on a modelization of the poloidal field coils and divertor coils for the 2D interpolation and extrapolation of discrete magnetic measurements in a tokamak. The method is generic and can be used to provide the Cauchy boundary conditions needed as input by a fixed domain equilibrium reconstruction code like EQUINOX. It can also be used to extrapolate the magnetic measurements in order to compute the plasma boundary itself. The proposed method and algorithm are detailed in [4] and results from numerous numerical experiments are presented. The method is foreseen to be used in the real-time plasma control loop on the WEST tokamak.

- Contact: Blaise Faugeras

CELTIQUE Project-Team

5. New Software and Platforms

5.1. JSCert

Certified JavaScript
FUNCTIONAL DESCRIPTION

The JSCert project aims to really understand JavaScript. JSCert itself is a mechanised specification of JavaScript, written in the Coq proof assistant, which closely follows the ECMAScript 5 English standard. JSRef is a reference interpreter for JavaScript in OCaml , which has been proved correct with respect to JSCert and tested with the Test 262 test suite.

- Participants: Martin Bodin and Alan Schmitt
- Partner: Imperial College London
- Contact: Alan Schmitt
- URL: http://jscert.org/

5.2. Jacal

JAvaCard AnaLyseur
KEYWORDS: JavaCard - Certification - Static program analysis - AFSCM
FUNCTIONAL DESCRIPTION

Jacal is a JAvaCard AnaLyseur developed on top of the SAWJA platform. This software verifies automatically that Javacard programs conform with the security guidelines issued by the AFSCM (Association Française du Sans Contact Mobile). Jacal is based on the theory of abstract interpretation and combines several object-oriented and numeric analyses to automatically infer sophisticated invariants about the program behaviour. The result of the analysis is thereafter harvest to check that it is sufficient to ensure the desired security properties.

- Participants: Delphine Demange, David Pichardie, Thomas Jensen and Frédéric Besson
- Contact: Thomas Jensen

5.3. Javalib

FUNCTIONAL DESCRIPTION

Javalib is an efficient library to parse Java .class files into OCaml data structures, thus enabling the OCaml programmer to extract information from class files, to manipulate and to generate valid .class files.

- Participants: Frédéric Besson, David Pichardie and Laurent Guillo
- Contact: David Pichardie
- URL: http://sawja.inria.fr/

5.4. SAWJA

Static Analysis Workshop for Java
KEYWORDS: Security - Software - Code review
FUNCTIONAL DESCRIPTION

Sawja is a library written in OCaml, relying on Javalib to provide a high level representation of Java bytecode programs. It name comes from Static Analysis Workshop for JAva. Whereas Javalib is dedicated to isolated classes, Sawja handles bytecode programs with their class hierarchy and with control flow algorithms.

Moreover, Sawja provides some stackless intermediate representations of code, called JBir and A3Bir. The transformation algorithm, common to these representations, has been formalized and proved to be semantics-preserving.

- Participants: Frédéric Besson, David Pichardie and Laurent Guillo
- Contact: Frédéric Besson
- URL: http://sawja.inria.fr/

5.5. Timbuk

KEYWORDS: Demonstration - Ocaml - Vérification de programmes - Tree Automata
FUNCTIONAL DESCRIPTION

Timbuk is a collection of tools for achieving proofs of reachability over Term Rewriting Systems and for manipulating Tree Automata (bottom-up non-deterministic finite tree automata)

- Participant: Thomas Genet
- Contact: Thomas Genet
- URL: http://www.irisa.fr/celtique/genet/timbuk/

5.6. CompCertSSA

KEYWORDS: Verified compilation - Single Static Assignment form - Optimization - Coq - OCaml
FUNCTIONAL DESCRIPTION

CompCertSSA is built on top of the C CompCert verified compiler, by adding a SSA-based middle-end (conversion to SSA, SSA-based optimizations, destruction of SSA). It is verified in the Coq proof assistant.

- Participant: Delphine Demange, David Pichardie, Yon Fernandez de Retana, Leo Stefanesco
- Contact: Delphine Demange
- URL: http://compcertssa.gforge.inria.fr/

Chroma Team

6. New Software and Platforms

6.1. CUDA-HSBOF

- Participants: Lukas Rummelhard, Christian Laugier and Amaury Nègre
- Contact: Amaury Nègre

6.2. DATMO (Detection and Tracking of Moving Objects)

- Authors: Trong Tuan Vu and Christian Laugier
- Contact: Christian Laugier

6.3. E.R.C.I.

Estimation du risque de collision aux intersections

- Participants: Stéphanie Lefevre, Christian Laugier and Javier Ibanez-Guzman
- Contact: Christian Laugier

6.4. Embedded Perception

FUNCTIONAL DESCRIPTION

The method for computing occupancy grids from a stereoscopic sensor, developped in the e-motion team, has been implemented on GPU, using NVIDIA CUDA. This allows a real time implementation and an online processing within the Lexus experimental platform.

- Participants: Amaury Nègre, Christian Laugier and Mathias Perrollaz
- Contact: Christian Laugier

6.5. GPU BOF

Bayesian Occupancy Filter on GPU

- Participants: Yong Mao, Christian Laugier, Amaury Nègre and Mathias Perrollaz
- Contact: Christian Laugier

6.6. GPU Stro Occupancy Grid

GPU Stereo Occupancy Grid

- Participants: Amaury Nègre and Mathias Perrollaz
- Contact: Christian Laugier

6.7. VI-SFM

FUNCTIONAL DESCRIPTION

Experimentary the closed Form Solution for usual-initial data fusion agains real and simulated fusion

- Authors: Jacques Kaiser and Agostino Martinelli
- Contact: Agostino Martinelli

6.8. kinetics

- Contact: Jilles Dibangoye

CIDRE Project-Team

6. New Software and Platforms

6.1. Blare

To detect intrusion using information flows.
KEYWORDS: Cybersecurity - Intrusion Detection Systems (IDS) - Data Leakage Protection
SCIENTIFIC DESCRIPTION

Blare implements our approach of illegal information flow detection at the OS level for a single node and a set of nodes.
FUNCTIONAL DESCRIPTION

Blare IDS is a set of tools that implements our approach to illegal information flow detection at the OS level for a single node and a set of nodes.

- Partner: CentraleSupélec
- Contact: Frédéric Tronel
- URL: http://blare-ids.org

6.2. ELVIS

Extensible Log VISualization
KEYWORDS: Visualization - Cybersecurity - Intrusion Detection Systems (IDS) - Cyber attack - Forensics
SCIENTIFIC DESCRIPTION

The studies that were performed last year clearly showed that there was an important need for technologies that would allow analysts to handle in a consistent way the various types of log files that they have to study in order to detect intrusion or to perform forensic analysis. Consequently, we proposed this year ELVis, a security-oriented log visualization system that allows the analyst to import its log files and to obtain automatically a relevant representation of their content based on the type of the fields they are made of. First, a summary view is proposed. This summary displays in an adequate manner each field according to its type (i.e. categorical, ordinal, geographical, etc.). Then, the analyst can select one or more fields to obtain some details about it. A relevant representation is then automatically selected by the tool according to the types of the fields that were selected.

ELVis [35] has been presented in VizSec 2013 (part of Vis 2013) in October in Atlanta. A working prototype is currently being tuned in order to perform field trials with our partners in DGA-MI. Next year, we are planing to perform research on how various log files can be combined in the same representation. In the PANOPTESEC project, we will also perform some research on visualization for security monitoring in the context of SCADA systems.
FUNCTIONAL DESCRIPTION

ELVIS is a log visualization tool that allows analyst-friendly log explorations through automated selection of adequate representations. Many log formats can be used and it is quite simple to add new ones. ELVis has been presented in VizSec 2013 (part of Vis 2013) in October in Atlanta.

- Participant: Nicolas Prigent
- Partner: CentraleSupélec
- Contact: Nicolas Prigent

6.3. GEPETO

GEoPrivacy-Enhancing TOolkit

KEYWORDS: Privacy - Mobility
SCIENTIFIC DESCRIPTION

(GEoPrivacy-Enhancing TOolkit) is an open source software for managing location data (currently in development in cooperation with LAAS). GEPETO can be used to visualize, sanitize, perform inference attacks and measure the utility of a particular geolocated dataset. For each of these actions, a set of different techniques and algorithms can be applied. The global objective of GEPETO is to enable a user to design, tune, experiment and evaluate various sanitization algorithms and inference attacks as well as visualizing the following results and evaluating the resulting trade-off between privacy and utility. An engineer (Izabela Moïse) has contributed to the development of a distributed version of GEPETO based on the MapReduce paradigm and the Hadoop framework that is able to analyze datasets composed of millions of mobility traces in a few minutes [30] .
FUNCTIONAL DESCRIPTION

GEPETO is an open source software for managing location data. GEPETO can be used to visualize, sanitize, perform inference attacks, and measures the utility of a particular geolocated dataset.

- Partners: Université de Rennes 1 - CNRS
- Contact: Sébastien Gambs
- URL: https://gforge.inria.fr/projects/gepeto/

6.4. GNG

Security Supervision by Alert Correlation
KEYWORDS: Intrusion Detection Systems (IDS) - SIEM
SCIENTIFIC DESCRIPTION

GNG is an intrusion detection system that correlates different sources (such as different logs) in order to identify attacks against the system. The attack scenarios are defined using the Attack Description Langage (ADeLe) proposed by our team, and are internally translated to attack recognition automatons. GNG intends to define time efficient algorithms based on these automatons to recognize complex attack scenarios.

- Partner: CentraleSupélec
- Contact: Eric Totel
- URL: http://www.rennes.supelec.fr/ren/perso/etotel/GNG/index.html

6.5. JBlare

FUNCTIONAL DESCRIPTION

JBlare is a Java Virtual Machine (JVM) hypervisor, able to track information flows inside Java programs. Being a modified JVM, it runs vanilla java applications. A cooperation mode with KBlare affords both IDS more precision. JBlare can use hybrid analysis combining dynamic analysis with static analysis using Soot.

- Contact: Guillaume Hiet
- URL: https://www.blare-ids.org/flavors/jblare/

6.6. Netzob

FUNCTIONAL DESCRIPTION

Netzob is an opensource tool for reverse engineering, traffic generation and fuzzing of communication protocols. This tool allows to infer the message format (vocabulary) and the state machine (grammar) of a protocol through passive and active processes. Its objective is to bring state of art academic researches to the operational field, by leveraging bio-informatic and grammatical inferring algorithms in a semi-automatic manner.

- Participant: Georges Bossert
- Contact: Ludovic Mé
- URL: http://www.netzob.org/

6.7. GroddDroid

Automatic Triggering of Android Malware
KEYWORDS: Malware analysis
SCIENTIFIC DESCRIPTION GroddDroid is a tool dedicated to the automatic triggering of suspicious code in Android applications. GroddDroid copes with a classical problem in dynamic analysis which is the triggering of malicious actions. To avoid dynamic analysis, malware authors develop some protections that delay the malicious executions. GroddDroid overrides these protections by modifying the bytecode of the infected applications and reconstructing the application. The modified application can thus be executed and monitored.

- Partner: CentraleSupélec
- Contact: Valérie Viet Triem Tong
- URL: http://kharon.gforge.inria.fr/grodddroid.html

CLIME Project-Team

5. New Software and Platforms

5.1. Data assimilation library: Verdandi

Participants: Nicolas Claude, Vivien Mallet, Gautier Bureau [M3DISIM], Dominique Chapelle [M3DISIM], Sébastien Gilles [M3DISIM], Philippe Moireau [M3DISIM].

The leading idea is to develop a data assimilation library (see the web site http://verdandi.sourceforge.net/) intended to be generic, at least for high-dimensional systems. Data assimilation methods, developed and used by several teams at Inria, are generic enough to be coded independently of the system to which they are applied. Therefore these methods can be put together in a library aiming at:

- making easier the application of methods to a great number of problems,
- making the developments perennial and sharing them,
- improving the broadcast of data assimilation works.

An object-oriented language (C++) has been chosen for the core of the library. A high-level interface to Python is automatically built. The design study raised many questions, related to high dimensional scientific computing, the limits of the object contents and their interfaces. The chosen object-oriented design is mainly based on three class hierarchies: the methods, the observation managers and the models. Several base facilities have also been included, for message exchanges between the objects, output saves, logging capabilities, computing with sparse matrices.

In 2015, version 1.7 was released. We introduced an implementation of nudging. A level-set observation manager was added. Further tests were included. We added the option to build Verdandi as a library.

5.2. Image processing library: Heimdali

Participants: Isabelle Herlin, Dominique Béréziat [UPMC], David Froger [SED].

The initial aim of the image processing library Heimdali was to develop a library based on standard and open source tools, and mostly dedicated to satellite acquisitions.

The leading idea of the library is to allow the following issues:

- making easier the sharing and development of image assimilation softwares. For that purpose, the installation is easily achieved with the package manager Conda.
- developing generic tools for image processing and image assimilation based on ITK (Insight Segmentation and Registration Toolkit http://www.itk.org).
- in reverse, providing tools to ITK and contribute to the ITK community.

The main components of Heimdali concern:

- the pre/post processing of image sequences,
- the image assimilation with numerical models,
- the visualization of image sequences.

In 2015, additional functions were introduced in the library in order to allow more pre/post processing tools.

5.3. Polyphemus

Participants: Vivien Mallet, Sylvain Doré [CEREA], Karine Sartelet [CEREA], Yelva Roustan [CEREA].

Polyphemus (see the web site http://cerea.enpc.fr/polyphemus/) is a modeling system for air quality. As such, it is designed to yield up-to-date simulations in a reliable framework: data assimilation, ensemble forecasts and daily forecasts. Its completeness makes it suitable for use in many applications: photochemistry, aerosols, radionuclides, etc. It is able to handle simulations from local to continental scales, with several physical models. It is divided into three main parts:

- libraries that gather data processing tools (SeldonData), physical parameterizations (AtmoData) and post-processing abilities (AtmoPy);
- programs for physical pre-processing and chemistry-transport models (Polair3D, Castor, two Gaussian models, a Lagrangian model);
- model drivers and observation modules for model coupling, ensemble forecasting and data assimilation.

Fig. 1 depicts a typical result produced by Polyphemus.

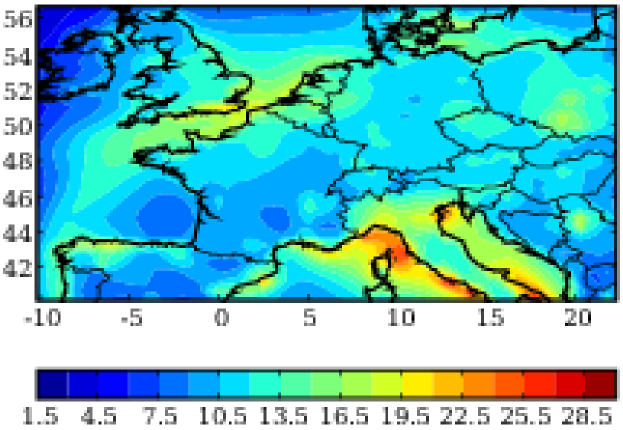


Figure 1. Map of the relative standard deviation (or spread, %) of an ensemble built with Polyphemus (ozone simulations, $\mu g\ m^{-3}$). The standard deviations are averaged over the summer of 2001. They provide an estimation of the simulation uncertainties.

Clime is involved in the overall design of the system and in the development of advanced methods in model coupling, data assimilation and uncertainty quantification (through model drivers and post-processing).

In 2015, version 1.9 was released, with all previous developments on the interface between Verdandi and Polyphemus. The other improvements were developed by CEREA on aerosol modeling.

COAST Project-Team

4. New Software and Platforms

4.1. Replication Benchmarker

Participants: Pascal Urso [contact], Mehdi Ahmed Nacer, Gérald Oster.

The Replication Benchmarker is a performance evaluation framework for optimistic replication mechanisms used in collaborative applications. It contains a library of implementation of several CRDT (Commutative Replicated Data Type) and OT (Operational Transformation) algorithms for different data types: text, set, trees. The framework is able to evaluate the performance of comparable algorithms on different corpus of events traces. These events traces can be produced randomly according to different parameters, can be extracted from real real-time editing session that have been recorded, or can be automatically extracted from distributed version control repositories such as the one produced with Git. Performances of the algorithms are measured in term of execution time, memory footprint and merge result quality (compared to manual merge history stored in git repositories). The source code of this evaluation framework is available at https://github.com/coast-team/replication-benchmarker/.

4.2. MUTE

Participants: Claudia-Lavinia Ignat, Luc André, François Charoy, Gérald Oster [contact].

MUTE (Multi-User Text Editor) is a web-based text editing tool that allows to edit documents collaboratively in real-time. It implements our recent work on collaborative editing algorithms and more specifically the LOGOOTSPLIT+ approach [17]. Compared to existing web-based collaborative text editing tool this editor does not require a powerful central server since the server is not performing any computation and acts as a simple broadcast server. Our editor offers support for working offline while still being able to reconnect at a later time. This prototype is distributed under the term of GNU GPLv3 licence and is freely available at https://github.com/coast-team/mute-demo/. A demo server is hosted at http://www.coedit.re/.

4.3. OpenPaaS POC

Participants: Olivier Perrin [contact], Ahmed Bouchami.

The OpenPaaS Proof of Concept was presented during the final review of the FSN OpenPaaS project. Our contribution was dedicated to the authentication mechanism, and to the authorization framework. These two functionalities was delivered thanks to two RESTful services. The authentication service wrapped the LemonLDAP::NG product within a fully RESTful service, while the authorization service uses the reputation of people within the Enterprise Social Network, and computes the decision/rejection of access based on the trust level of the subject requesting the access. The source code can be obtained via request addressed to Olivier Perrin.

COATI Project-Team

6. New Software and Platforms

6.1. Grph

Participants: Luc Hogie [Contact], Nathann Cohen, David Coudert.

FUNCTIONAL DESCRIPTION

GRPH is an open-source Java library for the manipulation of graphs. In 2015, the library has been maintained and augmented for users needs, especially with a new algorithm for iterating over the cycles of a given graph. This was requested by the EPI AOSTE for the TimeSquare tool.

URL: http://www.i3s.unice.fr/~hogie/grph/

6.2. JourneyPlanner

Participant: Marco Biazzini [Contact].

FUNCTIONAL DESCRIPTION

JourneyPlanner is a Java implementation of a recursive algorithm to solve a TSP problem on small dense graphs, where non-trivial constraints must be satisfied, that make commonly used paradigms (as dynamic programming) unfit to the task.
This work is done in collaboration with the R&D service of the "Train Transportation" division of Amadeus.

6.3. Sagemath

Participants: David Coudert [Contact], Nathann Cohen.

SCIENTIFIC DESCRIPTION

Sagemath is a free open-source mathematics software system initially created by William Stein (Professor of mathematics at Washington University). It builds on top of many existing open-source packages: NumPy, SciPy, matplotlib, Sympy, Maxima, GAP, FLINT, R and many more. Access their combined power through a common, Python-based language or directly via interfaces or wrappers.

OUR CONTRIBUTION

We contribute the addition of new graph algorithms to Sagemath, along with their documentation and the improvement of underlying data structures.

URL : http://www.sagemath.org/

6.4. TripPlanner

Participants: David Coudert [Contact], Stéphane Pérennes.

FUNCTIONAL DESCRIPTION

TripPlanner is a tool for computing a minimum cost trip across multiple cities when neither the order in which to visit the cities nor the sojourn duration in these cities are fully specified. The cost of a trip includes both the price of all airplane tickets necessarily for the trip plus the price of the hotels (both costs depend on the exact travel date) at which the user will sojourn. The trip planner is also able to compute the k cheapest trips.

TripPlanner is written in Python and uses the linear programming interface of Sagemath.

This work is done in collaboration with the R&D service of the "Train Transportation" division of Amadeus.

BNF Antepedia Deposit 2015-09-23-16-11-18

6.5. Platforms

6.5.1. BigGraphs

Participants: Luc Hogie [Contact], Nicolas Chleq [SED-SOP], Michel Syska [Coordinator], David Coudert, Paul Bertot, Flavian Jacquot, Arnaud Legout [DIANA], Fabrice Huet [SCALE], Éric Madelaine [SCALE].

FUNCTIONAL DESCRIPTION

The objective of BigGraphs is to provide a distributed platform for very large graphs processing. A typical data set for testing purpose is a sample of the Twitter graph with 3 millions of nodes and 200 millions of edges. Last year we started the project with the evaluation of existing middlewares (GraphX/Spark and Giraph/Hadoop). After having tested some useful algorithms (written in the BSP model) we decided to develop our own platform.

This platform is based on the existing BIGGRPH library and this year we have focused on the quality and the improvement of the code. In particular we have designed strong test suites and some non trivial bugs have been fixed. We also have implemented specific data structures for BSP and support for distributed debugging. This comes along with the implementation of algorithms such as BFS or strongly connected components that are run on the NEF cluster.

This project is a joint work of the three EPI COATI, DIANA and SCALE and is supported by an ADT grant.

URL: http://www.i3s.unice.fr/~hogie/software/index.php?name=grph

The following software are useful tools that bring basic services to the platform (they are not dedicated to BIGGRPH).

JAC-A-BOO: is a framework aiming at facilitating the deployment of distributed Java scientific applications over clusters and is used to start BIGGRPH. computers.

LDJO: (Live Distributed Java Objects) is a framework for the development and the deployment of Java distributed data structures

OCTOJUS: provides an object-oriented RPC (Remote Procedure Call) implementation in Java

Participants : Luc Hogie [Contact], Nicolas Chleq

URL : http://www.i3s.unice.fr/~hogie/ {jacaboo,ldjo,octojus}

COFFEE Project-Team

5. New Software and Platforms

5.1. NS2DDV

The code NS2DDV is developed jointly with the team SIMPAF, of the Inria Research Centre Lille Nord Europe. It is devoted to the simulation of non-homogeneous viscous flows, in two-dimensional geometries. The code is based on an original hybrid Finite Volume/Finite Element scheme; it works on unstructured meshes and can include mesh refinements strategies. Further details can be found in the research papers J. Comput. Phys., 227, 4671–4696, 2008 and J. Comput. Phys., 229 (17), 6027–6046, 2010. The code exists in two versions: a `Matlab` public version, a `C++` prototype version allowing more ambitious simulations. Both versions are still subject to developments. The current versions is restricted to incompressible flows but on-going progress are concerned with the simulation of avalanches. The source code of the public version is downloadable and several benchmarks tests can be reproduced directly.

- Contact: Emmanuel Creusé
- URL: math.univ-lille1.fr/~simpaf/SITE-NS2DDV/home.html
- The code has been subject to an APP deposit many years ago, but we never received any registration number.

5.2. Compass

for Computing Parallel Architecture to Speed up Simulation is a parallel code for the discretization of polyphasic flows by Finite Volumes methods. The code is mainly devoted to applications in porous media. It works on quite general polyhedral meshes. A first step in the code development has been made during the 2012 edition of CEMRACS and then pursued by C. Guichard, R. Masson and R. Eymard in 2013. A first version of the code has been deposited at the Agency for the Protection of Programs (APP). This current version of `ComPASS` has been tested on a gas storage two phase flow benchmark with GDFSuez using the Vertex Approximate Gradient spatial discretization. The results have shown a very good parallel scalability on the CICADA Cluster at UNS with a few millions of cells and up to 1024 cores. The objective is to develop a generic simulator for multiphase Darcy flows. This simulator will implement advanced finite volume methods on general 3D meshes and on heterogeneous anisotropic media, taking into account discrete fracture networks represented as interfaces of codimension one and coupled with the surrounding matrix. It will be able to treat a large range of multiphase Darcy flow models accounting for thermodynamical equilibrium and the coupling with an energy conservation equation. The simulator will run on massively parallel architectures with a few thousands of cores. It will be applied to several type of industrial applications starting with the simulation of high energy geothermal systems as a carbon-free source of power production.

- Participants: Roland Masson, Cindy Guichard, Feng Xing and Robert Eymard, Thierry Goudon,
- Contact: Roland Masson
- URL: math.unice.fr/~massonr/
- The code has been subject to an APP deposit a few years ago, but we never received any registration number.

5.3. SimBiof

We are developing numerical methods, currently by using Finite Differences approaches, for the simulation of biofilms growth. The underlying system of PDEs takes the form of multiphase flows equations with conservation constraints and vanishing phases. The numerical experiments have permitted to bring out the influence of physical parameters on the multidimensional growth dynamics.

- Contact: Magali Ribot

5.4. AP_PartFlow

We are developing experimental codes, mainly based on Finite Differences, for the simulation of particulate flows. A particular attention is paid to guaranty the asymptotic properties of the scheme, with respect to relaxation parameters.

- Contact: Thierry Goudon

COMETE Project-Team

6. New Software and Platforms

6.1. Location Guard

Participants: Konstantinos Chatzikokolakis [correspondant], Marco Stronati.

https://github.com/chatziko/location-guard

The purpose of Location Guard is to protect the user's location during the use of a location-based service, in an easy and intuitive way that makes it available to the general public. Various modern applications, running either on smartphones or on the web, allow third parties to obtain the user's location. A smartphone application can obtain this information from the operating system using a system call, while web application obtain it from the browser using a JavaScript call.

Although both mobile operating systems and browsers require the user's permission to disclose location information, the user faces an "all-or-nothing" choice: either disclose his exact location and give up his privacy, or stop using the application. This forces many users to disclose their location, although ideally they would like to enjoy some privacy.

The API level of a browser or an operating system is an ideal place for integrating a location obfuscation technique, in a way that is easy to understand for the average user, and readily available to all applications. When an application asks for the user's location, the browser or operating system can ask the user's permission, but including the option to provide an obfuscated location instead of the real one! Different levels of obfuscation can be also offered, so that the user can chose to provide more accurate location to applications that really need it, and more noisy location to those that don't.

In 2015, Location Guard matured with several additions and fixes throughout the year, and was selected by Mozilla as the pick of the month for June 2015, confirming the users' general interest in location privacy.

Moreover in 2015 we set the foundations for actively using Location Guard as a platform for performing research on location privacy. Since location data are sensitive, since the creation of Location Guard we chose to collect no data whatsoever from the users. However, such data are invaluable for research purposes. As a consequence, we created a framework for *locally* collecting data at the user's machine, perform an analysis also locally, and collect back only the results of the analysis for research purposes.

COMMANDS Project-Team

6. New Software and Platforms

6.1. BOCOP

Boite à Outils pour le Contrôle OPtimal

KEYWORDS: Energy management - Numerical optimization - Biology - Identification - Dynamic Optimization - Transportation

FUNCTIONAL DESCRIPTION

Bocop is an open-source toolbox for solving optimal control problems, with collaborations with industrial and academic partners. Optimal control (optimization of dynamical systems governed by differential equations) has numerous applications in transportation, energy, process optimization, energy and biology. Bocop includes a module for parameter identification and a graphical interface, and runs under Linux / Windows / Mac.

- Participants: Joseph Frédéric Bonnans, Pierre Martinon, Olivier Tissot and Benjamin Heymann
- Contact: Pierre Martinon
- URL: http://bocop.org

6.2. Bocop Avion

KEYWORDS: Optimization - Aeronautics

FUNCTIONAL DESCRIPTION

Optimize the climb speeds and associated fuel consumption for the flight planning of civil airplanes.

- Participants: Joseph Frédéric Bonnans, Pierre Martinon, Stéphan Maindrault, Cindie Andrieu, Pierre Jouniaux and Karim Tekkal
- Contact: Pierre Martinon

6.3. Bocop HJB

- Participants: Joseph Frédéric Bonnans, Pierre Martinon, Benjamin Heymann and Olivier Tissot
- Contact: Joseph Frédéric Bonnans
- URL: http://bocop.org

COMPSYS Project-Team

6. New Software and Platforms

6.1. Aspic

Accelerated Symbolic Polyhedral Invariant Generation
KEYWORDS: Abstract Interpretation - Invariant Generation
FUNCTIONAL DESCRIPTION

Aspic is an invariant generator for general counter automata. Combined with C2fsm (a tool developed by P. Feautrier in Compsys), it can be used to derive invariants for numerical C programs, and also to prove safety. It is also part of the WTC toolsuite (see http://compsys-tools.ens-lyon.fr/wtc/index.html), a tool chain to compute worse-case time complexity of a given sequential program.

Aspic implements the theoretical results of Laure Gonnord's PhD thesis on acceleration techniques and has been maintained since 2007.

- Participant: Laure Gonnord
- Contact: Laure Gonnord
- URL: http://laure.gonnord.org/pro/aspic/aspic.html

6.2. DCC

DPN C Compiler
KEYWORDS: Polyhedral compilation - Automatic parallelization - High-level synthesis
FUNCTIONAL DESCRIPTION

Dcc (Data-aware process network C compiler) analyzes a sequential regular program written in C and generates an equivalent architecture of parallel computer as a communicating process network (Data-aware Process Network, DPN). Internal communications (channels) and external communications (external memory) are automatically handled while fitting optimally the characteristics of the global memory (latency and throughput). The parallelism can be tuned. Dcc has been registered at the APP ("Agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria license.

- Participants: Christophe Alias and Alexandru Plesco
- Contact: Christophe Alias

6.3. Lattifold

Lattice-based Memory Folding
KEYWORDS: Polyhedral compilation - Euclidean Lattices
FUNCTIONAL DESCRIPTION

Implements advanced lattice-based memory folding techniques. The idea is to reduce memory footprint of multidimensional arrays by reducing the size of each dimension. Given a relation denoting conflicting array cells, it produces a new mapping based on affine functions bounded by moduli. The moduli induces memory reuse and bound memory accesses to a tighter area, allowing to reduce the array size without loss of correctness.

- Partner: ENS Lyon
- Contact: Alexandre Isoard

6.4. OpenOrdo

OpenStream scheduler

FUNCTIONAL DESCRIPTION

Finding polynomial schedules for the streaming language OpenStream. Main use: detecting deadlocks.

- Contact: Paul Feautrier

6.5. PoCo

Polyhedral Compilation library
KEYWORDS: Polyhedral compilation - Automatic parallelization
FUNCTIONAL DESCRIPTION

PoCo (Polyhedral Compilation library) is a compilation framework allowing to develop parallelizing compilers for regular programs. PoCo features many state-of-the-art polyhedral program analysis (dependences, affine scheduling, code generation) and a symbolic calculator on execution traces (represented as convex polyhedra). PoCo has been registered at the APP ("agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria license.

- Participant: Christophe Alias
- Contact: Christophe Alias

6.6. PolyOrdo

Polynomial Scheduler
FUNCTIONAL DESCRIPTION

Computes a polynomial schedule for a sequential polyhedral program having no affine schedule. Uses algorithms for finding positive polynomials in semi-algebraic sets. Status: proof of concept software.

- Contact: Paul Feautrier

6.7. PPCG-ParamTiling

Parametric Tiling Extension for PPCG
KEYWORDS: Source-to-source compiler - Polyhedral compilation
FUNCTIONAL DESCRIPTION

PPCG is a source-to-source compiler, based on polyhedral techniques, targeting GPU architectures. It involves automatic parallelization and tiling using polyhedral techniques. This version replaces the static tiling of PPCG by a fully parametric tiling and code generator. It allows to choose tile sizes at run time when the memory size is known. It also provides a symbolic expression of memory usage depending on the problem size and the tile sizes.

- Partner: ENS Lyon
- Contact: Alexandre Isoard

6.8. Termite

Termination of C programs
KEYWORDS: Abstract Interpretation - Termination
FUNCTIONAL DESCRIPTION

TERMITE is the implementation of our new algorithm "Counter-example based generation of ranking functions" (see Section 7.4). Based on LLVM and Pagai (a tool that generates invariants), the tool automatically generates a ranking function for each *head of loop*.

TERMITE represents 3000 lines of OCaml and is now available via the opam installer.

- Participants: Laure Gonnord, Gabriel Radanne (PPS, Univ Paris 7), David Monniaux (CNRS/Verimag).
- Contact: Laure Gonnord
- URL: https://termite-analyser.github.io/

6.9. Vaphor

Validation of C programs with arrays with Horn Clauses

KEYWORDS: Abstract Interpretation - Safety - Array Programs
FUNCTIONAL DESCRIPTION

VAPHOR (Validation of Programs with Horn Clauses) is the implementation of our new algorithm "An encoding of array verification problems into array-free Horn clauses" (see Section 7.3). The tool implements a translation from a C-like imperative language into Horn clauses in the SMT-lib Format.

VAPHOR represents 2000 lines of OCaml and its development is under consolidation.

- Participants: Laure Gonnord, David Monniaux (CNRS/Verimag).
- Contact: Laure Gonnord
- URL: not yet published, under consolidation.

CONVECS Project-Team

5. New Software and Platforms

5.1. The CADP Toolbox

Participants: Hubert Garavel [correspondent], Frédéric Lang, Radu Mateescu, Wendelin Serwe.

We maintain and enhance CADP (*Construction and Analysis of Distributed Processes* – formerly known as *CAESAR/ALDEBARAN Development Package*) [1], a toolbox for protocols and distributed systems engineering [0]. In this toolbox, we develop and maintain the following tools:

- CAESAR.ADT [42] is a compiler that translates LOTOS abstract data types into C types and C functions. The translation involves pattern-matching compiling techniques and automatic recognition of usual types (integers, enumerations, tuples, etc.), which are implemented optimally.
- CAESAR [47], [46] is a compiler that translates LOTOS processes into either C code (for rapid prototyping and testing purposes) or finite graphs (for verification purposes). The translation is done using several intermediate steps, among which the construction of a Petri net extended with typed variables, data handling features, and atomic transitions.
- OPEN/CAESAR [43] is a generic software environment for developing tools that explore graphs on the fly (for instance, simulation, verification, and test generation tools). Such tools can be developed independently of any particular high level language. In this respect, OPEN/CAESAR plays a central role in CADP by connecting language-oriented tools with model-oriented tools. OPEN/CAESAR consists of a set of 16 code libraries with their programming interfaces, such as:
  - CAESAR_GRAPH, which provides the programming interface for graph exploration,
  - CAESAR_HASH, which contains several hash functions,
  - CAESAR_SOLVE, which resolves Boolean equation systems on the fly,
  - CAESAR_STACK, which implements stacks for depth-first search exploration, and
  - CAESAR_TABLE, which handles tables of states, transitions, labels, etc.

  A number of on-the-fly analysis tools have been developed within the OPEN/CAESAR environment, among which:
  - BISIMULATOR, which checks bisimulation equivalences and preorders,
  - CUNCTATOR, which performs steady-state simulation of continuous-time Markov chains,
  - DETERMINATOR, which eliminates stochastic nondeterminism in normal, probabilistic, or stochastic systems,
  - DISTRIBUTOR, which generates the graph of reachable states using several machines,
  - EVALUATOR, which evaluates MCL formulas,
  - EXECUTOR, which performs random execution,
  - EXHIBITOR, which searches for execution sequences matching a given regular expression,
  - GENERATOR, which constructs the graph of reachable states,
  - PROJECTOR, which computes abstractions of communicating systems,
  - REDUCTOR, which constructs and minimizes the graph of reachable states modulo various equivalence relations,

---

[0] http://cadp.inria.fr

  - SIMULATOR, XSIMULATOR, and OCIS, which enable interactive simulation, and
  - TERMINATOR, which searches for deadlock states.
- BCG (*Binary Coded Graphs*) is both a file format for storing very large graphs on disk (using efficient compression techniques) and a software environment for handling this format. BCG also plays a key role in CADP as many tools rely on this format for their inputs/outputs. The BCG environment consists of various libraries with their programming interfaces, and of several tools, such as:
  - BCG_CMP, which compares two graphs,
  - BCG_DRAW, which builds a two-dimensional view of a graph,
  - BCG_EDIT, which allows the graph layout produced by BCG_DRAW to be modified interactively,
  - BCG_GRAPH, which generates various forms of practically useful graphs,
  - BCG_INFO, which displays various statistical information about a graph,
  - BCG_IO, which performs conversions between BCG and many other graph formats,
  - BCG_LABELS, which hides and/or renames (using regular expressions) the transition labels of a graph,
  - BCG_MIN, which minimizes a graph modulo strong or branching equivalences (and can also deal with probabilistic and stochastic systems),
  - BCG_STEADY, which performs steady-state numerical analysis of (extended) continuous-time Markov chains,
  - BCG_TRANSIENT, which performs transient numerical analysis of (extended) continuous-time Markov chains, and
  - XTL (*eXecutable Temporal Language*), which is a high level, functional language for programming exploration algorithms on BCG graphs. XTL provides primitives to handle states, transitions, labels, *successor* and *predecessor* functions, etc.

    For instance, one can define recursive functions on sets of states, which allow evaluation and diagnostic generation fixed point algorithms for usual temporal logics (such as HML [51], CTL [39], ACTL [41], etc.) to be defined in XTL.
- PBG (*Partitioned BCG Graph*) is a file format implementing the theoretical concept of *Partitioned LTS* [45] and providing a unified access to a graph partitioned in fragments distributed over a set of remote machines, possibly located in different countries. The PBG format is supported by several tools, such as:
  - PBG_CP, PBG_MV, and PBG_RM, which facilitate standard operations (copying, moving, and removing) on PBG files, maintaining consistency during these operations,
  - PBG_MERGE (formerly known as BCG_MERGE), which transforms a distributed graph into a monolithic one represented in BCG format,
  - PBG_INFO, which displays various statistical information about a distributed graph.
- The connection between explicit models (such as BCG graphs) and implicit models (explored on the fly) is ensured by OPEN/CAESAR-compliant compilers, e.g.:
  - BCG_OPEN, for models represented as BCG graphs,
  - CAESAR.OPEN, for models expressed as LOTOS descriptions,
  - EXP.OPEN, for models expressed as communicating automata,
  - FSP.OPEN, for models expressed as FSP [56] descriptions,
  - LNT.OPEN, for models expressed as LNT descriptions, and
  - SEQ.OPEN, for models represented as sets of execution traces.

The CADP toolbox also includes TGV (*Test Generation based on Verification*), which has been developed by the VERIMAG laboratory (Grenoble) and the VERTECS project-team at Inria Rennes – Bretagne-Atlantique.

The CADP tools are well-integrated and can be accessed easily using either the EUCALYPTUS graphical interface or the SVL [44] scripting language. Both EUCALYPTUS and SVL provide users with an easy and uniform access to the CADP tools by performing file format conversions automatically whenever needed and by supplying appropriate command-line options as the tools are invoked.

5.2. The PMC Partial Model Checker

Participants: Radu Mateescu, Frédéric Lang.

We develop a tool named PMC (*Partial Model Checker*, see § 6.4), which performs the compositional model checking of dataless MCL formulas on networks of communicating automata described in the EXP language.

PMC can be freely downloaded from the CONVECS Web site [0].

---

[0] http://convecs.inria.fr/software/pmc

CORSE Team

5. New Software and Platforms

5.1. Tirex

TIREX is an extensible, textual intermediate code representation that is intended to be used as an exchange format for compilers and other tools working on low level code. In the scope of the TIREX project we have developed tools for generating TIREX code from higher level languages such as C, as well as a number of static analyses and transformations.

Work on the TIREX project consisted of two main parts, firstly the cleanup and maintenance of the existing tools and web site and, secondly, implementing new backends for emitting TIREX.

The existing TIREX transormation and analysis tools as well the web site have been updated to make sure they work with the newest versions of their respective platforms (Java and PHP). They have also been refactored to make better use of newer or safer APIs. This work also included a redesign of the web site of the TIREX project and a rewrite of the build system.

The existing Open64 based backend has been updated to comply with the TIREX v2 specification so its output can be used with the rest of the tool chain.

We have also developed two new backends allowing us to generate TIREX code from any language the LLVM frontends support (including C, C++ and LLVM IR) as well as directly from assembly code. Preliminary work for generating TIREX directly from binaries has also been done, and the assembly backend is designed to allow most of its code to be reused for this purpose. These new developments required a partial rewrite of LLVMs internal machine description system to expose more machine information in an easily accessible manner. As a positive side effect we were able to reuse several parts used in earlier stages of the LLVM pipeline to write a simple type analysis on machine code used in the assembly backend. We also implemented a control flow reconstruction pass in the assembly backend to improve the quality of the generated code.

Lastly we have adopted continuous integration and started curating a regression test suite for our new developments.

5.2. LLVM plugins

Work has been started on multiple plugins for the LLVM compiler framework that implement the code optimization that have been elaborated by the team. While being work in progress this already provides us with crucial information for program analysis such as data-dependencies.

- Polly pointer disambiguation (publicly available): Status: Published. Description: A llvm-Polly patch that generates versioned SCoP, where the optimized version is guarded by run-time tests to validate that there are no hazardous aliasing.
- More on pointer disambiguation (to STMicroelectronics): Status: Implemented. Allows the use of malloc identifiers to quickly evaluate possible aliasing at run-time.
- Dynamic-dependence graph (to STMicroelectronics): Status: Under development. The run-time process is close to completion. Requires to treat function calls as sub-loops to allow optimization of recursive functions. The static analysis is capable of reading the trace file. The next step is to use a memory model to identify code transformations that would have better memory locality.

5.3. The klang-omp OpenMP compiler

Klang-Omp is a C and C++ source-to-source OpenMP compiler based on LLVM framework and on Intel's Clang-OMP front-end. It translates OpenMP directives into calls to task-based runtime system APIs. Klang-Omp currently targets both the StarPU runtime and the Kaapi runtime. The compiler supports independent tasks as defined by the 3.1 revision of the OpenMP specification as well as dependent tasks introduced with OpenMP 4. It also has been extended to support the omp target construct, making OpenMP applications able to offload computation to accelerators. This support also relies on the StarPU and XKaapi accelerator support capabilities. This work has been funded by the KSTAR Inria ADT project, involving the AVALON, STORM, MOAIS and CORSE Inria team. While the KSTAR project will end in January 2016, the klang-omp compiler will still be maintained and extended to support future OpenMP-oriented research actions, such as the ones promoted by the HEAVEN Persyval project.

5.4. mcGDB: Debugging of Multithreaded Applications

mcGDB is a new debugger for multithreaded applications. It implements a novel approach for interactive debugging named Programming Model-Centric Debugging. mcGDB raises interactive debugging to the level of programming models, by capturing and interpreting events generated during the application execution (e.g. through breakpointed API function calls). This new approach debugging is applied to four different programming models: software components (ST/NPM), Data flow (ST/PEDF), OpenCL and OpenMP. MCGDB was initialy developped by Kevin Pouget with STMicromectronics (CIFRE thesis). mcGDG uses the Temanejo graphical interface to display task graphs. mcGDB is currently extended in the DEMA/Nano2017 project with ST Microelectronics, Inria/Parkas and UPMC.

5.5. BOAST: Metaprogramming of Computing Kernels

BOAST aims at providing a framework to metaprogram, benchmark and validate computing kernels. BOAST is a programming framework dedicated to code generation and autotuning. This software allows the transformation from code written in the BOAST DSL to classical HPC targets like FORTRAN, C, OpenMP, OpenCL or CUDA. It also enables the meta-programming of optimization that can be (de)activated when needed. BOAST can also benchmark and do non regression tests on the generated kernels. This approach gives, both, performance gains and improved performance portability.

BOAST was used to generate and optimize the computing kernels of two scientific applications:

- BigDFT
- SPECFEM

BOAST can be dowloaded at this address https://forge.imag.fr/projects/boast/.

CQFD Project-Team

6. New Software and Platforms

6.1. Package PCAmixdata

FUNCTIONAL DESCRIPTION

Mixed data type arise when observations are described by a mixture of numerical and categorical variables. The R package PCAmixdata extends standard multivariate analysis methods to incorporate this type of data. The key techniques included in the package are PCAmix (PCA of a mixture of numerical and categorical variables), PCArot (rotation in PCAmix) and MFAmix (multiple factor analysis with mixed data within a dataset). The MFAmix procedure handles a mixture of numerical and categorical variables within a group - something which was not possible in the standard MFA procedure. We also included techniques to project new observations onto the principal components of the three methods in the new version of the package.

- Participants: Marie Chavent, Amaury Labenne, Jérome Saracco
- Contact: Marie Chavent
- URL: https://cran.r-project.org/web/packages/PCAmixdata/index.html

6.2. Package divclust

FUNCTIONAL DESCRIPTION DIVCLUS-T is a divisive hierarchical clustering algorithm based on a monothetic bipartitional approach allowing the dendrogram of the hierarchy to be read as a decision tree. It is designed for numerical, categorical (ordered or not) or mixed data. Like the Ward agglomerative hierarchical clustering algorithm and the k-means partitioning algorithm, it is based on the minimization of the inertia criterion. However, it provides a simple and natural monothetic interpretation of the clusters. Indeed, each cluster is decribed by set of binary questions. The inertia criterion is calculated on all the principal components of PCAmix (and then on standardized data in the numerical case).

- Participants: Marie Chavent, Marc Fuentes
- Contact: Marie Chavent
- URL: https://github.com/chavent/divclust

6.3. Package ClustGeo

FUNCTIONAL DESCRIPTION This R package is dedicated to the clustering of objects with geographical positions. The clustering method implemented in this package allows the geographical constraints of proximity to be taken into account within the ascendant hierarchical clustering.

- Marie Chavent, Amaury Labenne, Vanessa Kuentz, Jérome Saracco
- Contact: Amaury Labenne
- URL: https://cran.r-project.org/web/packages/ClustGeo/index.html

6.4. Package QuantifQuantile

FUNCTIONAL DESCRIPTION This R package is dedicated to the estimation of conditional quantiles using optimal quantization. It allows the construction of an optimal grid of N quantizers, the estimation of conditional quantiles and the data driven selection of the size N of the grid. Graphical illustrations are available for the selection of N and of resulting estimated curves or surfaces when the dimension of the covariate is one or two.

- Isabelle Charlier, Jérôme Saracco
- Contact: Isabelle Charlier
- URL: https://cran.r-project.org/web/packages/QuantifQuantile/index.html

6.5. Biips: Software for Bayesian Inference with Interacting Particle Systems

FUNCTIONAL DESCRIPTION

Biips is a software platform for automatic Bayesian inference with interacting particle systems. Biips allows users to define their statistical model in the probabilistic programming BUGS language, as well as to add custom functions or samplers within this language. Then it runs sequential Monte Carlo based algorithms (particle filters, particle independent Metropolis-Hastings, particle marginal Metropolis-Hastings) in a black-box manner so that to approximate the posterior distribution of interest as well as the marginal likelihood. The software is developed in C++ with interfaces with the softwares R, Matlab and Octave.

- Participants: François Caron, Adrien Todeschini and Pierrick Legrand
- Contact: Adrien Todeschini
- URL: http://biips.gforge.inria.fr

6.6. VCN: Software for analysis of VCN

FUNCTIONAL DESCRIPTION

VCN is a software for the analysis of the vigilance of the patient based on the analysis of the EEG signals. The code is written in Matlab and provides an interface easy to use for someone without informatics skills.

- Participants: Pierrick Legrand, Julien Clauzel, Laurent Vezard, Charlotte Rodriguez, Borjan Geshkovski.
- Contact: Pierrick Legrand

6.7. EMGView: Software for visualisation and time-frequency analysis of bio signals

FUNCTIONAL DESCRIPTION

EMGView is a software for the visualisation and the analysis of bio-signals. The code is written in Matlab and provides an interface easy to use for someone without informatics skills.

- Participants: Luis Herrera, Eric Grivel, Pierrick Legrand, Gregory Barriere
- Contact: Pierrick Legrand

CRYPT Team (section vide)

CTRL-A Team

6. New Software and Platforms

6.1. Heptagon/BZR

We want to produce results concretely usable by third parties, either in cooperative projects, or by free diffusion of tools. One perspective is to build tool boxes for the design of continuous control solutions for computing systems: it will be explored in the future. A readily available result concerns discrete control and programming.

FUNCTIONAL DESCRIPTION

Heptagon is an experimental language for the implementation of embedded real-time reactive systems. It is developed inside the Synchronics large-scale initiative, in collaboration with Inria Rhones-Alpes. It is essentially a subset of Lucid Synchrone, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

- Participants: Adrien Guatto, Marc Pouzet, Cédric Pasteur, Léonard Gérard, Brice Gelineau, Gwenaël Delaval and Eric Rutten
- Contact: Gwenaël Delaval
- URL: http://bzr.inria.fr

HEPTAGON has been used to build BZR [0], which is an extension of the former with contracts constructs. These contracts allow to express dynamic temporal properties on the inputs and outputs of HEPTAGON node. These properties are then enforced, within the compilation of a BZR program, by discrete controller synthesis, using the SIGALI tool [0]. The synthesized controller is itself generated in HEPTAGON, allowing its analysis and compilation towards different target languages (C, Java, VHDL).

Heptagon/BZR has been recently integrated with the ReaX verification and controller synthesis tool. The ReaX tool allows the handling of numerico-boolean programs by using abstract interpretation for controller synthesis.

Prospects about Heptagon/BZR lie in developping methodological and programming tools for : precise diagnosis in case of controller synthesis failure ; identification of relevant domain of abstractions, in relation with the use of the ReaX tool ; integration in various execution platforms (Fractal, reconfigurable FPGA, etc.)

---

[0] http://bzr.inria.fr

[0] http://www.irisa.fr/vertecs/Logiciels/sigali.html

DAHU Project-Team (section vide)

DANTE Project-Team

6. New Software and Platforms

6.1. GraSP

Graph Signal Processing
KEYWORDS: Matlab - LaTeX - Graph - Graph visualization - Signal processing - GNU Octave
FUNCTIONAL DESCRIPTION

Matlab / GNU Octave toolbox to manipulate and visualize signals on graphs. LaTeX package to draw signals.

- Contact: Benjamin Girault
- URL: http://perso.ens-lyon.fr/benjamin.girault/

6.2. IoT-LAB aggregation-tools

KEYWORD: Internet of things
FUNCTIONAL DESCRIPTION

IoT-LAB aggregation-tools allow aggregating data results from many nodes at a time. It connects to several tcp connections and handle the received data.

- Participant: Gaetan Harter
- Contact: Éric Fleury
- URL: https://github.com/iot-lab/aggregation-tools

6.3. IoT-LAB cli-tools

KEYWORD: Internet of things
FUNCTIONAL DESCRIPTION

IoT-LAB cli-tools provide a basic set of operations for managing IoT-LAB experiments from the command-line.

- Participants: Gaetan Harter and Frédéric Saint-Marcel
- Contact: Éric Fleury
- URL: https://github.com/iot-lab/cli-tools

6.4. IoT-LAB gateway

KEYWORD: Internet of things
FUNCTIONAL DESCRIPTION

IoT-LAB software embedded on a IoT-LAB gateway node new generation provides the local management of the experiment on that node. It is a software bridge between the IoT-LAB server, the user open node and the control node.

- Contact: Frédéric Saint-Marcel
- URL: https://github.com/iot-lab/iot-lab-gateway

6.5. IoT-LAB robots

KEYWORDS: Internet of things - Robotics
FUNCTIONAL DESCRIPTION

IoT-LAB robots is an embedded robot controler on a Turtlebot2 providing the IoT-LAB node mobility functionnality

- Partner: Université de Strasbourg
- Contact: Frédéric Saint-Marcel

6.6. Queueing Systems

KEYWORDS: Performance Evaluation - Queueing Models
FUNCTIONAL DESCRIPTION

This tool aims at providing a simple web interface to promote the use of our proposed solutions to numerically solve classical queueing systems.

- Participants: Thomas Begin and Alexandre Brandwajn
- Contact: Thomas Begin
- URL: http://queueing-systems.ens-lyon.fr/

6.7. WSNet

KEYWORD: Network simulator
FUNCTIONAL DESCRIPTION

The WSNet-3.0 project objective is to develop the next evolution of the WSNet simulator. It is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalabiliy, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation.

- Participants: Rodrigue Domga Komguem, Quentin Lampin, Alexandre Mouradian and Fabrice Valois
- Partner: CEA-LETI
- Contact: Fabrice Valois
- URL: https://gforge.inria.fr/projects/wsnet-3/

6.8. Platforms

6.8.1. FIT IoT-LAB

FUNCTIONAL DESCRIPTION

IoT-LAB provides full control of network IoT nodes and direct access to the gateways to which nodes are connected, allowing researchers to monitor nodes energy consumption and network-related metrics, e.g. end-to-end delay, throughput or overhead. The facility offers quick experiments deployment, along with easy evaluation, results collection and analysis. Defining complementary testbeds with different node types, topologies and environments allows for coverage of a wide range of real-life use-cases.

- Partner: FIT is one of 52 winning projects from the first wave of the French Ministry of Higher Education and Research's "Équipements d'Excellence" (Equipex) research grant programme. Th eFIT consortium is composed of: Université Pierre et Marie Curie (UPMC), Inria, Université de Strasbourg, Institut Mines Télécom and CNRS
- Contact: Éric Fleury
- URL: https://www.iot-lab.info/

DECENTRALISE Team

5. New Software and Platforms

5.1. GNUnet

GNUnet
KEYWORD: Privacy
FUNCTIONAL DESCRIPTION

GNUnet is a framework for secure peer-to-peer networking that does not use any centralized or otherwise trusted services. Our high-level goal is to provide a strong free software foundation for a global network that provides security and in particular respects privacy.

GNUnet started with an idea for anonymous censorship-resistant file-sharing, but has grown to incorporate other applications as well as many generic building blocks for secure networking applications. In particular, GNUnet now includes the GNU Name System, a privacy-preserving, decentralized public key infrastructure.

- Participants: Hans Grothoff, Florian Dold, Jeffrey Paul Burdges and Gabor Toth
- Partner: The GNU Project
- Contact: Hans Grothoff
- URL: https://gnunet.org/

5.2. MHD

GNU libmicrohttpd
KEYWORDS: Embedded - Web 2.0
FUNCTIONAL DESCRIPTION

GNU libmicrohttpd is a small C library that is supposed to make it easy to run an HTTP server as part of another application.

- Author: Hans Grothoff
- Contact: Hans Grothoff
- URL: http://www.gnu.org/software/libmicrohttpd/

5.3. Taler

GNU Taler
KEYWORD: Privacy
FUNCTIONAL DESCRIPTION

Taler is a new electronic payment system.

- Partner: The GNU Project
- Contact: Hans Grothoff
- URL: http://taler.net/

DEDUCTEAM Team

6. New Software and Platforms

6.1. Introduction

Deducteam develops several kinds of tools or libraries:

- Proof checkers:
  - Dedukti: proof checker for the $\lambda\Pi$-calculus modulo rewriting
  - Sukerujo: extension of Dedukti with syntactic constructions for records, strings, lists, etc.
  - Rainbow: CPF termination certificate verifier
- Tools for translating into Dedukti's proof format proofs coming from various other provers:
  - Coqine translates Coq proofs
  - Focalide translates Focalize proofs
  - Holide translates OpenTheory proofs (HOL-Light, HOL4, ProofPower)
  - Krajono translates Matita proofs
  - Sigmaid translates ς-calculus
- Automated theorem provers:
  - iProverModulo: theorem prover based on polarized resolution modulo
  - SuperZenon: extension of Zenon using superdeduction
  - ZenonArith: extension of Zenon using the simplex algorithm for arithmetic
  - ZenonModulo: extension of Zenon using deduction modulo and producing Dedukti proofs
  - Zipperposition: superposition prover featuring arithmetic and induction
  - HOT: automated termination prover for higher-order rewrite systems
- Libraries or generation tools:
  - CoLoR: Coq library on rewriting theory and termination
  - Logtk: library for first-order automated reasoning
  - mSat: modular SAT/SMT solver with proof output
  - Moca: generator of construction functions for types with relations on constructors

In the following, we only details software that received improvements in 2015.

In addition, Shuai Wang developed the ProofCloud prototype, a proof retrieval engine for verified higher order proofs. ProofCloud provides a fast proof searching service for mathematicians and computer scientists for the reuse of proofs and proof packages. Using ProofCloud, he conducted a statistical analysis of the OpenTheory repository.

6.2. Autotheo

Autotheo is a tool that transforms axiomatic theories into polarized rewriting systems, thus making them usable in iProver Modulo. It supports several strategies to orient the axioms, some of them being proved to be complete, in the sense that ordered polarized resolution modulo the resulting systems is refutationally complete, some others being merely heuristics. In practice, Autotheo takes a TPTP input file and produces an input file for iProver Modulo.

- Contact: Guillaume Burel
- URL: http://www.ensiie.fr/~guillaume.burel/blackandwhite_autotheo.html.en

In 2015, we extended Autotheo so that it prints a derivation of the transformation of the axioms into rewriting rules. This derivation is in TSTP format and includes the CNF conversions obtained from the prover E.

6.3. CoLoR

CoLoR is Coq library on rewriting theory and termination. It provides many definitions and theorems on various mathematical structures (quasi-ordered sets, relations, ordered semi-rings, etc.), data structures (lists, vectors, matrices, polynomials, finite graphs), term structures (strings, first-order terms, lambda-terms, etc.), transformation techniques (dependency pairs, semantic labeling, etc.) and (non-)termination criteria (polynomial and matrix interpretations, recursive path ordering, computability closure, etc.).

- Contact: Frédéric Blanqui
- URL: http://color.inria.fr/

In 2015, CoLoR has been enriched and improved in various ways:

- Its compilation time has been improved by about 20%.
- The results on computability have been extended to η-reduction.
- It has been enriched by a library on finite and infinite sets, and a proof of the infinite Ramsey's theorem [54].
- CoLoR is now available on OPAM.

6.4. Coqine

Coqine translates Coq proofs into Dedukti proofs.

- Contact: Guillaume Burel
- URL: http://www.ensiie.fr/~guillaume.burel/blackandwhite_coqInE.html.en

The addition of higher-order pattern matching in Dedukti allowed the encoding of universes.

6.5. Dedukti

Dedukti is a proof-checker for the $\lambda\Pi$-calculus modulo. As it can be parametrized by an arbitrary set of rewrite rules, defining an equivalence relation, this calculus can express many different theories. Dedukti has been created for this purpose: to allow the interoperability of different theories.

Dedukti's core is based on the standard algorithm for type-checking semi-full pure type systems and implements a state-of-the-art reduction machine inspired from Matita's and modified to deal with rewrite rules.

Dedukti's input language features term declarations and definitions (opaque or not) and rewrite rule definitions. A basic module system allows the user to organize his project in different files and compile them separately.

- Contact: Olivier Hermant
- URL: http://dedukti.gforge.inria.fr/

The new version of Dedukti (v2.5) brings two major improvements.

First the typing of rewrite rules has been completely reworked. It can now check a large class of rewrite rules including rules whose left-hand sides are not algebraic nor well-typed. Moreover the typing context do not need to be given with the rewrite rule anymore, as it is inferred by Dedukti, and therefore it is more convenient for the user.

Second, Dedukti can now be interfaced with automatic confluence checkers in order to check that the rewrite system generated by the rewrite rules together with beta reduction is confluent. This verification is important as the soundness of the program relies on this hypothesis.

6.6. Focalide

Focalide is an extension of the FoCaLize compiler which produces Dedukti files.

- Contact: Raphaël Cauderlier
- URL: http://deducteam.gforge.inria.fr/focalide/

Focalide has been improved to support FoCaLiZe proofs found by Zenon using the Dedukti backend for Zenon. This backend has been improved by a simple typing mechanism in order to work with Focalide. Focalide has also been updated again to work with the latest version of FoCaLiZe.

6.7. Holide

Holide translates HOL proofs to Dedukti proofs, using the OpenTheory standard (common to HOL Light and HOL4).

- Contact: Guillaume Burel
- URL: http://deducteam.gforge.inria.fr/holide/

Shuai Wang fixed a number of problems, especially in the translation of type variables, allowing us to translate more libraries.

6.8. iProverModulo

iProver Modulo is an extension of the automated theorem prover iProver originally developed by Konstantin Korovin at the University of Manchester. It implements ordered polarized resolution modulo, a refinement of the resolution method based on deduction modulo. It takes as input a proposition in predicate logic and a clausal rewriting system defining the theory in which the formula has to be proved. Normalization with respect to the term rewriting rules is performed very efficiently through translation into OCaml code, compilation and dynamic linking. Experiments have shown that ordered polarized resolution modulo dramatically improves proof search compared to using raw axioms. iProver Modulo is also able to produce proofs that can be checked by Dedukti, therefore improving confidence.

- Contact: Guillaume Burel
- URL: http://www.ensiie.fr/~guillaume.burel/blackandwhite_iProverModulo.html.en

In 2015, we improved its integration with Autotheo.

6.9. Krajono

Krajono translates Matita proofs into Dedukti proofs.

- Contact: Guillaume Burel
- URL: http://deducteam.gforge.inria.fr/krajono/

First working version able to translate the Matita library on arithmetics.

6.10. mSAT

mSAT is a modular, proof-producing, SAT and SMT core based on Alt-Ergo Zero, written in OCaml. The solver accepts user-defined terms, formulas and theory, making it a good tool for experimenting. This tool produces resolution proofs as trees in which the leaves are user-defined proof of lemmas.

- Contact: Guillaume Bury
- URL: https://github.com/Gbury/mSAT

mSAT now provides a functor for generating a McSat solver, outputs a model or a proof, and provides a push/pop functionality.

6.11. ZenonModulo

Zenon Modulo is an extension of the automated theorem prover Zenon. Compared to Super Zenon, it can deal with rewrite rules both over propositions and terms. Like Super Zenon, Zenon Modulo is able to deal with any first-order theory by means of a similar heuristic.

- Contact: Pierre Halmagrand
- URL: http://deducteam.gforge.inria.fr/zenonmodulo/

In 2015, we extended Zenon Modulo to polymorphism. Moreover, it can now take TPTP-TFF1 problems as input, and output Dedukti's proofs.

Guillaume Bury continued to improve an extension of Zenon with arithmetic.

6.12. Zipperposition

Zipperposition is an implementation of the superposition method that relies on the library Logtk for basic logic data structures and algorithms. Zipperposition is designed as a testbed for extensions to superposition, and can currently deal with polymorphic typed logic, integer arithmetic and total orderings.

- Contact: Simon Cruanes
- URL: http://deducteam.gforge.inria.fr/zipperposition/

In 2015, we extended Zipperposition to structural induction.

DEFI Project-Team

5. New Software and Platforms

5.1. FVforBlochTorrey

FUNCTIONAL DESCRIPTION

We developed two numerical codes to solve the multiple-compartments Bloch-Torrey partial differential equation in 2D and 3D to simulate the water proton magnetization of a sample under the influence of diffusion-encoding magnetic field gradient pulses.

We coupled the spatial discretization with an efficient time discretization adapted to diffusive problems called the (explicit) Runge-Kutta-Chebyshev method.

The version of the code using Finite Volume discretization on a Cartesian grid is complete (written by Jing-Rebecca Li). The version of the code using linear Finite Elements discretization is complete (written by Dang Van Nguyen and Jing-Rebecca Li).

- Contact: Jing Rebecca Li
- URL: http://www.cmap.polytechnique.fr/~jingrebeccali/

5.2. InvGIBC

A FreeFem++ routines for solving inverse Maxwell's problem for 3D shape identification using a gradient descent method.

- Contact: Houssem Haddar
- URL: http://www.cmap.polytechnique.fr/~haddar/

5.3. RODIN

FUNCTIONAL DESCRIPTION

In the framework of the RODIN project we continue to develop with our software partner ESI the codes Topolev and Geolev for topology and geometry shape optimization of mechanical structures using the level set method.

- Contact: Grégoire Allaire
- URL: http://www.cmap.polytechnique.fr/~allaire/

5.4. samplings-2d

This software solves forward and inverse problems for the Helmholtz equation in 2-D.

FUNCTIONAL DESCRIPTION

This software is written in Fortran 90 and is related to forward and inverse problems for the Helmholtz equation in 2-D. It includes three independent components. The first one solves to scattering problem using integral equation approach and supports piecewise-constant dielectrics and obstacles with impedance boundary conditions. The second one contains various samplings methods to solve the inverse scattering problem (LSM, RGLSM(s), Factorization, MuSiC) for near-field or far-field setting. The third component is a set of post processing functionalities to visualize the results

- Contact: Houssem Haddar
- URL: http://sourceforge.net/projects/samplings-2d/

5.5. Samplings-3d

FUNCTIONAL DESCRIPTION

This software is written in Fortran 90 and is related to forward and inverse problems for the Helmholtz equation in 3-D. It contains equivalent functionalities to samplings-2d in a 3-D setting.

- Contact: Houssem Haddar
- URL: http://www.cmap.polytechnique.fr/~haddar/

DEFROST Team

6. New Software and Platforms

6.1. SOFA

Simulation Open Framework Architecture
KEYWORDS: Physical simulation - Health - Biomechanics - GPU - Computer-assisted surgery
FUNCTIONAL DESCRIPTION

SOFA is an Open Source framework primarily targeted at real-time simulation, with an emphasis on medical simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows : the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods.

- Participants: Stéphane Cotin and Hervé Delingette
- Partner: IGG
- Contact: Stéphane Cotin
- URL: http://www.sofa-framework.org

6.2. Soft robot plugin for sofa

Our contribution consists in a new framework to simulate and control soft robots. This framework is based on a mechanical modeling of the robot elements combined with fast real-time direct/inverse FEM solvers. The keypoint of our approach is that the same modeling is used for interactive simulation of its behavior and interactive control of the fabricated robots. This plugin is being developped in the ADT project SORBET.

KEYWORDS: Simulation - Soft-Robot - Inverse models - Finite Element Method - Quadratic Programmings

- Participants: Eulalie Coevoet, Olivier Goury, Frédéric Largillière, Bruno Carrez, Damien Marchal, Jérémie Dequidt and Christian Duriez
- Contact: Eulalie Coevoet and Christian Duriez
- URL: https://project.inria.fr/softrobot/

6.3. Neurosurgery simulation

Vascular neurosurgery simulation based on SOFA Framework
KEYWORDS: Simulation - Health - Computer-assisted surgery

- Participants: Christian Duriez, Eulalie Coevoet, Laurent Thines and Jérémie Dequidt
- Partners: Université de Lille - CHRU Lille
- Contact: Christian Duriez

DEMAR Project-Team

4. New Software and Platforms

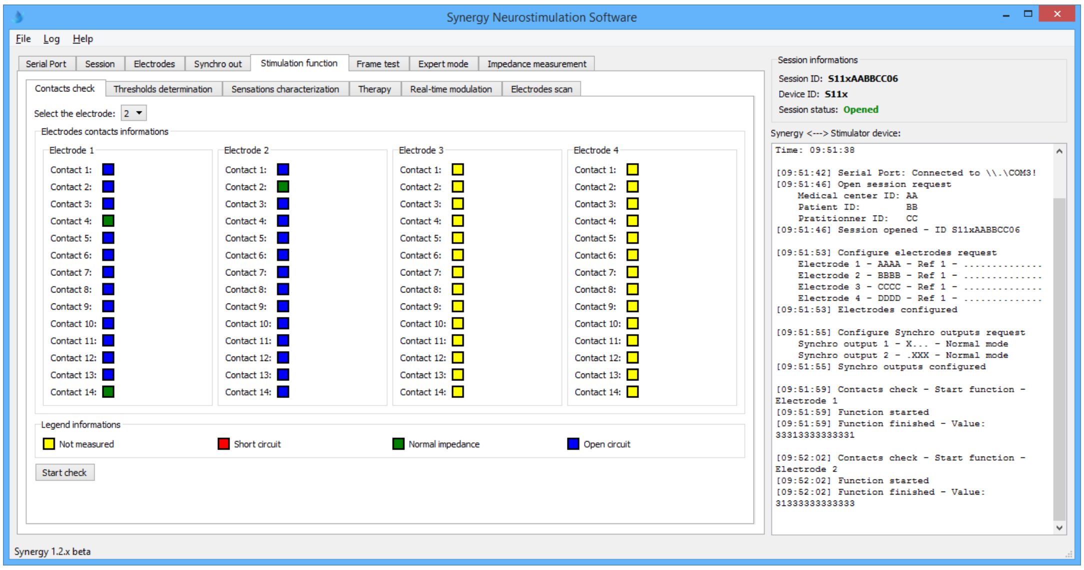
4.1. Synergy Neurostimulation Software

Participants: Arthur Hiairrassary, David Andreu, David Guiraud.

We have developed a specific software environment called Synergy Neurostimulation Software (fig.1), allowing to remotely manage a stimulation architecture based on one controller piloting a set of distributed stimulation units, connected by means of a dedicated network. The controller embeds the set of FES functions according to which it controls stimulation units, in real-time.

This FES distributed architecture is based on our last version of stimulation units that embed stimulation sequencing and a more efficient modulation mechanism.

Synergy Neurostimulation Software has been registered at the french Agence de Protection des Programmes (APP).



Select the electrode: 2

Electrodes contacts informations

	Electrode 1	Electrode 2	Electrode 3	Electrode 4
Contact 1:	🟦	🟦	🟨	🟨
Contact 2:	🟦	🟩	🟨	🟨
Contact 3:	🟦	🟦	🟨	🟨
Contact 4:	🟩	🟦	🟨	🟨
Contact 5:	🟦	🟦	🟨	🟨
Contact 6:	🟦	🟦	🟨	🟨
Contact 7:	🟦	🟦	🟨	🟨
Contact 8:	🟦	🟦	🟨	🟨
Contact 9:	🟦	🟦	🟨	🟨
Contact 10:	🟦	🟦	🟨	🟨
Contact 11:	🟦	🟦	🟨	🟨
Contact 12:	🟦	🟦	🟨	🟨
Contact 13:	🟦	🟦	🟨	🟨
Contact 14:	🟩	🟦	🟨	🟨

Legend informations

🟨 Not measured 🟥 Short circuit 🟩 Normal impedance 🟦 Open circuit

Session informations

Session ID: **S11xAABBCC06**
Device ID: **S11x**
Session status: **Opened**

Synergy <---> Stimulator device:

```
Time: 09:51:38

[09:51:42] Serial Port: Connected to \\.\COM3!
[09:51:46] Open session request
    Medical center ID: AA
    Patient ID:        BB
    Pratitionner ID:   CC
[09:51:46] Session opened - ID S11xAABBCC06

[09:51:53] Configure electrodes request
    Electrode 1 - AAAA - Ref 1 - ..............
    Electrode 2 - BBBB - Ref 1 - ..............
    Electrode 3 - CCCC - Ref 1 - ..............
    Electrode 4 - DDDD - Ref 1 - ..............
[09:51:53] Electrodes configured

[09:51:55] Configure Synchro outputs request
    Synchro output 1 - X... - Normal mode
    Synchro output 2 - .XXX - Normal mode
[09:51:55] Synchro outputs configured

[09:51:59] Contacts check - Start function -
Electrode 1
[09:51:59] Function started
[09:51:59] Function finished - Value:
33313333333331

[09:52:02] Contacts check - Start function -
Electrode 2
[09:52:02] Function started
[09:52:02] Function finished - Value:
31333333333333
```

Figure 1. Synergy Neuromodulation Software

4.2. HILECOP

High Level hardware Component Programming
FUNCTIONAL DESCRIPTION

Our SENIS (Stimulation Electrique Neurale dIStribuee) based FES architecture relies on distributed stimulation units (DSU) which are interconnected by means of a 2-wire based network. A DSU is a complex digital system since its embeds among others a dedicated processor (micro-machine with a specific reduced instruction set), a monitoring module and a 3-layer protocol stack. To face the complexity of the units digital part and to ease its prototyping on programmable digital devices (e.g. FPGA), we developed an approach for high level hardware component programming (HILECOP). To support the modularity and the reusability of sub-parts of complex hardware systems, the HILECOP methodology is based on components. An HILECOP component has: a Petri Net (PN) based behavior (fig.2), a set of functions whose execution is controlled by the PN, and a set of variables and signals. Its interface contains places and transitions from which its PN model can be inter-connected as well as signals it exports or imports. The interconnection of those components, from a behavioral point out view, consists in the interconnection of places and/or transitions according to well-defined mechanisms: interconnection by means of oriented arcs or by means of the "merging" operator (existing for both places and transitions).

The Eclipse-based version of HILECOP (registered at the french Agence de Protection des Programmes (APP)) has been refactored: for instance, the application ECore model, a new Eclipse E4 architecture and a set of new features (new link types and new views to connect components) have been developed.

Undergoing work concerns the integration, in the HILECOP tool, of the formalism evolutions that allow behavior agregation as well as exception handling, both for analysis and implementation sides.

Specification of GALS systems (Globally Asynchronous Locally Synchronous) is also an ongoing work, the aim being to take into account deployment properties like connecting different clocks to HILECOP components within a same FPGA, or on a set of interconnected FPGAs (and thus interconnecting them by means of asynchronous signals).

- Participants: Baptiste Colombani, David Andreu, Thierry Gil, Robin Passama
- Contact: David Andreu

4.3. MOS2SENS

Model Optimization and Simulation To Selective Electrical Neural Stimulation
KEYWORDS: Neurosciences - Health - Physiology
FUNCTIONAL DESCRIPTION

This model can predict nerve fiber activation through multipolar electrode stimulation. Furthermore the models provide an optimal current configuration to activate accurately the targeted muscle or organ (indeed a targeted group of fiber).

The new software MOS2SENS is an adjustment support tool for neuroprosthetics devices. It models and optimizes the current injected by multipolar CUFF electrodes inside the nerve in order to activate selective fiber targets in terms of spatial criterion.

- Participants: Melissa Dali, Olivier Rossel and David Guiraud
- Contact: David Guiraud

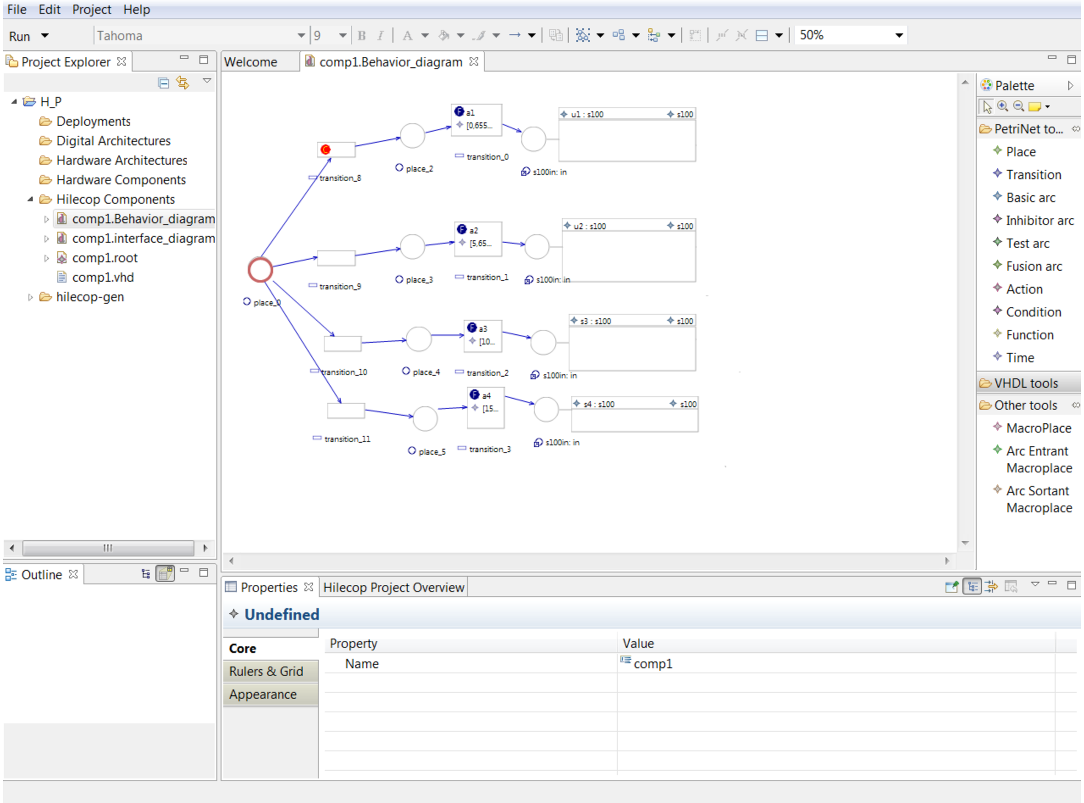
4.4. PALGate

KEYWORDS: Health - Home care - Handicap

- Contact: David Daney

4.5. PersoBalance

PersoBalance: A Personalized Balance Assessment in Home Rehabilitation
KEYWORDS: Health - Home care - Handicap



Property	Value
Name	comp1

Figure 2. HILECOP screenshot

4.5.1. PersoBalance: A Personalized Balance Assessment in Home Rehabilitation

Participants: Mitsuhiro Hayashibe, Alejandro Gonzalez [Euromov], Philippe Fraisse.

The objective of this software is to realize a personalized evaluation of the postural balance to be used in home-based rehabilitation, by using portable sensors such as Kinect and wii board. After the one time of identification, the system provide us the personalized estimation of the center of mass (CoM) for the whole body only with Kinect information, through Statically Equivalent Serial Chain method.

The first function is the adaptive identification interface for the CoM parameters based on Kalman filter which allows a subject to provide different postures interactively with minimized time length. The second function is the balance measure visualization (stable or instable) based on the identified model for each subject considering subject-specific body differences on the segment mass distribution.

Recently, this software was demonstrated at the event of Rencontre Inria-Industrie 13/10/2015 at Bordeaux. https://www.inria.fr/centre/bordeaux/innovation/rii-sante/demonstrations2 It is also filed at Software Catalogue of Inria. https://www.inria.fr/centre/bordeaux/innovation/rii-sante/catalogue-logiciels

PersoBalance is registered with the Agency for the Protection of Programs (APP) and deposited at the BNF (Bibliotheque Nationale de France). Its registration number is Antepedia Deposit 20150710154654.

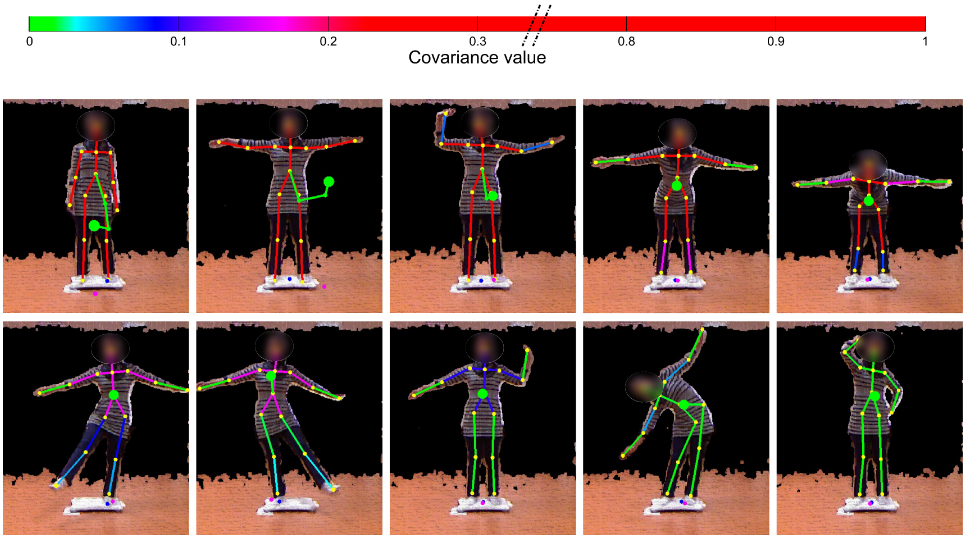


Figure 3. PersoBalance: A Personalized Balance Assessment in Home Rehabilitation: This scene shows the process how the CoM is being identified through different postures information with portable sensors.

4.6. SENISManager

Stimulation Electrique Neurale dIStribuee

FUNCTIONAL DESCRIPTION

SENISManager is a specific software environment allowing to remotely manage and control a network of DSUs, i.e. the distributed FES architecture. SENISManager performs self-detection of the architecture being deployed. This environment allows the manipulation of micro-programs from their edition to their remote control. It also allows the programming of control sequences executed by an external controller in charge of automatically piloting a stimulator.

- Participants: David Andreu and Robin Passama
- Contact: David Andreu

4.7. sensbiotk

KEYWORDS: Motion analysis - Sensors

SCIENTIFIC DESCRIPTION Sensbiotk is a toolbox in Python for the calibration, the acquisition, the analysis and visualization of motion capture Inertial Measurement Units (IMU). Motion and Gait parameter reconstruction algorithms are also available.

FUNCTIONAL DESCRIPTION

sensbiotk toolbox for Python. for the calibration, acquisition, analysis and visualization of motion capture using IMU

- Participants: Christine Azevedo Coste, Roger Pissard-Gibollet and Benoît Sijobert
- Contact: Roger Pissard Gibollet
- URL: http://sensbio.github.io/sensbiotk/

DIANA Project-Team

5. New Software and Platforms

5.1. ACQUA

Participants: Chadi Barakat [contact], Thierry Spetebroot, Nicolas Aguilera Miranda, Damien Saucez.

ACQUA is an Application for prediCting Quality of User experience at Internet Access. It was supported by the French ANR CMON project on collaborative monitoring and will be supported in 2016 by both the Inria ADT ACQUA and the ANR Project BottleNet. ACQUA presents a new way for the evaluation of the performance of Internet access. Starting from network-level measurements as the ones we often do today (bandwidth, delay, loss rates, etc), ACQUA targets the estimated quality of experience related to the different applications of interest to the user without the need to run them (e.g. estimated Skype quality, estimated video streaming quality). An application in ACQUA is a function that links the network-level measurements to the expected quality of experience. In its first version (the version available online), ACQUA was concentrating on delay measurements at the access and on the detection and estimation of the impact of delay anomalies (local problems, remote problems, etc). The current work is concentrating on using the ACQUA principle in the estimation and prediction of the quality of experience of main user's applications (see section 6.1.1 for more details). An Android version is under development supported by the Inria ADT ACQUA.

- URL: http://team.inria.fr/diana/acqua/
- Version: 1.1
- ACM: C.2.2, C.2.3
- Keywords: Internet measurement, Internet Access, Quality of Experience
- License: GPL (3)
- Type of human computer interaction: GUI for client, Web interface for experimentation
- OS/Middleware: MS Windows
- Required library or software: visual studio http://www.visualstudio.com/en-us/products/visual-studio-express-vs.aspx
- Programming language: C# for client, java for server, CGI and Dummynet for experimentation

5.2. ElectroSmart

Participants: Arnaud Legout [contact], Inderjeet Singh, Maksym Gabielkov.

The Internet and new devices such as smartphones have fundamentally changed the way people communicate, but this technological revolution comes at the price of a higher exposition of the general population to microwave electromagnetic fields (EMF). This exposition is a concern for health agencies and epidemiologists who want to understand the impact of such an exposition on health, for the general public who wants a higher transparency on its exposition and the health hazard it might represent, but also for cellular operators and regulation authorities who want to improve the cellular coverage while limiting the exposition, and for computer scientists who want to better understand the network connectivity in order to optimize communication protocols. Despite the fundamental importance to understand the exposition of the general public to EMF, it is poorly understood because of the formidable difficulty to measure, model, and analyze this exposition.

The goal of the ElectroSmart project is to develop the instrument, methods, and models to compute the exposition of the general public to microwave electromagnetic fields used by wireless protocols and infrastructures such as Wi-Fi, Bluetooth, or cellular. Using a pluri-disciplinary approach combining crowd-based measurements, in-lab experiments, and modeling using sparse and noisy data, we address challenges such as designing and implementing a measuring instrument leveraging on crowd-based measurements from mobile devices such as smartphones, modeling the exposition of the general public to EMF to compute the most accurate estimation of the exposition, and analyzing the evolution of the exposition to EMF with time. This technological breakthrough will have scientific, technical, and societal applications, notably on public health politics, by providing the scientific community and potential users with a unique measuring instrument, methods, and models to exploit the invaluable data gathered by the instrument.

This project has been supported by the Inria ADT ElectroSmart in 2014 and 2015 and will be supported by a Labex funding in the next two years.

In 2015, we released the first alpha version of the application for tests with real users (10 volunteers) and we published an associated Web site http://es.inria.fr.

- URL: http://es.inria.fr
- Version: 1.0alpha
- Keywords: background electromagnetic radiations
- License: Inria proprietary licence
- Type of human computer interaction: Android application
- OS/Middleware: Android
- Required library or software: Android
- Programming language: Java
- Documentation: javadoc

5.3. NEPI

Participants: Thierry Turletti [correspondant], Alina Ludmila Quereilhac, Thierry Parmentelat, Mario Antonio Zancanaro.

NEPI, the Network Experimentation Programming Interface, is a framework to describe and orchestrate network experiments on a variety of network experimentation platforms, including simulators, emulators, live testbeds, and testbed federations. NEPI is capable of supporting arbitrary platforms through the use of a generic network experiment description model, based on abstracting network experiments as a collection of arbitrary resource objects, and through the generalization of the experiment life cycle for all resources. The common resource life cycle consists of the sequence of operations deploy, start, stop, and release. Different resource objects can implement specific versions of those operations to adapt to any platform. NEPI resolves experiment orchestration as an online scheduling problem.

In the context of Alina Quereilhac PhD, we generalized in 2015 the network experiments automation framework for arbitrary evaluation platforms, and for scenarios targeting any networking research domain. The proposed approach is based on abstracting the experiment life cycle for different platforms into generic steps that are valid for simulators, emulators, and testbeds. Based on these steps, a generic experimentation architecture was proposed and implemented, composed of an experiment model, an experimentation interface, and an orchestration algorithm. Three main aspects of the framework were evaluated: its extensibility to support heterogeneous platforms, its efficiency to orchestrate experiments, and its flexibility to support diverse use cases for different networking research domains, including education, platform management, and experimentation with testbed federations, and cross-platform and multi-platform scenarios. The results show that the proposed approach can be used to efficiently automate experimentation on heterogeneous evaluation platforms, for a wide range of scenarios.

On a much more practical level, NEPI is now available in a version numbered 6, that can run within both python2 and python3 environments.

- URL: http://nepi.inria.fr
- Version: 6.0
- ACM: C.2.2, C.2.4
- Keywords: networking experimentation, simulation, emulation
- License: GPL (3)
- Type of human computer interaction: python library
- OS/Middleware: Linux
- Required library or software: matplotlib - graphviz (both optional)
- Programming language: python2 or python3

5.4. ns-3

Participants: Walid Dabbous [contact], Thierry Turletti.

ns-3 is a discrete-event network simulator for Internet systems, targeted primarily for research and educational use. ns-3 includes a solid event-driven simulation core as well as an object framework focused on simulation configuration and event tracing, a set of realistic 802.11 MAC and PHY models, an IPv4, UDP, and TCP stack and support for nsc (integration of Linux and BSD TCP/IP network stacks). ns-3 is free software, licensed under the GNU GPLv2 license, and it is publicly available for research, development, and use. Our team has been involved in ns-3 project since 2006 and we are founding member of the ns-3 consortium including Washington University, Georgia Tech, CTTC, INESC PORTO as executive members. In 2015, using the NEPI framework, we worked on the automation of ns-3 experiments in multi-host scenarios with three example cases: a) running parallel simulations on a cluster of hosts, b) running distributed simulations spanning multiple hosts, and c) integrating live and simulated networks.

- URL: http://www.nsnam.org
- Version: ns-3.21
- Keywords: networking event-driven simulation
- License: GPL (GPLv2)
- Type of human computer interaction: programmation C++/python, No GUI
- OS/Middleware: Linux, cygwin, osX
- Required library or software: standard C++ library: GPLv2
- Programming language: C++, python
- Documentation: doxygen

5.5. DCE

Participants: Thierry Turletti [contact], Walid Dabbous.

DCE enables developers and researchers to develop their protocols and applications in a fully controllable and deterministic environment, where tests can be repeated with reproducible results. It allows unmodified protocol implementations and application code to be tested over large and possibly complex network topologies through the ns-3 discrete-event network simulator. The single-process model used in the DCE virtualization core brings key features, such as the possibility to easily debug a distributed system over multiple simulated nodes without the need of a distributed and complex debugger. Examples of tested applications over DCE include Quagga, iperf, torrent, thttpd, CCNx and various Linux kernel versions (from 2.6.36 to 3.12 versions). DCE was initially developed by Mathieu Lacage during his PhD thesis and is maintained by engineers in the team in collaboration with Hajime Tazaki from University of Tokyo. Our effort on DCE was reduced in 2015 due to lack of resources, but DCE/ns-3 represents an important component of R2lab in particular for performance comparison and hybrid (real/simulation/emulation) experiments. DCE is free software, licensed under the GNU GPLv2 license, and is publicly available for research, development, and use.

- URL: https://www.nsnam.org/overview/projects/direct-code-execution/
- Version: DCE-1.7
- Keywords: emulation, virtualization, networking event-driven simulation
- License: GPL (GPLv2)
- Type of human computer interaction: programmation C/C++, No GUI
- OS/Middleware: Linux
- Required library or software: standard C++ library: GPLv2
- Programming language: C++, python
- Documentation: doxygen

5.6. OpenLISP

Participant: Damien Saucez [contact].

Among many options tackling the scalability issues of the current Internet routing architecture, the Locator/Identifier Separation Protocol (LISP) appears as a viable solution. LISP improves a network's scalability, flexibility, and traffic engineering, enabling mobility with limited overhead. As for any new technology, implementation and deployment are essential to gather and master the real benefits that it provides. We propose a complete open source implementation of the LISP control plane. Our implementation is deployed in the worldwide LISP Beta Network and the French LISP-Lab testbed, and includes the key standardized control plane features. Our control plane software is the companion of the existing OpenLISP dataplane implementation, allowing the deployment of a fully functional open source LISP network compatible with any implementation respecting the standards. As of 2015, OpenLISP is still used to provide connectivity between satellite sites of the LISP-Lab project and has been used as LISP implementation for PACAO, an overlay aiming at optimising Cloud access in distributed data-centers.

- http://www.lisp-lab.org/
- Version: 3.2
- ACM: C.2.1, C.2.2, C.2.6
- Keywords: routing, LISP, control-plane
- License: BSD
- Type of human computer interaction: XML, CLI
- OS/Middleware: POSIX
- Required library or software: Expat 2
- Programming language: C
- Documentation: Unix man
- Deployment: ddt-root.org

5.7. Platforms

5.7.1. Reproducible research laboratory ($\mathrm{R}^2\mathrm{LAB}$)

Scientific evaluation of network protocols requires that experiment results must be reproducible before they can be considered as valid. This is particularly difficult to obtain in the wireless networking domain, where characteristics of wireless channels are known to be variable, unpredictable and hardly controllable. We have built at Inria Sophia-Antipolis, in 2014, an anechoic chamber, with RF absorbers preventing radio waves reflections and with Faraday cage blocking external interferences. This lab, named $\mathrm{R}^2\mathrm{lab}$, represents an ideal environment for experiments reproducibility. $\mathrm{R}^2\mathrm{lab}$ has been announced for usage by the general public at the end of 2015. It was developed, and is now operated, in the context of the FIT ’Equipment of Excellence’ project, and as such, it is now federated with the other testbeds that are part of the FIT initiative. This testbed is for the long-haul, and is scheduled to remain operational until at least 2020. Future work, in addition to regular operations, includes adding new hardware capabilities to the wireless nodes, such as USRP for running Software Defined Radio, as well as possibly OpenAirInterface for supporting 5G-like experiments.

For more details see http://r2lab.inria.fr.

DICE Team

5. New Software and Platforms

5.1. BitBallot

The BitBallot voting protocol is designed to avoid the concentration of data by third party. The protocol allows users to cast their ballot on their mobile device, and then share only restricted amounts of their data with other peers to compute the tally. Unlike other protocols, voters pull data from others instead of pushing their own votes.

Convinced by the need of new election mechanisms, to support emerging forms of more continuous democracy, we are developing BitBallot, to allow elections with distributed tallying that incorporate individual verification. As such, it provides anonymity of the data sources, non interruptible run-time, global access to results, and non-predictability of results through partial communication spying. Cryptography is not essential to protect the privacy of the voters or the secrecy of the ballots. On the basis of this protocol, a SaaS platform that allows to run public tests online is under development.

- Contact: Stéphane Grumbach, Stéphane Frénot, Damien Reimert, Robert Riemann

5.2. C3PO

Social networks put together individuals with common interests and/or existing real-life relationships so that they can produce and share information. There is a strong interest of individuals towards these networks. They rely in general on a stable, centralized network infrastructure, and a user will always be provided with the same services no matter what their current context is. By contrast, the C3PO project (C3PO stands for Collaborative Creation of Contents and Publishing using Opportunistic networks) aims at promoting "spontaneous and ephemeral social networks" (SESN), built on top of a peer-to-peer distributed architecture leveraging ad-hoc mobile networks and the resources and services offered by mobile devices. As with traditional social networks, SESN can put together nomad individuals based on their affinities and common interests so that they can collaboratively work on tasks as part of a SESN. (Supported by an ANR project.)

- Contact: Stéphane Frénot, Damien Reimert

5.3. Fluxion

This joint project with Worldline aims at managing mobile code in complex Web architectures. We design a fast and reactive framework, transparently moving functions between running systems to cope with the load variation in high performance Web architectures. The Fluxion model is our approach to design mobile application modules that are a mix of functional programming and flow based reactive systems. We work on compilation techniques to transform a Javascript event-loop into a parallelized pipeline where each stage is made independent from the main event-loop.

- Contact: Stéphane Frénot, Etienne Brodu

5.4. Jumplyn

Jumplyn is a student project delivery platform. It offers a service based on three features: the ongoing management of the project, resources recommendation, and enhancement of the activity. Like any intermediation platform, it speaks directly to its users, students, and puts them in relation to relevant information.

- Contact: Stéphane Frénot, Stéphane Grumbach, Auguste Caen
- URL: http://www.jumplyn.com

DIONYSOS Project-Team

5. New Software and Platforms

5.1. IPv6 Test Toolkit

FUNCTIONAL DESCRIPTION

These test suites are developed using the TTCN-3 environment.

The packages contains the full Abstract Test Suites written in TTCN-3 and the source files for building the codecs and adapters with the help of T3DevKit.

- Participants: Cesar Pascal Viho
- Contact: Cesar Pascal Viho
- URL: http://www.irisa.fr/tipi

5.2. Passive Test Tool

- Participants: Cesar Pascal Viho
- Contact: Cesar Pascal Viho
- URL: http://www.irisa.fr/tipi

5.3. T3DevKit

SCIENTIFIC DESCRIPTION

We have built a toolkit for easing executing tests written in the standardized TTCN-3 test specification language. This toolkit is made of a C++ library together with a highly customizable CoDec generator that allows fast development of external components (that are required to execute a test suite) such as CoDec (for message Coding/Decoding), System and Platform Adapters. It also provides a framework for representing and manipulating TTCN-3 events so as to ease the production of test reports. The toolkit addresses issues that are not yet covered by ETSI standards while being fully compatible with the existing standard interfaces: TRI (Test Runtime Interfaces) and TCI (Test Control Interfaces), it has been tested with four TTCN-3 environments (IBM, Elvior, Danet and Go4IT) and on three different platforms (Linux, Windows and Cygwin).

FUNCTIONAL DESCRIPTION

T3DevKit is a free open source toolkit to ease the development of test suites in the TTCN-3 environment. It provides:

- a CoDec generator (t3cdgen) that automates the development process of the CoDec needed for coding TTCN-3 values into physically transmittable messages and decoding incoming messages
- a library (t3devlib) that provides an object oriented framework to manipulate TTCN-3 entities (values, ports, timers, external functions...)
- an implementation of the TRI and TCI standard interfaces
- default implementations for the system adapter (SA), platform adapter (PA), test management (TM), test logging (TL) and component handling (CH) modules
- default codecs
- built-in scripts for the generation of executable test suites, which are tool-independent and facilitate the distribution of test suite sources
- Participants: Cesar Pascal Viho
- Contact: Cesar Pascal Viho

5.4. Interoperability Assessment

Participant: César Viho.

Our experience in interoperability assessment (since 1996) and in using the TTCN-3 standard allowed us to develop a tool (called `ttproto`) that helps in: (i) experimenting new concepts for long term evolution of the TTCN-3 standard and (ii) facilitating new approaches and methods for interoperability assessment. For instance, new passive approaches that we developed have been implemented and validated using `ttproto`. This tool `ttproto` has been used to develop test suites for 6LoWPAN-ND (IPv6 for Low Power Networks) and CoAP (Constrained Application Protocol). The CoAP test suites have been successfully used for two Plugtest interoperability events organized by ETSI, IPSO Alliance and the FP7 PROBE-IT project. The tool `ttproto` and the test suites indicated above are freely available at http://www.irisa.fr/tipi.

5.5. Performance and dependability evaluation

Participants: Gerardo Rubino, Bruno Sericola, Bruno Tuffin.

We develop software tools for the evaluation of two classes of models: Markov models and reliability networks. The main objective is to quantify dependability aspects of the behaviors of the modeled systems, but other aspects of the systems can be handled (performance, performability, vulnerability). The tools are specialized libraries implementing numerical, Monte Carlo and Quasi-Monte Carlo algorithms.

One of these libraries has been developed for the Celar (DGA), and its goal is the evaluation of dependability and vulnerability metrics of wide area communication networks (WANs). The algorithms in this library can also evaluate the sensitivities of the implemented dependability measures with respect to the parameters characterizing the behavior of the components of the networks (nodes, lines).

We are also developing tools with the objective of building Markovian models and to compute bounds of asymptotic metrics such as the asymptotic availability of standard metrics of models in equilibrium, loss probabilities, blocking probabilities, mean backlogs, etc. A set of functions designed for dependability analysis is being built under the name `DependLib`.

We contribute to the development of SPNP (*Stochastic Petri Net Package*). SPNP is used by more than 200 companies and universities. The main designer is Duke University. Our contributions are on Monte Carlo methods. We plan to increase our participation in the development of this tool.

Pierre L'Ecuyer is also developing in Montreal a library, *Stochastic Simulation in Java* (SSJ), providing facilities for generating uniform and nonuniform random variates, computing different measures related to probability distributions, performing goodness-of-fit tests, applying quasi-Monte Carlo methods, collecting (elementary) statistics, and programming discrete-event simulations with both events and processes.

DISCO Project-Team

6. New Software and Platforms

6.1. OreAlgebraicAnalysis

FUNCTIONAL DESCRIPTION

OreAlgebraicAnalysis is a Mathematica implementation of algorithms available in the OreModules and the OreMorphisms packages (developed in Maple). OreAlgebraicAnalysis is based on the implementation of Grobner bases over Ore algebras available in the Mathematica HolonomicFunctions package developed by Christoph Koutschan (RICAM). OreAlgebraicAnalysis can handle larger classes of Ore algebras than the ones accessible in Maple, and thus we can study larger classes of linear functional systems. Finally, Mathematica internal design allows us to consider classes of systems which could not easily be considered in Maple such as generic linearizations of nonlinear functional systems defined by explicit nonlinear equations and systems containing transcendental functions (e.g., trigonometric functions, special functions). This package has been developed within the PHC Parrot project CASCAC.

- Participants: Alban Quadrat and Thomas Cluzeau
- Contact: Alban Quadrat
- URL: http://pages.saclay.inria.fr/alban.quadrat/OreAlgebraicAnalysis/index.html

6.2. OreModules

FUNCTIONAL DESCRIPTION

The OreModules package, based on the commercial Maple package Ore-algebra, is dedicated to the study of linear multidimensional systems defined over certain Ore algebras of functional operators (e.g., ordinary or partial differential systems, time-delay systems, discrete systems) and their applications in mathematical systems theory, control theory and mathematical physics.

- Participants: Frédéric Chyzak and Alban Quadrat
- Contact: Alban Quadrat
- URL: http://wwwb.math.rwth-aachen.de/OreModules/

6.3. OreMorphisms

FUNCTIONAL DESCRIPTION

The OreMorphisms package of OreModules is dedicated to the implementation of homological algebraic tools such as the computations of homomorphisms between two finitely presented modules over certain noncommutative polynomial algebras (Ore algebras), of kernel, coimage, image and cokernel of homomorphisms, Galois transformations of linear multidimensional systems and idempotents of endomorphism rings. Using the packages Stafford and Quillen-Suslin , the factorization, reduction and decomposition problems can be constructively studied for different classes of linear multidimensional systems. Many linear systems studied in engineering sciences, mathematical physics and control theory have been factorized, reduced and decomposed by means of the OreMorphisms package.

- Participants: Alban Quadrat and Thomas Cluzeau
- Contact: Alban Quadrat
- URL: http://pages.saclay.inria.fr/alban.quadrat/OreMorphisms/index.html

6.4. PurityFiltration

FUNCTIONAL DESCRIPTION

The PurityFiltration package, built upon the OreModules package, is an implementation of a new effective algorithm which computes the purity/grade filtration of linear functional systems (e.g., partial differential systems, differential time-delay systems, difference systems) and equivalent block-triangular matrices. This package is used to compute closed form solutions of over/underdetermined linear partial differential systems which cannot be integrated by the standard computer algebra systems such as Maple and Mathematica.

- Contact: Alban Quadrat
- URL: http://pages.saclay.inria.fr/alban.quadrat/OreAlgebraicAnalysis/index.html

6.5. QuillenSuslin

FUNCTIONAL DESCRIPTION

QuillenSuslin is a Maple implementation of a constructive version of the Quillen-Suslin Theorem. It provides an algorithm which computes a basis of a free module over a polynomial ring. In terms of matrices, this algorithm completes a unimodular rectangular matrix (e.g. a unimodular row) to an invertible matrix over the given polynomial ring with rational or integer coefficients. The package was also extended with Park's Algorithm to deal with unimodular rows over Laurent polynomial rings and with heuristic methods for localizations of polynomial rings.

- Participants: Alban Quadrat and Anna Fabiańska
- Contact: Alban Quadrat
- URL: http://wwwb.math.rwth-aachen.de/QuillenSuslin/

6.6. Stafford

FUNCTIONAL DESCRIPTION

The Stafford package of OreModules contains an implementation of two constructive versions of Stafford's famous but difficult theorem [96] stating that every ideal over the Weyl algebra An(k) (resp., Bn(k)) of partial differential operators with polynomial (resp., rational) coefficients over a field k of characteristic 0 (e.g., k=Q,R) can be generated by two generators. Based on this implementation and algorithmic results developed by the authors of the package, two algorithms which compute bases of free modules over the Weyl algebras An(Q) and Bn(Q) have been implemented. The rest of Stafford's results developed in [96] have recently been made constructive (e.g., computation of unimodular elements, decomposition of modules, Serre's splitting-off theorem, Stafford's reduction, Bass' cancellation theorem, minimal number of generators) and implemented in the Stafford package. The development of the Stafford package was motivated by applications to linear systems of partial differential equations with polynomial or rational coefficients (e.g., computation of injective parametrization, Monge problem, differential flatness, the reduction and decomposition problems and Serre's reduction problem). To our knowledge, the Stafford package is the only implementation of Stafford's theorems nowadays available.

- Participants: Alban Quadrat and Daniel Robertz
- Contact: Alban Quadrat
- URL: http://wwwb.math.rwth-aachen.de/OreModules/index_sub.html

6.7. YALTA

FUNCTIONAL DESCRIPTION

The YALTA toolbox is a Matlab toolbox dedicated to the study of classical and fractional systems with delay in the frequency-domain. Its objective is to provide basic but important information such as, for instance, the position of the neutral chains of poles and unstable poles, as well as the root locus with respect to the delay of the system. The corresponding algorithms are based on recent theoretical results and on classical continuation methods exploiting the particularities of the problem.

- Participants: Hugo Cavalera, Catherine Bonnet, Andre Fioravanti, Le Ha Vy Nguyen, Jim Pioche
- Contact: Catherine Bonnet
- URL: http://yalta-toolbox.gforge.inria.fr/

The YALTA toolbox is a Matlab toolbox dedicated to the study of classical and fractional systems with delay in the frequency-domain. Its objective is to provide basic but important information such as, for instance, the position of the neutral chains of poles and unstable poles, as well as the root locus with respect to the delay of the system. The corresponding algorithms are based on recent theoretical results (see, for instance, [78] and [85]) and on classical continuation methods exploiting the particularities of the problem [86], [87].

For classical delay systems, a Pade2 approximation scheme is available as well as a finite-dimensional approximation of the system.

Binaries are freely available at http://yalta-toolbox.gforge.inria.fr/.

The YALTA GUI (graphical user interface) is a graphical application developed in Python that interacts with the Matlab toolbox YALTA. User actions are performed through intuitive graphic elements (dialog boxes, icons, menus, scroll bars) in order to capitalize on the functionalities of YALTA. This software, still in development, is based on PyQt, a Python binding of the cross-platform GUI toolkit Qt (C++).

Recently, some features have been added. YALTA toolbox and YALTA GUI have been designed to support multi-languages settings (English and French languages currently available). Parallely, the implementation of the Pade2 approximation scheme has been improved. Finally, continuous integration processes and tools such as Jenkins Hudson have been configured and managed to ensure long-term software quality.

DIVERSE Project-Team

6. New Software and Platforms

6.1. FAMILIAR

FeAture Model scrIpt Language for manIpulation and Automatic Reasoning

KEYWORDS: Software line product - Configators - Customisation

SCIENTIFIC DESCRIPTION

FAMILIAR (for FeAture Model scrIpt Language for manIpulation and Automatic Reasoning) is a language for importing, exporting, composing, decomposing, editing, configuring, computing "diffs", refactoring, reverse engineering, testing, and reasoning about (multiple) feature models. All these operations can be combined to realize complex variability management tasks. A comprehensive environment is proposed as well as integration facilities with the Java ecosystem.

- Participants: Mathieu Acher, Guillaume Bécan, Sana Ben Nasr, Jose Galindo, Olivier Barais
- Contact: Mathieu Acher
- URL: http://familiar-project.github.com

6.2. OpenCompare

OpenCompare.org

KEYWORDS: product comparison matrix - tabular data - comparison

SCIENTIFIC DESCRIPTION

Product comparison matrices (PCMs) are tabular data: supported and unsupported features are documented for both describing the product itself and for discriminating one product compared to another. PCMs abound and constitute a rich source of knowledge for easily comparing and choosing product. Yet the current practice is suboptimal both for humans and computers, mainly due to unclear semantics, heterogeneous forms of data, and lack of dedicated support.

OpenCompare.org is a project for the collaborative edition, the sharing, the standardisation, and the open exploitation of PCMs. The goal of OpenCompare.org is to provide an integrated set of tools (e.g., APIs, visualizations, configurators, editors) for democratizing their creation, import, maintenance, and exploitation.

MatrixMiner is also part of opencompare. It is a tool for automatically synthesizing PCMs from a set of product descriptions written in natural language. MatrixMiner is capable of identifying and organizing features and values in a PCM despite the informality and absence of structure in the textual descriptions of products. More information here: https://matrix-miner.variability.io/

- Participants: Guillaume Bécan, Mathieu Acher, Sana Ben Nasr
- Contact: Mathieu Acher
- URL: http://opencompare.org

6.3. Kermeta

KEYWORDS: Eclipse - Model-driven engineering

SCIENTIFIC DESCRIPTION

Kermeta is used in several cases:

to give a precise semantic of the behavior of a metamodel, which then can be simulated,

to act as a model transformation language,

to act as a constraint language.

FUNCTIONAL DESCRIPTION

The Kermeta workbench is a powerful meta-programming environment based on an object-oriented DSL (Domain Specific Language) optimized for metamodel engineering. Kermeta is now integrated into Melange (see next tool), and will continue to be supported and developed under this new project with a broader scope.

- Participants: Zoé Drey, Cyril Faucher, Franck Fleurey, Jean Marc Jezequel, Pierre Alain Muller, Jim Steel, François Tanguy, Didier Vojtisek, Benoît Combemale, Olivier Barais, Arnaud Blouin, Benoit Baudry, Thomas Degueule, David Mendez Acuna, Erwan Bousse and Fabien Coulon
- Partners: Université de Rennes 1 - UHA
- Contact: Benoît Combemale
- URL: http://www.kermeta.org

6.4. Melange

KEYWORDS: Language workbench, Domain-Specific (Modeling) Language, Model-Driven Engineering, Model execution and debugging, Execution trace management

SCIENTIFIC DESCRIPTION

Melange is a follow-up of the executable metamodeling language Kermeta, which provides a tool-supported dedicated meta-language to safely assemble language modules, customize them and produce new DSMLs. Melange provides specific constructs to assemble together various abstract syntax and operational semantics artifacts into a DSML. DSMLs can then be used as first class entities to be reused, extended, restricted or adapted into other DSMLs. Melange relies on a particular model type system that statically ensures the structural correctness of the produced DSMLs, and specific subtyping relationships between DSMLs to reason about their substitutability. Newly produced DSMLs are correct by construction, ready for production (i.e., the result can be deployed and used as-is), and reusable in a new assembly.

Melange is a language workbench that support a modular and reusable approach for domain-specific language design and implementation.

FUNCTIONAL DESCRIPTION

Melange is a language workbench which helps language engineers to mashup their various language concerns as language design choices, to manage their variability, and support their reuse. It provides a modular and reusable approach for customizing, assembling and integrating DSMLs specifications and implementations. The language workbench embeds a model-oriented type system that provides model polymorphism and language substitutability, i.e. the possibility to manipulate a model through different interfaces and to define generic transformations that can be invoked on models written using different DSMLs. Melange also provides a dedicated meta-language where models are first-class citizens and languages are used to instantiate and manipulate them. By analogy with the class-based, object-oriented paradigm, Melange can be classified as a language-based, model-oriented programming language. Melange is tightly integrated with the Eclipse Modeling Framework ecosystem and relies on the meta-language Ecore for the definition of the abstract syntax of DSMLs. Executable meta-modeling is supported by weaving operational semantics defined with Kermeta (defined on top of Xtend). Melange is bundled as a set of Eclipse plug-ins.

- Participants: Thomas Degueule, Erwan Bousse, Fabien Coulon, Dorian Leroy, Didier Vojtisek, Olivier Barais, Arnaud Blouin, Benoit Combemale, Jean-Marc Jézéquel
- Partners: Université de Rennes 1
- Contact: Benoît Combemale
- URL: http://melange-lang.org

6.5. Kevoree

Kevoree Core C++

KEYWORDS: Embedded - Software Components - Software component - Dynamic adaptation

SCIENTIFIC DESCRIPTION

Kevoree is an open-source models@runtime platform (http://www.kevoree.org) to properly support the dynamic adaptation of distributed systems. Models@runtime basically pushes the idea of reflection [132] one step further by considering the reflection layer as a real model that can be uncoupled from the running architecture (e.g. for reasoning, validation, and simulation purposes) and later automatically resynchronized with its running instance.

Kevoree has been influenced by previous work that we carried out in the DiVA project [132] and the Entimid project [135] . With Kevoree we push our vision of models@runtime [131] farther. In particular, Kevoree provides a proper support for distributed models@runtime. To this aim we introduced the Node concept to model the infrastructure topology and the Group concept to model semantics of inter node communication during synchronization of the reflection model among nodes. Kevoree includes a Channel concept to allow for multiple communication semantics between remoteComponents deployed on heterogeneous nodes. All Kevoree concepts (Component, Channel, Node, Group) obey the object type design pattern to separate deployment artifacts from running artifacts. Kevoree supports multiple kinds of very different execution node technology (e.g. Java, Android, MiniCloud, FreeBSD, Arduino, ...).

Kevoree is distributed under the terms of the LGPL open source license.

Main competitors:

- the Fractal/Frascati eco-system (http://frascati.ow2.org).
- SpringSource Dynamic Module (http://spring.io/)
- GCM-Proactive (http://proactive.inria.fr/)
- OSGi (http://www.osgi.org)
- Chef
- Vagran (http://vagrantup.com/)

Main innovative features:

- distributed models@runtime platform (with a distributed reflection model and an extensible models@runtime dissemination set of strategies).
- Support for heterogeneous node type (from Cyber Physical System with few resources until cloud computing infrastructure).
- Fully automated provisioning model to correctly deploy software modules and their dependencies.
- Communication and concurrency access between software modules expressed at the model level (not in the module implementation).

Impact:

Several tutorials and courses have been performed this year at EJCP for French PhD student, at ECNU summer school for 82 chineese PhD students. See also the web page http://www.kevoree.org .

In 2015, we mainly created a new implementation in C# and we created an implementation for system containers for driving resources using Kevoree. We also use Kevoree in the context of Mohammed's PhD to create testing infrastructure on-demand.

Version: 5.3.1

Programming language: Java, Scala, Kermeta, Kotlin, Javascript, c#

FUNCTIONAL DESCRIPTION

Kevoree is an open-source models@runtime platform to properly support the dynamic adaptation of distributed systems. Models@runtime basically pushes the idea of reflection one step further by considering the reflection layer as a real model that can be uncoupled from the running architecture (e.g. for reasoning, validation, and simulation purposes) and later automatically resynchronized with its running instance.

- Participants: Olivier Barais, Johann Bourcier, Noël Plouzeau, Benoit Baudry, Maxime Tricoire, Jacky Bourgeois, Inti Gonzalez Herrera, Ivan Paez Anaya, Manuel Leduc, Francisco-Javier Acosta Padilla and Mohamed Boussaa
- Partner: Université de Rennes 1
- Contact: Olivier Barais
- URL: http://kevoree.org/

6.6. amiunique

KEYWORDS: Privacy - Browser fingerprinting

FUNCTIONAL DESCRIPTION

This web site aims at informing visitors about browser fingerprinting and possible tools to mitigate its effect, as well as at collecting data about the fingerprints that can be found on the web. It collects browser fingerprints with the explicit agreement of the users (they have to click on a button on the home page). Fingerprints are composed of 17 attributes, which include regular HTTP headers as well as the most recent state of the art techniques (canvas fingerprinting, WebGL information).

SCIENTIFIC DESCRIPTION

The amiunique web site has been deployed in the context of the DiverSE's research activities on browser fingerprinting and how software diversity can be leveraged in order to mitigate the impact of fingerprinting on the privacy of users. The construction of a dataset of genuine fingerprints is essential to understand in details how browser fingerprints can serve as unique identifiers and hence what should be modified in order to mitigate its impact privacy. This dataset also supports the large-scale investigation of the impact of web technology advances on fingerprinting. For example, we can analyze in details the impact of the HTML5 canvas element or the behavior of fingerprinting on mobile devices.

The whole source code of amiunique is open source and is distributed under the terms of the MIT license.

Similar sites:

- Panopticlick https://panopticlick.eff.org/
- BrowserSpy http://browserspy.dk/
- http://noc.to/

Main innovative features:

- canvas fingerprinting
- WebGL fingerprinting
- advanced JS features (platform, DNT, etc.)

Impact:

The website has been showcased in several professional forums in 2014 and 2015 (Open World Forum 2015, FOSSA'14, FIC'15, ICT'15) and it has been visited by more than 100000 unique visitors in one year.

Programming language: Java, JavaScript, Scala

- Participants: Pierre Laperdrix, Benoit Baudry
- Partner: INSA Rennes
- Contact: Benoit Baudry
- URL: https://amiunique.org/
- URL source code: https://github.com/DIVERSIFY-project/amiunique

DOLPHIN Project-Team

6. New Software and Platforms

6.1. COCO

COmparing Continuous Optimizers

KEYWORDS: Benchmarking - Numerical optimization - Black-box optimization - Stochastic optimization

6.1.1. SCIENTIFIC DESCRIPTION

COmparing Continuous Optimisers (COCO) is a tool for benchmarking algorithms for black-box optimisation. COCO facilitates systematic experimentation in the field of continuous optimization. COCO provides: (1) an experimental framework for testing the algorithms, (2) post-processing facilities for generating publication quality figures and tables, (3) LaTeX templates of articles which present the figures and tables in a single document. The COCO software is composed of two parts: (i) an interface available in different programming languages (C/C++, Java, Matlab/Octave, R, Python) which allows to run and log experiments on multiple test functions testbeds of functions (noisy and noiseless) are provided (ii) a Python tool for generating figures and tables that can be used in the LaTeX templates. In 2015, we extended the software towards multiobjective optimization and will provide a first release in early 2016.

6.1.2. FUNCTIONAL DESCRIPTION

The Coco Platform provides the functionality to automatically benchmark optimization algorithms for unbounded, unconstrained optimization problems in continuous domains. Benchmarking is a vital part of algorithm engineering and a necessary path to recommend algorithms for practical applications. The Coco platform releases algorithm developers and practitioners alike from (re-)writing test functions, logging, and plotting facilities by providing an easy-to-handle interface in several programming languages. The Coco platform has been developed since 2007 and has been used extensively within the “Blackbox Optimization Benchmarking (BBOB)” workshop series since 2009. Overall, 151 algorithms and algorithm variants by contributors from all over the world have been benchmarked with the platform so far and all data is publicly available for the research community. For 2016, a new suite of benchmark functions for bi-objective problems is expected to build the basis of the next BBOB workshop at GECCO 2016 for which a new software release is planned for January.

- Participants: Dimo Brockhoff, Arnaud Liefooghe, Thanh-Do Tran, Dejan Tušar, Tea Tušar (all Dolphin), Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara, Asma Atamna, Phillipe Sampaio, and Duc Manh Nguyen (all TAO team)
- Partners: TU Dortmund University, Germany and Czech Technical University, Czech Republic
- Contact: Dimo Brockhoff
- URL: http://coco.gforge.inria.fr/, https://github.com/numbbo/coco

6.2. MO-Mine

SCIENTIFIC DESCRIPTION

MO-Mineclust is the first package of the platform and is dedicated to clustering (unsupervised classification). Indeed, it is well-known that clustering may be seen as a bi-objective optimization problem as the goal is both to minimize distances between data belonging to a same cluster, while maximizing distances between data belonging to different clusters. Several models (objective functions used,...) and engines (optimization algorithms) have been implemented. The framework searches, for a given dataset, the best association of model/engine/parameter without specifiing the number of clusters. MO-Mineclust shows very interesting behavior and shows that the choice of the model and the engine has a great importance in the performance of the method and depends on the dataset to analyze.

FUNCTIONAL DESCRIPTION

MO-Mine is a process of tests and evaluations of multi-objective optimisation algorithms for data mining. MO-Mine platform will provide data sets (literature + synthetics benchmarks), data mining (Features selection, Clustering, Classification and Association rules) algorithms based on multi-objective metaheuristics (Evolutionary algorithm), validation methods and tools to compare algorithms. MO-Mine is based on evolutionary algorithms implemented in ParadisEO and adapted to solve problem of data mining. MO-Mine proposed to users to compare their own methods with different approaches following protocols clearly identified and shared.

- Participants: B. Fisset, L. Jourdan and C. Dhaenens
- Contact: Laetitia Jourdan
- URL: http://mo-mine.gforge.inria.fr/doku.php

6.3. ParadisEO

KEYWORD: Parallelisation
SCIENTIFIC DESCRIPTION

ParadisEO (PARallel and DIStributed Evolving Objects) is a C++ white-box object-oriented framework dedicated to the flexible design of metaheuristics. Based on EO, a template-based ANSI-C++ compliant evolutionary computation library, it is composed of four modules: * Paradiseo-EO provides tools for the development of population-based metaheuristic (Genetic algorithm, Genetic programming, Particle Swarm Optimization (PSO)...) * Paradiseo-MO provides tools for the development of single solution-based metaheuristics (Hill-Climbing, Tabu Search, Simulated annealing, Iterative Local Search (ILS), Incremental evaluation, partial neighborhood...) * Paradiseo-MOEO provides tools for the design of Multi-objective metaheuristics (MO fitness assignment shemes, MO diversity assignment shemes, Elitism, Performance metrics, Easy-to-use standard evolutionary algorithms...) * Paradiseo-PEO provides tools for the design of parallel and distributed metaheuristics (Parallel evaluation, Parallel evaluation function, Island model) Furthermore, ParadisEO also introduces tools for the design of distributed, hybrid and cooperative models: * High level hybrid metaheuristics: coevolutionary and relay model * Low level hybrid metaheuristics: coevolutionary and relay model

FUNCTIONAL DESCRIPTION

Paradiseo is a software framework for metaheuristics (optimisation algorithms aimed at solving difficult optimisation problems). It facilitates the use, development and comparison of classic, multi-objective, parallel or hybrid metaheuristics.

- Partners: CNRS - Université Lille 1
- Contact: El-Ghazali Talbi
- URL: http://paradiseo.gforge.inria.fr/

6.4. VRPsolve

KEYWORDS: C++ - Mobile Computing, Transportation - Optimization

- Participants: Clive Ferret-Canape, Arnaud Liefooghe and Sébastien Vérel
- Contact: Arnaud Liefooghe
- URL: http://gforge.inria.fr/projects/vrpsolve (limited access)

SCIENTIFIC DESCRIPTION

VRPsolve is a software for solving vehicle routing problems dealing with last-mile delivery issues that arise as we approach the final customer. When modeling and solving combinatorial optimization problems, especially problems related to the transport of goods and people, the resulting models are generally subject to a specific development in order to be validated, as industrial needs are highly dependent of the application domain. However, a set of conventional objectives and constraints, such as vehicles capacities, incompatible parcels, time windows, are now commonly encountered. In addition to being efficient and effective, VRPsolve differentiates from other tools by allowing to quickly and conveniently integrate ad-hoc constraints and objectives into a generic software. Indeed, VRPsolve effectively deal with industrial last-mile delivery vehicle routing problems and is able to cope with multiple objectives and a large number of constraints by using advanced optimization algorithms which are usually not available with existing softwares. In addition, VRPsolve allows industrial collaborations to be addressed by solving real-world problems requiring geographic information systems (GIS).

FUNCTIONAL DESCRIPTION

The current release includes the following functional and technical specifications:

- A modular architecture which allows for an easy integration into a global information system (with respect to data standards, weak coupling with external libraries, etc),
- An independent geographic information system with graphic display,
- A resolution engine based on metaheuristics (running in a high-performance computing mode),
- The possibility of coupling with other optimization solvers and frameworks like Paradiseo (in order to enable a quick prototyping of new optimization algorithms),
- Objective- and constraint-handling that can be easily configured by the user,
- Software engineering (build system testing, continuous integration, etc).

6.5. Platforms

6.5.1. Grid'5000

The Grid'5000 experimental platform is a scientific instrument to support computer science research related to distributed systems, including parallel processing, high performance computing, cloud computing, operating systems, peer-to-peer systems and networks. It is distributed on 10 sites in France and Luxembourg, including Lyon. Grid'5000 is a unique platform as it offers to researchers many and varied hardware resources and a complete software stack to conduct complex experiments, ensure reproducibility and ease understanding of results.

- Participants: F. Desprez, F. Huet, E. Jeannot, Y. Jegou, A. Lebre, L. Lefevre, F. Loui, D. Margery, N. Melab, J-M. Menaud, P. Neyron, L. Nussbaum, C. Perez, J-M. Pierson, O. Richard., S. Varette.
- Contact: Frédéric Desprez
- URL: https://www.grid5000.fr/mediawiki/index.php/Grid5000:Home

DRACULA Project-Team

5. New Software and Platforms

5.1. CelDyn

KEYWORDS: Modeling - Bioinformatics - Biology
FUNCTIONAL DESCRIPTION

Software "Celdyn" is developed in order to model cell population dynamics for biological applications. Cells are represented either as soft spheres or they can have more complex structure. Cells can divide, move, interact with each other or with the surrounding medium. Different cell types can be introduced. When cells divide, the types of daughter cells are specified. A user interface is developed.

- Participants: Nikolai Bessonov, Vitaly Volpert, Alen Tosenberger and Laurent Pujo-Menjouet
- Contact: Vitaly Volpert

DREAM Project-Team

6. New Software and Platforms

6.1. Platforms

The Dream project-team, in collaboration with their applicative partners, has proposed and maintains several important software platforms for its main research topics.

6.1.1. Platform: Environmental decision-support systems

Participants: Marie-Odile Cordier, Christine Largouët, Véronique Masson.

6.1.1.1. SACADEAU

Système d'Acquisition des Connaissances pour l'Aide à la Décision sur la qualité de l'EAU

FUNCTIONAL DESCRIPTION

the Sacadeau system is an environmental decision software that implements the Sacadeau transfer model. The Sacadeau simulation model couples two qualitative models, a transfer model describing the pesticide transfer through the catchment and a management model describing the farmer decisions. Giving as inputs a climate file, a topological description of a catchment, and a cadastral repartition of the plots, the Sacadeau model simulates the application of herbicides by the farmers on the maize plots, and the transfer of these pollutants through the catchment until the river. The two main simulated processes are the runoff and the leaching. The output of the model simulation is the quantity of herbicides arriving daily to the stream and its concentration at the outlets. The originality of the model is the representation of water and pesticide runoffs with tree structures where leaves and roots are respectively up-streams and down-streams of the catchment.

- Contact: Véronique Masson
- URL: http://www.irisa.fr/dream/SACADEAU/

6.1.1.2. EcoMata

FUNCTIONAL DESCRIPTION

The EcoMata tool-box provides means for qualitative modeling and exploring ecosystems and for aiding to design environmental guidelines.We have proposed a new qualitative approach for ecosystem modeling based on timed automata (TA) formalism combined to a high-level query language for exploring scenarios.

- Participants: Marie-Odile Cordier, Yulong Zhao, Christine Largouët and Thomas Guyet
- Contact: Christine Largouët
- URL: https://team.inria.fr/dream/fr/ecomata/

6.1.1.3. PaturMata

KEYWORDS: Bioinformatics - Biology

SCIENTIFIC DESCRIPTION

In the PaturMata software, users can create a pasture system description by entering herds and plots information. For each herd, the only parameter is the number of animals. For each plot, users should enter the surface, the density, the herb height, the distance to the milking shed, a herb growth profile and an accessibility degree.

Users then specify pasturing and fertilization strategies. Finally, users can launch a pasture execution. PaturMata displays the results and a detailed trace of pasture. Users can launch a batch of different strategies and compare the results in order to find the best pasture strategy.

PaturMata is developed in Java (Swing for the GUI) and the model-checker that is called for the timed properties verification is UPPAAL .

FUNCTIONAL DESCRIPTION

The Paturmata tool-box provides means for qualitative modeling and exploring agrosystems, specifically management of herd based on pasture. The system is modelled using a hierarchical hybrid model described in timed automata formalism.

- Contact: Christine Largouët

6.1.2. Platform: Pattern Mining

Participants: Thomas Guyet, René Quiniou.

6.1.2.1. QTempIntMiner

Temporal pattern mining in sequences
SCIENTIFIC DESCRIPTION

The QTempIntMiner data mining software implements several algorithms (QTIAPRIORI and QTIPREFIXSPAN). The software is mainly implemented in Matlab. It uses the Mixmod toolbox to compute multi-dimensional Gaussian distributions. The main features of QTEMPINTMINER are:

- a tool for generating synthetic noisy sequences of temporal events,
- an implementation of the QTEMPINTMINER, QTIAPRIORI and QTIPREFIXSPAN algorithms,
- a graphical interface that enables the user to generate or import data set and to define the parameters of the algorithm and that displays the extracted temporal patterns.
- a sequence transformer to process long sequences of temporal events. Long sequences are transformed into a database of short temporal sequences that are used as input instances for the available algorithms.

The software includes one new algorithm based on the separation of the set of interval to extract more efficiently but less accurately the time interval in temporal patterns. This new algorithm version is still under evaluation on simulated and real datasets.

This year, an APP deposit of the early version (in Matlab) of this framework has been done. In parallel, we started the developement of a C++ version of the framework.

- Participants: Thomas Guyet and René Quiniou
- Partner: AGROCAMPUS
- Contact: Thomas Guyet
- URL: http://www.irisa.fr/dream/QTempIntMiner/

6.1.3. Platform: Diagnostic and Monitoring Systems

Participants: Marie-Odile Cordier, René Quiniou, Sophie Robin, Laurence Rozé.

6.1.3.1. ManageYourself

FUNCTIONAL DESCRIPTION

The ManageYourself software comes from a collaborative project between Dream and the Telelogos company aiming at monitoring smartphones from a stream of observations made on the smartphone state.

Today's smartphones are able to perform calls, as well as to realize much more complex activities. They are small computers. But as in computers, the set of applications embedded on the smartphone can lead to problems. The aim of the project ManageYourself is to monitor smartphones in order to avoid problems or to detect problems and to repair them. To this end, a model of the martphone system is learned and updated incrementally.

- Contact: Laurence Rozé

6.1.3.2. Odisseptale

KEYWORDS: Biology - Health
FUNCTIONAL DESCRIPTION

The Odisseptale software implements disease detectors using monitoring of data provided by sensors placed on calves or cows. Sensors record streams of data such as body temperature, physical activity, feeding behavior, etc. These data are transmitted regularly to a monitoring software that aims to detect if a noticeable change has occurred on the data streams. Several detectors can be simultaneously active and each contribute to the final decision (detection of a disease). Two kinds of detectors have been implemented: a generic detector based on adaptive CUSUM and a symbolic pattern-based detector. Odisseptale provides also facilities for parameter setting and performance evaluation.

- Contact: René Quiniou

6.2. TraceSquiz

FUNCTIONAL DESCRIPTION

TraceSquiz is a software developped in collaboration with STMicroelectronics. Its goal is to reduce the volume of execution trace captured during endurance tests of multimedia applications. It uses anomaly detection techniques to "learn" regular parts of the trace and only capture the irregular ones. The software is written in C++.

- Participants: Alexandre Termier, Serge Vladimir Emteu Tchagou, René Quiniou
- Contact: Serge Vladimir Emteu Tchagou

DREAMPAL Project-Team

5. New Software and Platforms

5.1. HoMade

KEYWORDS: SoC - Multicore - Softcore
FUNCTIONAL DESCRIPTION

HoMade is a softcore processor. The current version is reflective (i.e., the program it executes is self-modifiable), and statically configurable, dynamically reconfigurable multi-processors are the next steps. Users have to add to it the functionality they need in their applications via IPs. We have also being developing a library of IPs for the most common processor functions (ALU, registers, ...). All the design is in VHDL except for some schematic specifications.

- Participant: Jean Luc Dekeyser
- Partner: LIFL
- Contact: Jean Luc Dekeyser
- URL: https://sites.google.com/site/homadeguideen/home

5.2. JHomade

FUNCTIONAL DESCRIPTION

JHomade is a software suite written in JAVA, including compilers and tools for the HoMade processor. It allows us to compile HiHope programs to Homade machine code and load the resulting binaries on FPGA boards. It was first released in 2013. The second version in 2014 includes several new features, like a C-frontend, a few optimizations (automatic inlining and more compact byte-code), a binary decoder and a code-generator for VHDL simulation. New features of the HiHope language are described in [19].

- Contact: Frédéric Guyomarch
- URL: https://gforge.inria.fr/frs/?group_id=3646

DYLISS Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: Bioinformatics - Linked data - Networks - Semantic Web - Omics
FUNCTIONAL DESCRIPTION

This tool was designed in 2015 in the framework of the MIRNadapt project. Biological studies and bioinformatical analysis produce numerous heterogeneous data, calling for their integration. AskOmics is an integration and interrogation software relying on an RDF model and the SPARQL query language. Its purpose is to obtain quick answers to biological questions demanding currently hours of manual search in several spreadsheet results files. New study perpectives will arise from these answers and from this integration work. Using AskOmics, we integrated an omic dataset borrowed from the MiRNAdapt ANR project that aims to describe the networks of the genes involved in aphids adaptation to seasons. AskOmics allows biologists to integrate and interrogate themselves their data without needing any knowledge about RDF and SPARQL. The query process consists in linking sets of biological entities as nodes in a graphical interface, optionaly specifying biological attributes for these nodes. The graph is then converted inton a SPARQL query to provide the user an answer to his biological questions. The answers are the elements of the sets that match the query contraints.

- Participants: Charles Bettembourg, Anthony Bretaudeau, Olivier Dameron, Aurélie Evrard, Yvanne Chaussin, Anne Siegel, Fabrice Legeai
- Partners: INRA IGEPP
- Contact: Fabrice Legeai
- URL: http://bipaa.genouest.org/askomics_aphid/

6.2. VIRALpro

FUNCTIONAL DESCRIPTION

VIRALpro is a predictor capable of identifying capsid and tail protein sequences using support vector machines (SVM) with an estimated accuracy between 90% and 97%. Predictions are based on the protein amino acid composition, on the protein predicted secondary structure, as predicted by SSpro, and on a boosted linear combination of HMM e-values obtained from 3,380 HMMs built from multiple sequence alignments of specific fragments - called contact fragments - of both capsid and tail sequences. This tool was designed in the context of a 2015 Explorer Program visit at University of California, Irvine

- Participants: Clovis Galiez, François Coste
- Partner: Pierre Baldi, University of California, Irvine
- Contact: Clovis Galiez

6.3. Shogen

KEYWORDS: Systems Biology - Bioinformatics - Genomics
FUNCTIONAL DESCRIPTION

This ASP-based software aims at identifying every segments of consecutive genes in a bacterial genome with a maximum number of genes that participates in a given metabolic pathway. Through this selection, the shogen tool deciphers putative sets of genes that (1) take an active part in metabolic pathways while being closely connected via metabolic networks and (2) are consecutive on each of the genomes involved. In practice, our approach connects genomic and metabolic knowledge by considering the genome organization and the biochemical reactions catalyzed by enzymes encoded by its genes. The underline parsimonious principle assumes that genes must be jointly regulated to activate a metabolic reaction cascade, and should be close enough in the genome organization. In 2015, the tool was simplified to handle standardized data formats, enabling its application to the modelling of a bacterial community [17]

- Participants: Philippe Bordron, Damien Eveillard, Alejandro Maass and Anne Siegel
- Partners: LINA - University of Chile
- Contact: Anne Siegel
- URL: http://aspforbiology.genouest.org/wiki.php/Software%20&%20Biological%20applications

6.4. Caspo

Cell ASP Optimizer
FUNCTIONAL DESCRIPTION

Cell ASP Optimizer (caspo) is a pipeline for automated reasoning on logical signaling networks. The main underlying issue is that inherent experimental noise is considered, so that many different logical networks can be compatible with a set of experimental observations. Caspo-learn performs an automated inference of logical networks from experimental data. It identifies admissible large-scale families of logic models without any a priori bias, thus saving a lot of efforts. Next, once a family a logical networks has been identified, caspo-design can suggest or design new experiments in order to reduce the uncertainty associated to this family. Finally, caspo-control computes intervention strategies (i.e. inclusion minimal sets of knock-ins and knock-outs) that force a set of target species or compounds into a desired steady state. In 2015, the tool was extended to compute experimental design proposition [23], and to handle time-series datasets [31].

- Participants: Santiago Videla, Carito Guziolowski, Sven Thiele, Thomas Cokelaer, Torsten Schaub, Anne Siegel, Loic Paulevé and Max Ostrowski
- Partners: Ecole Centrale de Nantes - University of Potsdam - EMBL - LRI - Laboratoire de Recherche en Informatique
- Contact: Anne Siegel
- URL: http://bioasp.github.io/caspo/

6.5. Platforms and toolboxes

Among others, a goal of the team is to facilitate interplays between tools for biological data analysis and integration. Our tools are based on formal systems. They aim at guiding the user to progressively reduce the space of models (families of sequences of genes or proteins, families of keys actors involved in a system response, dynamical models) which are compatible with both knowledge and experimental observations.

Most of our tools are available both as stand-alone software and through portals such as Mobyle or Galaxy interfaces. Tools are developed in collaboration with the GenOuest resource and data center hosted in the IRISA laboratory, including their computer facilities [more info].

We present here three toolboxes which each contains complementary tools with respect to their targeted sub-domain of bioinformatics.

6.5.1. Integrative Biology: (constraint-based) toolbox for network filtering

The goal is to offer a toolbox for the reconstruction of networks from genome, literature and large-scale observation data (expression data, metabolomics...) in order to elucidate the main regulators of an observed phenotype. Most of the optimization issues are addressed with Answer Set Programming.

MeMap and MeMerge. We develop a workflow for the **Au**tomatic **Re**construction of **Me**tabolic networks (AuReMe). In this workflow, we use heterogeneous sources of data with identifiers from different namespaces. MeMap (**Me**tabolic network **Mapp**ing) consists in mapping identifiers from different namespaces to a unified namespace. Then, MeMerge (**Me**tabolic network **Merge**) merges two metabolic networks previously mapped on the same namespace. [web server].

meneco [*input*: draft metabolic network & metabolic profiles. *output*: metabolic network]. It is a qualitative approach to elaborate the biosynthetic capacities of metabolic networks and solve incompleteness of large-scale metabolic networks. Since November 2015, a new version of Meneco has been available with Python 3, and a new functionality of topological producibility checking has been set up. [82] [60] [python package][web server].

shogen [*input*: genome & metabolic network. *output* : functional regulatory modules]. This software is able to identify genome portions which contain a large density of genes coding for enzymes that regulate successive reactions of metabolic pathways. See section 6.3 for details. [55][python package].

lombarde [*input*: genome, modules & several gene-expression datasets. *output*: oriented regulation network]. This tool is useful to enhance key causalities within a regulatory transcriptional network when it is challenged by several environmental perturbations. In 2015, the tool was simplified to handle standardized data formats. [41] [web server].

ingranalysis [*input*: signed regulation network & one gene-expression dataset. *output*: network repair gene-expression prediction] This tool is an extension to the bioquali tool. It proposes a range of different operations for altering experimental data and/or a biological network in order to re-establish their mutual consistency, an indispensable prerequisite for automated prediction. For accomplishing repair and prediction, we take advantage of the distinguished modeling and reasoning capacities of Answer Set Programming. The tool has evolved to the *iggy* tool recently [5] [21] [Python package][web server].

6.5.2. Dynamics and invariant-based prediction

We develop tools predicting some characteristics of a biological system behavior from incomplete sets of parameters or observations.

cadbiom. Based on Guarded transition semantic, this software provides a formal framework to help the modeling of biological systems such as cell signaling network. It allows investigating synchronization events in biological networks. [software][web server].

caspo: Cell ASP Optimizer This soft provides an easy to use software for learning Boolean logic models describing the immediate-early response of protein signaling networks. See Sec. 6.4 for details. The tool is included in the cellNopt package [0]. [python package][web server].

nutritionAnalyzer. This tool is dedicated to the computation of allocation for an extremal flux distribution. It allows quantifying the precursor composition of each system output (AIO) and to discuss the biological relevance of a set of flux in a given metabolic network by computing the extremal values of AIO coefficients. This approach enables to discriminate diets without making any assumption on the internal behaviour of the system [40][webserver][software and doc].

POGG. The POGG software allows scoring the importance and sensibility of regulatory interactions with a biological system with respect to the observation of a time-series quantitative phenotype. This is done by solving nonlinear problems to infer and explore the family of weighted Markov chains having a relevant asymptotic behavior at the population scale. Its possible application fields are systems biology, sensitive interactions, maximal entropy models, natural language processing. It results from our collaboration with the LINA-Nantes [2][matlab package].

6.5.3. Sequence annotation

We develop tools for discovery and search of complex signatures within biological sequences.

---

[0] http://www.cellnopt.org/

Logol Logol is a swiss-army-knife for pattern matching on DNA/RNA/Protein sequences, using a high-level grammar to permit a large expressivity [48]. In 2015, the efficiency of the tool was improved by slight evolutions of the underlying grammar. Possible fields of application are the detection of mutated binding sites or stem-loop identification (e.g. in CRISPR [0] [10]) [software].

Protomata learner Protomata software suite provides a grammatical inference framework for learning the specific signature of a functional protein family from unaligned sequences by partial and local multiple alignment and automata modeling. In 2015, motivated by the characterization of viral protein sequences during the internship of Maud Jusot [38], we have begun a refactoring of the parsing part of Protomata and we implemented a new mode returning the sum of the scores over all paths (Forward score), besides the classical score on best path (Viterbi score), to improve parsing's sensitivity on divergent but conserved families of sequences. [web server].

6.5.4. Integration of toolboxes and platforms in webservices

Most of our software were designed as "bricks" that can be combined through workflow application such as Mobyle. It worths considering them into larger dedicated environments to benefit from the expertise of other research groups.

Plateform for data storage, expertise sharing and application inventory In collaboration with the GenOuest ressource center, the BII plateform (Bio Investigation Index) is a good way to enhance knowledge and expertise sharing, improve the visibility on the team's work in progress and record the History of the team's discoveries and main results. It enables experiment reproducibility, reporting on experiment process details, storing all scripts and softwares (in the corresponding versions) and linking all input files, results and not reproducible intermediate data. [web access].

Web servers In collaboration with the GenOuest ressource center, most our tools are made available through several web portals.

- The **mobyle@GenOuest portal** is the generic web server of our ressource center. It hosts the ingranalysis, meneco, caspo, lombarde and shogun tools [website].
- The **Mobyle@Biotempo server** is a mobyle portal for system biology with formal approaches. It hosts the memap, memerge, meneco, ingranalysis, cadbiom and pogg tools [website].
- The **GenOuest galaxy portal** now provides access to most tools for integrative biology and sequence annotation (access on demand).

Dr Motif This resource aims at the integration of different software commonly used in pattern discovery and matching. This resource also integrates Dyliss pattern search and discovery software.

ASP4biology and BioASP It is a meta-package to create a powerful environment of biological data integration and analysis in system biology, based on knowledge representation and combinatorial optimization technologies (ASP). It provides a collection of python applications which encapsulates ASP tools and several encodings making them easy to use by non-expert users out-of-the-box. [Python package][website].

ASP encodings repository This suite comprises projects related to applications of Answer Set Programming using Potassco systems (the Potsdam Answer Set Solving Collection, bundles tools for Answer Set Programming developed at the University of Potsdam). These are usually a set of encodings possibly including auxiliary software and scripts [respository].

---

[0] http://crispi.genouest.org/

DYOGENE Project-Team

6. New Software and Platforms

6.1. CloNES

CLOsed queueing Networks Exact Sampling
FUNCTIONAL DESCRIPTION

Clones is a Matlab toolbox for exact sampling of closed queueing networks.

- Participant: Christelle Rovetta
- Contact: Christelle Rovetta
- URL: http://www.di.ens.fr/~rovetta/Clones/index.html

ECUADOR Project-Team

5. New Software and Platforms

5.1. AIRONUM

SCIENTIFIC DESCRIPTION

Aironum is an experimental software that solves the unsteady compressible Navier-Stokes equations with k-, LES-VMS and hybrid turbulence modelling on parallel platforms, using MPI. The mesh model is unstructured tetrahedrization, with possible mesh motion.

FUNCTIONAL DESCRIPTION

Aironum was developed by Inria and University of Montpellier. It is used by Inria, University of Montpellier and University of Pisa (I). Aironum is used as an experimental platform for:

- Numerical approximation of compressible flows, such as upwind mixed element volume approximation with superconvergence on regular meshes.
- Numerical solution algorithms for the implicit time advancing of the compressible Navier-Stokes equations, such as parallel scalable deflated additive Schwarz algorithms.
- Turbulence modelling such as the Variational Multiscale Large eddy Simulation and its hybridization with RANS statistical models.
- Participant: Alain Dervieux
- Contact: Alain Dervieux
- URL: http://www-sop.inria.fr/tropics/aironum

5.2. TAPENADE

KEYWORDS: Static analysis - Optimization - Compilation - Gradients

SCIENTIFIC DESCRIPTION

Tapenade implements the results of our research about models and static analyses for AD. For a full specification and description, see [10]. AD produces analytical derivatives, that are exact up to machine precision. Adjoint AD computes gradients at a cost which is independent from the number of input variables. Tapenade performs sophisticated flow- and context-sensitive data-flow analysis on the complete source program to produce an efficient differentiated code. Analyses include Type-Checking, Read-Write analysis, Pointer analysis. AD-specific analyses include:

- Activity analysis: Detects variables whose derivative is either null or useless, to reduce the number of derivative instructions.
- Adjoint Liveness analysis: Detects the source statements that are dead code for the computation of derivatives.
- TBR analysis: In Adjoint AD, reduces the set of source variables that need to be recovered.

FUNCTIONAL DESCRIPTION

Tapenade transforms an original program into a new program that computes derivatives of the original program. Tapenade accepts source programs written in Fortran77, Fortran90, or C. Tapenade can differentiate in tangent, vector tangent, adjoint, and vector adjoint modes. Tapenade can be downloaded and installed on most architectures. Alternatively, it can be used as a web server. Higher-order derivatives can be obtained through repeated application.

- Participants: Laurent Hascoët, Valérie Pascual, Ala Taftaf
- Contact: Laurent Hascoët
- URL: http://www-sop.inria.fr/tropics/tapenade.html

ERABLE Project-Team

5. New Software and Platforms

5.1. AcypiCyc

FUNCTIONAL DESCRIPTION

Database of the metabolic network of *Acyrthosiphon pisum*.

- Participants: Patrice Baa Puyoule, Hubert Charles, Stefano Colella, Ludovic Cottret, Marie-France Sagot, Augusto Vellozo and Amélie Veron
- Contact: Hubert Charles
- URL: http://acypicyc.cycadsys.org/

5.2. AlViE

FUNCTIONAL DESCRIPTION

ALVIE is a post-mortem algorithm visualisation Java environment, which is based on the interesting event paradigm. The current distribution of ALVIE includes more than forty visualisations. Almost all visualisations include the representation of the corresponding algorithm C-like pseudo-code. The ALVIE distribution allows a programmer to develop new algorithms with their corresponding visualisation: the included Java class library, indeed, makes the creation of a visualisation quite an easy task (once the interesting events have been identified).

- Participants: Pierluigi Crescenzi, Giorgio Gambosi, Roberto Grossi, Carlo Nocentini, Tommaso Papini, Walter Verdese
- Contact: Pierluigi Crescenzi
- URL: http://javamm.sourceforge.net/piluc/software/alvie.html

5.3. Cassis

FUNCTIONAL DESCRIPTION

Algorithm for precisely detecting genomic rearrangement breakpoints.

- Participants: Christian Baudet, Christian Gautier, Claire Lemaitre, Marie-France Sagot, Eric Tannier
- Contact: Christian Baudet (not Inria), Claire Lemaitre (Inria GenScale), Marie-France Sagot (Inria ERABLE)
- URL: http://pbil.univ-lyon1.fr/software/Cassis/

5.4. Cidane

FUNCTIONAL DESCRIPTIONCIDANE is a novel framework for genome-based transcript reconstruction and quantification from RNA-seq reads.

- Participants: Stefan Canzar, Sandra Andreotti, David Weese, Kurt Reinert, Gunnar Klau
- Contact: Stefan Canzar (not Inria)
- URL: http://ccb.jhu.edu/software/cidane/

5.5. Coala

FUNCTIONAL DESCRIPTION

COALA stands for “CO-evolution Assessment by a Likelihood-free Approach”. It is thus a likelihood-free method for the co-phylogeny reconstruction problem which is based on an Approximative Bayesian Computation (ABC).

- Participants: Christian Baudet, Pierluigi Crescenzi, Beatrice Donati, Christian Gautier, Catherine Matias, Marie-France Sagot, Blerina Sinaimeri
- Contact: Christian Baudet (not Inria), Marie-France Sagot and Blerina Sinaimeri
- URL: http://coala.gforge.inria.fr/

5.6. CophyTrees

FUNCTIONAL DESCRIPTION

COPHYTREES is a visualisator for host-parasite and gene-specie trees evolution..

- Participants: Laurent Bulteau
- Contact: Laurent Bulteau (not Inria), Blerina Sinaimeri (for Inria)
- URL: http://eucalypt.gforge.inria.fr/viewer.html

5.7. C3Part & Isofun

FUNCTIONAL DESCRIPTION

The C3PART / ISOFUN package implements a generic approach to the local alignment of two or more graphs representing biological data, such as genomes, metabolic pathways or protein-protein interactions, in order to infer a functional coupling between them. It is based on the notion of “common connected components” between graphs.

- Participants: Frédéric Boyer, Yves-Pol Deniélou, Anne Morgat, Marie-France Sagot and Alain Viari
- Contact: Alain Viari
- URL: http://www.inrialpes.fr/helix/people/viari/lxgraph/index.html

5.8. CycADS

FUNCTIONAL DESCRIPTION

Cyc annotation database system.

- Participants: Patrice Baa Puyoule, Hubert Charles, Stefano Colella, Ludovic Cottret, Marie-France Sagot and Augusto Vellozo
- Contact: Hubert Charles
- URL: http://www.cycadsys.org/

5.9. Dinghy

FUNCTIONAL DESCRIPTION

DINGHY is a visualisation program for network pathways of up to 150 reactions.

- Participants: Laurent Bulteau, Alice Julien-Laferrière, Delphine Parrot
- Contact: Laurent Bulteau (not Inria), Alice Julien-Laferrière, Delphine Parrot
- URL: http://dinghy.gforge.inria.fr/

5.10. Eucalypt

FUNCTIONAL DESCRIPTION

EUCALYPT stands for “EnUmerator of Co-evolutionary Associations in PoLYnomial-Time delay”. It is an algorithm for enumerating all optimal (possibly time-unfeasible) mappings of a parasite tree unto a host tree.

- Participants: Christian Baudet, Pierluigi Crescenzi, Beatrice Donati, Pierluigi Crescenzi, Marie-France Sagot, Blerina Sinaimeri,
- Contact: Christian Baudet (not Inria), Beatrice Donati (not Inria), and Marie-France Sagot
- URL: http://eucalypt.gforge.inria.fr/index.html

5.11. Gobbolino & Touché

FUNCTIONAL DESCRIPTION

GOBBOLINO and TOUCHÉ were designed to solve the metabolic stories problem, which consists in finding all maximal directed acyclic subgraphs of a directed graph G whose sources and targets belong to a subset of the nodes of G, called the black nodes. Biologically, stories correspond to alternative metabolic pathways that may explain some stress that affected the metabolites corresponding to the black nodes by changing their concentration (measured by metabolomics experiments).

- Participants: Vicente Acuña, Etienne Birmelé, Ludovic Cottret, Pierluigi Crescenzi, Fabien Jourdan, Vincent Lacroix, Alberto Marchetti-Spaccamela, Andrea Marino, Paulo Vieira Milreu, Marie-France Sagot, Leen Stougie
- Contact: Paulo Vieira Milreu (not Inria), Marie-France Sagot
- URL: http://gforge.inria.fr/projects/gobbolino

5.12. HapCol

FUNCTIONAL DESCRIPTION

A fast and memory-efficient DP approach for haplotype assembly from long reads that works until 25x coverage, solves a constrained minimum error correction problem exactly.

- Participants: Paola Bonizzoni, Riccardo Dondi, Gunnar Klau, Yuri Pirola, Nadia Pisanti, Simone Zaccaria
- Contact: Gunnar Klau, Nadia Pisanti, Paola Bonizzoni (not Inria)
- URL: https://github.com/AlgoLab/HapCol

5.13. KisSNP & DiscoSNP

FUNCTIONAL DESCRIPTION

Algorithm for identifying SNPs without a reference genome by comparing raw reads. KISSNP has now given birth to DISCOSNP in a work involving V. Lacroix from ERABLE and the GenScale Inria Team at Rennes.

- Participants: Vincent Lacroix, Pierre Peterlongo
- Contact: Pierre Peterlongo (EPI GenScale)

5.14. KisSplice & KisSplice2igv7

FUNCTIONAL DESCRIPTION

Enables to analyse RNA-seq data with or without a reference genome. It is an exact local transcriptome assembler, which can identify SNPs, indels and alternative splicing events. It can deal with an arbitrary number of biological conditions, and will quantify each variant in each condition. KISSPLICE2IGV is a pipeline that combines the outputs of KISSPLICE to a reference transcriptome (obtained with a full-length transcriptome assembler or a reference database). It provides a visualisation of the events found by KISSPLICE in a longer context using a genome browser (IGV).

- Participants: Lilia Brinza, Alice Julien-Laferrière, Janice Kielbassa, Vincent Lacroix, Leandro Ishi Soares de Lima, Camille Marchet, Vincent Miele, Gustavo Sacomoto
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/

5.15. kissDE

FUNCTIONAL DESCRIPTION

KISSDE is an R Package enabling to test if a variant (genomic variant or splice variant) is enriched in a condition. It takes as input a table of read counts obtained from NGS data pre-processing and gives as output a list of condition specific variants.

- Participants: Lilia Brinza, Janice Kielbassa, Vincent Lacroix, Camille Marchet and Vincent Miele
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kissDE/

5.16. KisSplice2RefTranscriptome

FUNCTIONAL DESCRIPTION

KISSPLICE2REFTRANSCRIPTOME enables to combine the output of KISSPLICE with the output of a full-length transcriptome assembler, thus allowing to predict a functional impact for the positioned SNPs, and to intersect these results with condition-specific SNPs. Overall, starting from RNAseq data only, we obtain a list of condition-specific SNPs stratified by functional impact.

- Participants: Mathilde Boutigny, Vincent Lacroix, Hélène Lopez-Maestre
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kiss2rt/

5.17. KisSplice2RefGenome

FUNCTIONAL DESCRIPTION

KISSPLICE (see above) identifies variations in RNAseq data, without a reference genome. In many applications however, a reference genome is available. KISSPLICE2REFGENOME enables to facilitate the interpretation of KISSPLICE's results after mapping them to a reference genome.

- Participants: Alice Julien-Laferrière, Vincent Lacroix, Camille Marchet, Camille Sessegolo
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kiss2refgenome/

5.18. Lasagne

FUNCTIONAL DESCRIPTION

LASAGNE is a Java application which allows the user to compute distance measures on graphs by making a clever use either of the breadth-first search or of the Dijkstra algorithm. In particular, the current version of LASAGNE can compute the exact value of the diameter of a graph: the graph can be directed or undirected and it can be weighted or unweighted. Moreover, LASAGNE can compute an approximation of the distance distribution of an undirected unweighted graph. These two features are integrated within a graphical user interface along with other features, such as computing the maximum (strongly) connected component of a graph.

- Participants: Pierluigi Crescenzi, Roberto Grossi, Michel Habib, Claudio Imbrenda, Leonardo Lanzi, Andrea Marino
- Contact: Pierluigi Crescenzi
- URL: http://lasagne-unifi.sourceforge.net/

5.19. MeDuSa

FUNCTIONAL DESCRIPTION

MEDUSA (Multi-Draft based Scaffolder) is an algorithm for genome scaffolding. It exploits information obtained from a set of (draft or closed) genomes from related organisms to determine the correct order and orientation of the contigs.

- Participants: Emmanuelle Bosi, Sara Brunetti, Pierluigi Crescenzi, Beatrice Donati, Renato Fani, Marco Fondi, Marco Galardini, Pietro Lió, Marie-France Sagot,
- Contact: Pierluigi Crescenzi, Marco Fondi (not Inria)
- URL: http://combo.dbe.unifi.it/medusa

5.20. MetExplore

FUNCTIONAL DESCRIPTION

Web server to link metabolomic experiments and genome-scale metabolic networks.

- Participants: Michael Barrett, Hubert Charles, Ludovic Cottret, Fabien Jourdan, Marie-France Sagot, Florence Vinson, David Wildridge
- Contact: Fabien Jourdan (not Inria), Marie-France Sagot
- URL: http://metexplore.toulouse.inra.fr/metexplore/

5.21. Migal

FUNCTIONAL DESCRIPTION

Algorithm for comparing RNA structures.

- Participants: Julien Allali and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://www-igm.univ-mlv.fr/~allali/logiciels/index.en.php

5.22. Mirinho

FUNCTIONAL DESCRIPTION

Predicts, at a genome-wide scale, microRNA candidates.

- Participants: Christian Gautier, Cyril Fournier, Christine Gaspin, Susan Higashi, Marie-France Sagot
- Contact: Susan Higashi (not Inria), Marie-France Sagot
- URL: http://mirinho.gforge.inria.fr/

5.23. Motus & MotusWEB

FUNCTIONAL DESCRIPTION

Algorithm for searching and inferring coloured motifs in metabolic networks (web-based version - offers different functionalities from the downloadable version).

- Participants: Ludovic Cottret, Fabien Jourdan, Vincent Lacroix, Odile Rogier and Marie-France Sagot
- Contact: Vincent Lacroix
- URL: http://doua.prabi.fr/software/motus and http://pbil.univ-lyon1.fr/software/motus_web/

5.24. PhEVER

FUNCTIONAL DESCRIPTION

Database of homologous gene families built from the complete genomes of all available viruses, prokaryotes and eukaryotes and aimed at the detection of virus/virus and virus/host lateral gene transfers.

- Participants: Christian Gautier, Vincent Lotteau, Leonor Palmeira, Simon Penel, Chantal Rabourdin-Combe
- Contact: Christian Gautier, Leonor Palmeira (not EPI)
- URL: http://pbil.univ-lyon1.fr/databases/phever

5.25. PepLine

FUNCTIONAL DESCRIPTION

Pipeline for the high-throughput analysis of proteomic data.

- Participant: Jérôme Garin, Alain Viari
- Contact: Alain Viari

5.26. Pitufo and family

FUNCTIONAL DESCRIPTION

Algorithms to enumerate all minimal sets of precursors of target compounds in a metabolic network.

- Participants: Vicente Acuña Aguayo, Ludovic Cottret, Alberto Marchetti-Spaccamela, Fabio Henrique Viduani Martinez, Paulo Vieira Milreu, Marie-France Sagot, Leen Stougie
- Contact: Paulo Vieira Milreu (not Inria), Marie-France Sagot
- URL: https://sites.google.com/site/pitufosoftware/home

5.27. RepSeek

FUNCTIONAL DESCRIPTION

Finding approximate repeats in large DNA sequences.

- Participants: Guillaume Achaz, Eric Coissac, Alain Viari
- Contact: Guillaume Achaz (not Inria), Alain Viari
- URL: http://wwwabi.snv.jussieu.fr/public/RepSeek/

5.28. Rime

FUNCTIONAL DESCRIPTION

RIME detects long similar fragments occurring at least twice in a set of biological sequences.

- Participants: Maria Federico, Pierre Peterlongo, Nadia Pisanti, Marie-France Sagot
- Contact: Maria Federico (not Inria), Nadia Pisanti, Marie-France Sagot
- URL: https://code.google.com/p/repeat-identification-rime/

5.29. Smile

FUNCTIONAL DESCRIPTION

Motif inference algorithm taking as input a set of biological sequences.

- Participants: Laurent Marsan, Marie-France Sagot
- Contact: Marie-France Sagot
- URL: Not available

5.30. UniPathway

FUNCTIONAL DESCRIPTION

Database of manually curated pathways developed with the Swiss-Prot group.

- Participants: Eric Coissac, Anne Morgat, Alain Viari
- Contact: Anne Morgat
- URL: http://www.unipathway.org/

5.31. WhatsHap and pWH

FUNCTIONAL DESCRIPTION

WHATSHAP is a DP approach for haplotype assembly from long reads that works until 20x coverage, solves the minimum error correction problem exactly. PWH is a parallelisation of the core dynamic programming algorithm of WHATSHAP done by M. Aldinucci, A. Bracciali, T. Marschall, M. Patterson, N. Pisanti, and M. Torquati.

- Participants: Gunnar Klau, Tobias Marschall, Murray Patterson, Nadia Pisanti, Alexander Schönhuth, Leen Stougie, Leo van Iersel
- Contact: Alexander Schönhuth(not Inria), Gunnar Klau, Nadia Pisanti
- URL: https://bitbucket.org/whatshap/whatshap

ESTASYS Team

5. New Software and Platforms

5.1. PLASMA Lab

Platform for Learning and Advanced Statistical Model checking Algorithms
KEYWORDS: Model Checking - Statistical - Model Checker - Runtime Analysis - Statistics
SCIENTIFIC DESCRIPTION

Statistical model checking (SMC) is a fast emerging technology for industrial scale verification and optimisation problems. Plasma was conceived to have high performance and be extensible, using a proprietary virtual machine. Since SMC requires only an executable semantics and is not constrained by decidability, we can easily implement different modelling languages and logics.
FUNCTIONAL DESCRIPTION

Plasma-Lab is a formal verification tool for complex embeded systems. It uses statistical model checking, and applies to complex problems coming from the area of security, cyber physical systems, or privacy.

- Participants: Axel Legay, Sean Sedwards, Louis-Marie Traonouez, Jean Quilbeuf
- Contact: Axel Legay
- URL: https://project.inria.fr/plasma-lab

5.2. PyECDAR

KEYWORDS: Timed input - Output automata
SCIENTIFIC DESCRIPTION

The tool has been originally developed to analyze the robustness of timed specifications, in extension of the tool Ecdar. As Ecdar , it allows to compose components specifications based on Timed I/O Automata (TIOA), and it implements timed game algorithms for checking consistency and compatibility. Additionally, it features original methods for checking the robustness of these specifications.

The tool has been later extended to analyse adaptive systems. It therefore implements original algorithms for checking featured timed games against requirements expressed in the timed AdaCTL logic.

The tool is written in Python with around 3’000 lines of code. It uses a Python console as user interface, from which it can load TIOA components from XML files written in the UPPAAL format, and design complex systems by combining the components using a simple algebra. Then, it can analyze these systems, transform them and save them in a new XML file.
FUNCTIONAL DESCRIPTION

PyEcdar is a free software that analyses timed games and timed specifications. The goal of the tool is to allow a fast prototyping of new analysis techniques. It currently allows to solve timed games based on timed automata models. These can be extended with adaptive features to represent dynamicity and to model software product lines.

- Participants: Louis-Marie Traonouez and Axel Legay
- Contact: Louis-Marie Traonouez
- URL: https://project.inria.fr/pyecdar/

5.3. Quail

FUNCTIONAL DESCRIPTION

Privacy is a central issue for Systems of Systems and interconnected objects. We propose QUAIL, a tool that can be used to quantify privacy of components. QUAIL is the only tool able to perform an arbitrary-precision quantitative analysis of the security of a system depending on private information. Thanks to its Markovian semantics model, QUAIL computes the correlation between the system's observable output and the private information, obtaining the amount of bits of the secret that the attacker will infer by observing the output.

- Participants: Fabrizio Biondi, Axel Legay, Louis-Marie Traonouez and Andrzej Wasowski
- Contact: Axel Legay
- URL: https://project.inria.fr/quail/

EVA Team

6. New Software and Platforms

6.1. OpenWSN (Software)

Participants: Thomas Watteyne, Tengfei Chang, Malisa Vucinic, Jonathan Muñoz.

OpenWSN (http://www.openwsn.org/) is an open-source implementation of a fully standards-based protocol stack for the Internet of Things. It has become the de-facto implementation of the IEEE802.15.4e TSCH standard, has a vibrant community of academic and industrial users, and is the reference implementation of the work we do in the IETF 6TiSCH standardization working group.

The OpenWSN ADT started in 2015, with Research Engineer Tengfei Chang who joined the EVA team.

Highlights for 2015:

- Development:
  - Moving the project from UC Berkeley to Inria (**Thomas Watteyne**)
  - Implementation of a layer-2 security based on AES-128 and CCM* (Malisa Vucinic)
  - Implementation of draft-ietf-6tisch-minimal (Tengfei Chang)
  - Implementation of draft-dujovne-6tisch-6top-sf0 (Tengfei Chang)
  - Implementation of draft-wang-6tisch-6top-sublayer (Tengfei Chang)
  - Creation of "Golden Image" used as a reference during interoperability testing (Tengfei Chang)
- Recognition:
  - OpenWSN was selected by ETSI as the reference implementation for IETF 6TiSCH-related standards. It is therefore the base for the ETSI's Golden Device for 6TiSCH standards, including IEEE802.15.4e TSCH, 6LoWPAN and RPL.
- Events:
  - **Tutorial**
    OpenWSN & OpenMote: Hands-on Tutorial on Open Source Industrial IoT. Thomas Watteyne, Xavier Vilajosana, Pere Tuset. IEEE Global Telecommunications Conference (GLOBECOM), San Diego, CA, USA, 6-10 December 2015.
  - **Tutorial**
    OpenWSN Tutorial [presented by Xavi Vilsajosana] Workshop Internet Of Things / Equipex FIT IoT-LAB, Lille, France, 15 October 2015.
  - **Hackathon**
    OpenWSN/6TiSCH Hackathon, Czech Republic, 19 July 2015.
  - **Interop event**
    First ETSI 6TiSCH plugtest (interop event) in Prague, Czech Republic, 17-18 July 2015.

6.2. OPERA and OCARI (Software)

Participants: Erwan Livolant, Pascale Minet.

The OPERA software was developed by the Hipercom2 team in the OCARI project (see https://ocari.org/). It includes EOLSR, an energy efficient routing protocol and OSERENA, a coloring algorithm optimized for dense wireless networks. It was registered by the APP. In 2013, OPERA has been made available for download as an open software from the InriaGForge site: https://gforge.inria.fr/scm/?group_id=4665

In 2014, OPERA has been ported on a more powerful platform based on the Atmel transceiver AT86RF233 and on a 32 bits microcontroler Cortex M3. More details and documentation about this software are available in the website made by the Eva team: http://opera.gforge.inria.fr/index.html

In 2015, Erwan Livolant maintained the code and corrected some bugs.

6.3. CONNEXION (Software)

Participants: Ines Khoufi, Pascale Minet, Erwan Livolant.

These developments are part of the CONNEXION project. In 2015, Ines khoufi developped two softwares:

- a distributed algorithm, called OA-DVFA, to deploy autonomous and mobile sensor nodes to ensure full coverage of a 2-D area with unknown obstacles. It is based on virtual forces and virtual grid.
- an algorithm, called MRDS, to compute the tours of mobile robots in charge of placing static sensor nodes at the positions given (e.g. points of interest). This is a multi-objective optimization problem: to minimize the deployment duration, to balance the durations of robots tours and to minimize the number of robots used. A genetic heuristic is used to solve this problem.

With regard to the wireless sensor network OCARI, in 2015 we designed and developed the mobility support for OCARI. The solution proposed to support mobility in the OCARI network is simple and limits the overhead induced by mobile nodes. This mobility support is designed to be efficient in its use of resources (e.g. bandwidth, energy, memory). The properties of energy efficiency, determinism, latency and robustness provided by OCARI to static wireless sensor nodes are ensured. In the absence of mobile nodes, the OCARI network behaves exactly as without mobility support and exhibits exactly the same performances. Similarly, the overhead induced by mobile sinks is paid only if mobile sinks are present. Data gathering by the static sink, being the most important objective of the OCARI network from the application point of view, its performances are not altered by mobility support. Data gathering by a mobile sink is a new functionality provided by mobility support. This mobility support has been demonstrated with a mobile robot embedding a sensor node and transfering its data to the static sink via router nodes that depend on the position of the robot.

With Telecom ParisTech, the integration of OCARI in a Service-Oriented Architecture using the OPC-UA/ROSA middleware went on. More precisely, we developed the creation of services corresponding to newly available physical sensor measurements and the suppression of services that are no longer available.

Erwan Livolant developed an OCARI frame dissector plugin for Wireshark (https://www.wireshark.org) available from the Git repository at OCARI website (https://www.ocari.org/gitlab/tools/wireshark.git). This tool displays the contents of the packets sniffed for the MAC, the NWK and the Application layers, taking into account the specificities of OCARI.

6.4. SAHARA (Software)

Participants: Erwan Livolant, Pascale Minet.

Erwan Livolant developed a SAHARA frame dissector plugin for Wireshark (https://www.wireshark.org). This tool displays the contents of the packets sniffed for the MAC and the NWK layers, taking into account the specificities of the SAHARA project.

6.5. FIT IoT-LAB (Platform)

Participant: Thomas Watteyne.

Note well: IoT-lab is NOT strictly speaking a project of Inria-EVA. It is a large project which runs from 2011 to 2021 and which involves the following other partners Inria (Lille, Sophia-Antipolis, Grenoble), INSA, UPMC, Institut Télécom Paris, Institut Télécom Evry, LSIIT Strasbourg. This section highlight Inria-EVA activity and contribution to the IoT-lab testbed in 2015.

- The Paris-Rocquencourt deployment has been stable throughout 2015.
- Thomas Watteyne and the OpenWSN community have been using the platform (all sites, not just Rocquencourt) extensively throughout 2015. Highlights include:
  - Nicola Accettura (then postdoc at UC Berkeley) created scripts to automate running OpenWSN on the IoT-lab, under the co-supervision of Thomas Watteyne and Prof. Kris Pister. Source code is available at https://github.com/openwsn-berkeley/openwsn-on-iotlab.
  - This work was presented during the OpenWSN hackathon held in conjunction with the IETF93 standardization meeting in Prague in July 2015.
  - Prof. Diego Dujovne from Universidad Diego Portales (Chile) visited Thomas Watteyne in July 2015 to work on the Mercator project (https://github.com/openwsn-berkeley/mercator) to collect Dense Wireless Connectivity Datasets for the IoT on the IoT-lab.
- The Inria-EVA team supported the IoT-lab admin team to remove malfunctioning batteries from the Inria-Rocquencourt deployment in December 2015.
- Thomas Watteyne integrated the IoT-lab admin team in December 2015. Together, they are working on a smaller test deployment with the Inria-EVA premises at Inria-Paris, on which development will be done to:
  - Allow commercial hardware to be plugged into the IoT-lab gateways.
  - Allow multiple motes to be plugged into the same IoT-lab gateway.
  - Use the IoT-lab for deploying and verifying the correct functioning of the OpenWSN implementation on all supported hardware board.
  - Use the IoT-lab for deploying and verifying the correct functioning of the OpenWSN implementation at small/medium/large scale.
- The activities above are lead by Tengfei Chang from the Inria-EVA team, under the supervision of Thomas Watteyne, and in close collaboration with the IoT-lab core team.

EX-SITU Team

6. New Software and Platforms

6.1. New Software

6.1.1. WildOS

Participant: Michel Beaudouin-Lafon [correspondant].

WildOS is middleware designed to support applications that run in an interactive room, such as our WILD and WILDER rooms, with various interaction resources, including a tiled wall display, a motion tracking system, interactive tabletops, tablets, smartphones and custom-made or 3d printed interactive devices. The conceptual model of WildOS is a *platform*, such as the WILD or WILDER room, that can be described as a set of devices on which one or more applications can be run.

WildOS consists of a server running on a machine that has network access to all the machines involved in the platform, and a set of clients running on the various interaction resources, such as a display cluster or a tablet. Once *WildOS* is running, applications can be started and stopped and devices can be added to or removed from the platform.

WildOS relies on Web technologies, most notably Javascript and node.js, as well as node-webkit and HTML5. This makes it inherently portable (it is currently tested on Mac OS X and Linux). While applications can be developed only with these Web technologies, it is also possible to bridge to existing applications developed in other environments if they provide sufficient access for remote control. Sample applications include a web browser, an image viewer, a window manager, and the BrainTwister application developed in collaboration with neuroanatomists at NeuroSpin.

WildOS is used for several research projects at ExSitu and by other partners of the Digiscope project. It was also deployed on several of Google's interactive rooms in Mountain View, Dublin and Paris. It is available under on Open Source licence at https://bitbucket.org/mblinsitu/wildos.

- ACM: H.5.2 [User Interfaces]: Graphical user interfaces (GUI)
- Software benefit: helps development of multisurface applications.
- OS/Middleware: Crossplatform
- Required library or software: node.js, node-webkit
- Programming language: Javascript

6.1.2. Unity Cluster

Participants: Cédric Fleury [correspondant], Jean-Baptiste Louvet.

Unity Cluster is middleware to distribute any Unity 3D (https://unity3d.com/) application on a cluster of computers that run in interactive rooms, such as our WILD and WILDER rooms, or immersive CAVES (Computer-Augmented Virtual Environments). Users can interact the the application with various interaction resources.

Unity Cluster provides an easy solution for running existing Unity 3D applications on any display that requires a rendering cluster with several computers. *Unity Cluster* is based on a master-slave architecture: The master computer runs the main application and the physical simulation as well as manages the input; the slave computers receive updates from the master and render small parts of the 3D scene. *Unity Cluster* manages data distribution and synchronization among the computers to obtain a consistent image on the entire wall-sized display surface.

Unity Cluster can also deform the displayed images according to the user's position in order to match the viewing frustum defined by the user's head and the four corners of the screens. This respects the motion parallax of the 3D scene, giving users a better sense of depth.

Unity Cluster is composed of a set of C Sharp scripts that manage the network connection, data distribution, and the deformation of the viewing frustum. In order to distribute an existing application on the rendering cluster, all scripts must be embedded into a Unity package that is included in an existing Unity project.

- ACM: C.2.4 [Distributed Systems]: Distributed applications, I.3.7 [3D Graphics and Realism]: Virtual reality
- Software benefit: adapts existing Unity 3D application to a rendering cluster of an interactive room.
- OS/Middleware: Crossplatform
- Required library or software: Unity 3D
- Programming language: C Sharp

6.2. Platforms

6.2.1. WILDER

Participants: Michel Beaudouin-Lafon [correspondant], Cédric Fleury, Olivier Gladin, Rémi Hellequin, Stéphane Huot, Amani Kooli, Monireh Sanaei, Gabriel Tezier, Jonathan Thorpe.

WILDER (Figure 1) is our second experimental ultra-high-resolution interactive environment, which follows the WILD platform developed in 2009 [2]. It features a wall-sized display with seventy-five 20" LCD screens, i.e. a 5m50 x 1m80 (18' x 6') wall displaying 14 400 x 4 800 = 69 million pixels, powered by a 10-computer cluster and two front-end computers. The platform also features a camera-based motion tracking system that lets users interact with the wall, as well as the surrounding space, with various mobile devices. The display uses a multitouch frame (the largest of its kind in the world) to make the entire wall touch sensitive.

WILDER was inaugurated in June, 2015. It is one of the ten platforms of the Digiscope Equipment of Excellence and, in combination with WILD and the other Digiscope rooms, provides a unique experimental environment for collaborative interaction.

In addition to using WILD and WILDER for our research, we have also developed software architectures and toolkits, such as WildOS and Unity Cluster, that enable developers to run applications on these multi-device, cluster-based systems.

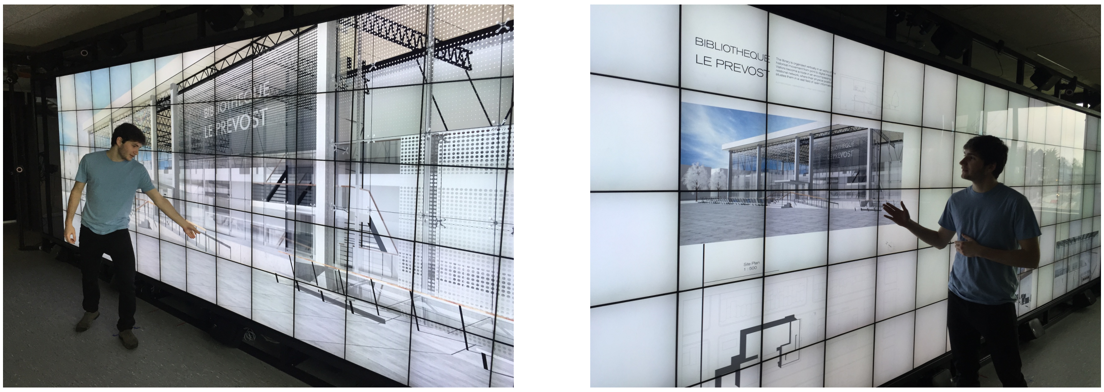


Figure 1. The WILDER platform.

EXMO Project-Team

6. New Software and Platforms

6.1. Alignment API

Participants: Jérôme Euzenat [Correspondent], Jérôme David, Nicolas Guillouet, Armen Inants.

We have designed a format for expressing alignments in a uniform way [2]. The goal of this format is to share available alignments on the web. It should help systems using alignments, e.g., mediators, translators, to take advantage of any matching algorithm and it will help matching algorithms to be used in many different tasks. This format is expressed in RDF, so it is freely extensible.

The API itself [2] is a JAVA description of tools for accessing the common format. It defines five main interfaces (OntologyNetwork, Alignment, Cell, Relation and Evaluator).

We provide an implementation for this API which can be used for producing transformations, rules or bridge axioms independently from the algorithm which produced the alignment. The proposed implementation features:

- a base implementation of the interfaces with all useful facilities;
- a library of algebras of relations;
- a library of sample matchers;
- a library of renderers (XSLT, RDF, SKOS, SWRL, OWL, C-OWL, SPARQL);
- a library of evaluators (various generalisation of precision/recall, precision/recall graphs);
- a flexible test generation framework which allows for generating evaluation datasets;
- a library of wrappers for several ontology API;
- a parser for the format.

To instanciate the API, it is sufficient to refine the base implementation by implementing the `align()` method. Doing so, the new implementation will benefit from all the services already implemented in the base implementation.

In 2015, we further integrated the implementation of link keys and their transformations into SPARQL queries (§3.3). We developed the transformation aspect of the EDOAL language. Finally, we provided the interface with alignment algebras into the API implementation (§7.1.2).

We have developed, on top of the Alignment API, an Alignment server that can be used by remote clients for matching ontologies and for storing and sharing alignments. It is developed as an extensible platform which allows to plug-in new interfaces. The Alignment server can be accessed through HTML, web service (SOAP and REST) and agent communication interfaces. It has been used this year in the Ready4SmartCities project (§9.2.1.1) [14], [20].

The Alignment API is used in the Ontology Alignment Evaluation Initiative data and result processing (§7.1.1). It is also used by more than 50 other teams worldwide.

The Alignment API is freely available since december 2003, under the LGPL licence, at http://alignapi.gforge.inria.fr.

6.2. The OntoSim library

Participants: Jérôme David [Correspondent], Jérôme Euzenat.

OntoSim is an API library offering similarity and distance measures between ontology entities as well as between ontologies themselves. It materialises our work towards better ontology proximity measures.

There are many reasons for measuring a distance between ontologies. For example, in semantic social networks, when a peer looks for particular information, it could be more appropriate to send queries to peers having closer ontologies because it will be easier to translate them and it is more likely that such a peer has the information of interest. OntoSim provides a framework for designing various kinds of similarities. In particular, we distinguish similarities in the ontology space from those in the alignment space. The latter ones use available alignments in an ontology network while the former only rely on ontology data. OntoSim is provided with 4 entity measures which can be combined using various aggregation schemes (average linkage, Hausdorff, maximum weight coupling, etc.), 2 kinds of vector space measures (boolean and TFIDF), and 4 alignment space measures. It also features original comparison methods such as agreement/disagreement measures. In addition, the framework embeds external similarity libraries which can be combined to our own.

In 2015, OntoSim only supported a maintenance upgrade.

OntoSim is based on an ontology interface allowing for using ontology parsed with different APIs. It is written in JAVA and is available, under the LGPL licence, at http://ontosim.gforge.inria.fr.

FLOWERS Project-Team

6. New Software and Platforms

6.1. Poppy project

6.1.1. Introduction

- Participants: Matthieu Lapeyre, Pierre Rouanet, Nicolas Rabault, Theo Segonds, Jonathan Grizou and Pierre-Yves Oudeyer
- Contact: Pierre-Yves Oudeyer
- URL: https://www.poppy-project.org/

The Poppy Project develops open-sources 3D printed robots platforms based on robust, flexible, easy-to-use and reproduce hardware and software. In particular, the use of 3D printing and rapid prototyping technologies is a central aspect of this project, and makes it easy and fast not only to reproduce the platform, but also to explore morphological variants. Poppy targets three domains of use: science, education and art.

6.1.2. Poppy Ergo Jr (hardware)

Poppy Ergo Jr is a new open hardware robot developped by the Poppy Project to explore the use of robots in classroom for learning robotic and computer science. It is a 6-Dofs arm designed to be both expressiv and low-cost. This is achieved by the use of FDM 3D printing, low cost Robotis XL-320 actuators. In addition we have added a Pi camera so the robot can detect object, faces or QR codes.

The Ergo Jr is controlled by the pypot software running on a Raspberry pi 2. The communication between the Raspberry pi and the actuators is made possible by the Pixl board we have designed.

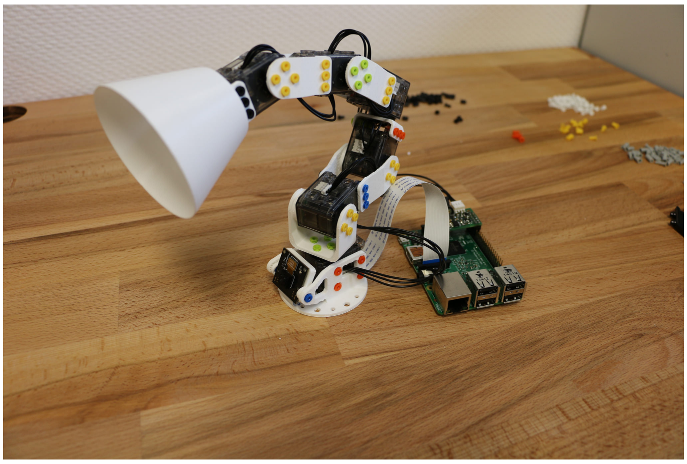


Figure 1. The new open hardware Poppy Ergo Jr, 6-DoFs arm robot for education

The sources are availables on the following web platforms:

- Github repository: https://github.com/poppy-project/poppy-ergo-jr
- CAD files: https://cad.onshape.com/documents/10951c2120eb4209abfff972/w/2b2ed99178db4a72aa4ebcc9

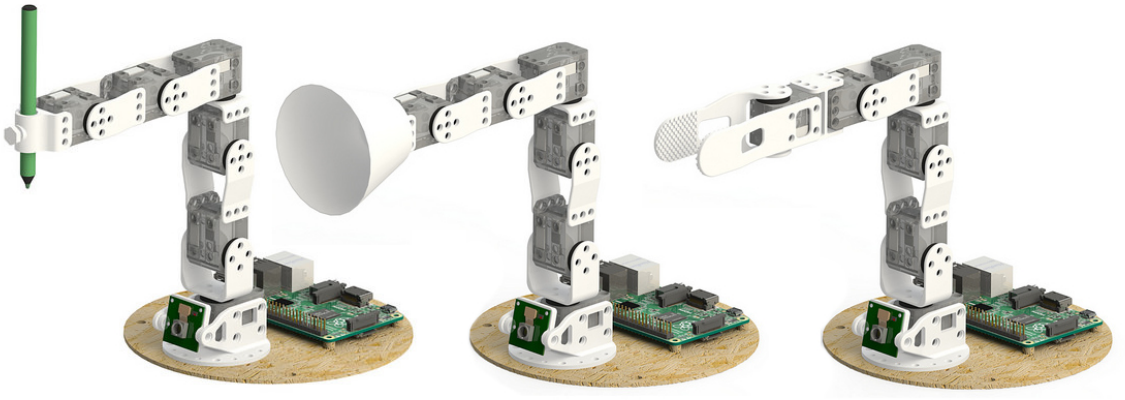


Figure 2. The Ergo Jr has 3 tools, a pen holder, a lampshade and a gripper

The Poppy Ergo Jr has several 3D printed tools to extend its capabilities. There are currently the lampshade, the gripper and a pen holder.

6.1.3. Pixl (Electronics)

Pixl is a tiny board used to create low cost robots based on raspbery pi and XL320 motors. This board have bean created by the Poppy project team. Pixl have 2 main features, the power part, and the communication part :

- The power part allow the user to plug an 7V AC/DC converter directly into the Pixl. This power will be distributed to all XL320 motors and will be converted to 5V for the raspberry pi.
- The communication part convert full duplex to half duplex and vice versa. The half duplex part switch between RX and TX automatically. Another connector allow the user to connect his XL320 network.

6.1.4. Poppy Com

FUNCTIONAL DESCRIPTION

Poppy-com is a low level library who manage the new poppy system communication protocol. This work in progress library, writen in C/C++, is completely open-source and available on github. Atctually poppy-com work with Atmel ATMEGA series microcontroler and a test version can be run on X86 architectures. His main objectiv is to give access to the user at the lowest level of code. Each poppy system module run this code to be detected into the robt network and to comunicate with others modules. Users can write theire owns code and write it in any module. With this new level the user can create basic behavior directly into a poppy system module.

- Bootloader : The bootloader have to manage robot network discovery, auto-addressing, module specific firmware update validation, and user code update.
- User : The user side have a small part of code dedicated to the module management like motor management routines, sensors synchronizations, numerical treatment of signals... The empty memory of each modules can be used by the user and he can add his own code to manage his robot.

This library will be compatible with the Arduino univers, that allow non expert people to use it anyway. To simplify the robot functionality developpement and function execution localization we want to try to create a way to write a code for all a robot modules on only one code. Each function of this code could be redirected in a specific module, the execution can be completely distributed.

- Participants: Pierre Rouanet, Matthieu Lapeyre, Nicolas Rabault and Pierre-Yves Oudeyer
- Contact: Pierre-Yves Oudeyer
- URL: https://www.poppy-project.org/
- Contact: Nicolas Rabault
- URL: https://github.com/poppy-project/poppy-com

6.1.5. Poppy System

FUNCTIONAL DESCRIPTION

In the Poppy project we are working on the Poppy System which is a new modular and open-source robotic architecture. It is designed to help people create and build custom robots. It permits, in a similar approach as Lego, building robots or smart objects using standardized elements.

Poppy System is an unified system where each essential robotic components (actuators, sensors, ...) is an independant module, connected with other through standardized interfaces:

- Unified mechanical interfaces which simplifies the assembly process and the design of 3D printable parts.
- Unified communication between elements using the same connector and bus for each module.
- Unified software makes it easy to program each module independantly.

The current Poppy robots (Humanoid, Torso, Ergo) will be updated using this novel architecture.

Our ambition is to create an ecosystem around this system so communities can develop custom modules, following the Poppy System standards, which can be compatible with all other Poppy robots.

6.1.6. Pypot

SCIENTIFIC DESCRIPTION

Pypot is a framework developed to make it easy and fast to control custom robots based on dynamixel motors. This framework provides different levels of abstraction corresponding to different types of use. More precisely, you can use pypot to:

- directly control robotis motors through a USB2serial device,
- define the structure of your particular robot and control it through high-level commands,
- define primitives and easily combine them to create complex behavior.

Pypot is part of the Poppy project. It is the core library used by the different Poppy robots. This abstraction layer allows to seamlessly switch from one of the Poppy robot to another. It also provides a common set of tools, such as forward and inverse kinematics, simple computer vision, recording and replaying moves, or easy access to the autonomous exploration library Explauto.

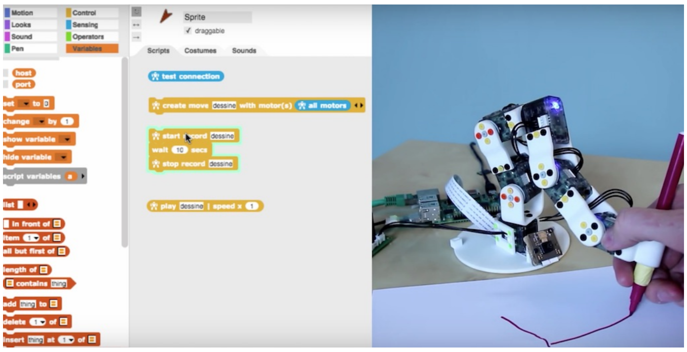
To extend pypot application domains and connection to outside world, it also provides an HTTP REST API. On top of providing an easy way to connect to smart sensors or connected devices, it is notably used to connect to Snap! a variant of the well-known Scratch visual programming language.

FUNCTIONAL DESCRIPTION

Pypot has been entirely written in Python to allow for fast development, easy deployment and quick scripting by non-necessary expert developers. It can also benefits from the scientific and machine learning libraries existing in Python. The serial communication is handled through the standard library and thus allows for rather high performance (10ms sensorimotor loop). It is crossed-platform and has been tested on Linux, Windows and Mac OS.

Pypot is also compatible with the V-REP simulator. This allows the transparent switch from a real robot to its simulated equivalent without having to modify the code.

Finally, it has been developed to permit an easy and fast extension to other types of motors and sensors.



```
test connection

create move dessine with motor(s) all motors

start record dessine
wait 10 secs
stop record dessine

play dessine | speed x 1
```

Figure 3. Example of using pypot to program a robot to reproduce a drawn shape

It works with Python 2.7 or Python 3.3 or later. It has also been adapted to the Raspberry-Pi board.

CONNECTION WITH THE VISUAL PROGRAMMING LANGUAGE SNAP!

Pypot has been connected to Snap!, a variant of the famous Scratch visual language, developed for teaching computer science to children. It is based on blocks that can be dragged-and-drop, and assembled to write scripts.

Thanks to the Snap! HTTP block, a connection can be made to pypot allowing users to directly control robots through their visual interfaces. A set of dedicated Snap! blocks have been designed, such as *set motor position* or *get motor temperature*.

Figure 4. Using Snap! to program a robot by demonstration and create complex choreographies

Snap! is also used as a tool for programming the robot by demonstration. Thanks to *record* and *play* blocks, users can easily trigger kinesthetic recording of the robots (or only subpart such as one arm). They can then be played or "mixed" - either played in sequence or in parallel - with other recordings to compose complex choreographies. The moves are encoded as a model of mixture of gaussians (GMM) which allows the definition of clean mathematical operators for combining them.

This tool has been developed and used in collaboration with artists who investigate the concept of robotic moves.

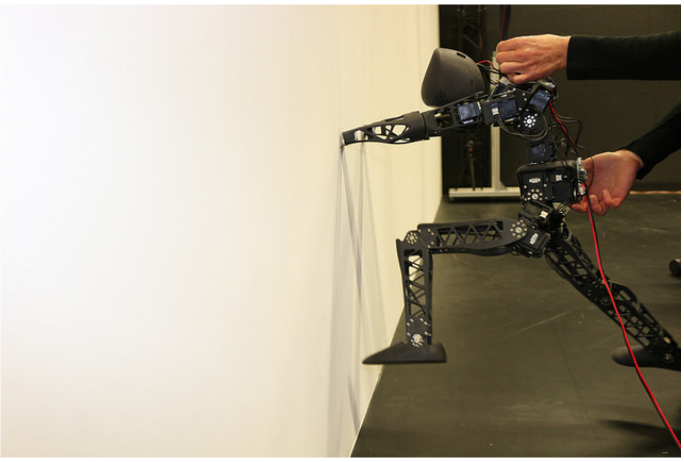


Figure 5. Artistic project exploring the concept of robotic move.

DISSEMINATION AND CONTRIBUTION

The pypot source file are released under the GPLv3 license and can be accessed on Github. They have been downloaded about 50k times (source Python Package Index) and forked about 50 times (source Github).

18 contributors have participated to its development.

Pypot are also largely based on jupyter notebooks to provide examples, tutorials or scientific experiments.

- Participants: Pierre Rouanet, Theo Segonds, Matthieu Lapeyre
- Contact: Pierre Rouanet
- URL: https://github.com/poppy-project/pypot

6.1.7. Inverse kinematics library

FUNCTIONAL DESCRIPTION

IKPy is a Python Inverse Kinematics library, designed to be simple to use and extend. It provides Forward and Inverse kinematics functionalities, bundled with helper tools such as 3D plotting of the kinematics chains. Being written entirely in Python, IKPy is lightweight and is based on numpy and scipy for fast optimization. IKPy is compatible with many robots, by automatically parsing URDF files. It also supports other (such as DH-parameters) and custom representations. Moreover, it provides a framework to easily implement new Inverse Kinematics strategies. Originally developed for the Poppy project, it can also be used as a standalone library. IKPy is open-source, and can be found at: https://github.com/Phylliade/ikpy

- Participants: Pierre Manceron, Pierre Rouanet, Pierre-Yves Oudeyer
- Contact: Pierre Rouanet
- URL: https://github.com/Phylliade/ikpy

6.2. Tools for robot learning, control and perception

6.2.1. CARROMAN

FUNCTIONAL DESCRIPTION

This software implements a control architecture for the Meka humanoid robot. It integrates the Stanford Whole Body Control in the M3 architecture provided with the Meka robot, and provides clear and easy to use interfaces through the URBI scripting language. This software provides a modular library of control modes and basic skills for manipulating objects, detecting objects and humans which other research projects can reuse, extend and enhance. An example would be to locate a cylindrical object on a table using stereo vision, and grasping it using position and force control.

- Contact: David Filliat

6.2.2. DMP-BBO

Black-Box Optimization for Dynamic Movement Primitives

FUNCTIONAL DESCRIPTION

The DMP-BBO Matlab library is a direct consequence of the insight that black-box optimization outperforms reinforcement learning when using policies represented as Dynamic Movement Primitives. It implements several variants of the PIBB algorithm for direct policy search. The `dmp_bbo` C++ library (https://github.com/stulp/dmpbbo) has been extended to include the "unified model for regression", see Section 7.2.3 . The implementation of several of the function approximators have been made real-time compatible.

- Participant: Freek Stulp
- Contact: Freek Stulp
- URL: https://github.com/stulp/dmpbbo

6.2.3. DyNAMoS

FUNCTIONAL DESCRIPTION

This simulation software comes in the form of a PYTHON module and allows a user to define and simulate complex neural architectures while making use of the parallelism inherent to modern multi-core processors. A special focus lies on on-line learning, processing inputs one by one, in contrast to batch processing of whole databases at a time.

- Participants: Alexander Gepperth and Mathieu Lefort
- Contact: Mathieu Lefort

6.2.4. Multimodal Concept Learning with Non-negative Matrix Factorization

FUNCTIONAL DESCRIPTION

The python code provides a minimum set of tools and associated libraries to reproduce the experiments in [98] , together with the choreography datasets. The code is primarily intended for reproduction of the mulimodal learning experiment mentioned above. It has already been reused in several experimentations by other member of the team and is expected to play an important role in further collaborations. It is also expected that the public availability of the code encourages further experimentation by other scientists with data coming from other domains, thus increasing both the impact of the aforementioned publication and the knowledge on the algorithm behaviors.

- Participant: Olivier Mangin
- Contact: Olivier Mangin
- URL: https://github.com/omangin/multimodal

6.2.5. Explorers

FUNCTIONAL DESCRIPTION

The Explorers framework is aimed at creating, testing and comparing autonomous exploration strategies for sensorimotor spaces in robots. The framework is largely strategy-agnostic, and is aimed as expressing motor babbling, goal babbling and intrinsically motivated exploration algorithms, among other. It is also able to express strategies that feature transfer learning, such as the reuse algorithm.

- Participants: Pierre-Yves Oudeyer and Fabien Benureau
- Contact: Pierre-Yves Oudeyer
- URL: https://github.com/humm/explorers

6.2.6. Of 3-D point cloud

FUNCTIONAL DESCRIPTION

This software scans the 3-D point cloud of a scene to find objects and match them against a database of known objects. The process consists in 3 stages. The segmentation step finds the objects in the point cloud, the feature extraction computes discriminating properties to be used in the classification stage for object recognition.

- Participants: David Filliat, Alexander Gepperth and Louis-Charles Caron
- Contact: Alexander Gepperth

6.2.7. OptiTrack

FUNCTIONAL DESCRIPTION

This python library allows you to connect to an OptiTrack from NaturalPoint. This camera permits the tracking of 3D markers efficiently and robustly. With this library, you can connect to the Motive software used by the OptiTrack and retrieve the 3D position and orientation of all your tracked markers directly from python.

- Participant: Pierre Rouanet
- Contact: Pierre Rouanet

6.2.8. PEDDETECT

FUNCTIONAL DESCRIPTION

PEDDETECT implements real-time person detection in indoor or outdoor environments. It can grab image data directly from one or several USB cameras, as well as from pre-recorded video streams. It detects mulitple persons in 800x600 color images at frame rates of >15Hz, depending on available GPU power. In addition, it also classifies the pose of detected persons in one of the four categories "seen from the front", "seen from the back", "facing left" and "facing right". The software makes use of advanced feature computation and nonlinear SVM techniques which are accelerated using the CUDA interface to GPU programming to achieve high frame rates. It was developed in the context of an ongoing collaboration with Honda Research Institute USA, Inc.

- Participant: Alexander Gepperth
- Contact: Alexander Gepperth

6.2.9. pyStreamPlayer

FUNCTIONAL DESCRIPTION

This Python software is intended to facilitate the application of machine learning algorithms by avoiding to work directly with an embodied agent but instead with data recorded in such an agent. Assuming that non-synchronous data from multiple sensors (e.g., camera, Kinect, laser etc.) have been recorded according to a flexible format defined by the pyStreamPlayer architecture, pyStreamPlayer can replay these data while retaining the exact temporal relations between different sensor measurements. As long as the current task does not involve the generation of actions, this software allows to process sensor data as if it was coming from an agent which is usually considerably easier. At the same time, pyStreamPlayer allows to replay arbitrary supplementary information such as, e.g., object information, as if it was coming from a sensor. In this way, supervision information can be stored and accessed together with sensory measurements using an unified interface. pyStreamPlayer has been used to facilitate real-world object recognition tasks, and several of the major databases in this field (CalTech Pedestrian database, HRI RoadTraffic traffic objects database, CVC person database, KITTI traffic objects database) have been converted to the pyStreamPlaer format and now serve as a source of training and test data for learning algorithms.

- Participant: Alexander Gepperth
- Contact: Alexander Gepperth

6.2.10. Aversive++

FUNCTIONAL DESCRIPTION

Aversive++ is a C++ library that eases microcontroller programming. Its aim is to provide an interface simple enough to be able to create complex applications, and optimized enough to enable small microcontrollers to execute these applications. The other aspect of this library is to be multiplatform. Indeed, it is designed to provide the same API for a simulator (named SASIAE) and for AVR-based and ARM-based microcontrollers.

- Participants: Loïc Dauphin
- Contact: Loïc Dauphin
- Website: http://aversiveplusplus.com/

6.3. Explauto: Autonomous Exploration and Learning Benchmarking

An autonomous exploration library

SCIENTIFIC DESCRIPTION

An important challenge in Developmental Robotics is how robots can efficiently learn sensorimotor mappings by experience, i.e. the mappings between the motor actions they make and the sensory effects they produce. This can be a robot learning how arm movements make physical objects move, or how movements of a virtual vocal tract modulates vocalization sounds. The way the robot will collects its own sensorimotor experience have a strong impact on learning efficiency because for most robotic systems the involved spaces are high dimensional, the mapping between them is non-linear and redundant, and there is limited time allowed for learning. If robots explore the world in an unorganized manner, e.g. randomly, learning algorithms will be often ineffective because very sparse data points will be collected. Data are precious due to the high dimensionality and the limited time, whereas data are not equally useful due to non-linearity and redundancy. This is why learning has to be guided using efficient exploration strategies, allowing the robot to actively drive its own interaction with the environment in order to gather maximally informative data to feed the sensorimotor model.

In the recent year, work in developmental learning has explored various families of algorithmic principles which allow the efficient guiding of learning and exploration.

Explauto is a framework developed to study, model and simulate curiosity-driven learning and exploration in virtual and robotic agents. Explauto's scientific roots trace back from Intelligent Adaptive Curiosity algorithmic architecture [120], which has been extended to a more general family of autonomous exploration architecture by [73] and recently expressed as a compact and unified formalism [114]. The library is detailed in [115].

In Explauto, the strategies to explore sensorimotor models are called interest models. They implements the active exploration process, where sensorimotor experiments are chosen to improve the forward or inverse prediction of the sensorimotor model. The simplest strategy is to randomly draw goals tin the motor or sensory space. More efficient strategies are based on the active choice of learning experiments that maximize learning progress, for e.g. improvement of predictions or of competences to reach goals [120]. This automatically drives the system to explore and learn first easy skills, and then explore skills of progressively increasing complexity. Both random and learning progress models can act either on the motor or on the sensory space, resulting in motor babbling or goal babbling strategies.

- Motor babbling consists in sampling commands in the motor space according to a given strategy (random or learning progress), predicting the expected sensory consequence, executing the command through the environment and observing the actual sensory effect. Both sensorimotor and interest models are finally updated according to this experience.
- Goal babbling consists in sampling goals in the sensory effect space and to use the current state of the sensorimotor model to infer a motor action supposed to reach the goals (inverse prediction). The robot/agent then executes the command through the environment and observes the actual sensory effect. Both sensorimotor and interest models are finally updated according to this experience.

It has been shown that this second strategy allows a progressive covering of the reachable sensory space much more uniformly than in a motor babbling strategy, where the agent samples directly in the motor space [73].

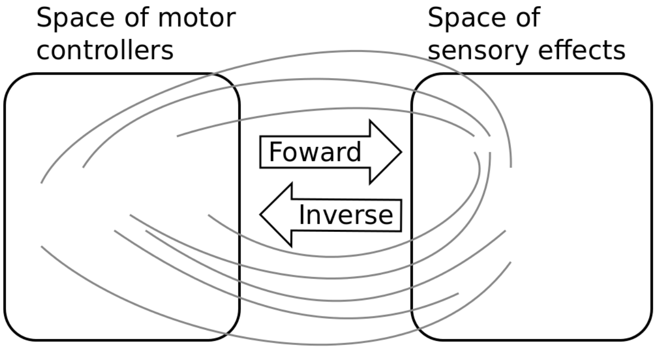


Figure 6. Complex sensorimotor mappings involve a high dimensional sensorimotor spaces. For the sake of visualization, the motor M and sensory S spaces are only 2D each in this example. The relationship between M and S is non-linear, dividing the sensorimotor space into regions of unequal stability: small regions of S can be reached very precisely by large regions of M, or large regions in S can be very sensitive to variations in M.: s as well as a non-linear and redundant relationship. This non-linearity can imply redundancy, where the same sensory effect can be attained using distinct regions in M.

FUNCTIONAL DESCRIPTION

This library provides high-level API for an easy definition of:

- Virtual and robotics setups (Environment level),
- Sensorimotor learning iterative models (Sensorimotor level),
- Active choice of sensorimotor experiments (Interest level).

The library comes with several built-in environments. Two of them corresponds to simulated environments: a multi-DoF arm acting on a 2D plan, and an under-actuated torque-controlled pendulum. The third one allows to control real robots based on Dynamixel actuators using the Pypot library.

Learning sensorimotor mappings involves machine learning algorithms, which are typically regression algorithms to learn forward models, from motor controllers to sensory effects, and optimization algorithms to learn inverse models, from sensory effects, or goals, to the motor programs allowing to reach them. We call these sensorimotor learning algorithms sensorimotor models. The library comes with several built-in sensorimotor models: simple nearest-neighbor look-up, non-parametric models combining classical regressions and optimization algorithms, online mixtures of Gaussians, and discrete Lidstone distributions. Explauto sensorimotor models are online learning algorithms, i.e. they are trained iteratively during the interaction of the robot in the environment in which it evolves.

Explauto provides also a unified interface to define exploration strategies using the InterestModel class. The library comes with two built-in interest models: random sampling as well as sampling maximizing the learning progress in forward or inverse predictions.

This library has been used in many experiments including:

- the control of a 2D simulated arm,
- the exploration of the inverse kinematics of a poppy humanoid (both on the real robot and on the simulated version),
- accoustic model of a vocal tract.

Explauto is crossed-platform and has been tested on Linux, Windows and Mac OS. It has been released under the GPLv3 license.

- Participants: Pierre Rouanet, Clément Moulin-Frier, Sébastien Forestier, Pierre-Yves Oudeyer
- Contact: Pierre Rouanet
- URL: https://github.com/flowersteam/explauto

6.4. KidLearn: active teaching in Intelligent Tutoring Systems

KEYWORD: Automatic Learning
FUNCTIONAL DESCRIPTION

KidLearn is a software which adaptively personalize sequences of learning activities to the particularities of each individual student. It aims at proposing to the student the right activity at the right time, maximizing concurrently his learning progress and its motivation.

- Participants: Benjamin Clement, Pierre Yves Oudeyer, Didier Roy and Manuel Lopes
- Contact: Manuel Lopes
- URL: https://flowers.inria.fr/research/kidlearn/

6.5. Self-calibration BCI

KEYWORDS: Neurosciences - Health - Brain-Computer Interface
FUNCTIONAL DESCRIPTION

Self-calibration BCI is a Matlab library which allows a robot to be instructed a new task by a human using communicative signals initially totally unknown to the robot. It is was extended and improved in the context of EEG-based brain-machine interfaces (BMIs).

It results in a BCI based control of sequential tasks with feedback signals that do not require any calibration process. As a by-product, the method provides an unsupervised way to train a decoder with the same performance than state-of-the-art supervised classifiers, while keeping the system operational and solving, with a lower performance during the first steps, the unknown task. The algorithm has been tested with online experiments, showing that the users were able to guide from scratch an agent to a desired position.

- Participants: Manuel Lopes, Jonathan Grizou and Pierre-Yves Oudeyer
- Contact: Jonathan Grizou
- URL: https://github.com/flowersteam/self_calibration_BCI_plosOne_2015/

6.6. Platforms

6.6.1. Platform: Collaborative assemblies with Baxter

- Participant: Yoan Mollard, Baptiste Busch, Thibaut Munzer
- Contact: Yoan Mollard

FUNCTIONAL DESCRIPTION This platform is a set of software components and hardware robotic components designed as an experimental setup for performing scientific experiments with the Baxter robot illustrating human-robot collaboration. It comes with a set of capabilities (pick objects, handover, hold objects in place, ...) and physical objects (screwdriver, landmarks, camera mounts, ...) created on purpose or hacked to serve these capabilities. The initial capabilities focus on industrial activities and allow the robot to provide assistance to workers in manufacturing factories for their daily tasks (pieces fetching, screwing, assembly, ...). We simulated an industrial environment with a trolley acting as a feeder where all spare parts are initially located, a workspace for the worker and 7 spare parts composing a wooden toolbox that users and robot will handle for their collaborative tasks. This industrial environment is the one of the 3rd hand project, but the platform and its capabilities will progessively be improved and enriched to be used for other projects. The picture 7 illustrates the experimental setup.

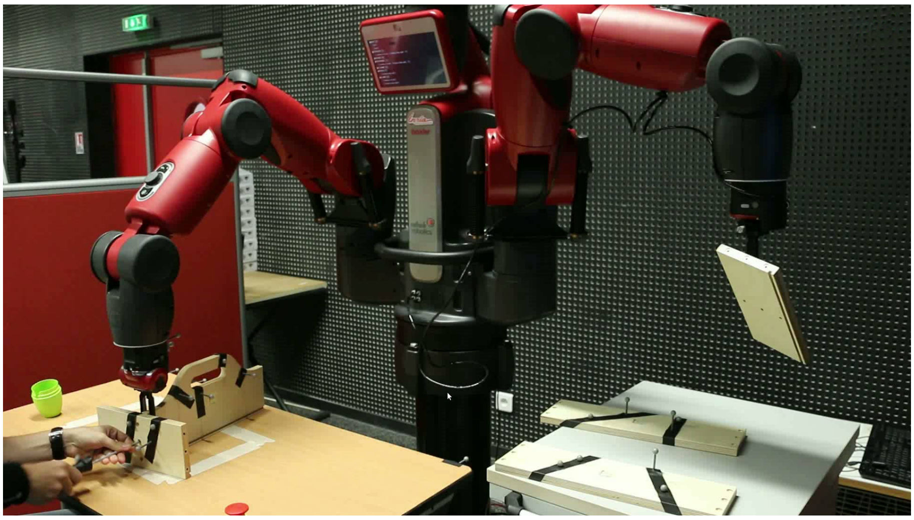


Figure 7. Experimental setup for human-robot collaborative assemblies of a wooden toolbox

FLUMINANCE Project-Team

5. New Software and Platforms

5.1. 2DLayeredMotion

Estimation of 2D independent mesoscale layered atmospheric motion fields
FUNCTIONAL DESCRIPTION

This software enables to estimate a stack of 2D horizontal wind fields corresponding to a mesoscale dynamics of atmospheric pressure layers. This estimator is formulated as the minimization of a global energy function. It relies on a vertical decomposition of the atmosphere into pressure layers. This estimator uses pressure data and classification clouds maps and top of clouds pressure maps (or infra-red images). All these images are routinely supplied by the EUMETSAT consortium which handles the Meteosat and MSG satellite data distribution. The energy function relies on a data model built from the integration of the mass conservation on each layer. The estimator also includes a simplified and filtered shallow water dynamical model as temporal smoother and second-order div-curl spatial regularizer. The estimator may also incorporate correlation-based vector fields as additional observations. These correlation vectors are also routinely provided by the Eumetsat consortium.

- Participant: Etienne Mémin
- Contact: Etienne Mémin
- URL: http://fluid.irisa.fr/index.html

5.2. 3DLayeredMotion

Estimation of 3D interconnected layered atmospheric motion fields
FUNCTIONAL DESCRIPTION

This software extends the previous 2D version. It allows the recovery of 3D wind fields from satellite image sequences. As with the previous techniques, the atmosphere is decomposed into a stack of pressure layers. The estimation relies also on pressure data and classification clouds maps and top of clouds pressure maps. In order to recover the 3D missing velocity information, physical knowledge on 3D mass exchanges between layers has been introduced in the data model. The corresponding data model appears to be a generalization of the previous data model constructed from a vertical integration of the continuity equation.

- Contact: Etienne Mémin
- URL: http://fluid.irisa.fr

5.3. DenseMotion

Estimation of 2D dense motion fields
FUNCTIONAL DESCRIPTION

This code allows the computation from two consecutive images of a dense motion field. The estimator is expressed as a global energy function minimization. The code enables the choice of different data models and different regularization functionals depending on the targeted application. Generic motion estimators for video sequences or fluid flows dedicated estimators can be set up. This software allows in addition the users to specify additional correlation based matching measurements. It enables also the inclusion of a temporal smoothing prior relying on a velocity vorticity formulation of the Navier-Stoke equation for Fluid motion analysis applications. The different variants of this code correspond to research studies that have been published in IEEE transaction on Pattern Analysis and machine Intelligence, Experiments in Fluids, IEEE transaction on Image Processing, IEEE transaction on Geo-Science end Remote Sensing. The binary of this code can be freely downloaded on the FLUID web site http://fluid.irisa.fr.

- Participants: Étienne Mémin and Thomas Corpetti
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.4. Low-Order-Motion - Estimation of low order representation of fluid motion

Low order description and estimation of 2D dense motion fields
FUNCTIONAL DESCRIPTION This code enables the estimation of a low order representation of a fluid motion field from two consecutive images.The fluid motion representation is obtained using a discretization of the vorticity and divergence maps through regularized Dirac measure. The irrotational and solenoidal components of the motion fields are expressed as linear combinations of basis functions obtained through the Biot-Savart law. The coefficient values and the basis function parameters are formalized as the minimizer of a functional relying on an intensity variation model obtained from an integrated version of the mass conservation principle of fluid mechanics.

- Participants: Étienne Mémin and Anne Cuzol
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.5. TYPHOON

GPU implementation of wavelet based motion estimator for Lidar data. This code is developped in coproperty between Inria and Chico.
FUNCTIONAL DESCRIPTION Typhoon is a motion estimation software specialized in fluid motion estimation. It is based on a dense optical flow technique associated to a multiscale wavelet representation of the estimated motion.

- Participants: Pierre Dérian, Christopher Mauzey and Étienne Mémin
- Contact: Étienne Mémin

FOCUS Project-Team

6. New Software and Platforms

6.1. AIOCJ

SCIENTIFIC DESCRIPTION

AIOCJ is an open-source choreography programming language for developing adaptive systems. It allows one to program adaptive distributed systems based on message passing. AIOCJ comes as a plugin for Eclipse, AIOCJ-ecl, allowing to edit descriptions of distributed systems as adaptive interaction-oriented choreographies (AIOC). From interaction-oriented choreographies the description of single participants can be automatically derived. Adaptation is specified by rules allowing to replace predetermined parts of the AIOC with a new behaviour. A suitable protocol ensures that all the participants are updated in a coordinated way. As a result, the distributed system follows the specification given by the AIOC under all changing sets of adaptation rules and environment conditions. In particular, the system is always deadlock free. AIOCJ can interact with external services, seen as functions, by specifying their URL and the protocol they support (HTTP, SOAP, ...). Deadlock-freedom guarantees of the application are preserved provided that those services do not block.

- Contact: Saverio Giallorenzo
- URL: http://www.cs.unibo.it/projects/jolie/aiocj.html

6.2. DF4ABS

Deadlock Framework for ABS

SCIENTIFIC DESCRIPTION

We have prototyped a framework for statically detecting deadlocks in a concurrent object-oriented language with asynchronous method calls and cooperative scheduling of method activations (the language is ABS, which has been developed in the EU project HATS and currently extended with primitives for cloud-computing in the EU project ENVISAGE. ABS is very similar to ASP, developed by the OASIS team.). Since this language features recursion and dynamic resource creation, deadlock detection is extremely complex and state-of-the-art solutions either give imprecise answers or do not scale. In order to augment precision and scalability we propose a modular framework that allows several techniques to be combined. The basic component of the framework is a front-end inference algorithm that extracts abstract behavioural descriptions of methods that retain resource dependency information. Then these behavioural descriptions are analysed by a back-end that uses a fix-point technique to derive in a deterministic way the deadlock information.

- Contact: Elena Giachino
- URL: http://df4abs.nws.cs.unibo.it/

6.3. HoCA

Higher-Order Complexity Analysis

SCIENTIFIC DESCRIPTION

Over the last decade, various tools for the static analysis of resource properties of programs have emerged. In particular, the rewriting community has recently developed several tools for the time complexity analysis of term rewrite systems. These tools have matured and are nowadays able to treat non-trivial programs, in a fully automatic setting. However, none of these automatic complexity analysers can deal with higher-order functions, a pervasive feature of functional programs.

Our tool HoCA (Higher-Order Complexity Analyser) overcomes this limitation by translating higher-order programs – in the form of side-effect free OCaml programs – into equivalent first-order rewrite systems. At the heart of our tool lies Reynold's defunctionalization technique. Defunctionalization however is not enough. Resulting programs have a recursive structure too complicated to be analysed automatically in all but trivial cases. To overcome this issue, HoCA integrates a handful of well established program transformation techniques, noteworthy dead-code elimination, inlining, instantiation and uncurrying. All these techniques have been specifically suited to the methods integrated in modern first-order complexity analysers. Of course, the complete transformation pipeline underlying our tool is not only proven semantically correct, but also to reflect the runtime behavior. This way, a complexity bound on the resulting first-order program can be relayed back reliably to the higher-order program of interest.
A detailed description of HoCA is available on http://arxiv.org/abs/1506.05043

- Contact: Ugo Dal Lago
- URL: http://cbr.uibk.ac.at/tools/hoca/

6.4. JOLIE

Java Orchestration Language Interpreter Engine
SCIENTIFIC DESCRIPTION

Jolie is a service-oriented programming language. Jolie can be used to program services that interact over the Internet using different communication protocols.

Differently from other Web Services programming languages such as WS-BPEL, Jolie is based on a user-friendly C/Java-like syntax (more readable than the verbose XML syntax of WS-BPEL) and, moreover, the language is equipped with a formal operational semantics. This language is used for the *proof of concepts* developed around Focus activities. For instance, contract theories can be exploited for checking the conformance of a Jolie program with respect to a given contract.
Developments in 2015: Jolie has transitioned from version 1.1 to version 1.4.1. The releases are the result of more than 400 commits with hundreds of bug fixes and enhancements. Highlights include: a new web site and documentation, a new pre-compiled installer, 2 new IDEs as plugins for the editors Sublime Text and Atom, a transition from SouceForge to GitHub, introduction of new behavioural and architectural constructs, structured support for the development of REST applications, introduction of the construct of internal services: embedded Jolie services defined directly within the embedder program (internal services offer a convenient way of reusing code as in procedural programming, without breaking the principle that such code should be easily exported to an external microservice), increased compliance with protocol standards (foremost HTTP, SSL), enhanced stability and performances. Moreover, 2015 has seen the development of Jolie Redeployment Optimiser (JRO), a tool for the automatic and optimised deployment of microservices written in Jolie. JRO uses Zephyrus, a state-of-the-art tool that automatically generates configurations starting from partial and abstract descriptions of the target application. Given the output configuration from Zephyrus, JRO interacts with Jolie Enterprise, an administrative tool for the deployment of Jolie services on remote nodes, to deploy the wanted architecture.

- Contact: Fabrizio Montesi, Saverio Giallorenzo
- URL: http://www.jolie-lang.org/

6.5. SRA

Static Resource Analyzer for ABS
SCIENTIFIC DESCRIPTION

We prototype a static analysis technique that computes upper bounds of virtual machine usages in a concurrent language with explicit acquire and release operations of virtual machines. In our language it is possible to delegate other (ad-hoc or third party) concurrent code to release virtual machines (by passing them as arguments of invocations, a feature that is used by Amazon Elastic Cloud Computing or by the Docker FiWare). Our technique is modular and consists of (i) a type system associating programs with behavioural descriptions that record relevant information for resource usage (creations, releases, and concurrent operations), (ii) a translation function that takes behavioural types and returns cost equations, and (iii) an automatic off-the-shelf solver for the cost equations.

- Contact: Elena Giachino
- URL: http://sra.cs.unibo.it/

6.6. SUNNY-CP

SCIENTIFIC DESCRIPTION

Within the Constraint Programming paradigm, a portfolio solver combines different constraint solvers in order to create a globally better solver. Sunny-cp is a parallel parallel portfolio solver capable of solving Constraint (Satisfaction/Optimization) Problems defined in the MiniZinc language. It essentially implements the SUNNY algorithm introduced in the team. Sunny-cp is built on top of state-of-the-art constraint solvers, including: Choco, Chuffed, CPX, G12/LazyFD, G12/FD, G12/Gurobi, G12/CBC, Gecode, HaifaCSP, iZplus, MinisatID, Opturion, OR-Tools

SUNNY-CP is a portfolio solver for solving both Constraint Satisfaction Problems and Constraint Optimization Problems. The goal of SUNNY-CP is to provide a flexible, configurable, and usable CP portfolio solver that can be set up and executed just like a regular individual CP solver.

- Contact: Roberto Amadini
- URL: https://github.com/CP-Unibo/sunny-cp

6.7. Blender

SCIENTIFIC DESCRIPTION

The various tools developed in the Aeolus project (Zephyrus, Metis, Armonic) have been combined in this software which represents an integrated solution for the declarative specification of cloud applications, and its subsequent automatic deployment on an OpenStack cloud system. In particular, a web-based interface is used to specify the basic software artifacts to include in the application, indicate their level of replication, and specify co-installability conflicts (i.e. when two components cannot be installed on the same virtual machines). The tool Zephyrus is then used to synthesize the final architecture of the application, the tool Metis indicates the plan of configuration actions, and the Armonic platform provides the library of components and the low-level scripts to actually install and configure the entire application.

- Partners: IRILL - Mandriva
- Contact: Gianluigi Zavattaro
- URL: https://github.com/aeolus-project/blender

FUN Project-Team

6. New Software and Platforms

6.1. IoT-LAB robots

KEYWORDS: Internet of things - Robotics
FUNCTIONAL DESCRIPTION

IoT-LAB robots is an embedded robot controller on a Turtlebot2 providing the IoT-LAB node mobility functionality.

- Partner: Université de Strasbourg

6.2. FIT IoT-Lab

Participants: Raymond Borenstein, Nathalie Mitton [correspondant], Julien Vandaele.

FIT IoT-LAB is a very large scale open testbed that features over 2700 wireless sensor nodes and more than 200 robots spread across six different sites in France. Nodes are either fixed or mobile and can be allocated in various topologies throughout all sites. A variety of wireless sensors are available, with different processor architectures (MSP430, STM32 and Cortex-A8) and different wireless chips (802.15.4 PHY at 800 MHz or 2.4 GHz). In addition, "open nodes" can receive custom wireless sensors for inclusion in IoT-LAB testbed. This platform is completely open and can be used by any one wishing to run experiment on wireless sensors and robots.

The Lille site displays 3 subsets of the platforms:

- Euratechnologies : this site features 256 WSN430 sensor nodes operating in the 2.4GHz band. 64 nodes are mobile, embedded on mobile trains.
- Haute Borne : this site features 256 M3 sensor nodes operating in the 2.4GHz band and 64 mobile robots (32 turtlebots and 32 wifibots) completely remotely programmable.
- Opennodes : this site will feature (opening beginning 2015) 64 hardware open slots to allow any one to plug his own hardware and benefits from the platform debugging and monitoring tools.

GALAAD2 Team

5. New Software and Platforms

5.1. AXEL

KEYWORDS: CAO - Algebraic geometric modeler
SCIENTIFIC DESCRIPTION

Axel is an algebraic geometric modeler that aims at providing “algebraic modeling” tools for the manipulation and computation with curves, surfaces or volumes described by semi-algebraic representations. These include parametric and implicit representations of geometric objects. Axel also provides algorithms to compute intersection points or curves, singularities of algebraic curves or surfaces, certified topology of curves and surfaces, etc. A plugin mechanism allows to extend easily the data types and functions available in the plateform.
FUNCTIONAL DESCRIPTION

Axel is a cross platform software to visualize, manipulate and compute 3D objects. It is composed of a main application and several plugins. The main application provides atomic geometric data and processes, a viewer based on VTK, a GUI to handle objects, to select data, to apply process on them and to visualize the results. The plugins provides more data with their reader, writer, converter and interactors, more processes on the new or atomic data. It is written in C++ and thanks to a wrapping system using SWIG, its data structures and algorithms can be integrated into C# programs, as well as Python. The software is distributed as a source package, as well as binary packages for Linux, MacOSX and Windows.

- Participants: Nicolas Douillet, Anaïs Ducoffe, Valentin Michelet, Bernard Mourrain, Meriadeg Perrinel, Stéphane Chau and Julien Wintz
- Contact: Bernard Mourrain
- URL: http://axel.inria.fr/

Collaboration with Elisa Berrini (MyCFD, Sophia), Tor Dokken (Gotools library, Oslo, Norway), Angelos Mantzaflaris (GISMO library, Linz, Austria), Laura Saini (Post-Doc GALAAD/Missler, TopSolid), Gang Xu (Hangzhou Dianzi University, China).

5.2. Mathemagix

SCIENTIFIC DESCRIPTION

The project aims at building a bridge between symbolic computation and numerical analysis. It is structured by collaborative software developments of different groups in the domain of algebraic and symbolic-numeric computation.

In this framework, we are working more specifically on the following components:

realroot: a set of solvers using subdivision methods to isolate the roots of polynomial equations in one or several variables, continued fraction expansion of roots of univariate polynomials, Bernstein basis representation of univariate and multivariate polynomials and related algorithms, exact computation with real algebraic numbers, sign evaluation, comparison, certified numerical approximation.

shape: tools to manipulate curves and surfaces of different types including parameterized, implicit with different type of coefficients, algorithms to compute their topology, intersection points or curves, self-intersection locus, singularities, ...

These packages are integrated from the former library Synaps (SYmbolic Numeric APplicationS) dedicated to symbolic and numerical computations. There are also used in the algebraic-geometric modeler axel .
FUNCTIONAL DESCRIPTION

Mathemagix is a free computer algebra system which consists of a general purpose interpreter, which can be used for non-mathematical tasks as well, and efficient modules on algebraic objects. It includes the development of standard libraries for basic arithmetic on dense and sparse objects (numbers, univariate and multivariate polynomials, power series, matrices, etc., based on FFT and other fast algorithms). These developments, based on C++, offer generic programming without losing effectiveness, via the parameterization of the code (template) and the control of their instantiations.

- Participants: Bernard Mourrain, Grégoire Lecerf, Philippe Trebuchet and Joris Van Der Hoeven
- Contact: Bernard Mourrain
- URL: http://www.mathemagix.org/

GALEN Project-Team

6. New Software and Platforms

6.1. DISD

Dense Image and Surface Descriptors
FUNCTIONAL DESCRIPTION

Scale-Invariant Descriptor, Scale-Invariant Heat Kernel Signatures DISD implements the SID, SI-HKS and ISC descriptors. SID (Scale-Invariant Descriptor) is a densely computable, scale- and rotation- invariant descriptor. We use a log-polar grid around every point to turn rotation/scalings into translation, and then use the Fourier Transform Modulus (FTM) to achieve invariance. SI-HKS (Scale-Invariant Heat Kernel Signatures) extract scale-invariant shape signatures by exploiting the fact that surface scaling amounts to multiplication and scaling of a properly sampled HKS descriptor. We apply the FTM trick on HKS to achieve invariance to scale changes. ISC (Intrinsic Shape Context) constructs a net-like grid around every surface point by shooting outwards and tracking geodesics. This allows us to build a meta-descriptor on top of HKS/SI-HKS that takes neighborhood into account, while being invariant to surface isometries.

- Participants: Iasonas Kokkinos and Eduard Trulls
- Contact: Iasonas Kokkinos
- URL: http://vision.mas.ecp.fr/Personnel/iasonas/descriptors.html

6.2. DPMS

FUNCTIONAL DESCRIPTION

Dpms implements branch-and-bound object detection, cutting down the complexity of detection from linear in the number of pixels to logarithmic.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos
- URL: http://cvn.ecp.fr/personnel/iasonas/dpms.html

6.3. DROP

KEYWORDS: Health - Merging - Registration of 2D and 3D multimodal images - Medical imaging
FUNCTIONAL DESCRIPTION

Drop is a software programme that registers images originating from one or more modes by quickly and efficiently calculating a non-rigid / deformable field of deformation. Drop is a new, quick and effective registration tool based on new algorithms that do not require a cost function derivative.

- Partner: Centrale Paris
- Contact: Nikolaos Paragyios
- URL: http://campar.in.tum.de/Main/Drop

6.4. FastPD

KEYWORD: Medical imaging
FUNCTIONAL DESCRIPTION

FastPD is an optimization platform in C++ for the computer vision and medical imaging community.

- Contact: Nikolaos Paragyios
- URL: http://www.csd.uoc.gr/~komod/FastPD/

6.5. GraPeS

Grammar Parser for Shapes

FUNCTIONAL DESCRIPTION It is a software for parsing facade images using shape grammars. Grapes implement a parsing methods based on Reinforcement Learning principles. It optimizes simultaneously the topology of the parse tree as well as the associated parameters. GraPeS comes along with predefined shape grammars as XML files and defines three kinds of rewards. However, it also offers the possibility to create new grammars and to provide custom rewards in text files, widening the scope of potential applications. The name of the software comes from the aspect of the parse tree of the binary split grammars involved in the process.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos
- URL: http://vision.mas.ecp.fr/Personnel/teboul/grapesPage/index.php

6.6. HOAP-SVM

High-Order Average Precision SVM

SCIENTIFIC DESCRIPTION

We consider the problem of using high-order information (for example, persons in the same image tend to perform the same action) to improve the accuracy of ranking (specifically, average precision). We develop two learning frameworks. The high-order binary SVM (HOB-SVM) optimizes a convex upper bound of the surrogate 0-1 loss function. The high-order average precision SVM (HOAP-SVM) optimizes a difference-of-convex upper bound on the average precision loss function.

Authors of the research paper: Puneet K. Dokania, A. Behl, C. V. Jawahar and M. Pawan Kumar

FUNCTIONAL DESCRIPTION

The software provides a convenient API for learning to rank with high-order information. The samples are ranked according to a score that is proportional to the difference of max-marginals of the positive and the negative class. The parameters of the score function are computed by minimizing an upper bound on the average precision loss. The software also provides an instantiation of the API for ranking samples according to their relevance to an action, using the poselet features. The following learning algorithms are included in the API:

(1) Multiclass-SVM (2) AP-SVM (3) High Order Binary SVM (HOB-SVM) (4) High Order AP-SVM (HOAP-SVM) (5) M4 Learning (unpublished work)

The API is developed in C/C++ by Puneet K. Dokania.

- Participants: Puneet Dokania and Pawan Kumar
- Contact: Puneet Dokania
- URL: http://puneetkdokania.github.io/projects/ranking-highorder/ranking-highorder.html

6.7. LBSD

Learning-Based Symmetry Detection

FUNCTIONAL DESCRIPTION

LBSD implements the learning-based approach to symmetry detection. It includes the code for running a detector, alongside with the ground-truth symmetry annotations that we have introduced for the Berkeley Segmentation Dataset (BSD) benchmark.

- Participant: Stavros Tsogkas
- Contact: Stavros Tsogkas
- URL: https://github.com/tsogkas/oid_1.0

6.8. TeXMeG

FUNCTIONAL DESCRIPTION

Texture, modulation, generative models, segmentation, TeXMeG is a front-end for texture analysis and edge detection platform in Matlab that relies on Gabor filtering and image demodulation. Includes frequency- and time- based definition of Gabor- and other Quadrature-pair filterbanks, demodulation with the Regularized Energy Separation Algorithm and Texture/Edge/Smooth classification based on MDL criterion.

- Participant: Iasonas Kokkinos
- Contact: Iasonas Kokkinos
- URL: http://cvsp.cs.ntua.gr/software/texture/

6.9. mrf-registration

KEYWORDS: Health - Medical imaging
FUNCTIONAL DESCRIPTION

Deformable image and volume registration, is a deformable registration platform in C++ for the medical imaging community. This is the first publicly available platform which contains most of the existing metrics to perform registration under the same concept. The platform is used for clinical research from approximately 3,000 users worldwide.

- Participant: Nikolaos Paragyios
- Contact: Nikolaos Paragyios
- URL: http://www.mrf-registration.net/

GALLIUM Project-Team

6. New Software and Platforms

6.1. CompCert

Participants: Xavier Leroy [**contact**], Sandrine Blazy [team Celtique], Jacques-Henri Jourdan, Bernhard Schommer [AbsInt GmbH].

The CompCert project investigates the formal verification of realistic compilers usable for critical embedded software. Such verified compilers come with a mathematical, machine-checked proof that the generated executable code behaves exactly as prescribed by the semantics of the source program. By ruling out the possibility of compiler-introduced bugs, verified compilers strengthen the guarantees that can be obtained by applying formal methods to source programs. AbsInt Angewandte Informatik GmbH sells a commercial version of CompCert with long-term maintenance.

- URL: http://compcert.inria.fr/ (academic), http://www.absint.com/compcert/ (commercial).

6.2. Diy

Participants: Luc Maranget [**contact**], Jade Alglave [Microsoft Research, Cambridge], Keryan Didier.

The **diy** suite (for “Do It Yourself”) provides a set of tools for testing shared memory models: the **litmus** tool for running tests on hardware, various generators for producing tests from concise specifications, and **herd**, a memory model simulator. Tests are small programs written in x86, Power, ARM or generic (LISA) assembler that can thus be generated from concise specification, run on hardware, or simulated on top of memory models. Test results can be handled and compared using additional tools. Recent versions also take a subset of the C language as input, so as to test and simulate the C11 model.

- URL: http://diy.inria.fr/

6.3. Menhir

Participants: François Pottier [**contact**], Yann Régis-Gianas [Université Paris Diderot].

Menhir is a LR(1) parser generator for the OCaml programming language. That is, Menhir compiles LR(1) grammar specifications down to OCaml code.

- URL: http://gallium.inria.fr/~fpottier/menhir/

6.4. OCaml

Participants: Damien Doligez [**contact**], Alain Frisch [LexiFi], Jacques Garrigue [Nagoya University], Fabrice Le Fessant, Xavier Leroy, Luc Maranget, Gabriel Scherer, Mark Shinwell [Jane Street], Leo White [Jane Street], Jeremy Yallop [OCaml Labs, Cambridge University].

The OCaml language is a functional programming language that combines safety with expressiveness through the use of a precise and flexible type system with automatic type inference. The OCaml system is a comprehensive implementation of this language, featuring two compilers (a bytecode compiler, for fast prototyping and interactive use, and a native-code compiler producing efficient machine code for x86, ARM, PowerPC and SPARC), a debugger, a documentation generator, a compilation manager, a package manager, and many libraries contributed by the user community.

- URL: http://ocaml.org/

6.5. PASL

Participants: Mike Rainey [**contact**], Arthur Charguéraud, Umut Acar.

PASL is a C++ library for writing parallel programs targeting the broadly available multicore computers. The library provides a high level interface and can still guarantee very good efficiency and performance, primarily due to its scheduling and automatic granularity control mechanisms.

- URL: http://deepsea.inria.fr/pasl/

6.6. Zenon

Participants: Damien Doligez [**contact**], Guillaume Bury [CNAM], David Delahaye [CNAM], Pierre Halmagrand [team DEDUCTEAM], Olivier Hermant [MINES ParisTech].

Zenon is an automatic theorem prover based on the tableaux method. Given a first-order statement as input, it outputs a fully formal proof in the form of a Coq proof script. It has special rules for efficient handling of equality and arbitrary transitive relations. Although still in the prototype stage, it already gives satisfying results on standard automatic-proving benchmarks.

Zenon is designed to be easy to interface with front-end tools (for example integration in an interactive proof assistant), and also to be easily retargeted to output scripts for different frameworks (for example, Isabelle and Dedukti).

- URL: http://opam.ocaml.org/packages/zenon/zenon.0.8.0/

GAMMA3 Project-Team

4. New Software and Platforms

4.1. ABL4FLO

FUNCTIONAL DESCRIPTION

KEYWORDS: Boundary layer, Hybrid meshes
SCIENTIFIC DESCRIPTION

Automatic boundary layer mesh generation for complex geometries

FUNCTIONAL DESCRIPTION

ABL4FLO is designed to generate 3D adapted boundary layer meshes by using a cavity-based operator.

- Participant: Adrien Loseille
- Contact: Adrien Loseille
- URL: https://www.rocq.inria.fr/gamma/Adrien.Loseille/index.php?page=softwares

4.2. AMA4FLO

FUNCTIONAL DESCRIPTION

KEYWORDS: Anisotropic mesh adaptation, Surface and volume remeshing, Non manifold geometries
SCIENTIFIC DESCRIPTION

Robust and automatic generation of anisotropic meshes in 3D

FUNCTIONAL DESCRIPTION

AMA4FLO is designed to generate adapted meshes with respect to a provided anisotropic sizing field. The surface and the volume mesh is adapted simultaneously to guarantee that a 3D valid mesh is provided on output.

- Participant: Adrien Loseille
- Contact: Adrien Loseille
- URL: https://www.rocq.inria.fr/gamma/Adrien.Loseille/index.php?page=softwares

4.3. BL2D

KEYWORDS: Automatic mesher - Delaunay - Anisotropic - Planar domain

SCIENTIFIC DESCRIPTION

The meshing method is of controled Delaunay type, isotropic or anisotropic. The internal point generation follows an advancing-front logic, and their connection is realised as in a classical Delaunay approach. Quadrilaterals are obtained by a pairing process. The direct construction of degree 2 elements has been made possible via the control of the domain boundary mesh, in order to ensure the desired compatibility.

FUNCTIONAL DESCRIPTION

Planar mesh generator (isotropic or anisotropic, adaptive).

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: https://www.rocq.inria.fr/gamma/Patrick.Laug/logiciels/logiciels.html

4.4. BL2D-ABAQ

KEYWORDS: Automatic mesher - Delaunay - Anisotropic - Planar domain - error estimation - interpolation

SCIENTIFIC DESCRIPTION

The meshing method is the same as BL2D (see above) in an adaptive process. An error estimation (*a posteriori*) of a solution at the nodes of the current mesh results in a size map. A new mesh satisfying these size specifications (made continuous) is built, and the solution is interpolated on the new mesh.

FUNCTIONAL DESCRIPTION

Planar mesh generator (isotropic or anisotropic, adaptive) for deformable domains, interacting with the ABAQUS solver.

- Participants: Houman Borouchaki, Patrick Laug and Abel Cherouat
- Contact: Patrick Laug
- URL: https://www.rocq.inria.fr/gamma/Patrick.Laug/logiciels/logiciels.html

4.5. BLGEOL

KEYWORDS: Automatic mesher - Hex-dominant - Geologic structures

SCIENTIFIC DESCRIPTION

The aim is to generate hex-dominant meshes of geologic structures complying with different geometric constraints: surface topography (valleys, reliefs, rivers), geologic layers and underground workings. First, a reference 2D domain is obtained by projecting all the line constraints into a horizontal plane. Different size specifications are given for rivers, outcrop lines and workings. Using an adaptive methodology, the size variation is bounded by a specified threshold in order to obtain a high quality quad-dominant mesh. Secondly, a hex-dominant mesh of the geological medium is generated by a vertical extrusion, taking into account the surfaces found (interfaces between two layers, top or bottom faces of underground workings). The generation of volume elements follows a global order established on the whole set of surfaces to ensure the conformity of the resulting mesh.

FUNCTIONAL DESCRIPTION

Hex-dominant mesher of geologic structures and storage facilities.

- Participants: Patrick Laug and Houman Borouchaki
- Contact: Patrick Laug
- URL: https://www.rocq.inria.fr/gamma/Patrick.Laug/logiciels/logiciels.html

4.6. BLMOL

KEYWORDS: Automatic mesher - Molecular surface

SCIENTIFIC DESCRIPTION

To model a molecular surface, each constituting atom is idealized by a simple sphere. First, a boundary representation (B-rep) of the surface is obtained, i.e. a set of patches and the topological relations between them. Second, an appropriate parameterization and a metric map are computed for each patch. Third, meshes of the parametric domains are generated with respect to an induced metric map, using a combined advancing-front generalized-Delaunay approach. Finally these meshes are mapped onto the entire surface.

FUNCTIONAL DESCRIPTION

Molecular surface mesher.

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: https://www.rocq.inria.fr/gamma/Patrick.Laug/logiciels/logiciels.html

4.7. BLSURF

Keywords: Automatic mesher - parametric surface - CAD surface

Scientific Description

An indirect method for meshing parametric surfaces conforming to a user-specifiable size map is used. First, from this size specification, a Riemannian metric is defined so that the desired mesh is one with unit length edges with respect to the related Riemannian space (the so-called ‚Äòunit mesh‚Äô). Then, based on the intrinsic properties of the surface, the Riemannian structure is induced into the parametric space. Finally, a unit mesh is generated completely inside the parametric space such that it conforms to the metric of the induced Riemannian structure. This mesh is constructed using a combined advancing-front Delaunay approach applied within a Riemannian context.

Functional Description

CAD surface mesher.

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: https://www.rocq.inria.fr/gamma/Patrick.Laug/logiciels/logiciels.html

4.8. FEFLOA-REMESH

Keywords: Anisotropic mesh adaptation, Surface remeshing, Cavity-based operator

Scientific Description

Automatic generation of metric-aligned and metric-orthogonal anisotropic meshes in 3D

Functional Description

FEFLOA-REMESH is intended to generate adapted 2D, surface and volume meshes by using a unique cavity-based operator. The metric-aligned or metric-orthogonal approach is used to generate high quality surface and volume meshes independently of the anisotropy involved.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Adrien Loseille
- URL: https://www.rocq.inria.fr/gamma/Adrien.Loseille/index.php?page=softwares

4.9. GAMANIC 3D

Keywords: Tetrahedral mesh - Delaunay - Anisotropic size and direction control - Automatic Mesher

Scientific Description

Automatic tetrahedral mesher based on an anisotropic Delaunay type point insertion method. A metric field is provided specifying the desired size (edge length) and directional properties.

Functional Description

GAMANIC3D is a volume mesher governed by a (anisotropic) size and directional specification metric field.

- Participants: Houman Borouchaki, Paul Louis George, Frederic Hecht, √âric Saltel, Frédéric Alauzet and Adrien Loseille
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

4.10. GAMHIC 3D

Keywords: Tetrahedral mesh - Delaunay - Isotropic size control - Automatic Mesher

Scientific Description

Automatic tetrahedral mesher based on the Delaunay point insertion method. A metric field is provided specifying the desired size (edge length).

FUNCTIONAL DESCRIPTION

GAMHIC3D is a volume mesher governed by a (isotropic) size specification metric field.

- Participants: Houman Borouchaki, Paul Louis George, Frederic Hecht, √âric Saltel, Frédéric Alauzet and Adrien Loseille
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

4.11. GHS3D

KEYWORDS: Tetrahedral mesh - Delaunay - Automatic Mesher
SCIENTIFIC DESCRIPTION

Automatic tetrahedral mesher based on the Delaunay point insertion method.

FUNCTIONAL DESCRIPTION

GHS3D is an automatic volume mesher

- Participants: Paul Louis George, Houman Borouchaki, √âric Saltel, Frédéric Alauzet, Adrien Loseille and Frederic Hecht
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

4.12. HEXOTIC

KEYWORDS: Hexahedral mesh - Octree - Automatic mesher
SCIENTIFIC DESCRIPTION

Automatic full hexahedral mesher primarily based on an octree.

FUNCTIONAL DESCRIPTION

HEXOTIC is an automatic hexahedral mesher

- Contact: Loïc Maréchal
- URL: https://www.rocq.inria.fr/gamma/gamma/Membres/CIPD/Loic.Marechal/Research/Hexotic.html

4.13. Metrix

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Compute a metric field from a given solution field using various error estimates.

FUNCTIONAL DESCRIPTION

Metrix computes metric field from a given solution field using various error estimates. Available error estimates are feature-based and goal-oriented based error estimates for steady or unsteady fields. Metrix also performs operations on metrics: gradation, intersection, natural metric of a mesh.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.14. Nimbus 3D

KEYWORDS: Surface reconstruction - Point cloud
SCIENTIFIC DESCRIPTION

Given a point cloud, a surface is constructed primarily based on a Delaunay approach.

FUNCTIONAL DESCRIPTION

Nimbus3D is a surface reconstruction method piece of software

- Participants: Paul Louis George and Houman Borouchaki
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

4.15. VIZIR

KEYWORDS: Mesh and solution visualization
SCIENTIFIC DESCRIPTION

Interactive mesh and solution visualization for linear, and high order curved elements

FUNCTIONAL DESCRIPTION

VIZIR is intended to visualize and modify interactively simplicial, hybrid and high order curved meshes.

- Participants: Julien Castelneau, Adrien Loseille and Alexis Loyer
- Contact: Adrien Loseille
- URL: http://www-roc.inria.fr/gamma/gamma/vizir/

4.16. Wolf

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

General solver platform containing all the Wolf modules: Wolf-Bloom, Wolf-Elast, Wolf-Interpol, Wolf-MovMsh, Wolf-Nsc, Wolf-Shrimp, Wolf-Spyder and Wolf-Xfem.

FUNCTIONAL DESCRIPTION

Wolf is a general solver platform containing all the Wolf modules: Wolf-Bloom, Wolf-Elast, Wolf-Interpol, Wolf-MovMsh, Wolf-Nsc, Wolf-Shrimp, Wolf-Spyder and Wolf-Xfem.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.17. Wolf-Bloom

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Structured boundary layer mesh generator using a pushing approach.

FUNCTIONAL DESCRIPTION

Wolf-Bloom is a structured boundary layer mesh generator using a pushing approach. It start from an existing volume mesh and insert a structured boundary layer by pushing the volume mesh. The volume mesh deformation is solved with an elasticity analogy. Mesh-connectivity optimizations are performed to control volume mesh element quality.

- Participants: Frédéric Alauzet, Adrien Loseille and Dave Marcum
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.18. Wolf-Elast

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Linear elasticity solver using a P1 Finite-Element method.

FUNCTIONAL DESCRIPTION

Wolf-Elast is a linear elasticity solver using the P1 Finite-Element method. The Young and Poisson coefficient can be parametrized. The linear system is solved using the Conjugate Gradient method with the LUSGS preconditioner.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.19. Wolf-Interpol

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Software transferring scalar, vector and tensor fields from one mesh to another one.

FUNCTIONAL DESCRIPTION

Wolf-Interpol is a tool to transfer scalar, vector and tensor fields from one mesh to another one. Polynomial interpolation (from order 2 to 4) or conservative interpolation operators can be used. Wolf-Interpol also extract solutions along lines or surfaces.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.20. Wolf-MovMsh

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Moving mesh algorithm coupled with mesh-connectivity optimization.

FUNCTIONAL DESCRIPTION

Wolf-MovMsh is a moving mesh algorithm coupled with mesh-connectivity optimization. Mesh deformation is computed by means of a linear elasticity solver or a RBF interpolation. Smoothing and swapping mesh optimization are performed to maintain good mesh quality. It handles rigid bodies or deformable bodies, and also rigid or deformable regions of the domain.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.21. Wolf-Nsc

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Numerical flow solver solving the compressible Navier-Stokes equations.

FUNCTIONAL DESCRIPTION

Wolf-Nsc is numerical flow solver solving steady or unsteady turbulent compressible Euler and Navier-Stokes equations. The available turbulent models are the Spalart-Almaras and the Menter SST k-omega. A mixed finite volume - finite element numerical method is used for the discretization. Second order spatial accuracy is reached thanks to MUSCL type methods. Explicit or implicit time integration are available. It also resolved dual (adjoint) problem and compute error estimate for mesh adaptation.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.22. Wolf-Shrimp

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Mesh partitioner for parallel mesh generation and parallel computation.

FUNCTIONAL DESCRIPTION

Wolf-Shrimp is a generic mesh partitioner for parallel mesh generation and parallel computation. It can partition planar, surface (manifold and non manifold), and volume domain. Several partitioning methods are available: Hilbert-based, BFS, BFS with restart. It can work with or without weight function and can correct the partitions to have only one connected component.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.23. Wolf-Spyder

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Metric-based mesh quality optimizer using vertex smoothing and edge/face swapping.

FUNCTIONAL DESCRIPTION

Wolf-Spyder is a metric-based mesh quality optimizer using vertex smoothing and edge/face swapping.

- Participants: Frédéric Alauzet and Adrien Loseille
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

4.24. Wolf-Xfem

KEYWORD: Scientific calculation
SCIENTIFIC DESCRIPTION

Tool providing the mesh of the intersection between a surface mesh and a volume mesh.

FUNCTIONAL DESCRIPTION

Wolf-Xfem is a tool providing the mesh of the intersection between a surface mesh and a volume mesh.

- Participants: Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: https://www.rocq.inria.fr/gamma/Frederic.Alauzet/code_eng.html

GANG Project-Team

6. New Software and Platforms

6.1. Svvamp: Simulator of Various Voting Algorithms in Manipulating Populations

Svvamp is a Python package dedicated to the study of voting systems with an emphasis on manipulation analysis. Svvamp can generate datasets based on a large library of artificial models, or use any kind of real dataset as input. It currently implements more than 20 voting systems. Using state of the art algorithms, it can analyze multiple variants of tactical voting (e.g. absence of weak/strong Nash equilibrium). Svvamp is free software, under the GNU General Public License version 3. Its documentation includes installation procedure, tutorials, reference guide and instructions for new contributors.

Svvamp represents about ten thousands lines of code, and according to the Python Software Foundation, 2568 downloads have been reported in the last month (as of December, 10th, 2015). It is available at https://svvamp.readthedocs.org.

Svvamp [39] will be demonstrated in The Thirtieth Conference on Artificial Intelligence.

6.1.1. Svvamp self-assesment

A3: ambitious software, usable by people inside and outside the team but without a clear and strong dissemination and support action plan. So3up4: original software reusing known ideas and introducing a few new ideas / original software implementing a fair number of original ideas.

SM3: well-developed software, fairly extensive documentation, reasonable software engineering and testing, attention to usability, dissemination, bug fixes, and user feedback;

EM2: basic maintenance to keep the software alive;

SDL4: public source or binary distribution on the web, organized by the development team;

François Durand is the main contributor (4) in: a) design and architecture (DA) b) coding and debugging (CD) c) maintenance and support (MS) d) team/project management (TPM)

6.2. Big Graph Tools

The team is starting a software development activity around big graph manipulation. A preliminary library offering diameter and skeleton computation is available at https://who.rocq.inria.fr/Laurent.Viennot/dev/big-graph-tools/. This library was used to compute the diameters of the worldwide road network (200M edges) and the Twitter follower-followee graph (23G edges).

GECO Project-Team (section vide)

GENSCALE Project-Team

6. New Software and Platforms

6.1. HTS data processing

6.1.1. GATB: Genome Assembly & Analysis Tool Box

The GATB software toolbox aims to lighten the design of NGS algorithms. It offers a panel of high-level optimized building blocks to speed-up the development of NGS tools related to genome assembly and/or genome analysis. The underlying data structure is the de Bruijn graph, and the general parallelism model is multithreading. The GATB library targets standard computing resources such as current multicore processors (laptop computer, small server) with a few GB of memory. From high-level API, NGS programming designers can rapidly elaborate their own software based on domain state-of-the-art algorithms and data structures. The GATB library is written in C++.

Contact: Dominique Lavenier

URL: https://gatb.inria.fr/

6.1.2. LEON: Genomic Data Compression

Leon is a lossless compression software that achieves compression of DNA sequences of high throughput sequencing data, without the need of a reference genome. Techniques are derived from assembly principles that better exploit NGS data redundancy. A reference is built de novo from the set of reads as a probabilistic de-Bruijn graph stored in a Bloom filter. Each read is encoded as a path in this graph, storing only an anchoring kmer and a list of bifurcations indicating which path to follow in the graph. This new method will allow to have compressed read files containing its underlying de-Bruijn Graph, thus directly re-usable by many tools relying on this structure. Leon achieved the encoding of a *C. elegans* reads set with 0.7 bits per base, outperforming state of the art reference-free methods.

Contact: Claire Lemaitre

URL: https://gatb.inria.fr/software/leon/

6.1.3. BLOOCOO: Genomic Data Correction

Bloocoo is a k-mer spectrum-based read error corrector, designed to correct large datasets with a very low memory footprint. It uses the disk streaming k-mer counting algorithm included in the GATB library, and inserts solid k-mers in a bloom-filter. The correction procedure is similar to the Musket multistage approach. Bloocoo yields similar results while requiring far less memory: as an example, it can correct whole human genome re-sequencing reads at 70 x coverage with less than 4GB of memory.

Contact: Claire Lemaitre

URL: https://gatb.inria.fr/bloocoo-read-corrector/

6.1.4. DiscoSnp++: DISCOvering Single Nucleotide Polymorphism

DiscoSnp++ is designed for discovering Single Nucleotide Polymorphism (SNP) and insertions/deletions (indels) from raw set(s) of reads obtained with Next Generation Sequencers (NGS). The number of input read sets is not constrained, it can be one, two, or more. No other data as reference genome or annotations are needed. The software is composed of three modules: (1) kissnp2, that detects SNPs and indels from read sets; (2) kissreads2, that enhances the kissnp2 results by providing for each variant a read coverage mean and a (phred) quality; (3) VCF_creator, that provides a file in the Variant Calling Format (VCF). A VCF file using or not a reference genome is also created.

Contact: Pierre Peterlongo

URL: http://colibread.inria.fr/software/discosnp/

6.1.5. MindTheGap: Detection of insertion

MindTheGap is a software that performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It takes as input a set of reads and a reference genome. It outputs two sets of FASTA sequences: one is the set of breakpoints of detected insertion sites, the other is the set of assembled insertions for each breakpoint. For each breakpoint, MindTheGap either returns a single insertion sequence (when there is no assembly ambiguity), or a set of candidate insertion sequences (due to ambiguities) or nothing at all (when the insertion is too complex to be assembled). MindTheGap performs de novo assembly using the de Bruijn Graph implementation of GATB. Hence, the computational resources required to run MindTheGap are significantly lower than that of other assemblers.

Contact: Claire Lemaitre

URL: http://mindthegap.genouest.org/

6.1.6. TakeABreak: Detection of inversion breakpoints

TakeABreak is a tool that can detect inversion breakpoints directly from raw NGS reads, without the need of any reference genome and without de novo assembling the genomes. Its implementation is based on the Genome Assembly Tool Box (GATB) library, and has a very limited memory impact allowing its usage on common desktop computers and acceptable runtime (Illumina reads simulated at 80x coverage from human chromosome 22 can be treated in less than two hours, with less than 1GB of memory).

Contact: Claire Lemaitre

URL: http://colibread.inria.fr/software/takeabreak/

6.2. Sequence comparison

6.2.1. PLAST: Parallel Local Alignment Search Tool

PLAST is a fast, accurate and NGS scalable bank-to-bank sequence similarity search tool providing significant accelerations of seeds-based heuristic comparison methods, such as the Blast suite. PLAST is fully designed to compare query and subject comprised of large sets of DNA, RNA and protein sequences. It is significantly faster than BLAST, while providing comparable sensitivity. PLAST contains a fully integrated data-filtering engine capable of selecting relevant hits with user-defined criteria (E-Value, identity, coverage, alignment length, etc.).

Contact: Dominique Lavenier

URL: https://plast.inria.fr

6.2.2. SIMKA: Comparison of metagenomic datasets

Simka rapidly compares a large number of metagenomics datasets using efficient kmer-based method. Datasets may contains hundreds of millions of NGS sequences. Kmers of each datasets are rapidly counted and identified to estimate the pairwise similarities between datasets. The output of Simka can be used for clustering purpose or for checking correlation between metadata.

Contact: Gaëtan Benoit

URL: https://gatb.inria.fr/software/simka/

6.2.3. BGREAT: read mapper on de-Bruijn graph

BGREAT maps reads on a de-Bruijn Graph, usually used for genome assembly. Mapping reads on graphs offers the possibility to conserve all the pieces of information lost during the assembly process and to avoid multi-mapping problems due to genomic repeats. BGREAT rewrites a read sequence as a succession of unitigs sequences. It can map millions of reads per CPU hour on a de-Bruijn graph built from a large set of human genomic reads.

Contact: Antoine Limasset

URL: http://github.com/Malfoy/BGREAT/

GEOMETRICA Project-Team

6. New Software and Platforms

6.1. GUDHI

Geometric Understanding in Higher Dimensions

SCIENTIFIC DESCRIPTION

The GUDHI open source library will provide the central data structures and algorithms that underly applications in geometry understanding in higher dimensions. It is intended to both help the development of new algorithmic solutions inside and outside the project, and to facilitate the transfer of results in applied fields.

FUNCTIONAL DESCRIPTION

The current release of the GUDHI library includes: – Data structures to represent, construct and manipulate simplicial complexes. – Algorithms to compute persistent homology and multi-field persistent homology. – Simplification methods via implicit representations. - A graphical user interface and several examples and datasets.
It also has improved performance, portability and documentation.

- Participants: Jean-Daniel Boissonnat, Marc Glisse, Anatole Moreau, Vincent Rouvreau and David Salinas
- Contact: Jean-Daniel Boissonnat
- URL: https://project.inria.fr/gudhi/software/

6.2. CGAL dD Triangulations

CGAL module: Triangulations in any dimension

KEYWORDS: Triangulation - Delaunay triangulation
FUNCTIONAL DESCRIPTION

This package of CGAL (Computational Geometry Algorithms Library, http://www.cgal.org) allows to compute triangulations and Delaunay triangulations in any dimension. Those triangulations are built incrementally and can be modified by insertion or removal of vertices.

- Participants: Samuel Hornus, Olivier Devillers and Clément Jamin
- Contact: Clément Jamin
- URL: http://doc.cgal.org/4.6/Triangulation/

6.3. CGAL Kernel_d

CGAL module: High-dimensional kernel Epick_d

FUNCTIONAL DESCRIPTION

Several functions were added in release 4.7 in preparation for a future alpha-complex implementation.

- Participants: Marc Glisse
- Contact: Marc Glisse
- URL: http://doc.cgal.org/4.7/Kernel_d/

6.4. R package TDA

Topological Data Analysis package for the R software

FUNCTIONAL DESCRIPTION

the R package TDA provides some tools for Topological Data Analysis. In particular, it includes implementations of functions that, given some data, provide topological information about the underlying space, such as the distance function, the distance to a measure, the kNN density estimator, the kernel density estimator, and the kernel distance.

- Participants: Clément Maria, Vincent Rouvreau
- Contact: Vincent Rouvreau
- URL: https://cran.r-project.org/web/packages/TDA/index.html

6.5. cgal Periodic Triangulations and Meshes

The CGAL library offers a package to compute the 3D periodic Delaunay triangulation of a point set in $\mathbb{R}^3$, more precisely the Delaunay triangulation of a point set in the 3-dimensional flat torus with cubic domain [49]. The package has been used in various fields. [0]

We have been extending this package in three directions:

First, a few new small functions have been added to the Delaunay triangulation class and integrated in CGAL 4.7.

We have developed and documented some new classes allowing to compute *weighted* periodic Delaunay triangulations. They have been submitted to the CGAL editorial board and accepted for inclusion in CGAL. The code still needs some polishing, and the testsuite must be completed, before a public distribution in CGAL.

We have continued our work to use this package together with the 3D mesh generation package of CGAL [48], in order to propose a construction of meshes of periodic volumes. Although last year's preliminary results were already convincing [50], [51], the work is not ready yet for being submitted to CGAL: the code requires to be completed, documented, and extensively tested.

- Participant : Aymeric Pellé
- Contact: Monique Teillaud (Vegas project-team)
- This work was done in the framework of the Inria ADT *(Action de Développement Technologique)* OrbiCGAL http://www.loria.fr/~teillaud/ADT-OrbiCGAL/

---

[0] see http://www.cgal.org/projects.html

GEOSTAT Project-Team

6. New Software and Platforms

6.1. Fluex

KEYWORDS: Signal - Signal processing

SCIENTIFIC DESCRIPTION

Fluex is a nonlinear signal processing software for 1D, 2D 3D and 3D+t general signals.

FUNCTIONAL DESCRIPTION

- Fluex is a library in nonlinear signal processing, written in C++, developed under Gforge, able to analyze turbulent and natural complex signals.
- Fluex is able to determine low level features in natural signals that cannot be determined using standard linear techniques.
- Participants: Hussein Yahia, Denis Arrivault, Rémi Paties.
- Contact: Hussein Yahia.
- URL: https://geostat.bordeaux.inria.fr/index.php/downloads.html.
- Fluex is deposited APP, Inter Deposit Digital Number: IDDN.FR.001.51.0028.000.S.P.2015.000.21000

6.2. FluidExponents

- Participants: Hussein Yahia and Antonio Turiel
- Contact: Hussein Yahia
- URL: https://geostat.bordeaux.inria.fr/index.php/downloads.html.

GRACE Project-Team

6. New Software and Platforms

6.1. Fast Compact Diffie-Hellman

KEYWORD: Cryptography
FUNCTIONAL DESCRIPTION

A competitive, high-speed, open implementation of the Diffie–Hellman protocol, targeting the 128-bit security level on Intel platforms. This download contains Magma files that demonstrate how to compute scalar multiplications on the x-line of an elliptic curve using endomorphisms. This accompanies the EuroCrypt 2014 paper by Costello, Hisil and Smith, the full version of which can be found here: http://eprint.iacr.org/2013/692 . The corresponding SUPERCOP-compatible crypto_dh application can be downloaded from http://hhisil.yasar.edu.tr/files/hisil20140318compact.tar.gz .

- Participant: Benjamin Smith
- Contact: Benjamin Smith
- URL: http://research.microsoft.com/en-us/downloads/ef32422a-af38-4c83-a033-a7aafbc1db55/

6.2. Platforms

6.2.1. ACTIS: Algorithmic Coding Theory in Sage

FUNCTIONAL DESCRIPTION

The aim of this project is to vastly improve the state of the error correcting library in Sage. The existing library does not present a good and usable API, and the provided algorithms are very basic, irrelevant, and outdated. We thus had two directions for improvement:

1. renewing the APIs to make them actually usable by researchers, and
2. incorporating efficient programs for decoding, like J. Nielsen's CodingLib, which contains many new algorithms.

After a year on the project, which started October 1st, 2014, we have been able to completely rethink and rewrite the API to a new structure able to support many mathematical constructions and integrate it in Sage. We also implemented numerous code classes and decoding algorithms, including cyclic codes over any finite field and list decoding of GRS codes, which are not available in Maple, Magma and Mathematica. As integrating code in Sage is a slow process, which requires external developers, we attended two Sage workshops (Sage Days 66 in Liège and Sage Days 70 in Berkeley) and welcomed one at Inria Saclay http://wiki.sagemath.org/GroupeUtilisateursParis#mercredi-1er-juillet-2015-module-de-codage-actis-pour-sage to spread the word on the project and meet the main Sage developers. We're now trusted members of the community, and we were able to integrate several patches in Sage.

- Contact: David Lucas
- URL: https://bitbucket.org/lucasdavid/sage_coding_project/wiki/Home
- One can check a full list of accepted and pending ACTIS patches for Sage here : http://trac.sagemath.org/ticket/18846.

GRAPHDECO Project-Team

6. New Software and Platforms

6.1. SWARPI

SWARPI (for Superpixel Warp for Image-based rendering)
FUNCTIONAL DESCRIPTION

This software package is the implementation of the publication and it was developed previously at REVES and now maintained by GRAPHDECO with public funding. The LINUX main software consists of two components: the depth synthesis step and the image-based runtime rendering step : a. depth synthesis step reads 3D points coming from the automated 3D reconstruction pipeline, together with images and calibrated cameras, and produces the superpixel decomposition and the depth synthesis algorithm. This package is provided as a set of C++ sources (for superpixel and depth) and matlab sources for depthSynth. b. The runtime rendering step is a C++ program (sources provided) which takes the result of the first step as input to allow interactive 3D navigation from pictures. The code uses multi-pass deferred shading with pixel and fragment shaders to perform the rendering.

- Participants: George Drettakis, Gaurav Chaurasia, Sylvain François Duchene and Olga Sorkine-Hornung
- Contact: George Drettakis

6.2. SWARPI-Unity

SWARPI-Unity (for Superpixel Warp for Image-based rendering for Unity)
This software package is the Unity port of the SWARPI used in the context of the CR-PLAY project.

- Participants: Jérôme Esnault, George Drettakis and Gaurav Chaurasia
- Contact: George Drettakis

6.3. SWARPI2-IBR-COMMON

SWARPI2-IBR-COMMON (for Superpixel Warp for Image-based rendering and common Image Based Rendering features)
This is the second version of SWARPI which is used internally for the research projects developed for Image-Based Rendering ([15]).

- Participants: George Drettakis, Gaurav Chaurasia, Jérôme Esnault and Sylvain François Duchene
- Contact: George Drettakis

6.4. CrossShade

CrossShade is an algorithm to estimate surface normals over a design sketch composed of vector curves representing silhouettes, boundaries and cross-sections. This algorithm has been developed in collaboration with U. of Toronto (Karan Singh) and U. British Columbia (A. Sheffer). We filed a patent on this technology and we have contacts with several companies about a potential transfer.

- Participants: Adrien Bousseau
- Contact: Adrien Bousseau

6.5. True2Form

True2Form is a sketch-based modeling system that reconstructs 3D curves from typical design sketches. This algorithm has been developed in collaboration with U. of Toronto (Karan Singh) and U. British Columbia (A. Sheffer). We filed a patent on this technology and we have contacts with several companies about a potential transfer.

- Participants: Adrien Bousseau
- Contact: Adrien Bousseau

GRAPHIK Project-Team

6. New Software and Platforms

6.1. DLGP 2.0

- Participants: Jean-François Baget, Michel Chein, Alain Gutierrez, Michel Leclère, Marie-Laure Mugnier, Swan Rocher and Clément Sipieter
- URL: http://graphik-team.github.io/graal/

DLGP (for Datalog+) is our textual format for the existential rules framework. This year, we extended it to ensure compatibility with Semantic Web languages. This required to include web notions such as IRIs and literals. A new parser was implemented, and is used in both Cogui (6.2) and Graal (6.3).

6.2. Cogui

Cogui is a tool for building and verifying knowledge bases. It is a freeware written in Java (version 1.6). Currently, it supports Conceptual Graphs and import/export in RDFS and Datalog+.

- Participants: Alain Gutierrez, Michel Leclère, Michel Chein, Marie-Laure Mugnier and Madalina Croitoru
- Contact: Michel Leclère (scientific contact) and Alain Gutierrez (technical contact)
- URL: http://www.lirmm.fr/cogui/

Objectives: Cogui is a visual tool for building conceptual graph knowledge bases (KB). It allows to create a KB, to edit its structure and content, and to control it. The KB can be serialized in the XML. Imports and exports from and to RDFS are also provided, as well as from and to the *Datalog+ (DLGP)* format that we defined for existential rules. Wizards allow to analyze and check facts with respect to some constraints, as well as to query them while taking into account inferences enabled by the ontology.

Users community:*Research:* MIMOS (National R&D center in information and communication technology, Malaysia http://www.mimos.my/), Defence R&D Canada, our partners in INRA, CIRAD, as well as a new collaboration with the Inria team Imagine. *Education:* Used in knowledge engineering in universities of Nice, Strasbourg, Montpellier, Sheffield, as well as in the engineering school of Tarbes.

Impact: internal use in several EU or National projects. We expect a broader audience by using Cogui as a graphical ontology modeling tool for our other software Graal, the communication being done through our DLGP format http://www.lirmm.fr/~mugnier/graphik/kiabora/downloads/datalog-plus_en.pdf.

State of the art: To the best of our knowledge, Cogui is the only ontology editing tool able to do reasoning with conceptual graph rules (equivalent to existential rules). Many tools exist for DLs and Semantic Web languages (e.g. Protégé http://protege.stanford.edu mainly designed for description logics and TopBraid Composer http://www.topquadrant.com/ designed for RDF and SPIN rules, which are rules without existential variables).

Misc.: Cogui is written in Java and has been part time developed since 2005 by Alain Gutierrez (approx. 50 man months). First developed as an interface communicating with the conceptual graph reasoner Cogitant http://cogitant.sourceforge.net/, it has become a standalone tool, integrating more and more reasoning features.

New features: This year, we mainly focused on improving the compatibility with the semantic web languages. The main improvements are the following:

- integration of the parser using our new textual format DLGP 2.0 (6.1).
- a new repository is available to store the projects. It facilitates collaborative work combined with a version control software (a feature developed for Qualinca combined with GIT).
- ergonomics: rule engine and query assistants have been redesigned, several graphical editor behaviors have been improved.
- A backward chaining rule evaluation algorithm, with lazy computation of rule bodies, has been developed for the kind of Datalog rules used in the system SudoQual.

6.3. GRAAL

In its current state, Graal allows storage of data via a generic interface in different storage paradigms and systems. Currently, the relational database management systems MySQL, PostgreSQL, Sqlite, and InMemory graph and LinkedList structures are implemented. The triple store Jena TDB and the graph database system Sparksee are coming soon. Graal also allows us to query this database taking into account an ontology represented by a set of existential rules. It provides forward chaining and query rewriting algorithms (building up on Mélanie König's PhD thesis) and a tool for the analysis of the properties of a set of rules which is an integration of Swan Rocher's tool Kiabora. The input and output of this software can be expressed in our Datalog-inspired format DLGP 2.0 (6.1), and can be translated from the semantic web language OWL2 or to RuleML. This software is designed in a modular way, hence it is possible to use only a subpart of Graal without embedding it all or to easily replace an implementation of a module by another.

FUNCTIONAL DESCRIPTION

Graal is intended to be a generic platform for ontology-based query answering with existential rules.

- Participants: Clément Sipieter, Swan Rocher, Jean-François Baget, Marie-Laure Mugnier, Michel Leclère
- Partner: LIRMM
- Contact: Marie-Laure Mugnier (scientific contact) and Clément Sipieter (technical contact)
- URL: http://graphik-team.github.io/graal/

Objectives: Graal is a generic platform for query answering under existential rules. It will integrate all algorithms designed in the team, and our ambition is to make it a reference platform in the research community, allowing for the integration of algorithms designed by other teams.

Users community: Graal is intended for use in research and education.

Impact: Due to the recent release of the first stable version, Graal has only been used for now in our projects. A related paper received the RuleML 2015 challenge award http://2015.ruleml.org/.

State of the art: To the best of our knowledge, the only other tool for reasoning with existential rules is Nyaya [0], a joint development from teams in Rome, Oxford, and Milan. It has been renamed IRIS+/- https://bitbucket.org/giorsi/nyaya.

Misc.: Graal is written in Java (around 30k lines of code, 30 man/months effort). It is mainly developed by Clément Sipieter (2 years Inria ADT funding) under the CeCILL licence (GPL compatible, see http://www.cecill.info/licences.fr.html). The development started 1.5 years ago from a prototype realized during Bruno Paiva's PhD thesis, and integrates work carried out by other PhD students (Mélanie König and Swan Rocher). Graal has been first presented at RuleML 2015 [23], [33], where it received a best paper award.

New features: Main features integrated in 2015 are query rewriting algorithms, projection algorithms, and translations to and from other languages (OWL2, RuleML).

Note that we do not detail here other software developments internal to our current projects and not publicly available.

---

[0] De Virgilio, R.; Orsi, G.; Tanca, L.; Torlone, R., "NYAYA: A System Supporting the Uniform Management of Large Sets of Semantic Data," in Data Engineering (ICDE), 2012 IEEE 28th International Conference on , vol., no., pp.1309-1312, 1-5 April 2012

HEPHAISTOS Project-Team

6. New Software and Platforms

6.1. ALIAS

Algorithms Library of Interval Analysis for Systems
FUNCTIONAL DESCRIPTION

The ALIAS library whose development started in 1998, is a collection of procedures based on interval analysis for systems solving and optimization.

ALIAS is made of two parts:

ALIAS-C++ : the C++ library (87 000 code lines) which is the core of the algorithms

ALIAS-Maple : the Maple interface for ALIAS-C++ (55 000 code lines). This interface allows one to specify a solving problem within Maple and get the results within the same Maple session. The role of this interface is not only to generate the C++ code automatically, but also to perform an analysis of the problem in order to improve the efficiency of the solver. Furthermore, a distributed implementation of the algorithms is available directly within the interface.

- Participants: Odile Pourtallier and Jean-Pierre Merlet
- Contact: Jean-Pierre Merlet
- URL: http://www-sop.inria.fr/hephaistos/developpements/main.html

HIEPACS Project-Team

6. New Software and Platforms

6.1. Introduction

We describe in this section the software that we are developing. The first list will be the main milestones of our project. The other software developments will be conducted in collaboration with academic partners or in collaboration with some industrial partners in the context of their private R&D or production activities. For all these software developments, we will use first the various (very) large parallel platforms available through GENCI in France (CCRT, CINES and IDRIS Computational Centers), and next the high-end parallel platforms that will be available via European and US initiatives or projects such that PRACE.

6.2. Chameleon

Participant: Emmanuel Agullo [corresponding member].

Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

6.3. MaPHyS

Participant: Emmanuel Agullo [corresponding member].

`MaPHyS` (Massivelly Parallel Hybrid Solver) is a software package that implements a parallel linear solver coupling direct and iterative approaches. The underlying idea is to apply to general unstructured linear systems domain decomposition ideas developed for the solution of linear systems arising from PDEs. The interface problem, associated with the so called Schur complement system, is solved using a block preconditioner with overlap between the blocks that is referred to as Algebraic Additive Schwarz.

The `MaPHyS` package is very much a first outcome of the research activity described in Section 3.3 . Finally, `MaPHyS` is a preconditioner that can be used to speed-up the convergence of any Krylov subspace method. We forsee to either embed in `MaPHyS` some Krylov solvers or to release them as standalone packages, in particular for the block variants that will be some outcome of the studies discussed in Section 3.3 .

`MaPHyS` can be found at http://maphys.gforge.inria.fr.

6.4. PaStiX

Participant: Pierre Ramet [corresponding member].

Complete and incomplete supernodal sparse parallel factorizations.

`PaStiX` (Parallel Sparse matriX package) is a scientific library that provides a high performance parallel solver for very large sparse linear systems based on block direct and block ILU(k) iterative methods. Numerical algorithms are implemented in single or double precision (real or complex): LLt (Cholesky), LDLt (Crout) and LU with static pivoting (for non symmetric matrices having a symmetric pattern).

The `PaStiX` library uses the graph partitioning and sparse matrix block ordering package `Scotch`. `PaStiX` is based on an efficient static scheduling and memory manager, in order to solve 3D problems with more than 50 million of unknowns. The mapping and scheduling algorithm handles a combination of 1D and 2D block distributions. This algorithm computes an efficient static scheduling of the block computations for our supernodal parallel solver which uses a local aggregation of contribution blocks. This can be done by taking into account very precisely the computational costs of the BLAS 3 primitives, the communication costs and the cost of local aggregations. We also improved this static computation and communication scheduling algorithm to anticipate the sending of partially aggregated blocks, in order to free memory dynamically. By doing this, we are able to reduce the aggregated memory overhead, while keeping good performance.

Another important point is that our study is suitable for any heterogeneous parallel/distributed architecture when its performance is predictable, such as clusters of multicore nodes. In particular, we now offer a high performance version with a low memory overhead for multicore node architectures, which fully exploits the advantage of shared memory by using an hybrid MPI-thread implementation.
Direct methods are numerically robust methods, but the very large three dimensional problems may lead to systems that would require a huge amount of memory despite any memory optimization. A studied approach consists in defining an adaptive blockwise incomplete factorization that is much more accurate (and numerically more robust) than the scalar incomplete factorizations commonly used to precondition iterative solvers. Such incomplete factorization can take advantage of the latest breakthroughs in sparse direct methods and particularly should be very competitive in CPU time (effective power used from processors and good scalability) while avoiding the memory limitation encountered by direct methods.

`PaStiX` is publicly available at http://pastix.gforge.inria.fr under the Inria CeCILL licence.

6.5. HIPS

Participant: Pierre Ramet [corresponding member].

Multilevel method, domain decomposition, Schur complement, parallel iterative solver.

`HIPS` (Hierarchical Iterative Parallel Solver) is a scientific library that provides an efficient parallel iterative solver for very large sparse linear systems.

The key point of the methods implemented in `HIPS` is to define an ordering and a partition of the unknowns that relies on a form of nested dissection ordering in which cross points in the separators play a special role (Hierarchical Interface Decomposition ordering). The subgraphs obtained by nested dissection correspond to the unknowns that are eliminated using a direct method and the Schur complement system on the remaining of the unknowns (that correspond to the interface between the sub-graphs viewed as sub-domains) is solved using an iterative method (GMRES or Conjugate Gradient at the time being). This special ordering and partitioning allows for the use of dense block algorithms both in the direct and iterative part of the solver and provides a high degree of parallelism to these algorithms. The code provides a hybrid method which blends direct and iterative solvers. `HIPS` exploits the partitioning and multistage ILU techniques to enable a highly parallel scheme where several subdomains can be assigned to the same process. It also provides a scalar preconditioner based on the multistage ILUT factorization.

`HIPS` can be used as a standalone program that reads a sparse linear system from a file ; it also provides an interface to be called from any C, C++ or Fortran code. It handles symmetric, unsymmetric, real or complex matrices. Thus, `HIPS` is a software library that provides several methods to build an efficient preconditioner in almost all situations.

`HIPS` is publicly available at http://hips.gforge.inria.fr under the Inria CeCILL licence.

6.6. MetaPart

Participant: Aurélien Esnard [corresponding member].

`MetaPart` is a library that adresses the challenge of (dynamic) load balancing for emerging complex parallel simulations, such as multi-physics or multi-scale coupling applications. First, it offers a uniform API over state-of-the-art (hyper-) graph partitioning software packages such as `Scotch`, `PaToH`, `METIS`, `Zoltan`, `Mondriaan`, etc. etc. Based upon this API, it provides a framework that facilitates the development and the evaluation of high-level partitioning methods, such as MxN repartitioning or coupling-aware partitioning (co-partitioning).

The framework is publicy available at Inria Gforge: http://metapart.gforge.inria.fr.

6.7. MPICPL

Participant: Aurélien Esnard [corresponding member].

MPICPL (MPI CouPLing) is a software library dedicated to the coupling of parallel legacy codes, that are based on the well-known MPI standard. It proposes a lightweight and comprehensive programing interface that simplifies the coupling of several MPI codes (2, 3 or more). MPICPL facilitates the deployment of these codes thanks to the *mpicplrun* tool and it interconnects them automatically through standard MPI inter-communicators. Moreover, it generates the universe communicator, that merges the world communicators of all coupled-codes. The coupling infrastructure is described by a simple XML file, that is just loaded by the *mpicplrun* tool.

MPICPL was developed by HIEPACS for the purpose of the ANR NOSSI. It uses advanced features of MPI2 standard. The framework is publicy available at Inria Gforge: http://mpicpl.gforge.inria.fr.

6.8. ScalFMM

Participant: Olivier Coulaud [corresponding member].

`ScalFMM` (Parallel Fast Multipole Library for Large Scale Simulations) is a software library to simulate N-body interactions using the Fast Multipole Method.

`ScalFMM` intends to offer all the functionalities needed to perform large parallel simulations while enabling an easy customization of the simulation components: kernels, particles and cells. It works in parallel in a shared/distributed memory model using OpenMP and MPI. The software architecture has been designed with two major objectives: being easy to maintain and easy to understand. There are two main parts: 1) the management of the octree and the parallelization of the method ; 2) the kernels. This new architecture allows us to easily add new FMM algorithm or kernels and new paradigm of parallelization. The code is extremely documented and the naming convention fully respected. Driven by its user-oriented philosophy, `ScalFMM` is using CMAKE as a compiler/installer tool. Even if `ScalFMM` is written in C++ it will support a C and fortran API soon.

The library offers two methods to compute interactions between bodies when the potential decays like $1/r$. The first method is the classical FMM based on spherical harmonic expansions and the second is the Black-Box method which is an independent kernel formulation (introduced by E. Darve at Stanford). With this method, we can now easily add new non oscillatory kernels in our library. For the classical method, two approaches are used to decrease the complexity of the operators. We consider either matrix formulation that allows us to use BLAS routines or rotation matrix to speed up the M2L operator.

The `ScalFMM` package is available at http://scalfmm.gforge.inria.fr

6.9. ViTE

Participant: Mathieu Faverge [corresponding member].

Visualization, Execution trace

`ViTE` is a trace explorer. It is a tool made to visualize execution traces of large parallel programs. It supports Pajé, a trace format created by Inria Grenoble, and OTF and OTF2 formats, developed by the University of Dresden and allows the programmer a simpler way to analyse, debug and/or profile large parallel applications. It is an open source software licenced under CeCILL-A.

The `ViTE` software is available at http://vite.gforge.inria.fr and has been developed in collaboration with the Inria Bordeaux - Sud-Ouest SED team, Telecom SudParis and Inria Grenoble.

In the same context we also contribute to the EZtrace and GTG libraries in collaboration with F. Trahay from Telecom SudParis. EZTrace (http://eztrace.gforge.inria.fr) is a tool that aims at generating automatically execution trace from HPC programs. It generates execution trace files thanks to the GTG library (http://gtg.gforge.inria.fr) that can be later interpreted by visualization tools such as `ViTE`.

6.10. Other software

For the materials physics applications, a lot of development will be done in the context of older ANR projects (NOSSI and OPTIDIS) in collaboration with LaBRI, CPMOH, IPREM, EPFL and with CEA Saclay and Bruyère-le-Châtel.

- **OptiDis**
  Participant: Olivier Coulaud [corresponding member].

  OptiDis is a new code for large scale dislocation dynamics simulations. Its aim is to simulate real life dislocation densities (up until 5.10^{22} dislocations/m^{-2}) in order to understand plastic deformation and study strain hardening. The main application is to observe and understand plastic deformation on irradiated zirconium. Zirconium alloys is the first containment barrier against the dissemination of radioactive elements. More precisely, with neutron irradiated zirconium alloys we are talking of channeling mechanism, which means to stick with the reality,more than tens of thousands of induced loops so 10^8 degrees of freedom in the simulation.

  The code is based on Numodis code developed at CEA Saclay and the `ScalFMM` library developed in our Inria project. The code is written in C++ language and using the last features of C++11. One of the main aspects is the hybrid parallelism MPI/OpenMP that gives the software the ability to scale on large cluster while the computation load rises. In order to achieve that, we use different levels of parallelism. First of all, the simulation box is spread over MPI processes, we then use a thinner level for threads, dividing the domain using an Octree representation. All theses parts are driven by the `ScalFMM` library. On the last level our data are stored in an adaptive structure absorbing dynamic of this kind of simulation and handling well task parallelism.

The two following packages are mainly designed and developed in the context of a US initiative led by ICL and to which we closely collaborate through the associate team MORSE.

- **PLASMA**
  Participant: Mathieu Faverge [corresponding member].

  The `PLASMA` (Parallel Linear Algebra for Scalable Multi-core Architectures) project aims at addressing the critical and highly disruptive situation that is facing the Linear Algebra and High Performance Computing community due to the introduction of multi-core architectures.

  The `PLASMA` ultimate goal is to create software frameworks that enable programmers to simplify the process of developing applications that can achieve both high performance and portability across a range of new architectures.

  The development of programming models that enforce asynchronous, out of order scheduling of operations is the concept used as the basis for the definition of a scalable yet highly efficient software framework for Computational Linear Algebra applications.

  The `PLASMA` library is available at http://icl.cs.utk.edu/plasma.

- **PaRSEC/DPLASMA**
  Participant: Mathieu Faverge [corresponding member].

  `PaRSEC` Parallel Runtime Scheduling and Execution Controller, is a generic framework for architecture aware scheduling and management of micro-tasks on distributed many-core heterogeneous architectures. Applications we consider can be expressed as a Direct Acyclic Graph of tasks with labeled edges designating data dependencies. DAGs are represented in a compact problem-size independent format that can be queried on-demand to discover data dependencies in a totally distributed fashion. `PaRSEC` assigns computation threads to the cores, overlaps communications and computations and uses a dynamic, fully-distributed scheduler based on architectural features such as NUMA nodes and algorithmic features such as data reuse.

  The framework includes libraries, a runtime system, and development tools to help application developers tackle the difficult task of porting their applications to highly heterogeneous and diverse environments.

DPLASMA (Distributed Parallel Linear Algebra Software for Multicore Architectures) is the leading implementation of a dense linear algebra package for distributed heterogeneous systems. It is designed to deliver sustained performance for distributed systems where each node featuring multiple sockets of multicore processors, and if available, accelerators like GPUs or Intel Xeon Phi. DPLASMA achieves this objective through the state of the art PaRSEC runtime, porting the PLASMA algorithms to the distributed memory realm.

The PaRSEC runtime and the DPLASMA library are available at http://icl.cs.utk.edu/parsec.

6.11. Platforms

6.11.1. PlaFRIM: an experimental parallel computing platform

PLAFRIM is an open experimental platform for research and development in modeling, simulations and high performance computing. This platform has been set up from 2009 under the leadership of Inria Bordeaux Sud-Ouest in collaboration with computer science and mathematics laboratories, respectively Labri and IMB with a strong support in the region Aquitaine. Since mid-2015, this platform is now open to laboratories involved in the CPU cluster and SMIs located in the region Aquitaine.

It aggregates different kinds of computational resources for research and development purposes. The latest technologies in terms of processors, memories and architecture are added when they are available on the market. It is now more than 2,500 cores (excluding GPU and Xeon Phi) that are available for all research teams of Inria Bordeaux, Labri and IMB. Those computers are in particular used by all the engineers who work in HiePACS and are advised by F. Rue from the SED.

The PlaFRIM platform initiative is coordinated by O. Coulaud.

HYBRID Project-Team

6. New Software and Platforms

6.1. OpenViBE

KEYWORDS: Brain-Computer Interface, EEG, Neuroscience, Interaction, Health, Neurofeedback

FUNCTIONAL DESCRIPTION

OpenViBE is a free and open-source software platform devoted to the design, test and use of Brain-Computer Interfaces (BCI). The platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. The key features of OpenViBE software are its modularity, its high-performance, its portability, its multiple-users facilities and its connection with high-end/VR displays. The "designer" of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge under the terms of the AGPL licence, and it was officially released in June 2009. Since then, the OpenViBE software has already been downloaded more than 40000 times, and it is used by numerous laboratories, projects, or individuals worldwide. More information, downloads, tutorials, videos, documentations are available on the OpenViBE website.

- Participants: Anatole Lécuyer, Jussi Tapio Lindgren, Jérôme Chabrol, Charles Garraud, and Marsel Mano
- Partners: Inria teams POTIOC, ATHENA and NEUROSYS
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

6.2. Statefinder

KEYWORDS: Brain-Computer Interface, EEG, Neuroscience, Interaction, Health, Neurofeedback, Welfare

FUNCTIONAL DESCRIPTION Statefinder is a software for determining the mental state of a user based on EEG signals analysis. It notably enables to classify between different different mental states on-line, using a preliminary training phase during which the EEG signals corresponding to these different mental states were recorded. This software was designed and used during the PhD of Mr. Laurent George, in Hybrid team. It has been transferred to Mensia Technologies startup company.

- Participants: Anatole Lécuyer
- Contact: Anatole Lécuyer

6.3. Pseudohaptik

KEYWORDS: User Interfaces, 3D web, Pseudo-Haptic, Deph Perception

FUNCTIONAL DESCRIPTION

PSEUDOHAPTIK is a software which enables to simulate pseudo-haptic effects notably for web applications. Pseudo-haptic feedback enables to simulate haptic properties such as feeling the texture or relief of an image using visual effects synchronized with the motion of the user. This software has been notably transferred to MBA Multimédia and Polymorph companies.

- Participants: Anatole Lécuyer, Ferran Argelaguet Sanz and Maud Marchal
- Contact: Anatole Lécuyer
- URL: https://team.inria.fr/hybrid/w3d-project/

6.4. Elastic_Images

KEYWORDS: User Interfaces, Depth Perception, 3D web, Pseudo-Haptic
FUNCTIONAL DESCRIPTION

Elastic_Images is a software which enables to simulate pseudo-haptic effects related to the elasticity or stiffness of 2D images, notably for web application purpose. This software has been transferred to MBA Multimédia and Polymorph companies.

- Participants: Anatole Lécuyer, Ferran Argelaguet Sanz and Maud Marchal
- Contact: Anatole Lécuyer
- URL: https://team.inria.fr/hybrid/w3d-project/

6.5. #FIVE

KEYWORDS: Virtual Reality, Collaboration, 3D Interaction
FUNCTIONAL DESCRIPTION

#FIVE is a set of software modules for the design of interactive and collaborative virtual environments. The user can focus on domain-specific aspects of his/her application (e.g., industry, medicine, etc). The #FIVE modules can then be used in a vast range of domains based on virtual reality and requiring interactive environments and collaboration - such as in training simulators for example when connected to the #SEVEN engine (see section 6.6).

- Participants: Thomas Boggini, Valérie Gouranton, Bruno Arnaldi, Florian Nouviale
- Contact: Florian Nouviale
- URL: https://hal.archives-ouvertes.fr/IRISA/hal-01147734v1

6.6. #SEVEN

KEYWORDS: Virtual Reality, Training, Scenario, Petri Net
FUNCTIONAL DESCRIPTION

#SEVEN is a scenario engines that enables the execution of complex scenarios for driving Virtual Reality training applications. #SEVEN's scenarios are based on an enhanced Petri net model that can describe and solve intricate event sequence. #SEVEN comes with an editor capable of creating, editing and remotely controlling and running such scenarios. #SEVEN is implemented in C# and can be used as a standalone application or as a library. An integration with the Unity3D engine, compatible with MiddleVR, also exists.

- Participants: Guillaume Claude, Valérie Gouranton, Bruno Arnaldi, Florian Nouviale
- Contact: Florian Nouviale
- URL: https://hal.archives-ouvertes.fr/hal-01086237

HYCOMES Team

5. New Software and Platforms

5.1. Flipflop

Test & Flip Net Synthesis Tool for the Inference of Technical Procedure Models

FUNCTIONAL DESCRIPTION

Flipflop is a Test and Flip net synthesis tool implementing a linear algebraic polynomial time algorithm. Computations are done in the Z/2Z ring. Test and Flip nets extend Elementary Net Systems by allowing test to zero, test to one and flip arcs. The effect of flip arcs is to complement the marking of the place. While the net synthesis problem has been proved to be NP hard for Elementary Net Systems, thanks to flip arcs, the synthesis of Test and Flip nets can be done in polynomial time. Test and flip nets have the required expressivity to give concise and accurate representations of surgical processes (models of types of surgical operations). Test and Flip nets can express causality and conflict relations. The tool takes as input either standard XES log files (a standard XML file format for process mining tools) or a specific XML file format for surgical applications. The output is a Test and Flip net, solution of the following synthesis problem: Given a finite input language (log file), compute a net, which language is the least language in the class of Test and Flip net languages, containing the input language.

- Contact: Benoît Caillaud
- URL: http://tinyurl.com/oql6f3y

5.2. MICA

Model Interface Compositional Analysis Library

KEYWORDS: Modal interfaces - Contract-based desing

SCIENTIFIC DESCRIPTION

In Mica, systems and interfaces are represented by extension. However, a careful design of the state and event heap enables the definition, composition and analysis of reasonably large systems and interfaces. The heap stores states and events in a hash table and ensures structural equality (there is no duplication). Therefore complex data-structures for states and events induce a very low overhead, as checking equality is done in constant time.

Thanks to the Inter module and the mica interactive environment, users can define complex systems and interfaces using Ocaml syntax. It is even possible to define parameterized components as Ocaml functions.

FUNCTIONAL DESCRIPTION

Mica is an Ocaml library implementing the Modal Interface algebra. The purpose of Modal Interfaces is to provide a formal support to contract based design methods in the field of system engineering. Modal Interfaces enable compositional reasoning methods on I/O reactive systems.

- Participant: Benoît Caillaud
- Contact: Benoît Caillaud
- URL: http://www.irisa.fr/s4/tools/mica/

5.3. TnF-C++

FUNCTIONAL DESCRIPTION

TnF-C++ is a robust and portable re-implementation of Flipflop, developed in 2014 and integrated in the S3PM toolchain. Both software have been designed in the context of the S3PM project on surgical procedure modeling and simulation,

- Contact: Benoît Caillaud
- URL: https://bitbucket.org/cpenet/tnf_cpp

I4S Project-Team

6. New Software and Platforms

6.1. Platform: PEGASE

Plate-forme Experte Générique pour Applications Sans-fil Embarquées
Keyword: SHM (Structural Health Monitoring)
Scientific Description

I4S is actually finalizing the setup of a new platform named PEGASE 2.0 as the technological successor of the previous PEGASE platform developed by IFSTTAR.

The new version of PEGASE keeps the best of its previous version in its main vocation, to be a generic high level Wireless Sensor Platofrm.

What does not change between PEGASE 1 and 2.0: Based on various feedback from application fields, results from real structures monitored by PEGASE, and due to the rapid obsolescence of electronic devices, the design of the new PEGASE platform has been launched in 2013. Some of the main functions of PEGASE does not change but are reinforced.

Software genericity: use of a Linux embedded OS to make any application developed independently from the hardware, to make the user able to manage the system without ant physical and heavy operations.

Hardware genericity: with a principle of daughter and mother boards, each redundant need is embedded (processing, memory, timing, GPS, energy, etc) which each pluggable daughter board implements a specific function (sensing, 3G, Ethernet, communication, signal processing and relay control).

Accurate time synchronization: based on an original GPS and PPS algorithm, PEGASE platform is one of the only board able to time-stamp data from sensors or any event with an accuracy of some micro-seconds Universal Time.

What's new on PEGASE 2 platform ?

Previous principles are maintained or extended. Full electronic design from scratch occurred in 2014 to maximise its capacities in terms efficiency, cost, energy consumption, etc. Its main characteristics are

Important software evolutions: the platform embedded a real Linux kernel (not
Functional Description

I4S is actually finalizing the setup of a new platform named PEGASE 2.0 as the technological successor of the previous PEGASE platform developed by IFSTTAR.

The new version of PEGASE keeps the best of its previous version in its main vocation, to be a generic high level Wireless Sensor Platofrm.

What does not change between PEGASE 1 and 2.0: Based on various feedback from application fields, results from real structures monitored by PEGASE, and due to the rapid obsolescence of electronic devices, the design of the new PEGASE platform has been launched in 2013. Some of the main functions of PEGASE does not change but are reinforced.

Software genericity: use of a Linux embedded OS to make any application developed independently from the hardware, to make the user able to manage the system without ant physical and heavy operations.

Hardware genericity: with a principle of daughter and mother boards, each redundant need is embedded (processing, memory, timing, GPS, energy, etc) which each pluggable daughter board implements a specific function (sensing, 3G, Ethernet, communication, signal processing and relay control).

Accurate time synchronization: based on an original GPS and PPS algorithm, PEGASE platform is one of the only board able to time-stamp data from sensors or any event with an accuracy of some micro-seconds Universal Time.

- Participants: Vincent Le Cam, Mathieu Le Pen, Laurent Mevel and Michael Doehler
- Contact: Michael Doehler
- URL: http://www.a3ip.com/joomla/index.php?option=com_content&view=article&id=12&Itemid=8

6.2. TDISTL

Time domain inverse scattering for transmission lines
KEYWORDS: Transmission lines - Problem inverse - Fault diagnosis
SCIENTIFIC DESCRIPTION

TDISTL is a time domain variant of the previously developed frequency domain software ISTL for numerical computations of the inverse scattering transform applied to electrical transmission lines. It provides an efficient solution to experimentally determining the distributed characteristic impedance of electrical transmission line from the time domain reflectogram (impulse response) measured at one end of the line. Its current applications are in the fields of electrical cable fault diagnosis. It is registered at Agence pour la Protection des Programmes (APP) under the number IDDN.FR.001.250014.000.S.P.2015.000.30705.

FUNCTIONAL DESCRIPTION

Computation of the distributed characteristic impedance of a transmission line from time domain reflectometry measurement

- Participants: Qinghua Zhang and Michel Sorine
- Contact: Qinghua Zhang

6.3. Cloud2SM

Cloud architecture design for Structural Monitoring with in-line Sensors and Models tasking
KEYWORDS: SHM, online physical models, Data Management, Multi-physics Sensing, GPGPU acceleration
SCIENTIFIC DESCRIPTION

From the past decades the monitoring of civil engineering structure became a major field of research and development process in the domains of modelling and integrated instrumentation. This increasing of interest can be attributed in part to the need of controlling the aging of such structures and on the other hand to the need to optimize maintenance costs. From this standpoint the project Cloud2SM (inria ADT) has been launched to develop a robust information system able to assess the long term monitoring of civil engineering structures as well as interfacing various sensors and data. The specificity of such architecture is to be based on the notion of data processing through physical or statistical models. Thus the data processing, whether material or mathematical, can be seen here as a resource of the main architecture. The project can be divided in various items:

- The sensors and their measurement process: Those items provide data to the main architecture and can embed storage or computational resources. Dependent of onboard capacity and the amount of data generated it can be distinguished heavy and light sensors.
- The storage resources: Based on the cloud concept this resource can store at least two types of data, raw data and processed ones.
- The computational resources: This item includes embedded “pseudo real time” resources as the dedicated computer cluster or computational resources.
- The models: Used for the conversion of raw data to meaningful data. Those types of resources inform the system of their needs they can be seen as independents blocks of the system.
- The user interface: This item can be divided in various HMI to assess maintaining operation on the sensors or pop-up some information to the user.
- The demonstrators: The structures themselves.

Beside those objective, the I4S ADT campaign has allowed the development of the first block of the architecture: the data acquisition system. Called Cloud2IR, this prototype implementation of generic sensor interface has been specialized for the long term thermal monitoring of civil engineering structure and opened the way to the development of a whole ecosystem of sensors

6.3.1. Cloud2IR

Cloud 2IR is a software dedicated to the structural health monitoring of civil engineering structures thanks to long term thermal imaging. Its particularity lies in the fact that it is based on a generic approach of the acquisition system concept and the format of the data. That allow it to apply to other types of sensor. Information can be obtained on the inria bil, https://bil.inria.fr/fr/software/view/2536/tab.

IBIS Project-Team

5. New Software and Platforms

5.1. Genetic Network Analyzer (GNA)

KEYWORDS: Bioinformatics - Gene regulatory networks - Qualitative simulation - Model checking
GENETIC NETWORK ANALYZER (GNA) is the implementation of methods for the qualitative modeling and simulation of gene regulatory networks developed in the IBIS project. The input of GNA consists of a model of the regulatory network in the form of a system of piecewise-linear differential equations (PLDEs), supplemented by inequality constraints on the parameters and initial conditions. From this information, GNA generates a state transition graph summarizing the qualitative dynamics of the system. In order to analyze large graphs, GNA allows the user to specify properties of the qualitative dynamics of a network in temporal logic, using high-level query templates, and to verify these properties on the state transition graph by means of standard model-checking tools, either locally installed or accessible through a remote web server. GNA is currently distributed by the company Genostar, but remains freely available for academic research purposes. The current version is GNA 8.7.1. In comparison with the previously distributed versions, GNA 8.7.1 has the following additional functionalities: (1) it supports the editing and visualization of regulatory networks, in an SBGN-compatible format, (2) it semi-automatically generates a prototype model from the network structure, thus accelerating the modeling process, and (3) it allows models to be exported in the SBML Qual standard.

- Participants: Hidde de Jong, Michel Page, François Rechenmann
- Partners: Genostar, Université Joseph Fourier, Université Pierre Mendès-France
- Contact: Hidde de Jong
- URL: http://www-helix.inrialpes.fr/gna

5.2. WellFARE

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling
WELLFARE is a Python library implementing linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. As input, WELLFARE reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various functions exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. WELLFARE is the computational core of the web application WELLINVERTER.

- Participants: Johannes Geiselmann, Hidde de Jong, Michel Page, Delphine Ropers, Valentin Zulkower
- Partners: Université Joseph Fourier, Université Pierre Mendès-France
- Contact: Hidde de Jong
- URL: https://github.com/ibis-inria/wellfare

5.3. WellInverter

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling

WELLINVERTER is a web application that implements linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. As input, WELLINVERTER reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various modules exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. The computational core of the web application consists of the Python library WELLFARE.

- Participants: Johannes Geiselmann, Hidde de Jong, Michel Page, Delphine Ropers, Valentin Zulkower
- Partners: Université Joseph Fourier, Université Pierre Mendès-France
- Contact: Hidde de Jong
- URL: http://ibis.inrialpes.fr/article1080.html

5.4. WellReader

WELLREADER is a program for the analysis of gene expression data obtained by means of fluorescent and luminescent reporter genes. WELLREADER reads data files in an XML format or in a format produced by microplate readers, and allows the user to detect outliers, perform background corrections and spline fits, compute promoter activities and protein concentrations, and compare expression profiles across different conditions. WELLREADER has been written in MATLAB and is available under an LGPL licence, both as source code (M files) and compiled code (platform-specific binary files).

- Participants: Johannes Geiselmann, Hidde de Jong, Michel Page, Delphine Ropers
- Partners: Université Joseph Fourier, Université Pierre Mendès-France
- Contact: Hidde de Jong
- URL: http://ibis.inrialpes.fr/article957.html

ILDA Team

6. New Software and Platforms

6.1. Smarties

FUNCTIONAL DESCRIPTION

The Smarties system provides an easy way to add mobile interactive support to collaborative applications for wall displays.

It consists of (i) a mobile interface that runs on mobile devices for input, (ii) a communication protocol between the mobiles and the wall application, and (iii) libraries that implement the protocol and handle synchronization, locking and input conflicts. The library presents the input as an event loop with callback functions and handles all communication between mobiles and wall application. Developers can customize the mobile interface from the wall application without modifying the mobile interface code.

On each mobile we find a set of cursor controllers associated with keyboards, widgets and clipboards. These controllers (pucks) can be shared by multiple collaborating users. They can control simple cursors on the wall application, or specific content (objects or groups of them). The developper can decide the types of widgets associated to pucks from the wall application side.

- Contact: Olivier Chapuis
- URL: http://smarties.lri.fr/

6.2. ZVTM

Zoomable Visual Transformation Machine

KEYWORDS: Information visualization - Data visualization - Geovisualization - Visualization - Big data - Graph visualization

FUNCTIONAL DESCRIPTION

ZVTM is a toolkit enabling the implementation of multi-scale interfaces for interactively navigating in large datasets displayed as 2D graphics.

ZVTM is used for browsing large databases in multiple domains: geographical information systems, control rooms of complex facilities, astronomy, power distribution systems.

The toolkit also enables the development of applications running on ultra-high-resolution wall-sized displays.

- Participants: Caroline Appert, Olivier Chapuis, Bruno Fruchard, Maria Jesus Lobo Gunther, Arnaud Prouzeau, Hande Ozaygen and Can Liu
- Contact: Emmanuel Pietriga
- URL: http://zvtm.sf.net

6.3. Platforms

6.3.1. Platform: WILDER

Ultra-high-resolution wall-sized displays [27] feature a very high pixel density over a large physical surface. Such platforms have properties that make them well-suited to the visualization of very large datasets. They can represent the data with a high level of detail while at the same time retaining context: users can transition from an overview of the data to a detailed view simply by physically moving in front of the wall display. Wall displays also offer good support for collaborative work, enabling multiple users to simultaneously visualize and interact with the displayed data. To make them interactive, wall-sized displays are increasingly coupled with input devices such as touch frames, motion-tracking systems and wireless multitouch devices, in order to enable multi-device and multi-user interaction with the displayed data. Application areas for such visualization platforms range from the monitoring of complex infrastructures and crisis management situations to tools for the exploratory visualization of scientific data.

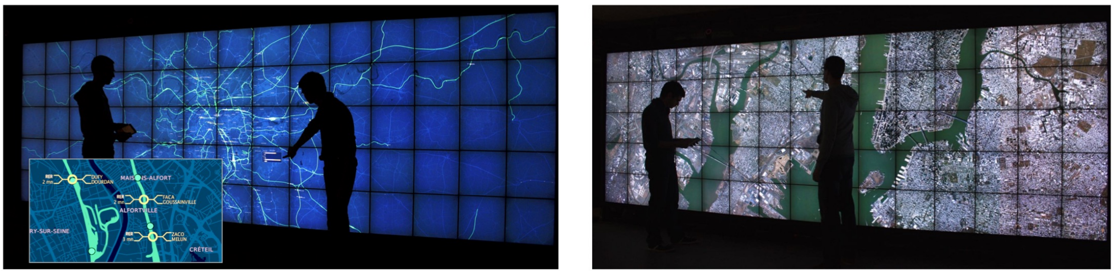


Figure 2. Geovisualization applications running on the WILDER platform. Real-time monitoring of railroad trafic in France (left), large-scale high-resolution orthoimagery visualization (right).

WILDER is the latest ultra-high-resolution wall-sized display set up at Inria Saclay, and is one of the nodes of the Digiscope EquipEx. We use this platform for multiple projects, both fundamental HCI research, and research and development activities for specific application areas such as geographical informations systems (Figure 2) and astronomy (see Figure 3).

6.3.2. Platform: ANDES

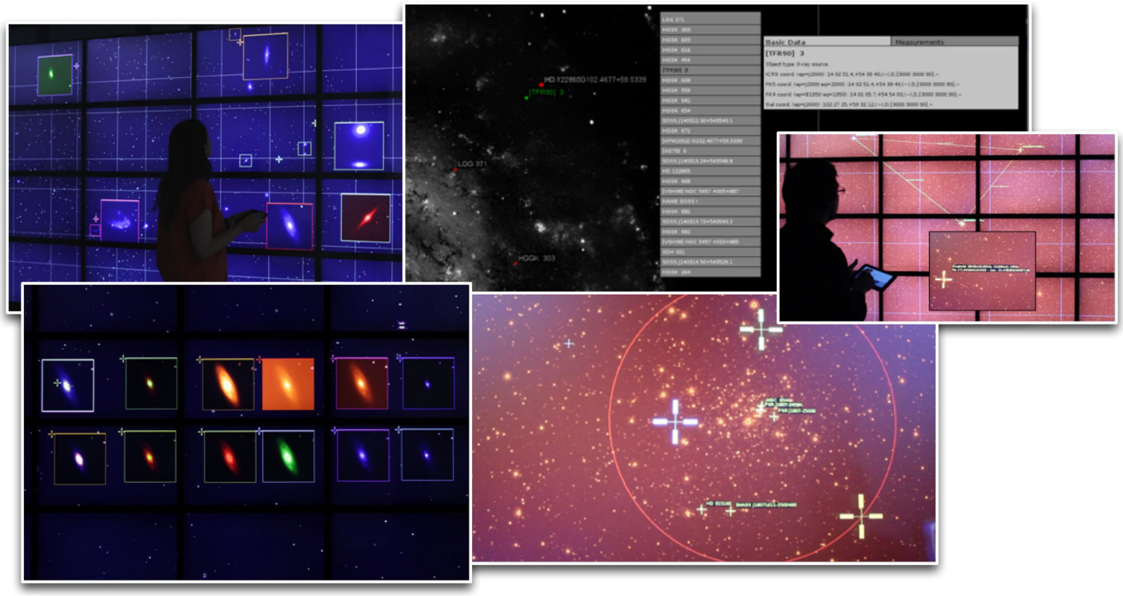


Figure 3. Visualization of high-dynamic-range FITS images and associated data catalogs in the domain of Astronomy on ANDES (collaboration with Inria Chile, Millenium Institute of Astrophysics, and Institut d'Astrophysique Spatiale).

ANDES is a platform similar to WILDER, set up at Inria in Santiago de Chile, that we use both as a research platform and as a showroom of our research and development activities. ANDES is the main platform used for our collaborative research project with the Millenium Institute of Astrophysics on the visualization of large FITS images (see Figure 3).

IMAGINE Project-Team

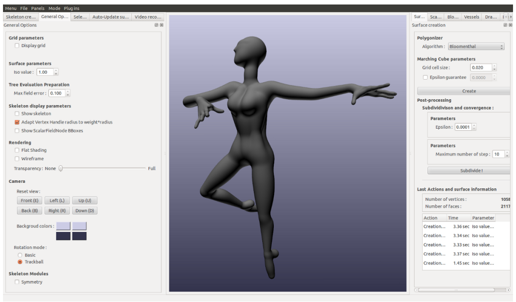
5. New Software and Platforms

5.1. Expressive

FUNCTIONAL DESCRIPTION

Expressive is a new C++ library created in 2013 for gathering and sharing the models and algorithms developed within the ERC Expressive project. It enables us to make our latest research results on new creative tools - such as high level models with intuitive, sketching or sculpting interfaces - soon available to the rest of the group and easily usable for our collaborators, such as Evelyne Hubert (Inria, Galaad) or Loic Barthe (IRIT, Toulouse). The most advanced part is a new version of Convol, a library dedicated to implicit modeling, with a main focus on integral surfaces along skeletons. Convol incorporates all the necessary material for constructive implicit modeling, a variety of blending operators and several methods for tessellating an implicit surface into a mesh, and for refining it in highly curved regions. The creation of new solid geometry can be performed by direct manipulation of skeletal primitives or through sketch-based modeling and multi-touch deformations.

- Participants: Marie-Paule Cani, Antoine Begault, Rémi Brouet, Even Entem, Thomas Delame, Ulysse Vimont and Cédric Zanni
- Contact: Marie-Paule Cani



Grid parameters
☐ Display grid

Surface parameters
Iso value : 1.00

Tree Evaluation Preparation
Max field error : 0.100

Skeleton display parameters
☐ Show skeleton
☑ Adapt Vertex Handle radius to weight*radius
☐ Show ScalarFieldNode BBoxes

Rendering
☐ Flat Shading
☐ Wireframe
Transparency : None Full

Camera
Reset view :
Backgroud colors :
Rotation mode :
○ Basic
● Trackball

Skeleton Modules
☐ Symmetry

Polygonizer
Algorithm : Bloomenthal

Marching Cube parameters
Grid cell size : 0.020
☐ Epsilon guarantee 0.0000

Post-processing
Subdividivison and convergence :
Parameters
Epsilon : 0.0001
Parameters
Maximum number of step : 10

Last Actions and surface information
Number of vertices : 1058
Number of faces : 2117

Action	Time	Parameter
Creation...	3.36 sec	Iso value...
Creation...	3.34 sec	Iso value...
Creation...	3.33 sec	Iso value...
Creation...	3.37 sec	Iso value...
Creation...	1.45 sec	Iso value...

Figure 2. GUI and Example of implicit surface and modeled with the Expressive platform.

5.2. MyCF

KEYWORDS: 3D modeling - Simulation - Health - Ontologies - Anatomy - Patientspecific - Medical imaging

FUNCTIONAL DESCRIPTION

My Corporis Fabrica (**MyCF**) is an anatomical knowledge ontology developed in our group. It relies on FMA (Foundational Model of Anatomy), developed under Creative Commons license (CC-by). MyCF browser is available on line, and is already in use for education and research in anatomy. Moreover, the MyCf's generic programming framework can be used for other domains, since the link it provides between semantic and 3D models matches several other research applications at IMAGINE.

- Participants: Olivier Palombi, Armelle Bauer, François Faure, Ali Hamadi Dicko
- Contact: Olivier Palombi
- URL: http://www.mycorporisfabrica.org

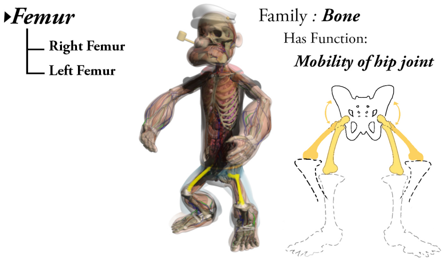


Figure 3. My Corporis Fabrica is an anatomical knowledge database developed in our team.

5.3. SOFA

Simulation Open Framework Architecture

KEYWORDS: Physical simulation - Health - Biomechanics - GPU - Computer-assisted surgery

FUNCTIONAL DESCRIPTION

SOFA is an Open Source framework primarily targeted at real-time simulation, with an emphasis on medical simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows : the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods.

- Participants: François Faure, Armelle Bauer, Olivier Carré, Matthieu Nesme, Romain Testylier.
- Contact: François Faure
- URL: http://www.sofa-framework.org

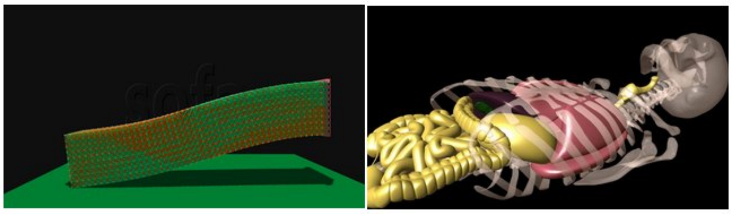


Figure 4. SOFA is an open source simulator for physically based modeling.

INDES Project-Team

5. New Software and Platforms

5.1. Web programming

Participants: Yoann Couillec, Colin Vidal, Vincent Prunet, Manuel Serrano [correspondant].

5.1.1. The HOP web programming environment

HOP is a higher-order language designed for programming interactive web applications such as web agendas, web galleries, music players, etc. It exposes a programming model based on two computation levels. The first one is in charge of executing the logic of an application while the second one is in charge of executing the graphical user interface. HOP separates the logic and the graphical user interface but it packages them together and it supports strong collaboration between the two engines. The two execution flows communicate through function calls and event loops. Both ends can initiate communications.

The HOP programming environment consists in a web *broker* that intuitively combines in a single architecture a web server and a web proxy. The broker embeds a HOP interpreter for executing server-side code and a HOP client-side compiler for generating the code that will get executed by the client.

An important effort is devoted to providing HOP with a realistic and efficient implementation. The HOP implementation is *validated* against web applications that are used on a daily-basis. In particular, we have developed HOP applications for authoring and projecting slides, editing calendars, reading RSS streams, or managing blogs.

HOP has won the software *open source contest* organized by the ACM Multimedia Conference 2007. It is released under the GPL license. It is available at http://hop.inria.fr.

- Participants: Manuel Serrano
- Contact: Manuel Serrano
- URL: http://hop.inria.fr

5.1.2. The Bigloo compiler

The programming environment for the Bigloo compiler [7] is available on the Inria Web site at the following URL: http://www-sop.inria.fr/teams/indes/fp/Bigloo. The distribution contains an optimizing compiler that delivers native code, JVM bytecode, and .NET CLR bytecode. It contains a debugger, a profiler, and various Bigloo development tools. The distribution also contains several user libraries that enable the implementation of realistic applications.

BIGLOO was initially designed for implementing compact stand-alone applications under Unix. Nowadays, it runs harmoniously under Linux and MacOSX. The effort initiated in 2002 for porting it to Microsoft Windows is pursued by external contributors. In addition to the native back-ends, the BIGLOO JVM back-end has enabled a new set of applications: Web services, Web browser plug-ins, cross platform development, etc. The new BIGLOO .NET CLR back-end that is fully operational since release 2.6e enables a smooth integration of Bigloo programs under the Microsoft .NET environment.

- Participants: Manuel Serrano
- Contact: Manuel Serrano
- URL: http://www-sop.inria.fr/teams/indes/fp/Bigloo

INFINE Team

5. New Software and Platforms

5.1. RIOT

KEYWORDS: Internet of things - Operating system - Internet protocols - Sensors - IoT - Wireless Sensor Networks

SCIENTIFIC DESCRIPTION

While requiring as low as 1,5kB of RAM and 5kB or ROM, the RIOT operating system offers both advanced capabilities such as real time and energy efficiency capabilities, as well as standard capabilities, such as a single API (partially POSIX compliant) across heterogeneous IoT hardware (8-bit, 16-bit and 32-bit low-power hardware). This API is developer-friendly in that it enables Linux-like developer experience which was not possible so far for embedded programming: multi-threading, standard C and C++ application programming and the use of standard debugging tools (gbd, valgrind etc.). On top of this, as expected from a modern OS, RIOT also provides standard connectivity capabilities, by means of several networks stacks that are readily available, such as a standard IPv6/6LoWPAN stack and a information-centric network stack (based on CCN).

FUNCTIONAL DESCRIPTION

RIOT is an open source operating system that provides an API and SDK for energy-, memory- and CPU-constrained IoT devices and similar communicating embedded systems. This API builds upon standard systems concepts (e.g. POSIX) and standard communication protocols (e.g. IPv6). RIOT thus allows the development of applications that collect sensor data and transmit it to the cloud over the Internet, using end-to-end communication means e.g. IPv6 communication from sensor to cloud servers, that can be protected by transport layer security (e.g. DTLS). This data can then be used for smart energy management for example.

An important part of the design of RIOT is that it can easily be ported to different hardware devices (tens of types of heterogeneous IoT devices are already supported), and it can easily be extended to support the latest evolution of communication standards (a wide range of protocols are already supported).

For example, RIOT already enables tests and experiements of arbitrary IoT applications and protocols on FIT IoT-Lab, which provides a large-scale infrastructure facility with 2700 nodes for testing remotely small wireless devices. Once validated, the code for such applications and protocols can then run on any other IoT device hardware supported by RIOT.

- Participants: Emmanuel Baccelli and Oliver Hahm
- Partner: Freie Universitaet Berlin
- Contact: Emmanuel Baccelli
- URL: http://www.riot-os.org

5.2. GardiNet (previously known as DragonNet)

FUNCTIONAL DESCRIPTION

GardiNet (previously known as DragonNet) is a generic framework for network coding in wireless networks. It is a initially result of the GETRF project of the Hipercom2 team.

It is based on intra-flow coding where the source divides the flow in a sequence of payloads of equal size (padding may be used). The design keys of DragonNet are simplicity and universality, GardiNet does not use explicit or implicit knowledge about the topology (such as the direction or distance to the source, the loss rate of the links, ...). Hence, it is perfectly suited to the most dynamic wireless networks. The protocol is distributed and requires minimal coordination. DragonNet architecture is modular, it is based on 5 building blocks (LIB, SIG, Protocol, SEW and DRAGON). Each block is almost independent. This makes DragonNet generic and hence adaptable to many application scenarios. DragonNet derives from a prior protocol called DRAGONCAST. Indeed, DragonNet shares the same principles and theoretical overview of DRAGONCAST. It enriches DRAGONCAST by the information base and signaling required to perform broadcast in wireless networks and in wireless sensor networks in particular.

- Participants: Cédric Adjih, Ichrak Amdouni, Hana Baccouch and Antonia Masucci
- Contact: Cédric Adjih
- URL: http://getrf.gforge.inria.fr/https://github.com/GardiNet/gardinet

5.3. MACACO

Mobile context-Adaptive CAching for COntent-centric networking
FUNCTIONAL DESCRIPTION

MACACOapp is developped in the context of the EU CHIST-ERA MACACO project. It consists in a mobile phone application that periodically samples phoneâs information on the mobility (through, e.g., GPS sensor, accelerometer and WiFi/Bluetooth/Cellular environment, connectivity type) and on the data traffic it generates (through, e.g., Internet browser history and applications data consumption). The information collected will be time-stamped and will be periodically sent to the central servers for analysis and visualization. We expect that (1) the collected information will allow us studying the correlation between mobility and content demand patterns and that (2) the results of this analysis will allow us inferring the best times and places to transfer content from/to usersâ phones location and/or from/to the wireless infrastructure closest to the usersâ phones location. Users will be also invited to fill a non-mandatory questionnaire relevant to this study. Our questionnaire collects information about the personality traits and application preferences of people. We expect that the information collected from questionnaire will allow us to analyse the correlation between users personality traits and their application preferences and interests. Userâs application preferences and interests will be inferred from the Internet browsing history and running app information obtained from the MACACO App.

- Participants: Aline Carneiro Viana, Katia Jaffres and Marco Fiore
- Contact: Aline Carneiro Viana
- URL: https://macaco.inria.fr/macacoapp/

INOCS Team (section vide)

IPSO Project-Team (section vide)

KERDATA Project-Team

6. New Software and Platforms

6.1. Major Software

6.1.1. BlobSeer

Participants: Alexandru Costan, Gabriel Antoniu, Luc Bougé, Loïc Cloatre.

Contact: Gabriel Antoniu.

Presentation: BlobSeer is the core software platform for many current cloud-oriented projects of the KerData team. It is a data storage service specifically designed to deal with the requirements of large-scale, data-intensive distributed applications that abstract data as huge sequences of bytes, called BLOBs (Binary Large OBjects). It provides a versatile versioning interface for manipulating BLOBs that enables reading, writing and appending to them.

BlobSeer offers both scalability and performance with respect to a series of issues typically associated with the data-intensive context: *scalable aggregation of storage space* from the participating nodes with minimal overhead, ability to store *huge data objects*, *efficient fine-grain access* to data subsets, *high throughput in spite of heavy access concurrency*, as well as *fault-tolerance*. This year we have mainly focused on the deployment in production of the BlobSeer software on IBM's cluster at Montpellier, in the context of the ANR MapReduce project. To this end, several bugs were solved, and several optimizations were brought to the communication layer of BlobSeer. To showcase the benefits of BlobSeer on this platform we focused on the Terasort benchmark. Currently, preliminary tests on Grid5000 with this benchmark show that BlobSeer performs better than HDFS for block sizes lower than 2 MB. We have also improved the continuous integration process of BlobSeer by deploying daily builds and automatic tests on Grid5000.

Users: Work is currently in progress in several formalized projects (see previous section) to integrate and leverage BlobSeer as a data storage back-end in the reference cloud environments: a) Microsoft Azure; b) the Nimbus cloud toolkit developed at Argonne National Lab (USA); and c) the OpenNebula IaaS cloud toolkit developed at UCM (Madrid).

URL: http://blobseer.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: This software is available on Inria's forge. Version 1.0 (released late 2010) registered with APP: IDDN.FR.001.310009.000.S.P.000.10700.

A *Technology Research Action* (ADT, *Action de recherche technologique*) was active for two years until January 2015, aiming to robustify the BlobSeer software and to make it a safely distributable product. This project is funded by Inria *Technological Development Office* (D2T, *Direction du Développement Technologique*).

6.1.2. Damaris

Participants: Matthieu Dorier, Gabriel Antoniu, Orçun Yildiz, Lokman Rahmani, Shadi Ibrahim.

Contact: Gabriel Antoniu.

Presentation: Damaris is a middleware for multicore SMP nodes enabling them to handle data transfers for storage and visualization efficiently. The key idea is to dedicate one or a few cores of each SMP node to the application I/O. It is developed within the framework of a collaboration between KerData and the *Joint Laboratory for Petascale Computing* (JLPC). Damaris enables efficient asynchronous I/O, hiding all I/O related overheads such as data compression and post-processing, as well as direct (*in-situ*) interactive visualization of the generated data. Version 1.0 was released in November 2014 and enables other approaches such as the use of dedicated nodes instead of dedicated cores.

Users: Damaris has been preliminarily evaluated at NCSA/UIUC (Urbana-Champaign, IL, USA) with the CM1 tornado simulation code. CM1 is one of the target applications of the Blue Waters supercomputer in production at, in the framework of the Inria-UIUC-ANL Joint Lab (JLPC). Damaris now has external users, including (to our knowledge) visualization specialists from NCSA and researchers from the France/Brazil Associated research team on Parallel Computing (joint team between Inria/LIG Grenoble and the UFRGS in Brazil). Damaris has been successfully integrated into four large-scale simulations (CM1, OLAM, Nek5000, GTC).

URL: http://damaris.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: This software is available on Inria's forge and registered with APP. Registration of the latest version with APP is in progress.

6.2. Other Software

6.2.1. Omnisc'IO

Participants: Matthieu Dorier, Shadi Ibrahim, Gabriel Antoniu.

Contact: Matthieu Dorier

Presentation: Omnisc'IO is a middleware integrated in the POSIX and MPI-I/O stacks to observe, model and predict the I/O behavior of any HPC application transparently. It is based on formal grammars, implementing a modified version of the Sequitur algorithm. Omnisc'IO has been used on Grid'5000 with the CM1 atmospheric simulation, the LAMMPS molecular dynamics simulation, the GTC fusion simulation and the Nek5000 CFD simulation. Omnisc'IO was subject to a publication at SC14.

Users: Omnisc'IO is currently used only within the KerData team and at Argonne National Lab.

URL: http://omniscio.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: Currently unavailable for distribution (subject to major changes). Version 1.0 (released in November 2015) registered with APP: IDDN.FR.001.540003.000.S.P.2015.000.10000.

6.2.2. JetStream

Participants: Radu Tudoran, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan

Presentation: JetStream is a middleware solution for batch-based, high-performance streaming across cloud data centers. JetStream implements a set of context-aware strategies for optimizing batch-based streaming, being able to self-adapt to changing conditions. Additionally, the system provides multi-route streaming across cloud data centers for aggregating bandwidth by leveraging the network parallelism. It enables easy deployment across .Net frameworks and seamless binding with event processing engines such as StreamInsight.

Users: JetStream is currently used at Microsoft Research ATLE Munich for the management of the Azure cloud infrastructure.

License: Microsoft Public License.

Status: Prototype and demo available.

6.2.3. OverFlow

Participants: Radu Tudoran, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan.

Presentation: OverFlow is a uniform data management system for scientific workflows running across geographically distributed sites, aiming to reap economic benefits from this geo-diversity. The software is environment-aware, as it monitors and models the global cloud infrastructure, offering high and predictable data handling performance for transfer cost and time, within and across sites. OverFlow proposes a set of pluggable services, grouped in a data-scientist cloud kit. They provide the applications with the possibility to monitor the underlying infrastructure, to exploit smart data compression, deduplication and geo-replication, to evaluate data management costs, to set a tradeoff between money and time, and optimize the transfer strategy accordingly. In 2015, OverFlow was extended with support for efficient metadata operations: the newly implemented strategies leverage workflow semantics in a 2-level metadata partitioning hierarchy that combines distribution and replication.

Users: Currently, OverFlow is used for data transfers by the Microsoft Research ATLE Munich team as well as for synthetic benchmarks at the Politehnica University of Bucharest.

License: GNU Lesser General Public License (LGPL) version 3.

Status: Registration of the latest version with APP is in progress

6.2.4. iHadoop

Participants: Tien Dat Phan, Shadi Ibrahim.

Contact: Shadi Ibrahim

Presentation: *iHadoop* is a Hadoop simulator developed in Java on top of SimGrid to simulate the behavior of Hadoop and therefore accurately predict the performance of Hadoop in normal scenarios and under failures. In 2015, iHadoop was extended to simulate the execution and predict the performance of multiple Map-Reduce applications, sharing the same Hadoop cluster. Two schedulers (Fifo, Fair) are now available in iHadoop.

Users: iHadoop is an internal software prototype, which was initially developed to validate our idea for exploring the behavior of Hadoop under failures. iHadoop has preliminarily evaluated within our group and it has shown very high accuracy when predicating the execution time of a Map-Reduce application. iHadoop was discussed with the SimGrid community during the SimGrid user days in Lyon (June 2015). We intend to add iHadoop to the contributions site of the SimGrid project and make it available to the SimGrid community.

License: GNU Lesser General Public License (LGPL) version 3.

Status: Available on Inria's forge. Registration of the latest version with APP is in progress.

LAGADIC Project-Team

6. New Software and Platforms

6.1. DESlam

Dense Egocentric SLAM
KEYWORDS: Deph Perception - Robotics - Localisation
FUNCTIONAL DESCRIPTION

This software proposes a full and self content solution to the dense Slam problem. Based on a generic RGB-D representation valid for various type of sensors (stereovision, multi-cameras, RGB-D sensors...), it provides a 3D textured representation of complex large indoor and outdoor environments and it allows localizing in real time (45Hz) a robot or a person carrying out a mobile camera.

- Participants: Maxime Meilland, Andrew Ian Comport and Patrick Rives
- Contact: Patrick Rives
- URL: http://team.inria.fr/lagadic

6.2. HandiViz

KEYWORDS: Health - Persons attendant - Handicap
FUNCTIONAL DESCRIPTION

The HandiViz software proposes a semi-autonomous navigation framework of a wheelchair relying on visual servoing.

It has been registered to the APP (“Agence de Protection des Programmes”) as an INSA software (IDDN.FR.001.440021.000.S.P.2013.000.10000) and is under GPL license.

- Participants: François Pasteau and Marie Babel
- Contact: Marie Babel
- URL: https://team.inria.fr/lagadic/

6.3. Perception360

Robot vision and 3D mapping with omnidirectional RGB-D sensors.
KEYWORDS: Depth Perception - 3D rendering - Computer vision - Robotics - Image registration - Sensors - Realistic rendering - 3D reconstruction - Localization
FUNCTIONAL DESCRIPTION

This software is a collection of libraries and applications for robot vision and 3D mapping with omnidirectional RGB-D sensors or standard perspective cameras. This project provides the functionality to do image acquisition, semantic annotation, dense registration, localization and 3D mapping. The omnidirectional RGB-D sensors used within this project have been developed in Inria Sophia-Antipolis by the team LAGADIC.

- Contact: Patrick Rives
- URL: https://team.inria.fr/lagadic/software-eng.html

6.4. Sinatrack

KEYWORDS: Computer vision - Robotics
FUNCTIONAL DESCRIPTION

Sinatrack is a tracking software that allows the 3D localization (translation and rotation) of an object with respect to a monocular camera. It allows to consider object with complex shape. The underlying approach is a model-based tracking techniques. It has been developed for satellite localization and on-orbit service applications but is also suitable for augmented reality purpose.

- Participants: Antoine Guillaume Petit, Éric Marchand and François Chaumette
- Contact: Éric Marchand
- URL: http://team.inria.fr/lagadic

6.5. UsTk

Ultrasound Toolkit
KEYWORDS: Echographic imagery - Image reconstruction - Active contours - Medical robotics
FUNCTIONAL DESCRIPTION

UsTk, standing for Ultrasound Toolkit, is a cross-platform library for two- and three-dimensional ultrasound image processing. Written in C++, UsTk provides tools for ultrasound image acquisition, processing and display of these images. Combined with the UsSimulator software that simulates a virtual ultrasound probe interacting with a 3D ultrasound volume and the UsGraphCut library that allows real-time segmentation of ultrasound images, it can serve as an useful framework for developing and testing new visual servoing approaches based on ultrasound images.

- Participants: Alexandre Krupa, Pierre Chatelain and Christophe Collewet
- Partners: Université de Rennes 1 - IRSTEA
- Contact: Alexandre Krupa
- URL: https://team.inria.fr/lagadic/

6.6. ViSP

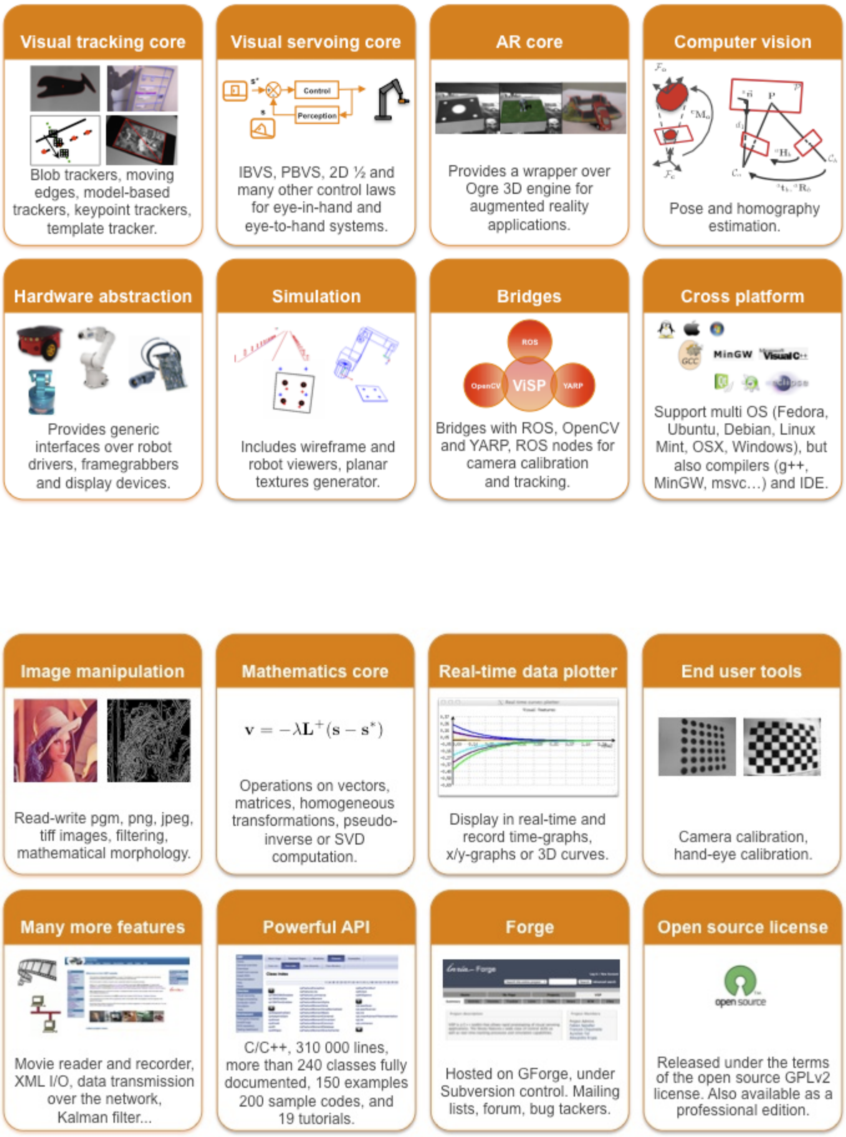
KEYWORDS: Augmented reality - Computer vision - Robotics - Visual servoing (VS)
SCIENTIFIC DESCRIPTION

Since 2005, we develop and release ViSP [5] , an open source library available from http://visp.inria.fr. ViSP standing for Visual Servoing Platform allows prototyping and developing applications using visual tracking and visual servoing techniques at the heart of the Lagadic research. ViSP was designed to be independent from the hardware, to be simple to use, expandable and cross-platform. ViSP allows to design vision-based tasks for eye-in-hand and eye-to-hand visual servoing that contains the most classical visual features that are used in practice. It involves a large set of elementary positioning tasks with respect to various visual features (points, segments, straight lines, circles, spheres, cylinders, image moments, pose...) that can be combined together, and image processing algorithms that allow tracking of visual cues (dots, segments, ellipses...) or 3D model-based tracking of known objects or template tracking. Simulation capabilities are also available.

FUNCTIONAL DESCRIPTION

ViSP provides simple ways to integrate and validate new algorithms with already existing tools. It follows a module-based software engineering design where data types, algorithms, sensors, viewers and user interaction are made available. Written in C++, ViSP is based on open-source cross-platform libraries (such as OpenCV) and builds with CMake. Several platforms are supported, including OSX, Windows and Linux. ViSP online documentation allows to ease learning. More than 250 fully documented classes organized in 16 different modules, with more than 200 examples and 35 tutorials are proposed to the user. ViSP is released under a dual licensing model. It is open-source with a GNU GPLv2 license. A professional edition license that replaces GNU GPLv2 is also available.

- Participants: François Chaumette, Éric Marchand, Fabien Spindler, Aurélien Yol and Souriya Trinh
- Partners: Université de Rennes 1 - CNRS
- Contact: Fabien Spindler
- URL: http://visp.inria.fr



Visual tracking core

Blob trackers, moving edges, model-based trackers, keypoint trackers, template tracker.

Visual servoing core

IBVS, PBVS, 2D ½ and many other control laws for eye-in-hand and eye-to-hand systems.

AR core

Provides a wrapper over Ogre 3D engine for augmented reality applications.

Computer vision

Pose and homography estimation.

Hardware abstraction

Provides generic interfaces over robot drivers, framegrabbers and display devices.

Simulation

Includes wireframe and robot viewers, planar textures generator.

Bridges

Bridges with ROS, OpenCV and YARP, ROS nodes for camera calibration and tracking.

Cross platform

Support multi OS (Fedora, Ubuntu, Debian, Linux Mint, OSX, Windows), but also compilers (g++, MinGW, msvc…) and IDE.

Image manipulation

Read-write pgm, png, jpeg, tiff images, filtering, mathematical morphology.

Mathematics core

$$\mathbf{v} = -\lambda \mathbf{L}^{+}(\mathbf{s} - \mathbf{s}^{*})$$

Operations on vectors, matrices, homogeneous transformations, pseudo-inverse or SVD computation.

Real-time data plotter

Display in real-time and record time-graphs, x/y-graphs or 3D curves.

End user tools

Camera calibration, hand-eye calibration.

Many more features

Movie reader and recorder, XML I/O, data transmission over the network, Kalman filter...

Powerful API

C/C++, 310 000 lines, more than 240 classes fully documented, 150 examples 200 sample codes, and 19 tutorials.

Forge

Hosted on GForge, under Subversion control. Mailing lists, forum, bug tackers.

Open source license

Released under the terms of the open source GPLv2 license. Also available as a professional edition.

Figure 1. This figure highlights ViSP main capabilities for visual tracking, visual servoing, and augmented reality that may benefit from computer vision algorithms. ViSP allows controlling specific platforms through hardware abstraction or in simulation. ViSP provides also bridges over other frameworks such as OpenCV and ROS. All these capabilities are cross-platform. Moreover, for easing the prototyping of applications, ViSP provides tools for image manipulation, mathematics, data plotting, camera calibration, and many other features. ViSP powerful API is fully documented and available on Inria's forge as an open source software under GPLv2 license.

This year, a new ViSP 2.10 release was produced in February. The corresponding source code tarball was downloaded 1290 times. With the help of the community, this release was packaged for Debian and Ubuntu 14.04. We also designed a new modular software architecture where ViSP capabilities are grouped in several modules (core, io, gui, vision...). As a result, the user will find several shared or static libraries, one for each module. In the mean time we continued our efforts to improve the software by ensuring the compatibility with third-party libraries that continue also to evolve like CMake and OpenCV. We also fixed some issues, allowed the markerless 3D model-based hybrid tracker to consider cylinders and introduce a new algorithm to determine face visibility. Moreover, we improve the object detection algorithm based on keypoints that is able to return the pose of a learned object. We improved the documentation by providing new tutorials and by updating the existing ones. ViSP 3.0.0 will be released these days.

Concerning ROS community, all the existing packages in "`vision_visp`" ROS stack (see http://wiki.ros.org/vision_visp) were updated and ported to jade build system. To ease ViSP usage in the ROS framework, the releases of the year were packaged for ROS.

ViSP is used in research labs in France, USA, Japan, Korea, India, China, Lebanon, Italy, Spain, Portugal, Hungary, Canada. For instance, it is used as a support in graduate courses at IFMA Clermont-Ferrand, University of Picardie in Amiens, Télécom Physique in Strasbourg and ESIR in Rennes.

6.7. bib2html

FUNCTIONAL DESCRIPTION

The purpose of this software is to automatically produce html pages from BibTEX files, and to provide access to the BibTEX entries by several criteria: year of publication, category of publication, keywords, author name. Moreover cross-linking is generating between pages to provide an easy navigation through the pages without going back to the index.

- Contact: Éric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html

6.8. Robot vision platform

Participant: Fabien Spindler [correspondant].

We exploit two industrial robotic systems built by Afma Robots in the nineties to validate our researches in visual servoing and active vision. The first one is a Gantry robot with six degrees of freedom, the other one is a cylindrical robot with four degrees of freedom (see Fig. 2). These robots are equipped with cameras. The Gantry robot allows also to embed grippers on its end-effector.

Five papers published by Lagadic in 2015 enclose results validated on this platform [30][53][29][31][50].

6.9. Mobile robotics platforms

Participants: Fabien Spindler [correspondant], Marie Babel, Patrick Rives.

6.9.1. Indoor mobile robots

For fast prototyping of algorithms in perception, control and autonomous navigation, the team uses Hannibal in Sophia Antipolis, a cart-like platform built by Neobotix (see Fig. 3 .a), and, in Rennes, a Robotino from Festo (see Fig. 3 .b) and a Pioneer 3DX from Adept (see Fig. 3 .c). These platforms are equipped with various sensors needed for Slam purposes, autonomous navigation and sensor-based control.

Moreover, to validate the researches in personally assisted living topic (see 7.3.3), we have in Rennes a six wheel electric wheelchair from Penny and Giles Drives Technology (see Fig. 3 .d) and a five wheel electric wheelchair from You-Q (see Fig. 3 .e). The control of the wheelchair is performed using a plug and play system between the joystick and the low level control of the wheelchair. Such a system lets us acquire the user intention through the joystick position and control the wheelchair by applying corrections to its motion. The wheelchairs have been fitted with cameras and eleven ultrasound sensors to perform the required servoing for assisting handicapped people.

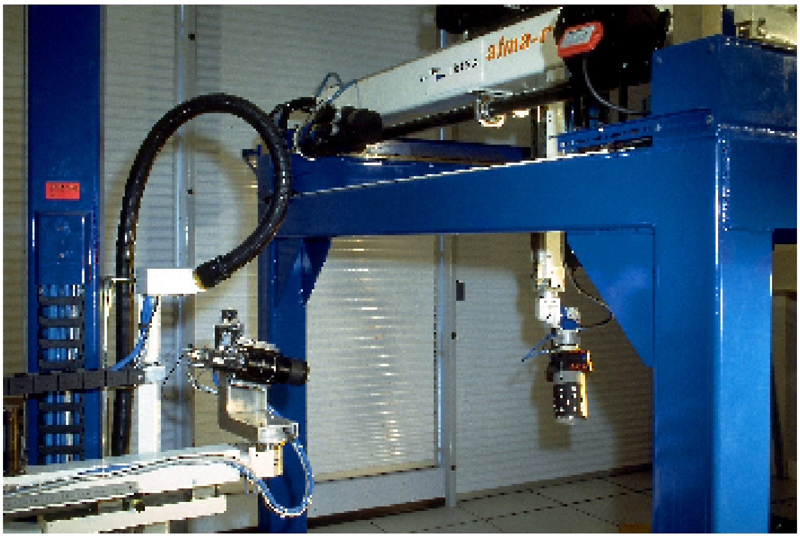


Figure 2. Lagadic robotics platform for vision-based manipulation

Note that 5 papers exploiting the indoors mobile robots were published this year [14][22][28][56][27].

6.9.2. Outdoor vehicles

The team exploits also Cycab urban electrical cars (see Figs. 3 .f and 3 .g). Two vehicles in Sophia Antipolis and one in Rennes are instrumented with cameras and range finders to validate researches in the domain of intelligent urban vehicle. Cycabs were used as experimental testbeds in several national projects in the past. This year we decided to donate the Cycab in Rennes to the INSA engineer school were it started a second live.

The camera rig can also be fixed to a standard car (see Fig. 4), which is driven at a variable speed depending on the road/traffic conditions, with an average of 30 km/h and a maximum speed of 80 km/h. The sequences are recorded at a frame rate of 20 Hz, where the six global shutter cameras of the stereo system are synchronized, producing spherical images with a resolution of 2048x665 (see fig. 4). Such sequences are fused offline to obtain maps that can be used later for localization or for scene rendering. (in a similar fashion to Google Street View) as we show in the accompanying video [0].

Four papers published by Lagadic in 2015 enclose experimental results obtained with these outdoor vehicles [20][37][10][42].

6.10. Medical robotics platform

Participants: Fabien Spindler [correspondant], Alexandre Krupa.

This testbed is of primary interest for researches and experiments concerning ultrasound visual servoing applied to probe positioning, soft tissue tracking or robotic needle insertion tasks described in Section 7.6 .

This platform is composed by two Adept Viper six degrees of freedom arms (see Fig. 5 .a). Ultrasound probes connected either to a SonoSite 180 Plus or an Ultrasonix SonixTouch imaging system can be mounted on a force torque sensor attached to each robot end-effector.

---

[0] video url:(www-sop.inria.fr/members/Renato-Jose.Martins/iros15.html)

(a) (b) (c)

(d) (e)

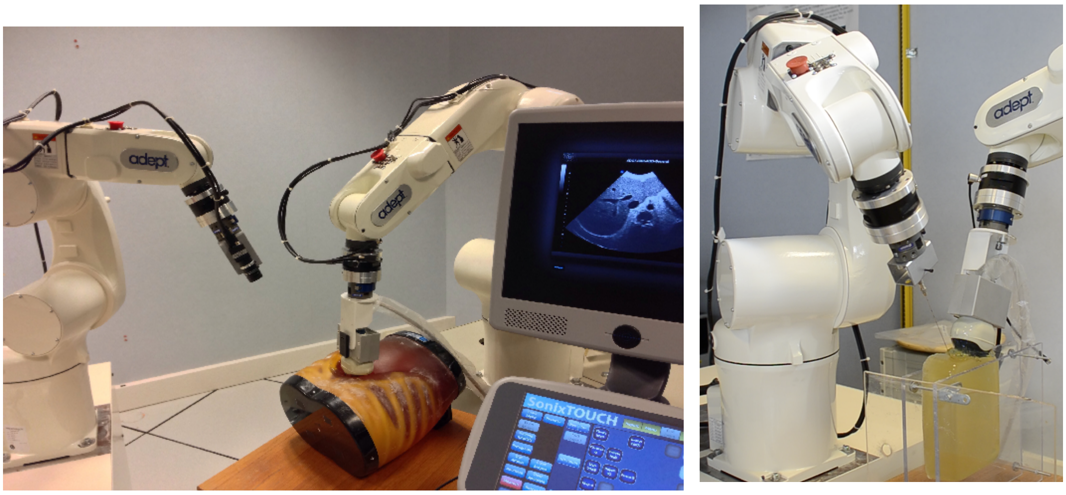
(f) (g)

Figure 3. a) Hannibal platform, b) Robotino, c) Pioneer P3-DX robot, d) wheelchair from Penny and Giles Drives Technology, e) wheelchair from You-Q , f) Cycab available in Rennes, g) one of the Cycabs available in Sophia Antipolis.

Figure 4. Globeye stereo sensor and acquisition system.

We designed an experimental setup to test an autonomous robotic needle insertion method based on visual servoing 7.6.2 . The experimental setup is composed with a gelatin phantom simulating soft tissues, a flexible biopsy needle actuated by an Adept Viper arm and a 3D ultrasound probe held by the second Adept Viper arm (see Fig. 5 .b).

This year, 5 papers enclose experimental results obtained with this platform [49][48][47][33][32].



(a) (b)

Figure 5. a) Lagadic medical robotics platforms. On the right Viper S850 robot arm equipped with a SonixTouch 3D ultrasound probe. On the left Viper S650 equipped with a tool changer that allows to attach a classical camera or biopsy needles. b) Robotic setup for autonomous needle insertion by visual servoing.

6.11. Humanoid robot platform

Participants: Giovanni Claudio, Fabien Spindler [correspondant].

Romeo is a humanoid robot from Aldebaran Robotics which is intended to be a genuine personal assistant and companion. For the moment only the upper part of the body (trunk, arms, neck, head, eyes) is working. This research platform is used to validate our researches in visual servoing and visual tracking. We continue to improve the work initiated last year to grasp a box and deliver it to a human introducing especially joint limits avoidance (see Fig. 6). We started also to work on a visual servoing framework able to control both arms to manipulate an object using only vision.

This year one paper encloses experimental results obtained with this platform [54].

6.12. Unmanned Aerial Vehicles (UAVs) platform

Participants: Thomas Bellavoir, Paolo Robuffo Giordano [correspondant].

From 2014, the team also started some activities involving perception and control for single and multiple quadrotor UAVs, especially thanks to a grant from “Rennes Métropole” (see Section 9.1.5) and the ANR project “SenseFly” (see Section 9.2.4). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (Fig. 7 .a), and one quadrotor from 3DRobotics, USA (Fig. 7 .b). The Mikrokopter quadrotors have been heavily customized by: (i) reprogramming from scratch the low-level attitude controller onboard the microcontroller of the quadrotors, (ii) equipping each quadrotor with an Odroid XU4 board (Fig. 7 .d)

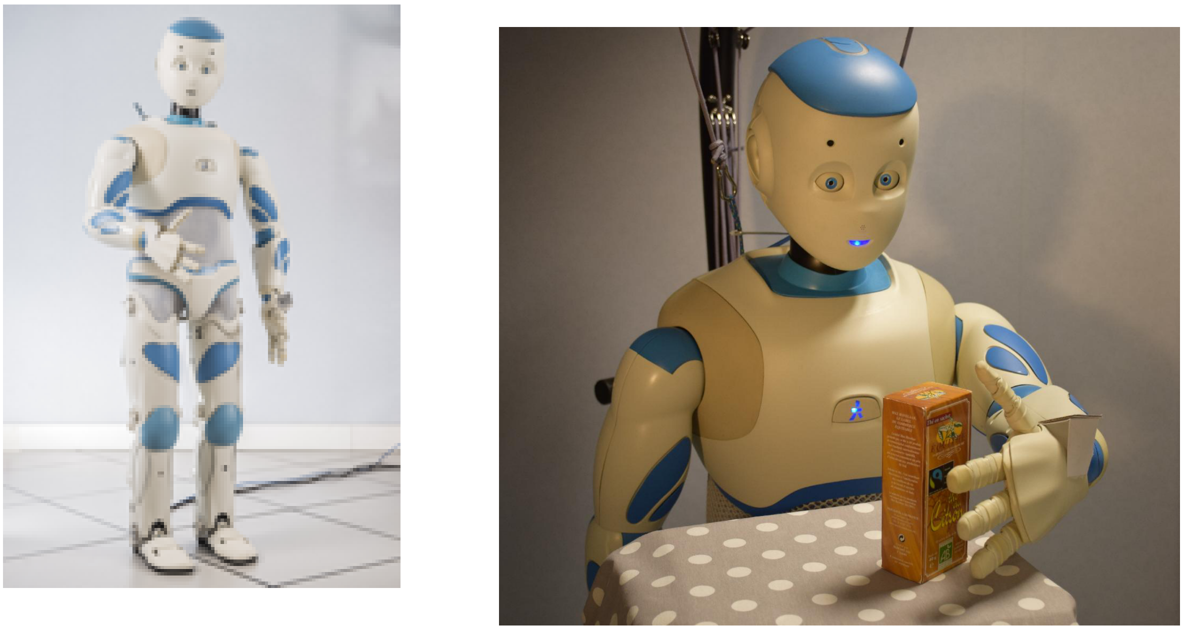
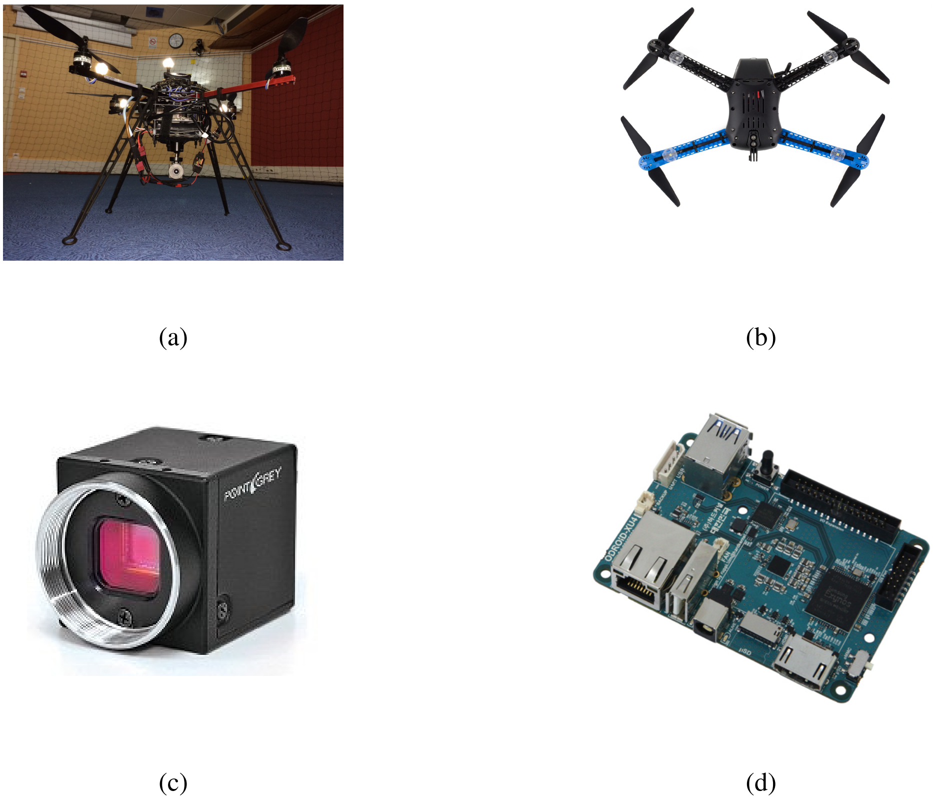


Figure 6. Romeo experimental platform.

running Linux Ubuntu and the TeleKyb software (the middleware used for managing the experiment flows and the communication among the UAVs and the base station), and (iii) purchasing the Flea Color USB3 cameras together with the gimbal needed to mount them on the UAVs (Fig. 7 .c). The quadrotor group will be used as robotic platforms for testing a number of single and multiple flight control schemes with a special attention on the use of onboard vision as main sensory modality.



(a) (b) (c) (d)

Figure 7. a) Quadrotor XL1 from Mikrokopter, b) Quadrotor Iris from 3DRobotics, c) Flea Color USB3 camera, d) Odroid XU4 board

LARSEN Team

6. New Software and Platforms

6.1. New Platforms

6.1.1. Experimental Room for Robotics

We collaborate on this experimental platform with Olivier Rochel (SED Inria Nancy - Grand Est).

Figure 2. Overview of the new experimental room.

A new room has been installed for the experiments of the ResiBots ERC project and of the Codyco FP7 project (Figure 2). This 100 m^2 room contains a 5.5 $\times$ 6 m experimental “arena” made with aluminium trusses.

It is equipped with:

- a 6D motion capture system (Optitrack), with 8 gibagit cameras (Prime 13);
- 4 high-power, studio lights;
- 3 mobile 19” racks (on wheels), which host the power supplies and the computers to control the robots;
- a 6-legged robot, used by the ResiBots project;
- an omnidirectional wheeled robot (Kuka Youbot), used by the ResiBots project;
- a hybrid, wheel-legged robot, used by the ResiBots project (loan by the Pierre and Marie Curie University);
- a Kinova robotic arm, used by the Codyco project.

The trusses support the motion capture system and the lights, and hold all the cables (network, power, etc.).

This room will also host the iCub humanoid robot that should be received in March 2016.

LEAR Project-Team

6. New Software and Platforms

6.1. Video descriptors

Participants: Heng Wang, Dan Oneata, Cordelia Schmid [correspondant], Jakob Verbeek.

We have developed and made on-line available software for video description based on dense trajectories and motion boundary histograms, which are presented in [9]. The trajectories capture the local motion information of the video. A state-of- the-art optical flow algorithm enables a robust and efficient extraction of the dense trajectories. Descriptors are aligned with the trajectories and based on motion boundary histograms (MBH) which are robust to camera motion. The code is available at http://lear.inrialpes.fr/~wang/improved_trajectories.

6.2. Patch CKN

Participants: Mattis Paulin, Julien Mairal, Matthijs Douze, Zaid Harchaoui, Florent Perronnin [Facebook], Cordelia Schmid.

This is an open-source software package implementing the image retrieval technique of [17]. It is available at http://lear.inrialpes.fr/people/paulin/projects/RomePatches/. The code relies on the software "Convolutional Kernel Networks" below.

6.3. Convolutional Kernel Networks

Participants: Julien Mairal, Piotr Koniusz, Zaid Harchaoui, Cordelia Schmid.

This is an open-source software package corresponding to a paper published at NIPS in 2014, available at http://ckn.gforge.inria.fr/, and which is continuously updated. In this software package, convolutional neural networks are learned in an unsupervised manner. We control what the non-linearities of the network are really doing: the network tries to approximate the kernel map of a reproducing kernel.

6.4. DeepFlow

Participants: Philippe Weinzaepfel, Jerome Revaud, Zaid Harchaoui, Cordelia Schmid.

We developed a package for the "deep flow" algorithm. "Deep flow" combines a standard variational framework with a our new matching algorithm "deep matching", presented in the publication [31]. The code for "deep matching" is in python and the code for "deep flow" in C. The code is available on-line at http://lear.inrialpes.fr/src/deepmatching. In 2015, we have released a GPU version of "deep matching".

6.5. EpicFlow

Participants: Jerome Revaud, Philippe Weinzaepfel, Zaid Harchaoui, Cordelia Schmid.

We developed a package for the EpicFlow method [18], [32]. EpicFlow computes a dense correspondence field by performing a sparse-to-dense interpolation from an initial sparse set of matches, leveraging contour cues using an edge-aware geodesic distance. The resulting dense correspondence field is fed as an initial optical flow estimate to a one-level variational energy minimization. The code is written in C/C++ and is available at http://lear.inrialpes.fr/src/epicflow.

6.6. Motion Boundaries Detection

Participants: Philippe Weinzaepfel, Jerome Revaud, Zaid Harchaoui, Cordelia Schmid.

We make our source code for detecting motion boundaries [23] publicly available. The method is based on structured random forest and leverages both appearance and motion cues at the patch level. The source code is written in Matlab with C++ Mex-file and is available at http://lear.inrialpes.fr/research/motionboundaries/

6.7. Pose estimation and segmentation of multiple people

Participants: Guillaume Seguin, Karteek Alahari, Josef Sivic, Ivan Laptev.

We developed a method to obtain a pixel-wise segmentation and pose estimation of multiple people in stereoscopic videos. The codebase is composed of a set of patches for the various components in our pipeline, as well as the full pose mask generation and segmentation. It is available for download on the project website: http://www.di.ens.fr/willow/research/stereoseg.

6.8. FlipFlop: Fast Lasso-based Isoform Prediction as a Flow Problem

Participants: Elsa Bernard [Institut Curie, Ecoles des Mines-ParisTech], Laurent Jacob [CNRS, LBBE Laboratory], Julien Mairal [correspondant], Jean-Philippe Vert [Institut Curie, Ecoles des Mines-ParisTech].

FlipFlop is an open-source software, implementing a fast method for de novo transcript discovery and abundance estimation from RNA-Seq data. It differs from classical approaches such as Cufflinks by simultaneously performing the identification and quantitation tasks using a penalized maximum likelihood approach, which leads to improved precision/recall. Other software taking this approach have an exponential complexity in the number of exons of a gene. We use a novel algorithm based on network flow formalism, which gives us a polynomial runtime. In practice, FlipFlop was shown to outperform penalized maximum likelihood based softwares in terms of speed and to perform transcript discovery in less than 1/2 second for large genes.

FlipFlop is a user friendly bioconductor R package, which was released in October 2014. It is freely available on the Bioconductor website under a GPL licence: http://bioconductor.org/packages/release/bioc/html/flipflop.html. In 2015, we released a new version to process multiple samples [4].

LEMON Team

6. New Software and Platforms

6.1. SW2D

Participants: Carole Delenne, Vincent Guinot.

Urban floods are usually simulated using two-dimensional shallow water models. A correct representation of the urban geometry and hydraulics would require that the average computational cell size be between 0.1 m and 1 m. The meshing and computation costs make the simulation of entire districts/conurbations impracticable in the current state of computer technology.

An alternative approach consists in upscaling the shallow water equations using averaging techniques. This leads to introducing storage and conveyance porosities, as well as additional source terms, in the mass and momentum balance equations. Various versions of porosity-based shallow water models have been proposed in the literature. The Shallow Water 2 Dimensions (SW2D) computational code embeds various finite volume discretizations of these models. Ituses fully unstructured meshes with arbitrary numbers of edges. The key features of the models and numerical techniques embedded in SW2D are

- specific momentum/energy dissipation models that are active only under transient conditions. Such models, that are not present in classical shallow water models, stem from the upscaling of the shallow water equations and prove essential in modeling the features of fast urban flow transients accurately
- modified HLLC solvers for an improved discretization of the momentum source terms stemming from porosity gradients
- higher-order reconstruction techniques that allow for faster and more stable calculations in the presence of wetting/drying fronts.

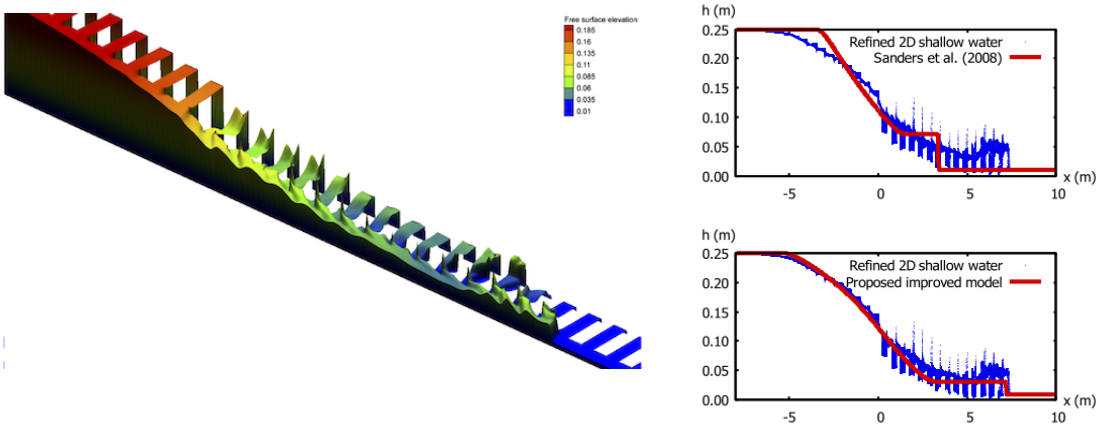


Figure 2. Propagation of a flood wave into a channel with lateral storage. Refined 2D simulation using the SW2D computational code

- Contact: Vincent Guinot
- URL: http://vincentguinot.free.fr

6.2. WindPoS

Participant: Antoine Rousseau.

The computation of the wind at small scale and the estimation of its uncertainties is of particular importance for applications such as wind energy resource estimation. To this aim, starting in 2005, we have developed a new method based on the combination of an existing Numerical Weather Prediction model providing a coarse prediction, and a Lagrangian Stochastic Model for turbulent flows. This Stochastic Downscaling Method (SDM) requires a specific modeling of the turbulence closure, and involves various simulation techniques whose combination is totally original (such as Poisson solvers, optimal transportation mass algorithm, original Euler scheme for confined Langevin stochastic processes, and stochastic particle methods).

In 2013, WindPoS became the kernel of the wind farm modeling of the Fundacion Inria Chile. In France, its development is going on through the collaborative Modéol project on the evaluation of wind potential.

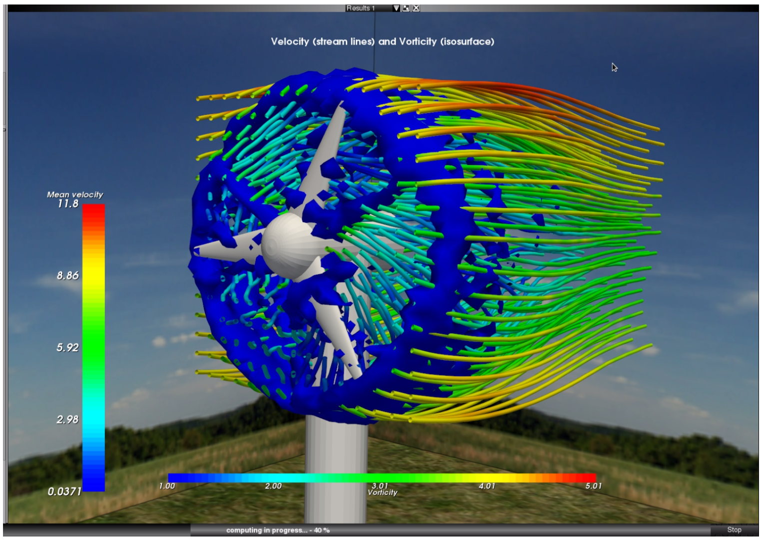


Figure 3. Velocity streamlines and vorticity around a wind mill (artistic view). WINDPOS Project.

This is a joint work with Mireille Bossy from the team TOSCA.

- Contact: Antoine ROUSSEAU
- URL: http://windpos.inria.fr

LFANT Project-Team

5. New Software and Platforms

5.1. APIP

Another Pairing Implementation in PARI
SCIENTIFIC DESCRIPTION

Apip , Another Pairing Implementation in PARI, is a library for computing standard and optimised variants of most cryptographic pairings.

The following pairings are available: Weil, Tate, ate and twisted ate, optimised versions (à la Vercauteren–Hess) of ate and twisted ate for selected curve families.

The following methods to compute the Miller part are implemented: standard Miller double-and-add method, standard Miller using a non-adjacent form, Boxall et al. version, Boxall et al. version using a non-adjacent form.

The final exponentiation part can be computed using one of the following variants: naive exponentiation, interleaved method, Avanzi–Mihailescu's method, Kato et al.'s method, Scott et al.'s method.

Part of the library has been included into PARI/GP proper.
FUNCTIONAL DESCRIPTION

APIP is a library for computing standard and optimised variants of most cryptographic pairings.

- Participant: Jérôme Milan
- Contact: Jérôme Milan
- URL: http://www.lix.polytechnique.fr/~milanj/apip/apip.xhtml

5.2. Arb

FUNCTIONAL DESCRIPTION

Arb is a C library for arbitrary-precision floating-point ball arithmetic. It supports real and complex numbers, polynomials, power series, matrices, and evaluation of many transcendental functions. All is done with automatic, rigorous error bounds. It has been accepted for inclusion in SageMath.

- Participant: Fredrik Johansson
- Contact: Fredrik Johansson
- URL: http://fredrikj.net/arb/

5.3. AVIsogenies

Abelian Varieties and Isogenies
FUNCTIONAL DESCRIPTION

AVIsogenies is a Magma package for working with abelian varieties, with a particular emphasis on explicit isogeny computation.

Its prominent feature is the computation of (l,l)-isogenies between Jacobian varieties of genus-two hyperelliptic curves over finite fields of characteristic coprime to l, practical runs have used values of l in the hundreds.

It can also be used to compute endomorphism rings of abelian surfaces, and find complete addition laws on them.

- Participants: Gaëtan Bisson, Romain Cosset and Damien Robert
- Contact: Damien Robert
- URL: http://avisogenies.gforge.inria.fr/

5.4. CM

FUNCTIONAL DESCRIPTION

The Cm software implements the construction of ring class fields of imaginary quadratic number fields and of elliptic curves with complex multiplication via floating point approximations. It consists of libraries that can be called from within a C program and of executable command line applications.

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/index.php?prog=cm&page=home

5.5. CMH

Computation of Igusa Class Polynomials

KEYWORDS: Mathematics - Cryptography - Number theory

FUNCTIONAL DESCRIPTION

Cmh computes Igusa class polynomials, parameterising two-dimensional abelian varieties (or, equivalently, Jacobians of hyperelliptic curves of genus 2) with given complex multiplication.

- Participants: Emmanuel Thomé, Andreas Enge and Regis Dupont
- Contact: Emmanuel Thomé
- URL: http://cmh.gforge.inria.fr

5.6. CUBIC

FUNCTIONAL DESCRIPTION

Cubic is a stand-alone program that prints out generating equations for cubic fields of either signature and bounded discriminant. It depends on the Pari library. The algorithm has quasi-linear time complexity in the size of the output.

- Participant: Karim Belabas
- Contact: Karim Belabas
- URL: http://www.math.u-bordeaux.fr/~belabas/research/software/cubic-1.2.tgz

5.7. Euclid

FUNCTIONAL DESCRIPTION

Euclid is a program to compute the Euclidean minimum of a number field. It is the practical implementation of the algorithm described in [38] . Some corresponding tables built with the algorithm are also available. Euclid is a stand-alone program depending on the PARI library.

- Participants: Pierre Lezowski and Jean-Paul Cerri
- Contact: Pierre Lezowski
- URL: http://www.math.u-bordeaux1.fr/~plezowsk/euclid/index.php

5.8. GNU MPC

FUNCTIONAL DESCRIPTION

Mpc is a C library for the arithmetic of complex numbers with arbitrarily high precision and correct rounding of the result. It is built upon and follows the same principles as Mpfr. The library is written by Andreas Enge, Philippe Théveny and Paul Zimmermann.

- Participants: Andreas Enge, Paul Zimmermann, Philippe Théveny and Mickaël Gastineau
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/

5.9. KleinianGroups

FUNCTIONAL DESCRIPTION

KleinianGroups is a Magma package that computes fundamental domains of arithmetic Kleinian groups.

- Participant: Aurel Page
- Contact: Aurel Page
- URL: http://www.normalesup.org/~page/Recherche/Logiciels/logiciels-en.html

5.10. MPFRCX

FUNCTIONAL DESCRIPTION

Mpfrcx is a library for the arithmetic of univariate polynomials over arbitrary precision real (Mpfr) or complex (Mpc) numbers, without control on the rounding. For the time being, only the few functions needed to implement the floating point approach to complex multiplication are implemented. On the other hand, these comprise asymptotically fast multiplication routines such as Toom-Cook and the FFT.

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/index.php?prog=mpfrcx

5.11. Nemo

FUNCTIONAL DESCRIPTION Nemo is a computer algebra package for the Julia programming language maintained by William Hart with code by William Hart, Tommy Hofmann, Claus Fieker, Fredrik Johansson, Oleksandr Motsak).

The features of Nemo include multiprecision integers and rationals, integers modulo n, p-adic numbers, finite fields (prime and non-prime order), number field arithmetic, maximal orders of number fields, arithmetic of ideals in maximal orders, arbitrary precision real and complex balls, generic polynomials, power series, fraction fields, residue rings and matrices.

- Participant: Fredrik Johansson
- Contact: William Hart
- URL: http://nemocas.org/

5.12. PARI/GP

FUNCTIONAL DESCRIPTION

PARI/GP is a widely used computer algebra system designed for fast computations in number theory (factorisation, algebraic number theory, elliptic curves, ...), but it also contains a large number of other useful functions to compute with mathematical entities such as matrices, polynomials, power series, algebraic numbers, etc., and many transcendental functions.

- Participants: Karim Belabas, Henri Cohen, Andreas Enge and Hamish Ivey-Law
- Contact: Karim Belabas
- URL: http://pari.math.u-bordeaux.fr/

LIFEWARE Project-Team

6. New Software and Platforms

6.1. BIOCHAM

The Biochemical Abstract Machine
KEYWORDS: Systems Biology - Bioinformatics
FUNCTIONAL DESCRIPTION

The Biochemical Abstract Machine (BIOCHAM) is a software environment for modeling and analyzing biochemical reaction systems, making simulations, performing static analyses, specifying behaviors in temporal logic.

- Participants: François Fages, François-Marie Floch, Thierry Martinez, Sylvain Soliman
- Contact: François Fages
- URL: http://lifeware.inria.fr/biocham/

6.2. BIOCHAM-WEB

KEYWORDS: Systems Biology - Bioinformatics
FUNCTIONAL DESCRIPTION

BIOCHAM-web is a web service which makes it possible to try BIOCHAM on line without any installation, through a spreadsheet.

- Participants: François Fages, François-Maris Floch and Thierry Martinez
- Contact: François Fages
- URL: http://lifeware.inria.fr/biocham/online/

6.3. CellStar

KEYWORDS: Systems Biology - Bioinformatics
FUNCTIONAL DESCRIPTION

In close collaboration with Kirill Batmanov, Cédric Lhoussaine and Cristian Versari from the LIFL (CNRS/Lille Univ) and with Pascal Hersen (MSC lab; CNRS/Paris 7), we developed CellStar, a tool-chain for image processing and analysis dedicated to segmentation and tracking of yeast cells in brightfield time-lapse microscopy movies. To estimate algorithm quality we developed a benchmark made of manually-verified images illustrating various situations. On this benchmark, CellStar outperformed 5 other state-of-the-art methods. The tool-chain is implemented in MATLAB and is provided together with the Python Yeast Image Toolkit benchmark tool.

- Participants: Pascal Hersen, Grégory Batt, Artémis Llamosi
- Contact: Grégory Batt
- URL: http://yeast-image-toolkit.biosim.eu/pmwiki.php

6.4. ClpZinc

FUNCTIONAL DESCRIPTION

CLP2Zinc is a rule-based modeling language for constraint programming. It extends the MiniZinc modeling language with Horn clauses which can be used to express search strategies as constraints in the model. This system is developed in the framework of the ANR Net-WMS-2 project and is a follow-up of the Rules2CP modeling language.

- Participants: Thierry Martinez, François Fages, Philippe Morignot and Sylvain Soliman
- Contact: Thierry Martinez
- URL: http://lifeware.inria.fr/~tmartine/clp2zinc/

LINKMEDIA Project-Team

5. New Software and Platforms

5.1. TermEx

Participant: Vincent Claveau [correspondent].

TermEx is a domain-independent terminology extraction system based on natural language processing and information retrieval concepts. This year, a new version (2.0) has been implemented that corresponds to a major rewriting in Python3 with support for English (in addition to French) and faster processing of documents in batch.

In 2015, TermEx has been licensed to a large company as a key component of the archiving process.

5.2. Experimental platform

Participant: Laurent Amsaleg [correspondent].

The experimental multimedia indexing platform (PIM) consists of dedicated equipments to experiment on very large collections of multimedia data. In 2015, no major evolution of PIM occurred and activities on the platform mainly consisted on maintenance. Due to the departure of Sébastien Campion, our former PIM manager, we have also initiated a reorganization of the responsibilities, in collaboration with SED.

5.3. A||GO multimedia web services

Participant: Guillaume Gravier [correspondent].

Available at http://allgo.irisa.fr, the A||GO platform allows for the easy deployment of the technology developed in the team as web services. The engineer hired by SED in October 2013 developed several new features that enable software providers to deploy autonomously their algorithm. In 2015, the team hired a development engineer to revamp the web service offer, making services interoperable and broadening the scope of services made available.

LINKS Team

6. New Software and Platforms

6.1. QuiX Tool suite

KEYWORDS: XML - JSon - Xproc - XSLT - Schematron - Xquery - NoSQL

SCIENTIFIC DESCRIPTION

The QuiX-Tool Suite provides tools to process XML streams and documents. The QuiX-Tool Suite is based on early algorithms: query answers are delivered as soon as possible and in all practical cases at the earliest time point. The QuiX-Tool Suite provides an implementation of the main XML standart over streams. XPath, XSLT, XQuery and XProc are W3C standarts while Schematron is an ISO one. The QuiX-Tool suite is developed in the Inria transfer project QuiXProc in cooperation with Innovimax. It includes among the others existing tools such as FXP and QuixPath, along with new tools, namely X-Fun. Both, a free and a professional version are available. The ownership of QuiX-Tool Suite is shared between Inria and Innovimax. The main application of QuiX-Tool Suite is its usage in QuiXProc, an professional implementation of the W3C pipeline language XProc owned by Innovimax.

The QuiXPath language is a large fragment of XPath with full support for the XML data model. The QuiXPath library provides a compiler from QuiXPath to FXP, which is a library for querying XML streams with a fragment of temporal logic.

The X-Fun language is a functional language for defining transformations between XML data trees, while providing shredding instructions. X-Fun can be understood as an extension of Frisch's XStream language with output shredding, while pattern matching is replaced by tree navigation with XPath expressions. The QuiX-Tool suite includes QuiXSLT, which is a compiler from XSLT into a fragment of X-Fun, which can be considered as the core of XSLT. It also provides QuiXSchematron, which is a compiler from Schematron to X-Fun, and QuiXQuery, which is a compiler from XQuery to X-Fun.

FUNCTIONAL DESCRIPTION

QuiX Tool suite reads and processes large XML files without loading the entire file in main memory. Instead of building a tree representation of the XML document, QuiXProc manages data as streams (sequence of opening and closing tags).

- Participants: Joachim Niehren and Tom Sebastian
- Partner: Innovimax
- Contact: Joachim Niehren
- URL: https://project.inria.fr/quix-tool-suite/

6.2. SmartHal

FUNCTIONAL DESCRIPTION

SmartHal is a better tool for querying the HAL bibliography database, while is based on Haltool queries. The idea is that a Haltool query returns an XML document that can be queried further. In order to do so, SmartHal provides a new query language. Its queries are conjunctions of Haltool queries (for a list of laboratories or authors) with expressive Boolean queries by which answers of Haltool queries can be refined. These Boolean refinement queries are automatically translated to XQuery and executed by Saxon. A java application for extraction from the command line is available.

- Participants: Guillaume Bagan and Joachim Nierhen
- Contact: Joachim Niehren
- URL: http://smarthal.lille.inria.fr/

6.3. X-FUN

KEYWORDS: XML - Transformation - Functional programming - Compilers - Programming language

FUNCTIONAL DESCRIPTION

X-FUN is a core language for implementing various XML, standards in a uniform manner. X-Fun is a higher-order functional programming language for transforming data trees based on node selection queries.

- Participants: Pavel Labath and Joachim Niehren
- Contact: Joachim Niehren

M3DISIM Team

6. New Software and Platforms

6.1. FELiScE

Finite Elements for Life SCiences and Engineering problems
KEYWORDS: Health - Cardiac - Finite elements - Cardiac Electrophysiology
FUNCTIONAL DESCRIPTION

FELISCE – standing for "Finite Elements for LIfe SCiences and Engineering" – is a new finite element code. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex cardiovascular models considered in the teams M3DISIM and REO – namely, involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena.

In FELISCE we have prepared a branch called HappyHeart, which aims at providing a user-friendly interface able to deal efficiently with complex cardiovascular simulations. Started in 2013, the code is already quite large (about 55,000 lines of code in almost 700 different files) and its core is about to be complete. It includes among others full HPC functionalities, high-order finite elements, physics coupling and topology capabilities. Our purpose will then be to use the library to implement the sophisticated cardiovascular models of the team and couple them with Verdandi (data assimilation library) to provide patient-specific simulations.

- Participants: Dominique Chapelle, Miguel Angel Fernandez Varela, Jean-Frédéric Gerbeau, Philippe Moireau, Marina Vidrascu, Sébastien Gilles, Sebastien Impériale and Gautier Bureau
- Contact: Sébastien Gilles
- URL: http://felisce.gforge.inria.fr

6.2. HeartLab

KEYWORDS: Simulation - Health - Cardiac - Image analysis - Computational geometry
SCIENTIFIC DESCRIPTION

The heartLab software is a library written in (64-bit compatible) Matlab and C (mex functions), designed to perform both simulation and estimation (based on various types of measurements, e.g. images) of the heart mechanical behavior. Started in 2006, it is already quite large (about 60,000 lines), and is used within various collaborations.

FUNCTIONAL DESCRIPTION

The code relies on OpenFEM – to which the team has previously contributed, see http://www.openfem.net – for the finite element computations, and the implementation was performed with a particular concern for modularity, since modeling and estimation use the same finite element operators. This modularity also allows to couple the code with other FEM solvers, such as LifeV and Mistral developed in the Reo team-project. In particular, we are now able to include perfusion and electrical coupling with LifeV using PVM, and fluid-structure interaction using Mistral.

We also included geometric data and tools in the code to define cardiac anatomical models compatible with the simulation requirements in terms of mesh quality, fiber direction data defined within each element, and the referencing necessary for handling boundary conditions and estimation, in particular. These geometries are analytical or come from computerized tomography (CT) or magnetic resonance (MR) image data of humans or animals.

We incorporated numerous non-linear data assimilation observation operators based on medical imaging post-processing to be able to now perform estimation with a large variety of medical imaging modalities. And recently we have worked on generalized micro-macro cardiac law using stochastic formulations.

- Participants: Radomir Chabiniok, Dominique Chapelle and Philippe Moireau
- Contact: Philippe Moireau
- URL: https://raweb.inria.fr/rapportsactivite/RA2013/m3disim/uid14.html

6.3. Verdandi

KEYWORDS: HPC - Model - Software Components - Partial differential equation

FUNCTIONAL DESCRIPTION

Verdandi is an open-source (LGPL) library for data assimilation. It includes various such methods for coupling one or several numerical models and observational data. Mainly targeted at large systems arising from the discretization of partial differential equations, the library is devised as generic, which allows for applications in a wide range of problems (biology and medicine, environment, image processing, etc.). Verdandi also includes tools to ease the application of data assimilation, in particular in the management of observations or for a priori uncertainty quantification. Implemented in C++, the library may be used with models implemented in Fortran, C, C++ or Python. Moreover, a Matlab module called VerdandinMatlab is developed in the team for pedagogical and test purposes.

- Participants: Nicolas Claude, Vivien Mallet, Dominique Chapelle, Philippe Moireau, Aurora Armiento and Gautier Bureau
- Contact: Vivien Mallet
- URL: http://verdandi.gforge.inria.fr/

MADYNES Project-Team

6. New Software and Platforms

6.1. Distem

KEYWORDS: Large scale - Experimentation - Virtualization - Emulation

It can be used to transform an homogenenous cluster (composed of identical nodes) into an experimental platform where nodes have different performance, and are linked together through a complex network topology, making it the ideal tool to benchmark applications targetting such environments.

- Participants: Luc Sarzyniec, Lucas Nussbaum and Tomasz Buchert
- Partners: CNRS - Université de Lorraine - Loria - Grid'5000 - Inria
- Contact: Lucas Nussbaum
- URL: http://distem.gforge.inria.fr

6.2. Escape

KEYWORDS: Security - Web - Privacy - TLS (Transport Layer Security)

Escape is a Firefox web browser add-on that offers the ability to bypass HTTPS firewalls that filter websites based on the SNI value of the TLS connection. In addition, it can be used to bypass legacy filtering of DNS requests. The extension is implemented in JavaScript and is based on another security add-on named Convergence.

- Participants: Shbair Wazen, Thibault Cholez, Antoine Goichot and Isabelle Chrisment
- Contact: Thibault Cholez
- URL: http://madynes.loria.fr/Research/Software#toc1

6.3. Flowoid

KEYWORDS: Android - NetFlow - Monitoring

Flowoid is a flow based monitoring probe dedicated to Android environments. It uses the NetFlow protocol to send to a collector, information related to the network activities of running Android applications. The information about each connection are grouped into records containing traditional properties including source IP address, destination IP address, bytes, packets, etc. In addition, Flowoid associates and sends for each NetFlow record a set of information related to the geographic location of the device, the name of the application that established the connection, the state of the device screen (ON, OFF, locked, unlocked) and the type of the traffic (foreground, background).

- Participants: Abdelkader Lahmadi, Frédéric Beck, Julien Vaubourg and Olivier Festor
- Contact: Abdelkader Lahmadi

6.4. Grid'5000 testbed

Grid'5000 is a scientific instrument designed to support experiment-driven research in all areas of computer science related to parallel, large-scale or distributed computing and networking. It gathers 10 sites, 25 clusters, 1200 nodes, for a total of 8000 cores. It provides its users with a fully reconfigurable environment (bare metal OS deployment with Kadeploy, network isolation with KaVLAN) and a strong focus on enabling high-quality, reproducible experiments.

- Participants: Luc Sarzyniec, Jérémie Gaidamour, Arthur Garnier, Clement Parisot, Emmanuel Jeanvoine, Lucas Nussbaum and Émile Morel
- Contact: Lucas Nussbaum
- URL: https://www.grid5000.fr/

6.5. Kadeploy

Kadeploy is a scalable, efficient and reliable deployment (provisioning) system for clusters and grids. It provides a set of tools for cloning, configuring (post installation) and managing cluster nodes. It can deploy a 300-nodes cluster in a few minutes, without intervention from the system administrator. It plays a key role on the Grid'5000 testbed (see below), where it allows users to reconfigure the software environment on the nodes, and is also used on a dozen of production clusters both inside and outside Inria.

- Participants: Emmanuel Jeanvoine, Lucas Nussbaum and Luc Sarzyniec
- Partners: CNRS - Université de Lorraine - Loria - Grid'5000 - Inria
- Contact: Emmanuel Jeanvoine
- URL: http://kadeploy3.gforge.inria.fr

6.6. MECSYCO suite

KEYWORDS: Modeling - Simulation - Simulator - Multi-model - Co-simulation - Multi-agent - Agent - Artefact

The MECSYCO suite (formerly AA4MM) is aiming at the modeling and simulation of complex systems. It provides concepts and tools to describe and then simulate a system as a set of heterogeneous models (namely a multi-model). It features MECSYCO-RE-java the Java implementation of the central part (core) and VisuAA4MM a visualization tool.

- Participants: Vincent Chevrier (Former LORIA Maia team), Laurent Ciarletta, Julien Siebert, Yannick Presse, Benjamin Segault, Benjamin Camus, Victorien Elvinger, Julien Vaubourg, Christine Bourjot, Benjamin Vouillaume and David Michel
- Partners: Université de Lorraine - Inria
- Contact: Vincent Chevrier

6.7. MPIGate

KEYWORDS: Internet of things - Home Automation - Health - Smart home - Home care - Connected object

MPIGate stands for Multi Protocol Interface GATEway for Tele-care, Environment Monitoring and Control. It is a set of softwares aiming at facilitating the development of both home automation and ambient assisted living applications thanks to the abstraction of heterogeneous sensor data and the facility of access to read and write functions over the devices plugged to the networks. This year, its evolution has mainly been carried out within SATELOR project and LAR project. Bluetooth Low Emission (BLE) has been integrated this year. It can be used by people working on home automation and ambient assisted living applications.

- Participants: Mandar Harshe and Ye-Qiong Song
- Contact: Yeqiong Song
- URL: http://mpigate.loria.fr/

6.8. Ruby-cute

KEYWORDS: Experimentation - HPC - Cloud

Ruby-Cute is a set of Commonly Used Tools for Experiments, or Critically Useful Tools for Experiments, depending on who you ask. It is a library aggregating various Ruby snippets useful in the context of (but not limited to) development of experiment software on distributed systems testbeds such as Grid'5000.

- Contact: Lucas Nussbaum
- URL: http://ruby-cute.github.io/

6.9. WISCAN

KEYWORDS: Network monitoring - Scanning

This tool allows to scan the entire IPv4 space in an efficient way. It relies on the Zmap (smap.io) while optimizing the randomness of the scanned IP addresses to avoid overloading destination networks and reduce the probability to scan two successive addresses of the same IP address block. Our approach to generate random permutation of IP addresses outperforms the approach used by Zmap in terms of the distribution of distance between successive IP addresses. Besides, our scan methodology can be distributed from multiple sources with few efforts.

- Contact: Jérôme François
- URL: http://gforge.inria.fr/projects/wiscan

6.10. XPFlow

XPFlow is an implementation of a new, workflow-inspired approach to control experiments involving large-scale computer installations. Such systems pose many difficult problems to researchers due to their complexity, their numerous constituents and scalability problems. The main idea of the approach consists in describing the experiment as a workflow and execute it using achievements of Business Process Management (BPM), workflow management techniques and scientific workflows.

- Participants: Tomasz Buchert and Lucas Nussbaum
- Contact: Lucas Nussbaum
- URL: http://xpflow.gforge.inria.fr/

6.11. Platforms

6.11.1. SCADA and IoT security assessment platform

Participants: Abdelkader Lahmadi [contact], Jérôme François, Olivier Festor.

SCADA *Supervisory Control and Data Acquisitions* refers to a centralized control and monitoring system for a variety of machinery and equipment involved with many industrial activities including: power generation and distribution, transportation, nuclear plants, manufacturing processes, etc. The most threaten accidents in SCADA networks are caused by targeted attacks, where adversaries exploit vulnerabilities available in software or network protocols components to disturb and make damage to the physical process. Therefore, it is important to provide new methods and tools for protecting SCADA networks from malicious cyber attacks targeting physical processes and infrastructures.

We are developing and maintaining a platform to assess and analyse the security of SCADA systems. The current version of the testbed combines real hardware Programmable Logic Controllers (PLCs) and simulation tools of physical processes. It also provides a set of tools that we have developed to capture and analyse control messages exchanged between a PLC and the physical processes. During the year 2015, we have received a regional funding to extend our platform with more devices and off-the-shelf solutions for home automation.

We have also extended the platform with IoT devices dedicated to home automation solutions (smart plugs, home boxes, lighting systems , door locks and detectors, etc). Our main goal is to rely on Software Defined Radio solution to evaluate the security of these devices and finding their communication protocol vulnerabilities.

MAESTRO Project-Team

6. New Software and Platforms

6.1. marmoteCore

Markov Modeling Tools and Environments - the Core
KEYWORDS: Modeling - Stochastic models - Markov model
FUNCTIONAL DESCRIPTION

marmoteCore is a C++ environment for modeling with Markov chains. It consists in a reduced set of high-level abstractions for constructing state spaces, transition structures and Markov chains (discrete-time and continuous-time). It provides the ability of constructing hierarchies of Markov models, from the most general to the particular, and equip each level with specifically optimized solution methods.

This software is developed within the ANR MARMOTE project: ANR-12-MONU-00019.

- Participants: Alain Jean-Marie, Issam Rabhi
- Partner: UVSQ
- Contact: Alain Jean-Marie
- URL: http://marmotecore.gforge.inria.fr/

6.2. ns-3

KEYWORDS: Simulation - Communication networks
FUNCTIONAL DESCRIPTION

ns-3 is a discrete-event network simulator for Internet systems, targeted primarily for research and educational use.

In the framework of the research project with ALSTOM Transport (see §8.1.3), we have extensively validated several modules of ns-3, related to the PHY and the MAC layers. We have implemented a directional antenna using 3-dimensional data for the radiation diagram. Modules related to the Automatic Train Protection function used in train systems have been implemented and validated. Last, we have developped objects that allow to generate easily simulation scenarios.

- Participants: Sara Alouf, Abdulhalim Dandoush, Giovanni Neglia and Alina Tuholukova

MAGIQUE-3D Project-Team

5. New Software and Platforms

5.1. Elasticus

SCIENTIFIC DESCRIPTION

Elasticus simulates acoustic and elastic wave propagation in 2D and in 3D, formulated as a first order system, using Discontinuous Galerkin Methods. The space discretization is based on two kind of basis functions, using Lagrange or Jacobi polynomials. Different kinds of fluxes (upwind and centered) are implemented, coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION

Elasticus is a sequential library, independent of DIVA and developed in Fortran, to simulate wave propagation in geophysical environment, based on a DG method. It is meant to help PhD students and post-doctoral fellows to easily implement their algorithms in the library. Thus, readability of the code is privileged over optimization of its performances. Developed features should be easily transferred in the computing platform of Total. Contrary to DIVA which only computes approximate solutions with P1, P2 and P3 elements, Elasticus manages arbitrary orders for the spatial discretization with DG method.

IMPROVEMENT

The various kinds of fluxes and the RK4 time schemes were implemented by Simon Ettouati. The elasto-acoustic coupling was implemented by Elvira Shishenina in the framework of her Master internship, in collaboration with Simon Ettouati and Lionel Boillot. The TTI elastic kernel as well as the Absorbing Boundary Conditions were developed by Lionel Boillot.

- Participants: Simon Ettouati, Julien Diaz, Lionel Boillot and Elvira Shishenina.
- Partner: TOTAL
- Contact: Julien Diaz

5.2. Hou10ni

SCIENTIFIC DESCRIPTION

Hou10ni simulates acoustic and elastic wave propagation in time domain and in harmonic domain, in 2D and in 3D, formulated as a second order system. It is also able to model elasto acoustic coupling. It is based on the second order formulation of the wave equation and the space discretization is achieved using Interior Penalty Discontinuous Galerkin (IPDG) Method. Recently, the harmonic domain solver has been extended to handle Hybridizable Discontinuous Galerkin Methods.

FUNCTIONAL DESCRIPTION

This software simulates the propagation of waves in heterogeneous 2D and 3D media in time-domain and in frequency domain. It is based on an Interior Penalty Discontinuous Galerkin Method (IPDGM) and allows for the use of meshes composed of cells of various order (p-adaptivity in space).

IMPROVEMENT

The main improvements are related to the frequency domain part. The Hybridizable Discontinuous Galerkin was implemented in 2D and in 3D elastodynamics by Marie Bonnasse Gahot in the framework of her PhD thesis. The IPDG Method was implemented in 3D acoustics and for the 3D elasto-acoustic coupling by Conrad Hillairet in the framework of his Master thesis. The Perfectly Matched Layers were optimized (the length of the layers and the amplitude of the absorption parameters are now automatically computed) by Andrew Wang in the framework of his two months internship.

- Participants: Julien Diaz, Marie Bonnasse Gahot, Conrad Hillairet and Lionel Boillot
- Contact: Julien Diaz

5.3. Montjoie

SCIENTIFIC DESCRIPTION

Montjoie is designed for the efficient solution of time-domain and time-harmonic linear partial differential equations using high-order finite element methods. This code is mainly written for quadrilateral/hexahedral finite elements, partial implementations of triangular/tetrahedral elements are provided. The equations solved by this code, come from the ”wave propagation” problems, particularly acoustic, electromagnetic, aeroacoustic, elastodynamic problems.

FUNCTIONAL DESCRIPTION

Montjoie is a code that provides a C++ framework for solving partial differential equations on unstructured meshes with finite element-like methods (continuous finite element, discontinuous Galerkin formulation, edge elements and facet elements). The handling of mixed elements (tetrahedra, prisms, pyramids and hexahedra) has been implemented for these different types of finite elements methods. Several applications are currently available : wave equation, elastodynamics, aeroacoustics, Maxwell’s equations.

IMPROVEMENT

This year, new high-order schemes (internship of Guillaume Marty and thesis of Mamadou N’diaye) have been implemented. The code has been strongly modified in order to obtain a fast compilation. The software has been used by Chloe team (through the internship of Laurene Hume) and compared to COMSOL providing a similar efficiency.

- Participants: Marc Duruflé, Juliette Chabassier, Mamadou N’diaye, Guillaume Marty
- Contact: Marc Duruflé
- URL: http://montjoie.gforge.inria.fr/

5.4. TMBM-DG

SCIENTIFIC DESCRIPTION

TMBM-DG simulates acoustic and elastic wave propagation in 2D and in 3D, formulated as a first order system, using Discontinuous Galerkin Methods. The space discretization is based on two kinds of basis functions, using Lagrange or Jacobi polynomials coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION

TMBM-DG is the follow up to DIVA-DG that we develop in collaboration with our partner Total. Its purpose is more general than DIVA-DG and should contains various DG schemes, basis functions and time schemes. It models wave propagation in acoustic media, elastic (isotropic and TTI) media and elasto-acoustic media, in two and three dimensions.

IMPROVEMENT

The first version of the code was recently developed jointly with our industrial partner Total. The main developer in MAGIQUE-3Dis Lionel Boillot.

- Participants: Lionel Boillot, Julien Diaz and Simon Ettouati
- Partner: TOTAL
- Contact: Julien Diaz

MAGNET Team

6. New Software and Platforms

6.1. CoRTex

Python library for noun phrase COreference Resolution in natural language TEXts
FUNCTIONAL DESCRIPTION

CoRTex is a LGPL-licensed Python library for Noun Phrase coreference resolution in natural language texts. This library contains implementations of various state-of-the-art coreference resolution algorithms, including those developed in our research. In addition, it provides a set of APIs and utilities for text preprocessing, reading the main annotation formats (ACE, CoNLL and MUC), and performing evaluation based on the main evaluation metrics (MUC, B-CUBED, and CEAF). As such, CoRTex provides benchmarks for researchers working on coreference resolution, but it is also of interest for developers who want to integrate a coreference resolution within a larger platform.

- Participants: Pascal Denis and David Chatel
- Contact: Pascal Denis
- URL: https://gforge.inria.fr/projects/cortex/

MAGRIT Project-Team

5. New Software and Platforms

5.1. Ltrack

The Inria development action LTrack aims at developing an Android platform in order to facilitate the transfer of some of our algorithms onto mobile devices. This year we finished developing an application that performs tracking by synthesis using the camera and the sensors of a mobile phone. User tests will start in January 2016 and we expect to submit the application to the Android Market in the middle of 2016.

- Contact: Marie-Odile Berger, Gilles Simon.

5.2. PoLAR

PoLAR (Portable Library for Augmented Reality) is a software library that offers powerful and state of the art visualization solutions under an API that is adapted and easy to use for a computer vision scientist. An ADT, also named PoLAR, started in October, 1st 2014 to sustain its development: a software engineer, Pierre-Jean Petitprez, was hired for two years.

After the code was made independent from our other research codes (RAlib), the library was ported to up-to-date versions of the supporting libraries: OpenSceneGraph 3.2 and Qt5.4. Heavy code refactoring was also carried out to set the core functionalities in conformity with the standards of the supporting libraries.

PoLAR was made available to the public in October 2015, and can be used under Linux or Windows at the moment.

Also this year, a research branch was developed to add the management of physics engines in PoLAR: so far, Bullet and Vega deformation engines were considered, the former being well integrated and the latter still being a work in progress.

- Contact: Erwan Kerrien, Pierre-Frédéric Villard.
- URL: http://polar.inria.fr

5.3. RAlib

RAlib is a library which contains the team's research development on image processing, registration (2D and 3D) and visualization. The library was extended over the period to integrate the Java code developed by Maxime Malgras during his Master's internship. Several applications either used internally or to demonstrate the team's work have been designed with this library.

- Contact: Erwan Kerrien, Gilles Simon

5.4. Reproducible research

Matlab software implementing the algorithms described in published articles is publicly available: NESIF (noise estimation by stacking images affected by illumination flickering) [15], ARPENOS (automated removal of quasi-periodic noise using frequency domain statistics) [14], and AC-ARPENOS (a-contrario automated removal of quasi periodic noise using frequency domain statistics) [22].

MAMBA Project-Team

6. New Software and Platforms

6.1. TiQuant

Tissue Quantifier

KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology

FUNCTIONAL DESCRIPTION

Systems biology and medicine on histological scales require the quantification of images from histological image modalities such as confocal laser scanning or bright field microscopy. The latter can be used to calibrate the initial state of a mathematical model, and to evaluate its explanatory value, which has been little recognised thus far. We generated a software for image analysis of histological material and demonstrated its use in analysing liver confocal micrografts, called TiQuant (Tissue Quantifier). The software is part of an analysis chain detailing protocols of imaging, image processing and analysis in liver tissue, allowing 3D reconstructions of liver lobules down to a resolution of less than a micrometer. The software has been made available to the public by publication in ref. [14], together with a new surface reconstruction algorithm based on the morphological Watershed algorithm. We validated that this algorithm allows reconstruction of cell shapes from nucleus and blood microvessel information, and demonstrated that it allows a reliable estimate of liver lobules, the smallest repetitive functional and micro-anatomical liver units, that besides in pig are not anatomically separated.

A separate 2D version of it (TI-Quant-BF-2D) has been used to analyse the invasion pattern of non-small cell lung cancer (NSCLC) cells *in vitro* [24] (see below).

- Contact: Dirk Drasdo
- URL: http://www.msysbio.com

6.2. TiSim

Tissue Simulator

KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology

FUNCTIONAL DESCRIPTION

We advanced the complementary software TiSim (Tissue Simulator) that will soon be provided. TiSim allows agent-based simulations of multicellular systems and can be directly used by processed image data provided by TiQuant.

The software has been tested over the whole year including almost all group members to prepare it for submission and will present a number of application example to introduce a potential user into the software. These will be monolayer and multicelluar spheroid growth, a multiscale modeling example and liver regeneration.

- Contact: Dirk Drasdo

MANAO Project-Team

6. New Software and Platforms

6.1. ALTA Lib

The ALTA Library

KEYWORDS: Statistic analysis - Fitting - Measures

FUNCTIONAL DESCRIPTION

ALTA is a multi-platform software library to analyze, fit and understand Bidirectional Reflection Distribution Functions (BRDFs). It provides a set of command line software to fit measured data to analytical forms, tools to understand models and data.

In 2015, we continued the development of ALTA and added different unit and integration tests to reach a new milestone with our first Beta version.

- Participants: Laurent Belcour, Romain Pacanowski, Xavier Granier and Pascal Barla
- Partner: LP2N (CNRS - UMR 5298)
- Contact: Romain Pacanowski
- URL: http://alta.gforge.inria.fr/

6.2. Elasticity Skinning

SCIENTIFIC DESCRIPTION

Geometric skinning techniques are very popular in the industry for their high performances, but fail to mimic realistic deformations. With elastic implicit skinning the skin stretches automatically (without skinning weights) and the vertices distribution is more pleasing. Our approach is more robust, for instance the angle's range of joints is larger than implicit skinning.

This software has been ported as a plugin for the Modo software (The Foundry) in collaboration with *Toulouse Tech Transfer*. This plugin has been bought by The Foundry, which maintains and sells it.

- Participants: Rodolphe Vaillant, Loïc Barthe, Florian Canezin, Gaël Guennebaud, Marie-Paule Cani, Damien Rohmer, Brian Wyvill, Olivier Gourmel and Mathias Paulin
- Partners: Université de Bordeaux - CNRS - INP Bordeaux - Université de Toulouse - Institut Polytechnique de Grenoble - Ecole Supérieure de Chimie Physique Electronique de Lyon
- Contact: Gaël Guennebaud
- URL: http://rodolphe-vaillant.fr/?e=59

6.3. Eigen

FUNCTIONAL DESCRIPTION

Eigen is an efficient and versatile C++ mathematical template library for linear algebra and related algorithms. In particular it provides fixed and dynamic size matrices and vectors, matrix decompositions (LU, LLT, LDLT, QR, eigenvalues, etc.), sparse matrices with iterative and direct solvers, some basic geometry features (transformations, quaternions, axis-angles, Euler angles, hyperplanes, lines, etc.), some non-linear solvers, automatic differentiations, etc. Thanks to expression templates, Eigen provides a very powerful and easy to use API. Explicit vectorization is performed for the SSE, AltiVec and ARM NEON instruction sets, with graceful fallback to non-vectorized code. Expression templates allow to perform global expression optimizations, and to remove unnecessary temporary objects.

In 2015, we released four revisions of the 3.2 branch, and the beta-1 of the next 3.3 version.

- Participant: Gaël Guennebaud
- Contact: Gaël Guennebaud
- URL: http://eigen.tuxfamily.org

6.4. HDRSee

KEYWORDS: OpenGL-GLSL HDR/LDR Viewer FUNCTIONAL DESCRIPTION HDRSee is a OpenGL/GLSL software that displays High Dynamic Range (HDR) and Low Dynamic Range (LDR) images. It is based on several libraries (e.g., glut, see below for full dependencies). To display HDR images, HDRSee implements a few tone-mapping operators. Moreover, it is designed with a plugin mechanism that let developers add, as easily as possible, their own tone-mapping operator. All tone-mapping operations are done using Graphics Hardware through pixel shader operations. The GUI currently used is nvWidgets.

- Participants: Romain Pacanowski, Xavier Granier.
- Partner: LP2N (CNRS - UMR 5298)
- Contact: Romain Pacanowski
- URL: http://mhdrviewer.gforge.inria.fr/

6.5. PFSTools

KEYWORD: HDR Merging, radiometric calibration, HDR tonemapping
FUNCTIONAL DESCRIPTION

The pfstools package is a set of command line programs for reading, writing, manipulating and viewing high-dynamic range (HDR) images and video frames. All programs in the package exchange data using a simple generic high dynamic range image format, pfs , and they use unix pipes to pass data between programs and to construct complex image processing operations.

pfstools comes with a library for reading and writing pfs files. The library can be used for writing custom applications that can integrate with the existing pfstools programs. It also offers a good integration with high-level mathematical programming languages, such as MATLAB or GNU Octave. pfstools can be used as an extension for MATLAB or Octave for reading and writing HDR images or simply to effectively store large matrices. The pfstools package integrates existing high dynamic range image formats by providing a simple data format that can be used to exchange data between applications. It is accompanied by the pfscalibration and pfstmo packages.

- Participants: Rafal Mantiuk, Ivo Ihrke
- Contact: Ivo Ihrke
- URL: http://pfstools.sourceforge.net/

6.6. Shiver

KEYWORD: HDR Viewer
FUNCTIONAL DESCRIPTION

Shiver is a Scientific HDR Image Viewer with a convenient GUI. It features fast display / zoom OpenGL capabilities, the comparison of several images in different tabs, LDR, HDR, and raw-support through a plugin architecture, and more.

In addition, Shiver is an image processing program providing the ability to execute algorithms that are programmed as plugins on one or more images. Different frontends like the command line or a QT-based graphical user interface are available. Depending on the frontend different work flows are possible.

The console frontend can be used, if no X11 server is available or a large number of images have to be processed. The QT Gui allows for intuitive work and a test of processing plugins. It allows for example pixel picking and a comfortable way to compare different processed images.

Available Shiver plugins implement, e.g., the CalTag system for automatically detecting checkerboard corners in camera calibration images.

- Participants: Ivo Ihrke
- Contact: Ivo Ihrke
- URL: http://sourceforge.net/projects/shiverfork/

6.7. Maori

KEYWORD: Matlab optical raytracing toolbox
FUNCTIONAL DESCRIPTION

The purpose of the Maori project is to provide a simple, extensible, optical raytracing library in Matlab that incorporates some modern concepts from computer graphics. In particular it features scene graph integration, a shader model, CSG objects and uses non-sequential raytracing as default. The goal is to provide a simple-to-use 3D system. In contrast to most commercial systems, 2D rotationally symmetric systems are treated as special cases of the 3D setting.

- Participants: Ivo Ihrke
- Contact: Ivo Ihrke

6.8. Patate Lib

KEYWORDS: Expressive rendering - Multi-scale analysis - Material appearance - Vector graphics - 2D animation
FUNCTIONAL DESCRIPTION

Patate is a header only C++/CUDA library for graphics applications. It provides a collection of Computer Graphics techniques that incorporate the latest innovations from Inria research teams working in the field. It strives for efficiency and ease-of-use by focusing on low-level core operators and key algorithms, organized in modules, each tackling a specific set of issues. The central goal of the library is to drastically reduce the time and efforts required to turn a research paper into a ready-to-use solution, for both commercial and academic purposes.

The library is still in its infancy and we are actively working on it to include the latest of our published research techniques. Modules will be dealing with graphics domains as varied as multi-scale analysis, material appearance, vector graphics, expressive rendering and 2D animation.

- Participants: Gaël Guennebaud, Pascal Barla, Simon Boyé, Gautier Ciaudo and Nicolas Mellado
- Contact: Gaël Guennebaud
- URL: http://patate.gforge.inria.fr/html/

6.9. Radiance Scaling for MeshLab

FUNCTIONAL DESCRIPTION The Radiance Scaling technique has received some interest in the Archaeology community, for enhancing details in carved stones in particular. For this reason, we have made it available as a plugin for the Open Source software Meshlab.

- Participants: Romain Vergne, Olivier Dumas and Pascal Barla
- Contact: Pascal Barla
- URL: http://manao.inria.fr/category/software/

MARELLE Project-Team

5. New Software and Platforms

5.1. Coq

KEYWORDS: Proof - Certification - Formalisation

FUNCTIONAL DESCRIPTION

Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

- Participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Denes, Stéphane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pédrot, Loïc Pottier, Matthias Puech, Yann Régis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliâtre
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Hugo Herbelin
- URL: http://coq.inria.fr/

Enrico Tassi and Maxime Dénès brought notable contributions to the Coq system in 2015. In particular, Enrico worked on the new user-interface that makes it possible to have several logical engines working on proofs simultaneously and Maxime Dénès supervised the release process for Coq 8.5, to be released in the early days of January.

In 2015, the Coq system is the object of intense activity within the Marelle project-team. Yves Bertot and Maxime Dénès are working at creating a consortium around this system, so that academic and industrial users find a suitable structure to voice there wishes for the evolution of the system, fund improvements, and coordinate developments for further improvement. This work is done in close collaboration with the $\pi.r^2$ project-team.

A first outcome of this animation work is the organization of regular events for developers to meet (coding sprints), the first of which happened in Sophia Antipolis in June 2015. Subsequently, Maxime Dénès was hired in Sophia Antipolis (in the Marelle project-team), and Matej Kosik was hired in Paris (in the $\pi.r^2$) team. A close collaboration was also set up with the Massachusetts Institute of Technology (MIT), with a software engineer to be hired at MIT to work on Coq in early 2016.

5.2. Easycrypt

FUNCTIONAL DESCRIPTION

EasyCrypt is a toolset for reasoning about relational properties of probabilistic computations with adversarial code. Its main application is the construction and verification of game-based cryptographic proofs. EasyCrypt can also be used for reasoning about differential privacy.

- Participants: Gilles Barthe, Benjamin Grégoire and Pierre-Yves Strub
- Contact: Gilles Barthe
- URL: https://www.easycrypt.info/trac/

5.3. Math-Components

Mathematical Components library
FUNCTIONAL DESCRIPTION

The Mathematical Components library is a set of Coq libraries that cover the mechanization of the proof of the Odd Order Theorem.

- Participants: Andrea Asperti, Jeremy Avigad, Yves Bertot, Cyril Cohen, François Garillot, Georges Gonthier, Stéphane Le Roux, Assia Mahboubi, Sidi Ould Biha, Ioana Pasca, Laurence Rideau, Alexey Solovyev, Enrico Tassi and Russell O'connor
- Contact: Assia Mahboubi
- URL: http://www.msr-inria.fr/projects/mathematical-components-2/

5.4. Ssreflect

FUNCTIONAL DESCRIPTION

Ssreflect is a tactic language extension to the Coq system, developed by the Mathematical Components team.

- Participants: Cyril Cohen, Yves Bertot, Laurence Rideau, Enrico Tassi and Laurent Théry
- Contact: Yves Bertot
- URL: http://ssr.msr-inria.inria.fr/

5.5. Zoocrypt

FUNCTIONAL DESCRIPTION

ZooCrypt is an automated tool for analyzing the security of padding-based public-key encryption schemes (i.e. schemes built from trapdoor permutations and hash functions). This years we extended the tool to be able to deal with schemes based on cyclic groups and bilinear maps.

- Participants: Benjamin Grégoire, Gilles Barthe and Pierre-Yves Strub
- Contact: Gilles Barthe
- URL: https://www.easycrypt.info/zoocrypt/

MATHERIALS Project-Team

5. New Software and Platforms

5.1. SIMOL

KEYWORDS: C++ - Statistical physics - Quantum chemistry - Molecular simulation - OpenMP
FUNCTIONAL DESCRIPTION

SIMOL (SIMulation of MOLecular systems) is a software written in C++. It is a research code aimed at testing new ideas and algorithms, and provides a unified development platform for the members of the project-team. It is composed of three parts: a common core of input/output functions, linear algebra, random number generators, etc; and two specific applicative branches: one for computational statistical physics and one for quantum chemistry. The methods implemented for computational statistical physics are based on discretizations of ergodic stochastic differential equations such as the Langevin dynamics and its overdamped limit. The systems that can be simulated range from a single isolated particle to Lennard-Jones fluids. For quantum chemistry, the building block is the Hartree-Fock model, solved via fixed-point iterations; and various refinements including greedy methods. A first release should be available in Spring 2016.

- Contact: Cédric Doucet

MATHRISK Project-Team

6. New Software and Platforms

6.1. PREMIA

KEYWORDS: Computational finance - Option pricing

SCIENTIFIC DESCRIPTION

Premia is a software designed for option pricing, hedging and financial model calibration. It is provided with it's C/C++ source code and an extensive scientific documentation. The Premia project keeps track of the most recent advances in the field of computational finance in a well-documented way. It focuses on the implementation of numerical analysis techniques for both probabilistic and deterministic numerical methods. An important feature of the platform Premia is the detailed documentation which provides extended references in option pricing.

Premia is thus a powerful tool to assist Research & Development professional teams in their day-to-day duty. It is also a useful support for academics who wish to perform tests on new algorithms or pricing methods without starting from scratch.

Besides being a single entry point for accessible overviews and basic implementations of various numerical methods, the aim of the Premia project is: 1 - to be a powerful testing platform for comparing different numerical methods between each other, 2 - to build a link between professional financial teams and academic researchers, 3 - to provide a useful teaching support for Master and PhD students in mathematical finance.

FUNCTIONAL DESCRIPTION

- Participants: Mathrisk project team and contributors
- Partners: Inria - Ecole des Ponts ParisTech - Université Paris-Est - Consortium Premia
- Contact: Agnès Sulem
- URL: http://www.premia.fr
- AMS: 91B28;65Cxx;65Fxx;65Lxx;65Pxx
- License: Licence Propriétaire (genuine license for the Consortium Premia)
- Type of human computer interaction: Console, interface in Nsp, Web interface
- OS/Middelware: Linux, Mac OS X, Windows
- APP: The development of Premia started in 1999 and 16 are released up to now and registered at the APP agency. Premia 16 has been registered on 0303/2015 under the number IDDN.FR.001.190010.013.S.C.2001.000.31000
- Programming language: C/C++ librairie Gtk
- Documentation: the PNL library is interfaced via doxygen
- Size of the software: 280580 lines for the Src part only, that is 11 Mbyte of code, 130400 lines for PNL, 105 Mbyte of PDF files of documentation.
- interfaces : Nsp for Windows/Linux/Mac, Excel, binding Python, and a Web interface.
- Publications: [12], [61], [69], [77], [80], [49], [59].

6.1.1. Content of Premia

Premia contains various numerical algorithms (Finite-differences, trees and Monte-Carlo) for pricing vanilla and exotic options on equities, interest rate, credit and energy derivatives.

1. **Equity derivatives:**

   The following models are considered:

Black-Scholes model (up to dimension 10), stochastic volatility models (Hull-White, Heston, Fouque-Papanicolaou-Sircar), models with jumps (Merton, Kou, Tempered stable processes, Variance gamma, Normal inverse Gaussian), Bates model.

For high dimensional American options, Premia provides the most recent Monte-Carlo algorithms: Longstaff-Schwartz, Barraquand-Martineau, Tsitsklis-Van Roy, Broadie-Glassermann, quantization methods and Malliavin calculus based methods.

Dynamic Hedging for Black-Scholes and jump models is available.

Calibration algorithms for some models with jumps, local volatility and stochastic volatility are implemented.

2. **Interest rate derivatives**

   The following models are considered:

   HJM and Libor Market Models (LMM): affine models, Hull-White, CIR++, Black-Karasinsky, Squared-Gaussian, Li-Ritchken-Sankarasubramanian, Bhar-Chiarella, Jump diffusion LMM, Markov functional LMM, LMM with stochastic volatility.

   Premia provides a calibration toolbox for Libor Market model using a database of swaptions and caps implied volatilities.

3. **Credit derivatives: Credit default swaps (CDS), Collateralized debt obligations (CDO)**

   Reduced form models and copula models are considered.

   Premia provides a toolbox for pricing CDOs using the most recent algorithms (Hull-White, Laurent-Gregory, El Karoui-Jiao, Yang-Zhang, Schönbucher)

4. **Hybrid products**

   A PDE solver for pricing derivatives on hybrid products like options on inflation and interest or change rates is implemented.

5. **Energy derivatives: swing options**

   Mean reverting and jump models are considered.

   Premia provides a toolbox for pricing swing options using finite differences, Monte-Carlo Malliavin-based approach and quantization algorithms.

6.1.2. Premia design

To facilitate contributions, a standardized numerical library (PNL) has been developed by J. Lelong under the LGPL since 2009, which offers a wide variety of high level numerical methods for dealing with linear algebra, numerical integration, optimization, random number generators, Fourier and Laplace transforms, and much more. Everyone who wishes to contribute is encouraged to base its code on PNL and providing such a unified numerical library has considerably eased the development of new algorithms which have become over the releases more and more sophisticated. J. Ph Chancelier, B. Lapeyre and J. Lelong are using Premia and Nsp for Constructing a Risk Management Benchmark for Testing Parallel Architecture [59].

Development of the PNL in 2015 (J. Lelong) . Release 1.70 and 1.71, PNL Library (http://pnl.gforge.inria.fr).

1. Release 1.72. of the *PNL* library (http://pnl.gforge.inria.fr/).
   1. Addition of a CMake module to include the library in other projects.
   2. Improvement of the `pnl_basis` module.
   3. Addition of the non central chi squared distribution to the random number generation toolbox.
   4. Addition of new functions in the linear algebra toolbox to build views.

6.1.3. Algorithms implemented in Premia in 2015

Premia 17 has been delivered to the consortium members in March 2015.

It contains the following new algorithms:

6.1.3.1. Commodities, FX, Insurance, Credit Risk

- Variables Annuities GLWB pricing in the Heston and Black-Scholes/Hull-White models with finite difference techniques.
- Variables Annuities GMAB, GMDB, GMMB pricing with Fourier-cosine techniques.
- A numerical scheme for the impulse control formulation for pricing variable annuities with a Guaranteed Minimum Withdrawal Benefit (GMWB) Z.Chen P.Forsyth
  Numerische Mathematik 109, 2008
- Managing Gap Risks in iCPPI for life insurance companies: A risk/return/cost analysis. A.Kalife S.Mouti L.Goudenege
  Insurance Markets and Companies: Analyses and Actuarial Computations, Issue 2 2014
- Simulating CVA on American Options. L. Abbas Turki, M.Mikou

6.1.3.2. Equity Derivatives

- Being particular about calibration. J.Guyon and P. Henry-Labordère.
  Risk magazine, Jan 2012.
- The Heston Stochastic-Local Volatility Model: Efficient Monte Carlo Simulation. A.W. van der Stoepb, L. A. Grzelakb, C. W. Oosterlee
  International Journal of Theoretical and Applied Finance, to appear
- On the Heston model with stochastic interest rates. L. Grzelak C.W.Oosterlee
  SIAM J. Fin. Math. 2,2011.
- Alternating direction implicit finite difference schemes for the Heston Hull-White partial differential equation.
  The Journal of Computational Finance Volume 16/Number 1, Fall 2012
- Pricing American options in the Heston Hull-White and Hull-White2d Models: an hybrid tree-finite difference approach. M.Briani, L.Caramellino, A.Zanette
- Efficient pricing of Asian options under Lévy processes based on Fourier cosine expansions. Part I: European-style products. B.Zhang C.W.Oosterlee.
  SIAM J. Financial Math., 4(1)
- Low-bias simulation scheme for the Heston model by Inverse Gaussian approximation. S. T. Tse J. W. L. Wan.
  Quantitative Finance, Volume 13, Issue 6, 2013
- Simple Simulation Scheme for CIR and Wishart Processes P. Baldi, C.Pisani
  International Journal of Theoretical and Applied Finance Vol. 16, No. 08, 2013
- Importance sampling for jump processes and applications to finance. L. Badouraly Kassim, J. Lelong and I. Loumrhari.
  Journal of Computational Finance, to appear
- A Wiener-Hopf Monte Carlo simulation technique for Lévy process. A. Kuznetsov, A.E.Kyprianou J. C. Pardo and K. van Schaik.
  The Annals of Applied Probability, Volume 21, Number 6, 2011.
- A Wiener-Hopf Monte Carlo simulation approach for pricing path-dependent options under Lévy process. O. Kudryavtsev
  Preprint.
- An Efficient Binomial Lattice Method for Step Double Barrier Options. E.Appolloni, M.Gaudenzi A.Zanette.
  International Journal of Applied and Theoretical Finance Vol.17, Issue No. 6, 2014.

The algorithms

- “Pricing American-Style Options by Monte Carlo Simulation : Alternatives to Ordinary Least Squares” by Stathis Tompaidis and Chunyu Yang
- “Value Function Approximation or Stopping Time Approximation : A comparison of Two Recent Numerical Methods for American Option Pricing using Simulation and Regression” by Lars Stentoft

implemented in 2015 by CélineLabart will be included in the following release.

Moreover, Jérome Lelong has performed the following tasks:

1. Add an importance sampling based code for jump diffusion models.
2. Improve the internal enumeration mechanism (PremiaEnum).
3. Update gnuplot files generation for reports.
4. Everyday maintenance to fix various bugs.
5. Clean the generation of the documentation process.

MAVERICK Project-Team

5. New Software and Platforms

5.1. Diffusion curves

KEYWORDS: Vector-based drawing - Shading
FUNCTIONAL DESCRIPTION

Diffusion Curves is a vector-based design tool for creating complex shaded images. This prototype is composed of the Windows binary, along with the required shader programs (ie. in source code).

- Participants: Joëlle Thollot, Pascal Barla, Adrien Bousseau and Alexandrina Orzan
- Partners: CNRS - LJK - INP Grenoble - Université Joseph-Fourier
- Contact: Joëlle Thollot
- URL: http://maverick.inria.fr/Publications/2008/OBWBTS08/index.php

5.2. Freestyle

FUNCTIONAL DESCRIPTION

Freestyle is a software for Non-Photorealistic Line Drawing rendering from 3D scenes. It is designed as a programmable interface to allow maximum control over the style of the final drawing: the user "programs" how the silhouettes and other feature lines from the 3D model should be turned into stylized strokes using a set of programmable operators dedicated to style description. This programmable approach, inspired by the shading languages available in photorealistic renderers such as Pixar's RenderMan, overcomes the limitations of integrated software with access to a limited number of parameters and permits the design of an infinite variety of rich and complex styles. The system currently focuses on pure line drawing as a first step. The style description language is Python augmented with our set of operators. Freestyle was developed in the framework of a research project dedicated to the study of stylized line drawing rendering from 3D scenes.

- Participant: Joëlle Thollot
- Contact: Joëlle Thollot
- URL: http://freestyle.sourceforge.net

5.3. GRATIN

FUNCTIONAL DESCRIPTION

Gratin is a node-based compositing software for creating, manipulating and animating 2D and 3D data. It uses an internal direct acyclic multi-graph and provides an intuitive user interface that allows to quickly design complex prototypes. Gratin has several properties that make it useful for researchers and students. (1) it works in real-time: everything is executed on the GPU, using OpenGL, GLSL and/or Cuda. (2) it is easily programmable: users can directly write GLSL scripts inside the interface, or create new C++ plugins that will be loaded as new nodes in the software. (3) all the parameters can be animated using keyframe curves to generate videos and demos. (4) the system allows to easily exchange nodes, group of nodes or full pipelines between people.

- Participants: Pascal Barla, Gautier Ciaudo and Romain Vergne
- Partner: UJF
- Contact: Romain Vergne
- URL: http://gratin.gforge.inria.fr

5.4. GigaVoxels

FUNCTIONAL DESCRIPTION

Gigavoxel is a software platform which goal is the real-time quality rendering of very large and very detailed scenes which couldn't fit memory. Performances permit showing details over deep zooms and walk through very crowdy scenes (which are rigid, for the moment). The principle is to represent data on the GPU as a Sparse Voxel Octree which multiscale voxels bricks are produced on demand only when necessary and only at the required resolution, and kept in a LRU cache. User defined producer lays accross CPU and GPU and can load, transform, or procedurally create the data. Another user defined function is called to shade each voxel according to the user-defined voxel content, so that it is user choice to distribute the appearance-making at creation (for faster rendering) or on the fly (for storageless thin procedural details). The efficient rendering is done using a GPU differential cone-tracing using the scale corresponding to the 3D-MIPmapping LOD, allowing quality rendering with one single ray per pixel. Data is produced in case of cache miss, and thus only whenever visible (accounting for view frustum and occlusion). Soft-shadows and depth-of-field is easily obtained using larger cones, and are indeed cheaper than unblurred rendering. Beside the representation, data management and base rendering algorithm themself, we also worked on realtime light transport, and on quality prefiltering of complex data. GigaVoxels is currently used for the quality real-time exploration of the detailed galaxy in ANR RTIGE.

- Participants: Cyril Crassin, Fabrice Neyret, Paul Gannay, Prashant Goswami, Jérémy Sinoir, Pascal Guehl and Eric Heitz
- Contact: Fabrice Neyret
- URL: http://gigavoxels.imag.fr

5.5. HQR: High Quality Renderer

KEYWORDS: Lighting simulation - Materials - Plug-in
FUNCTIONAL DESCRIPTION

HQR is a global lighting simulation platform. HQR software is based on the photon mapping method which is capable of solving the light balance equation and of giving a high quality solution. Through a graphical user interface, it reads X3D scenes using the X3DToolKit package developed at Maverick, it allows the user to tune several parameters, computes photon maps, and reconstructs information to obtain a high quality solution. HQR also accepts plugins which considerably eases the development of new algorithms for global illumination, those benefiting from the existing algorithms for handling materials, geometry and light sources.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: http://artis.imag.fr/~Cyril.Soler/HQR
- URL: https://launchpad.net/~csoler-users/+archive/ubuntu/hqr

5.6. Spherical harmonic library

KEYWORDS: Lighting simulation - Materials - Plug-in
FUNCTIONAL DESCRIPTION

The spherical harmonic library regroups a set of tools to decompose spherical functions in to spherical and rotated zonal harmonics. It also implements two spherical harmonic rotation formulas (Jan Kautz' ZXZXZ method, and the rotation formula derived in Cyril Soler's PhD thesis). A graphical tool called `shdisplay` is also included and allows to visualize and manipulate distributions of spherical harmonics.

- Participants: Cyril Soler
- Contact: Cyril Soler
- URL: https://launchpad.net/~csoler-users/+archive/ubuntu/ylm

5.7. MobiNet

KEYWORD: Simulation

FUNCTIONAL DESCRIPTION

The MobiNet software allows for the creation of simple applications such as video games, virtual physics experiments or pedagogical math illustrations. It relies on an intuitive graphical interface and language which allows the user to program a set of mobile objects (possibly through a network).

- Partners: CNRS - LJK - INP Grenoble - Inria - IREM - Cies
- Contact: Fabrice Neyret
- URL: http://mobinet.imag.fr/index.en.html

5.8. PLANTRAD

KEYWORDS: Bioinformatics - Biology

FUNCTIONAL DESCRIPTION

PlantRad is a software program for computing solutions to the equation of light equilibrium in a complex scene including vegetation. The technology used is hierarchical radiosity with clustering and instantiation. Thanks to the latter, PlantRad is capable of treating scenes with a very high geometric complexity (up to millions of polygons) such as plants or any kind of vegetation scene where a high degree of approximate self-similarity permits a significant gain in memory requirements.

- Participants: George Drettakis, François Sillion and Cyril Soler
- Contact: Cyril Soler
- URL: no URL available

5.9. PROLAND

PROcedural LANDscape

KEYWORDS: Real time - 3D - Realistic rendering - Masses of data - Atmosphere - Ocean

FUNCTIONAL DESCRIPTION

The goal of this platform is the real-time quality rendering and editing of large landscapes. All features can work with planet-sized terrains, for all viewpoints from ground to space.

- Participants: Antoine Begault, Eric Bruneton and Guillaume Piolet
- Contact: Fabrice Neyret
- URL: http://proland.imag.fr/

5.10. Vrender

FUNCTIONAL DESCRIPTION

The VRender library is a simple tool to render the content of an OpenGL window to a vectorial device such as Postscript, XFig, and soon SVG. The main usage of such a library is to make clean vectorial drawings for publications, books, etc.

In practice, VRender replaces the z-buffer based hidden surface removal of OpenGL by sorting the geometric primitives so that they can be rendered in a back-to-front order, possibly cutting them into pieces to solve cycles.

VRender is also responsible for the vectorial snapshot feature of the QGLViewer library.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: http://artis.imag.fr/Software/VRender/

Maxplus Team

6. New Software and Platforms

6.1. Boîte à outil Maxplus de SCILAB/Maxplus toolbox of Scilab

Trois chercheurs du groupe (S. Gaubert, J.-P. Quadrat, et G. Cohen) ont développé (à partir d'une première version réalisée par M. Mc Gettrick) la *boîte à outils Maxplus* de Scilab, qui est téléchargeable librement parmi les contributions du site Scilab, et qui est maintenant intégrée par défaut dans Scicoslab. Cette boîte à outils implémente l'ensemble du calcul numérique linéaire max-plus, elle comprend en particulier le stockage creux des matrices, et des algorithmes efficaces pour le calcul de la valeur propre basées sur les itérations sur les politiques. Elle a été utilisées par plusieurs chercheurs, voir notamment [66], [135]. Il faut aussi noter que le groupe de L. Hardouin, du LISA/Istia, a complété la boîte à outils Maxplus en interfaçant leur propre librairie C++, qui permet le calcul des séries de transfert de graphes d'événements temporisés.

English version

Three researchers of the team (S. Gaubert, J.-P. Quadrat, and G. Cohen, building on a preliminary version of M. McGettrick) have developed and released the *Maxplus toolbox* of Scilab, which is freely available among the contributions on the Scilab web site, and which is now included by default in Scicoslab. It implements all basic linear algebra functionalities, with a special attention to large sparse matrices, including efficient algorithms for eigenvalue computation based on policy iteration. The software has been used by several researchers in their work, including [66], [135]. It should be noted that the team of L. Hardouin, from LISA/Istia, has completed the toolbox by interfacing their own C++ library computing the transfer series of a timed event graph.

6.2. Itérations sur les politiques pour les jeux stochastiques à somme nulle/Policy iterations for zero sum stochastic games

L'algorithme d'itérations sur les politiques pour les jeux stochastiques à somme nulle pour le cas de paiements ergodiques (gain moyen par unité de temps), et dégénérés de type “multi-chaîne” a été introduit dans [84]. Plusieurs stages ont permis l'implémentation partielle en Scilab, C ou C++, et le test de ce type d'algorithmes (voir le travail de Vishesh Dhingra [101]), ou de son couplage avec la résolution de systèmes linéaires par des méthodes multigrilles algébriques (stage de Shantanu Gangal en 2007). Le travail de thèse de Sylvie Detournay a permis le développement d'un programme complet. Le code écrit par Sylvie Detournay (en C) a été déposé sur InriaGForge. Pour le moment il n'est accessible qu'aux membres de l'équipe.

English version

The policy iteration algorithm for zero sum repeated games with ergodic payoff (i.e. mean payoff per time unit), and in degenerate “multichain” cases, has been introduced in [84]. Several internships allowed us to implement in Scilab, C or C++, and to test such algorithms (see the work of Vishesh Dhingra [101]), or its combinaison with the resolution of linear systems by algebraic multigrid methods (internship of Shantanu Gangal in 2007). The PhD thesis work of Sylvie Detournay allowed us to develop a complete program. The program written by Sylvie Detournay (in C language) has been posted on InriaGForge. For the moment it can only be seen by members of the team.

6.3. TPLib: bibliothèque pour la manipulation de polyèdres tropicaux/TPLib: tropical polyhedra library

TPLib est une bibliothèque écrite en OCaml qui permet de manipuler des polyèdres tropicaux. Elle est distribuée sous license LGPL https://gforge.inria.fr/projects/tplib.

Cette bibliothèque implémente notamment des algorithmes permettant de passer d'une représentation externe d'un polyèdre à une représentation interne, ou inversement (voir §7.2.1 pour plus de détails). Elle permet aussi de réaliser d'autres opérations fondamentales, comme le calcul du complexe polyédral associé à un polyèdre donné (au sens de Develin et Sturmfels [97]), ou le calcul de cônes tangents tropicaux. Enfin, elle fournit toutes les primitives permettant d'utiliser les polyèdres tropicaux en tant que domaine abstrait numérique, afin de déterminer des invariants de programmes ou systèmes faisant intervenir les opérations $\min$ et $\max$ (voir [61]).

TPLib est utilisé dans le logiciel Polymake [116], développé à la Technische Universität Berlin (Allemagne). Ce dernier logiciel constitue une boite à outils permettant de manipuler des nombreux objets mathématiques (polytopes convexes, complexes polyédraux, graphes, matroïdes, polytopes tropicaux).

Le développement d'interfaces avec d'autres logiciels est désormais facilité grâce à la présence de *bindings* dans le langage C. Grâce à cela, un prototype d'interface a été réalisé entre TPLib et l'outil VerifyTAPN (https://launchpad.net/verifytapn), qui permet la vérification de réseaux de Pétri avec arcs temporisés. De même, une interface à la bibliothèque de domaines abstraits numériques APRON [127] est également en cours de développement.

English version

TPLib is a library written in OCaml, which allows to manipulate tropical polyhedra. It is distributed under LGPL https://gforge.inria.fr/projects/tplib.

This library implements algorithms allowing to pass from an external representation of a polyhedron to an internal description, or inversely (see §7.2.1 for more details). Besides, the library allows to perform several fundamental operations over tropical polyhedra, such as computing the associated polyhedral complex (see Develin and Sturmfels [97]), or determining the tropical tangent cone at any point. Finally, it provides all the primitives allowing to use tropical polyhedra as an numerical abstract domain, in order to determine program/system invariants involving the operations $\min$ and $\max$ (see [61]).

TPLib is used in the software Polymake [116], developed in Technische Universität Berlin (Germany). Polymake is a toolbox allowing to manipulate mathematic objects such as convex polytopes, polyhedral complexes, graphs, matroids, and tropical polytopes.

The development of further interfaces is now easier thanks to the distribution of bindings in C language. Using these bindings, a prototype of interface has been created between TPLib and the model-checker VerifyTAPN (https://launchpad.net/verifytapn), which allows the verification of timed-arc Petri Nets. An interface to the numerical abstract domain APRON [127] is also under development.

6.4. MPGLib

FUNCTIONAL DESCRIPTION

MPGLib is a library written in OCaml, which allows to manipulate tropical polyhedra.

This library implements algorithms allowing to pass from an external representation of a polyhedron to an internal description, or inversely. Besides, the library allows to perform several fundamental operations over tropical polyhedra, such as computing the associated polyhedral complex (see Develin and Sturmfels), or determining the tropical tangent cone at any point. Finally, it provides all the primitives allowing to use tropical polyhedra as an numerical abstract domain, in order to determine program/system invariants involving the operations min and max.

- Participant: Xavier Allamigeon
- Contact: Xavier Allamigeon
- https://gforge.inria.fr/projects/tplib

MCTAO Project-Team

5. New Software and Platforms

5.1. Hampath

KEYWORDS: Geometric control - Second order conditions - Differential homotopy - Ordinary differential equations

FUNCTIONAL DESCRIPTION

Hampath is a software developped to solve optimal control problems but also to study Hamiltonian flow.

- Participants: Jean-Baptiste Caillau, Olivier Cots and Joseph Gergaud
- Contact: Jean-Baptiste Caillau
- URL: http://cots.perso.enseeiht.fr/hampath/index.html

MEMPHIS Team

6. New Software and Platforms

6.1. New Software

6.1.1. NaSCar

This code is devoted to solve 3D-flows past moving and deformable bodies. The incompressible Navier-Stokes equations are solved on fixed grids, and the bodies are taken into account thanks to penalization and/or immersed boundary methods. The interface between the fluid and the bodies is tracked with a level set function or in a Lagrangian way. The numerical code is fully second order (time and space). The numerical method is based on projection schemes of Chorin-Temam type. The code is written in C language and use Petsc (http://www.mcs.anl.gov/petsc/petsc-as/) library for the resolution of large linear systems in parallel. NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.

- Main developper: M. Bergmann.
- Version: 1
- Keywords: numerical analysis, fluid mechanics, language C, PETSc
- Software benefit: flow around deformable obstacles, moving into a fluid.
- APP: in progress
- OS/Middelware: unix, linux, mac os
- Required library or software: PETSc item Programming language: C
- Documentation: in progress

6.1.2. NSMulti

The code is devoted to solve incompressible flows modeled by Navier-Stokes equations in two or three-dimensions. The equation of temperature can be added as well as Oldroyd-B model for viscous-elastic fluids. The two-dimensional version allows many sets of boundary conditions based on Dirichlet boundary condition, open boundary condition and periodic boundary condition. Bodies immersed in the fluid are taken into account by means of the volume penalization method as the code uses only uniform Cartesian meshes. The approximation is performed efficiently by a second order scheme for the linear terms and an upwind third order scheme for the convection terms. An efficient multigrid algorithm is used to accelerate the convergence. The whole code is written in FORTRAN 95 with MPI parallelization. When it is possible an hybrid MPI/OPEN MP parallelization is applied. The code yields the approximate solution at chosen times as well as the mean flow. In addition the time evolution of the main quantities at given points and global physical quantities such as the energy, the enstrophy, the lift, the drag are provided.

- Main developper: C.-H. Bruneau
- Version: 3
- Keywords: Incompressible flows, language FORTRAN95, MPI, OPEN MP.
- Software benefit : flow around solid or porous obstacles.
- APP: in progress
- OS/Middelware: unix, linux, mac os
- Required library or software: none
- Documentation: integrated

6.1.3. CoCoFlo

This is a research code to solve compressible multi-material flows modeled by conservation laws and hyperelatic constitutive models in three-dimensions. The whole code is written in FORTRAN 95 with MPI parallelization.

- Main developper: experimental code with contributions from past PhD students, mainly A. de Brauer and Y. Gorsse under the supervision of A. Iollo.
- Version: 0
- Keywords: Compressible material, language FORTRAN95, MPI, OPEN MP.
- Software benefit : impacts.
- APP: not foreseen
- OS/Middelware: unix, linux, mac os
- Required library or software: none
- Documentation: integrated

6.1.4. KOPPA

This code solves a polyatomic extension of the BGK or the ES-BGK models on octree meshes in parallel (Kinetic Octree Parallel Poly Atomic: KOPPA). It is a finite-volume code second-order accurate scheme in space and time with immersed boundaries. In collaboration with STORM team of Inria, Optimad and CINECA a porting on multi-integrated cores (XEON Phi for the moment) of this code is in progress.

- Main developper: F. Bernard
- Version: 0
- Keywords: Rarefied flows language C++, MPI, OPEN MP.
- Software benefit: simulation of non-equilibrium reentry flows, satellite nozzle plumes.
- APP: not foreseen at the moment
- OS/Middelware: unix, linux, mac os
- Required library or software: PABLO for octree.
- Documentation: integrated

MEPHYSTO Team

6. New Software and Platforms

6.1. MODULEF

FUNCTIONAL DESCRIPTION

The numerical method to approximate the constitutive laws for rubber elasticity derived from polymer physics are implemented in the Inria software Modulef.

It is based on : - algorithms from stochastic geometry to generate suitable polymer networks, - Delaunay tessellation algorithms to deal with steric effects (courtesy of the Inria project-team GAMMA2), - the introduction of 1-dimensional finite elements for the polymer-chains in Modulef.

- Participants: Marina Vidrascu and Antoine Gloria
- Contact: Marina Vidrascu
- URL: https://www.rocq.inria.fr/modulef/

MESCAL Project-Team

5. New Software and Platforms

5.1. CiGri

FUNCTIONAL DESCRIPTION

CiGri is a middleware which gathers the unused computing resource from intranet infrastructure and makes it available for the processing of large set of tasks. It manages the execution of large sets of parametric tasks on lightweight grid by submitting individual jobs to each batch scheduler. It is s associated to the OAR resource management system (batch scheduler). Users can easily monitor and control their set of jobs through a web portal. CiGri provides mechanisms to identify job error causes, to isolate faulty components and to resubmit jobs in a safer context.

- Contact: Olivier Richard
- URL: https://www.projet-plume.org/fiche/cigri

5.2. ComputeMode

ComputeMode: On-demand HPC cluster manager
KEYWORDS: HPC - Clusters - Operating system provisioning
FUNCTIONAL DESCRIPTION

ComputeMode is a on-demand HPC cluster manager, it allows deploying lightweight clustering framework on intranets.

ComputeMode is a software infrastructure that allows to extend or create a Grid through the aggregation of unused computing resources. For instance, a virtual cluster can be built using anyone's PC while not in use. Indeed, most PCs in large companies or university campus are idle at night, on weekends, and during vacations, training periods or business trips.

The main benefits of ComputeMode are the following

Easy deployment: the integration into an existing infrastructure is very easy: no modification is required on your PCs. ComputeMode comes as a software-only solution. The integration with major batch manager systems such as Sun Grid Engine, Platform LSF and Portable Batch System (PBS) can also be achieved. Seamless integration for the scientist: he/she submits unmodified computational jobs through his/her usual interface (batch submission engine), just like with any Beowulf type cluster. Seamless integration for the PC owner/user: ComputeMode runs when his/her PC is idle (night, weekends, ...) so annoyance is minimal if existant

Using ComputeMode, the life cycle of the PCs is basically split between 2 modes of operation a user mode, where the company's installation of Microsoft Windows or GNU/Linux remains a computation mode (hence the product name): uses a diskless boot of a GNU/Linux system and offers the PC's CPU power, RAM and connectivity to the Grid.

- Participants: Pierre Neyron, Olivier Richard and Bruno Bzeznik
- Partners: LIG - ANDRA
- Contact: Olivier Richard
- URL: http://computemode.imag.fr

5.3. Framesoc

FUNCTIONAL DESCRIPTION

Framesoc is the core software infrastructure of the SoC-Trace project. It provides a graphical user environment for execution-trace analysis, featuring interactive analysis views as Gantt charts or statistics views. It provides also a software library to store generic trace data, play with them, and build other analysis tools (e.g., Ocelotl).

- Participants: Jean-Marc Vincent and Arnaud Legrand
- Contact: Jean-Marc Vincent
- URL: http://soctrace-inria.github.io/framesoc/

5.4. GameSeer

FUNCTIONAL DESCRIPTION

GameSeer is a tool for students and researchers in game theory that uses Mathematica to generate phase portraits for normal form games under a variety of (user-customizable) evolutionary dynamics. The whole point behind GameSeer is to provide a dynamic graphical interface that allows the user to employ Mathematica's vast numerical capabilities from a simple and intuitive front-end. So, even if you've never used Mathematica before, you should be able to generate fully editable and customizable portraits quickly and painlessly.

- Contact: Panayotis Mertikopoulos
- URL: http://mescal.imag.fr/membres/panayotis.mertikopoulos/publications.html

5.5. KA-Tools

FUNCTIONAL DESCRIPTION

The KA-Tools is a software suite developed by MESCAL for exploitation of clusters and grids. It uses a parallelization technique based on spanning trees with a recursive starting of programs on nodes. Industrial collaborations were carried out with Mandrake, BULL, HP and Microsoft.

- Contact: Olivier Richard
- URL: http://ka-tools.imag.fr/

5.6. Kadeploy

KEYWORD: Operating system provisioning
FUNCTIONAL DESCRIPTION

Kadeploy is a scalable, efficient and reliable deployment system (cluster provisioning solution) for cluster and grid computing. It provides a set of tools for cloning, configuring (post installation) and managing cluster nodes. It can deploy a 300-nodes cluster in a few minutes, without intervention from the system administrator.

- Participants: Emmanuel Jeanvoine, Olivier Richard, Lucas Nussbaum and Luc Sarzyniec
- Partners: CNRS - Université de Lorraine - Loria - Grid'5000 - Inria
- Contact: Olivier Richard
- URL: http://kadeploy3.gforge.inria.fr

5.7. Kameleon

FUNCTIONAL DESCRIPTION

Kameleon is a simple but powerful tool to generate customized appliances. With Kameleon, you make your recipe that describes how to create step by step your own distribution. At start Kameleon is used to create custom kvm, docker, VirtualBox, ..., but as it is designed to be very generic you can probably do a lot more than that.

- Participant: Olivier Richard
- Partner: Grid'5000
- Contact: Olivier Richard
- URL: http://kameleon.imag.fr/

5.8. OAR

KEYWORDS: HPC - Cloud - Clusters - Resource manager - Light grid

SCIENTIFIC DESCRIPTION

This batch system is based on a database (PostgreSQL (preferred) or MySQL), a script language (Perl) and an optional scalable administrative tool (e.g. Taktuk). It is composed of modules which interact mainly via the database and are executed as independent programs. Therefore, formally, there is no API, the system interaction is completely defined by the database schema. This approach eases the development of specific modules. Indeed, each module (such as schedulers) may be developed in any language having a database access library.

FUNCTIONAL DESCRIPTION

OAR is a versatile resource and task manager (also called a batch scheduler) for HPC clusters, and other computing infrastructures (like distributed computing experimental testbeds where versatility is a key).

- Participants: Olivier Richard, Pierre Neyron, Salem Harrache and Bruno Bzeznik
- Partners: LIG - CNRS - Grid'5000 - CIMENT
- Contact: Olivier Richard
- URL: http://oar.imag.fr

5.9. Ocelotl

Multidimensional Overviews for Huge Trace Analysis

FUNCTIONAL DESCRIPTION

Ocelotl is an innovative visualization tool, which provides overviews for execution trace analysis by using a data aggregation technique. This technique enables to find anomalies in huge traces containing up to several billions of events, while keeping a fast computation time and providing a simple representation that does not overload the user.

- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Jean-Marc Vincent
- URL: http://soctrace-inria.github.io/ocelotl/

5.10. PEPS

FUNCTIONAL DESCRIPTION

The main objective of PEPS is to facilitate the solution of large discrete event systems, in situations where classical methods fail. PEPS may be applied to the modelling of computer systems, telecommunication systems, road traffic, or manufacturing systems.

- Participants: Luka Stanisic, Arnaud Legrand, Augustin Degomme, Jean-Marc Vincent and Florence Perronnin
- Contact: Arnaud Legrand
- URL: http://www-id.imag.fr/Logiciels/peps/

5.11. PSI

Perfect Simulator

FUNCTIONAL DESCRIPTION

Perfect simulator is a simulation software of markovian models. It is able to simulate discrete and continuous time models to provide a perfect sampling of the stationary distribution or directly a sampling of functional of this distribution by using coupling from the past. The simulation kernel is based on the CFTP algorithm, and the internal simulation of transitions on the Aliasing method.

- Contact: Arnaud Legrand
- URL: https://gforge.inria.fr/projects/psi/

5.12. Pajé

FUNCTIONAL DESCRIPTION

The Pajé generic tool provides interactive and scalable behavioral visualizations of parallel and distributed applications, helping to capture the dynamics of their executions, because of its genericity, it can be used unchanged in a large variety of contexts.

- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Jean-Marc Vincent
- URL: http://paje.sourceforge.net/

5.13. PajéNG

Pajé Next Generation

FUNCTIONAL DESCRIPTION

Pajé Next Generation is a re-implementation (in C++) and direct heir of the well-known Paje visualization tool for the analysis of execution traces (in the Paje File Format) through trace visualization (space/time view). The tool is released under the GNU General Public License 3. PajeNG comprises the libpaje library, the space-time visualization tool in pajeng and a set of auxiliary tools to manage Paje trace files (such as pj_dump and pj_validate).

- Participants: Jean-Marc Vincent and Arnaud Legrand
- Contact: Jean-Marc Vincent
- URL: https://github.com/schnorr/pajeng

5.14. SimGrid

KEYWORDS: Large-scale Emulators - Grid Computing - Distributed Applications

FUNCTIONAL DESCRIPTION

Scientific Instrument for the study of Large-Scale Distributed Systems. SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments.

- Participants: Jonathan Rouzaud-Cornabas, Frédéric Suter, Martin Quinson, Arnaud Legrand, Takahiro Hirofuchi, Adrien Lèbre, Jonathan Pastor, Mario Südholt, Flavien Quesnel, Luka Stanisic, Augustin Degomme, Jean-Marc Vincent and Florence Perronnin
- Partners: CNRS - Université de Nancy - University of Hawaii - Université de Reims Champagne-Ardenne - Femto-st
- Contact: Arnaud Legrand
- URL: http://simgrid.gforge.inria.fr/

5.15. Viva

FUNCTIONAL DESCRIPTION

Viva is an open-source tool used to analyze traces (in the Paje File Format) registered during the execution of parallel or distributed applications. The tool also serves as a sandbox to the development of new visualization techniques. Current features include: Temporal integration using dynamic time-intervals Spatial aggregation through hierarchical traces Interactive Graph Visualization with a force-directed algorithm, with viva Squarified Treemap to compare processes behavior on scale, with vv_treemap.

- Contact: Arnaud Legrand
- URL: https://github.com/schnorr/viva

5.16. Platforms

5.16.1. Grid'5000

The MESCAL project-team is involved in development and management of Grid'5000 platform. The Digitalis and IDPot clusters are integrated in Grid'5000 as well as of CIMENT.

5.16.2. Local cluster computing platforms: ICluster-2, IDPot, Digitalis

The MESCAL project-team manages a cluster computing center on the Grenoble campus. The center manages different architectures: a 48 bi-processors PC (ID-POT), and the center is involved with a cluster based on 110 bi-processors Itanium2 (ICluster-2) and another based on 34 bi-processor quad-core XEON (Digitalis) located at Inria. The three of them are integrated in the Grid'5000 grid platform.

More than 60 research projects in France have used the architectures, especially the 204 processors Icluster-2. Half of them have run typical numerical applications on this machine, the remainder has worked on middleware and new technology for cluster and grid computing. The Digitalis cluster is also meant to replace the Grimage platform in which the MOAIS project-team is very involved.

5.16.3. The Bull Machine

In the context of our collaboration with Bull the MESCAL project-team exploits a Novascale NUMA machine. The configuration is based on 8 Itanium II processors at 1.5 Ghz and 16 GB of RAM. This platform is mainly used by the Bull PhD students. This machine is also connected to the CIMENT Grid.

MEXICO Project-Team

6. New Software and Platforms

6.1. General Remark

The team's software and platform are the same as in 2014, namely

- COSMOS,
- MOLE,
- CosyVerif;

no major changes have occurred in 2015.

MIMESIS Team

5. New Software and Platforms

5.1. The SOFA Framework

5.1.1. Description

SOFA [0] is an open-source software framework targeted at real-time multi-physics simulation, with an emphasis on medical simulation. The idea of SOFA was initiated by members of the MIMESIS team, strongly supported by Inria and still actively developed within the MIMESIS team. Based on C++, the SOFA engine provides many algorithms, physiological models and anatomical data, made available within a plugin architecture. With its high level of modularity, SOFA appears to be an efficient tools to benchmark and develop new medical technologies using existing algorithms.

Figure 7. Logo of the SOFA framework

The SOFA framework relies on a multi-model representation which allows for having several representations (e.g. mechanical, thermal and visual) of the same object. Those different representations are connected together through a mechanism called mapping. With these features, it is also possible to have models of very different natures interacting with each other, for instance rigid bodies, deformable objects, and fluids. CPU and GPU implementations can be transparently combined to exploit the computational power of modern hardware architectures.

SOFA is at the heart of a number of research projects, including cardiac electro-physiology modeling, interventional radiology planning and guidance, planning for cryosurgery and deep brain stimulation, robotics, percutaneous procedures, laparoscopic surgery, non-rigid registration, etc. As a proof of its success, SOFA has been downloaded nearly 150,000 times, and is used today by many research groups around the world, as well as a number of companies. The mailing list used to exchange with the community includes several hundreds of researchers, from about 50 different institutions. SOFA is currently used by several industrial partners (Siemens Corporate Research, Epona Medical, Moog, SenseGraphics, etc.) and also provides the key technology on which our newly created start-up (InSimo) is relying. We strongly believe that today SOFA has become a reference for academic research, and is increasingly gaining recognition for product prototyping and development. The best illustration of this worldwide positioning is the role of SOFA in the challenge set by the HelpMeSee foundation to win the contract for the development of a very ambitious and high-risk project on cataract surgery simulation.

---

[0] More information about SOFA at http://www.sofa-framework.org

5.1.2. The SOFA Consortium

SOFA started ten years ago as an Inria collaborative research project. Now, SOFA includes many different functionalities, several companies rely on the framework as a physics engine and a large community rose over the years. To better meet the expectations of the community, Inria and the SOFA architects decided to create the SOFA Consortium in which the MIMESIS is strongly involved. The official kick-off of the Consortium took place in Strasbourg on the 25. November 2015.

Figure 8. The SOFA Consortium was created around the SOFA platform in 2015: here are some fields of application of SOFA

The **objectives of the SOFA Consortium** can be defined as:

- Represent the identity of SOFA,
- Structure and develop the community,
- Coordinate the development of SOFA to make it always more efficient and stable.

The Consortium has to represent the identity of SOFA. As a consequence, the first mission of the Consortium is to promote SOFA in conferences, forums or any other event. The Consortium must present SOFA to researchers and industrials and inform about all activities around the simulation platform and the available applications. By advertising all this work, the Consortium will bring more visibility to the entire SOFA community, encourage partnership and stimulate technology transfer.

Second, the Consortium now becomes a privileged contact point for any question or request. Members, users, beginners or any interested partner can contact us. We will find the answer to their needs and thus increase the interactions outside and within the community.

Third, the Consortium is in charge of coordinating the developments made in SOFA. Through regular meetings, and bi-annual technical committee, the Consortium makes sure the development follows the road map. Moreover, the Consortium sticks to the vision of SOFA as an open-source software, that has to become more and more stable and easy to use.

Finally, a free support is provided by the Consortium on the public version of SOFA, with the help of the entire SOFA community.

MIMETIC Project-Team

6. New Software and Platforms

6.1. AsymGait

Asymmetry index for clinical gait analysis based on depth images
KEYWORDS: Motion analysis - Kinect - Clinical analysis
SCIENTIFIC DESCRIPTION

The system uses depth images delivered by the Microsoft Kinect to retrieve the gait cycles first. To this end it is based on a analyzing the knees trajectories instead of the feet to obtain more robust gait event detection. Based on these cycles, the system computes a mean gait cycle model to decrease the effect of noise of the system. Asymmetry is then computed at each frame of the gait cycle as the spatial difference between the left and right parts of the body. This information is computed for each frame of the cycle.

FUNCTIONAL DESCRIPTION

AsymGait is a software package that works with Microsoft Kinect data, especially depth images, in order to carry-out clinical gait analysis. First is identifies the main gait events using the depth information (footstrike, toe-off) to isolate gait cycles. Then it computes a continuous asymmetry index within the gait cycle. Asymmetry is viewed as a spatial difference between the two sides of the body.

- Participants: Franck Multon and Edouard Auvinet
- Contact: Franck Multon

6.2. Cinematic Viewpoint Generator

KEYWORDS: Virtual Cinematography - Intelligent Gallery
FUNCTIONAL DESCRIPTION

The software, developed as an API, provides a mean to automatically compute a collection of viewpoints over one or two specified geometric entities, in a given 3D scene, at a given time. These viewpoints satisfy classical cinematographic framing conventions and guidelines including different shot scales (from extreme long shot to extreme close-up), different shot angles (internal, external, parallel, apex), and different screen compositions (thirds,fifths, symmetric of di-symmetric). The viewpoints allow to cover the range of possible framings for the specified entities. The computation of such viewpoints relies on a database of framings that are dynamically adapted to the 3D scene by using a manifold parametric representation and guarantee the visibility of the specified entities. The set of viewpoints is also automatically annotated with cinematographic tags such as shot scales, angles, compositions, relative placement of entities, line of interest.

- Participants: Emmanuel Badier, Christophe Lino and Marc Christie
- Partners: Université d'Udine - Université de Nantes - William Bares
- Contact: Marc Christie

6.3. Directors Lens Motion Builder

KEYWORDS: Previzualisation - Virtual cinematography - 3D animation
FUNCTIONAL DESCRIPTION

Directors Lens Motion Builder is a software plugin for Autodesk's Motion Builder animation tool. This plugin features a novel workflow to rapidly prototype cinematographic sequences in a 3D scene, and is dedicated to the 3D animation and movie previsualization industries. The workflow integrates the automated computation of viewpoints (using the Cinematic Viewpoint Generator) to interactively explore different framings of the scene, proposes means to interactively control framings in the image space, and proposes a technique to automatically retarget a camera trajectory from one scene to another while enforcing visual properties. The tool also proposes to edit the cinematographic sequence and export the animation. The software can be linked to different virtual camera systems available on the market.

- Participants: Emmanuel Badier, Christophe Lino and Marc Christie
- Partner: Université de Rennes 1
- Contact: Marc Christie

6.4. Kimea

Kinect IMprovement for Egronomics Assessment

KEYWORDS: Biomechanics - Motion analysis - Kinect

SCIENTIFIC DESCRIPTION

Kimea consists in correcting skeleton data delivered by a Microsoft Kinect in an ergonomics purpose. Kimea is able to manage most of the occlultations that can occur in real working situation, on workstations. To this end, Kimea relies on a database of examples/poses organized as a graph, in order to replace unreliable body segments reconstruction by poses that have already been measured on real subject. The potential pose candidates are used in an optimization framework.

FUNCTIONAL DESCRIPTION

Kimea gets Kinect data as input data (skeleton data) and correct most of measurement errors to carry-out ergonomic assessment at workstation.

- Participants: Franck Multon, Pierre Plantard and Hubert Shum
- Partner: Faurecia
- Contact: Franck Multon

6.5. Populate

SCIENTIFIC DESCRIPTION

Populate is a toolkit dedicated to task scheduling under time and space constraints in the field of behavioral animation. It is currently used to populate virtual cities with pedestrian performing different kind of activities implying travels between different locations. However the generic aspect of the algorithm and underlying representations enable its use in a wide range of applications that need to link activity, time and space. The main scheduling algorithm relies on the following inputs: an informed environment description, an activity an agent needs to perform and individual characteristics of this agent. The algorithm produces a valid task schedule compatible with time and spatial constraints imposed by the activity description and the environment. In this task schedule, time intervals relating to travel and task fulfilment are identified and locations where tasks should be performed are automatically selected.

FUNCTIONAL DESCRIPTION

The software provides the following functionalities:

- A high level XML dialect that is dedicated to the description of agents activities in terms of tasks and sub activities that can be combined with different kind of operators : sequential, without order, interlaced. This dialect also enables the description of time and location constraints associated to tasks.
- An XML dialect that enables the description of agent's personal characteristics.
- An informed graph describes the topology of the environment as well as the locations where tasks can be performed. A bridge between TopoPlan and Populate has also been designed. It provides an automatic analysis of an informed 3D environment that is used to generate an informed graph compatible with Populate.
- The generation of a valid task schedule based on the previously mentioned descriptions.

With a good configuration of agents characteristics (based on statistics), we demonstrated that tasks schedules produced by Populate are representative of human ones. In conjunction with TopoPlan, it has been used to populate a district of Paris as well as imaginary cities with several thousands of pedestrians navigating in real time.

- Participants: Fabrice Lamarche and Carl-Johan Jorgensen
- Contact: Fabrice Lamarche

6.6. The Theater

SCIENTIFIC DESCRIPTION

The Theater is a software framework to develop interactive scenarios in virtual 3D environements. The framework provides means to author and orchestrate 3D character behaviors and simulate them in real-time. The tools provides a basis to build a range of 3D applications, from simple simulations with reactive behaviors, to complex storytelling applications including narrative mechanisms such as flashbacks.

FUNCTIONAL DESCRIPTION

The Theater is Unity 3D application. XML descriptions are used to specify characters behaviors.

- Contact: Marc Christie

MIMOVE Team

6. New Software and Platforms

6.1. Introduction

In order to validate our research results and, in certain cases, make them available to specific communities or to the public, our research activities encompass the development of related software as surveyed below.

6.2. VSB: eVolution Service Bus for the Future Internet

Participants: Georgios Bouloukakis, Nikolaos Georgantas [contact], Maël Besson.

URL: https://tuleap.ow2.org/plugins/git/chorevolution/evolution-service-bus

The *eVolution Service Bus (VSB)* is a development and runtime environment dedicated to complex distributed applications of the Future Internet. Such applications are open, dynamic choreographies of extremely heterogeneous services and Things, including lightweight embedded systems (e.g., sensors, actuators and networks of them), mobile systems (e.g., smartphone applications), and resource-rich IT systems (e.g., systems hosted on enterprise servers and Cloud infrastructures). VSB's objective is to seamlessly interconnect, inside choreographies, services and Things that employ heterogeneous interaction protocols at the middleware level, e.g., SOAP Web services, REST Web services, and Things using CoAP (https://tools.ietf.org/html/rfc7252). This is based on runtime conversions between such protocols, with respect to their primitives and data type systems, while properly mapping between their semantics. This also includes mapping between the public interfaces of services/Things, regarding their operations and data, from the viewpoint of the middleware: the latter means that operations and data are converted based on their middleware-level semantics, while their business semantics remains transparent to the conversion.

VSB follows the well-known Enterprise Service Bus (ESB) paradigm. In this paradigm, a common intermediate bus protocol is used to facilitate interconnection between multiple heterogeneous middleware protocols. Conversion of each protocol to the common bus protocol is done by a component associated to the service/Thing in question and its middleware, called a Binding Component (BC), as it binds the service/Thing to the service bus. We introduce a generic architecture for VSB, which relies on the notion of *Generic Middleware (GM)* connector. GM abstracts interactions among peer components that employ the same middleware protocol through generic *post* and *get* operations, in a unifying fashion for any middleware protocol. We propose an API (application programming interface) for GM and a related generic interface description, which we call *GM-IDL*, for application components that (abstractly) employ GM. Concrete middleware protocols and related interface descriptions of application components that employ these middleware protocols can be mapped to GM API and GM-IDL, respectively. Based on these abstractions, we elaborate a generic architecture for BCs, as well as a related method for BC synthesis and refinement for a concrete choreography that includes services/Things with heterogeneous middleware protocols.

The eVolution Service Bus (VSB) presents a significant rethinking of the architecture and the implementation of a service bus destined to serve dynamic choreographies of services but also Things as first-class entities. More specifically, VSB presents the following advancements:

- VSB is a unified interoperability solution for both services and Things participating in choreographies;
- VSB is flexible and lightweight: it is a completely decentralized network of BCs that are deployed as necessary; hence, no BC is needed when a service/Thing employs the same middleware protocol as the one used as common bus protocol;
- Besides the client-server, publish/subscribe and tuple space paradigms, VSB also provides support for the data streaming paradigm;

- Different protocols can be introduced as VSB's common bus protocol with the same easiness as for integrating support for a new middleware protocol of a service/Thing; additionally, there is no need for relying on and/or providing a full-fledged ESB platform;
- While very modular, VSB's architecture includes only few levels of indirection in the processing of primitives when converting between protocols; this makes it simple, lightweight and fast;
- In VSB, mapping between a concrete middleware protocol and the GM paradigm can be performed in different ways, thus enabling to cover all possible interaction cases; there is no unique, fixed mapping limiting the applicability of the solution;
- BC synthesis follows a systematic method allowing for its automation.

VSB is being developed within the H2020 CHOReVOLUTION project (see § 8.2.1.1) with additional support from the iCONNECT Inria ADT (see § 8.1.1.1). It is also based on previous development carried out in the FP7 CHOReOS project (http://www.choreos.eu). VSB is available for download under open source license.

6.3. SoundCity: Urban-scale Noise Monitoring using the Urban Civics Middleware

Participants: Valérie Issarny [contact], Fadwa Rebhi, Animesh Pathak, Sara Hachem.

URL: http://urbancivics.com/soundcity_app.html

The interest in noise pollution and its effects, especially in terms of its influence on citizens' health, has been increasing throughout the years, as illustrated by the plethora of available research and health studies. Traditionally, cities perform periodic noise monitoring to assess the noisiness of neighborhoods and update their city planning policies accordingly. However, in its current state, noise monitoring for city planning takes place once every several years and leverages only a few static sensors (e.g., BruitParif activity, http://www.bruitparif.fr). Additionally, the outcome is not representative of citizens' personal exposure to noise as it is coarse grained and requires preplanning to determine where and when the sensing should take place. It is worth mentioning that, even if we assume that the city administration is able to use applications running on the smart phones of the city employees, gathering data by following a pre-determined spatio-temporal schedule – although an excellent strategy in terms of the quality of data gathered – would be expensive and cumbersome to organize.

Noise sensing is also complemented by data modeling approaches to generate maps that allow citizens and governments to visualize the distribution of noise over a region of interest. Those techniques range from basic data plotting to data assimilation techniques that leverage large scale data analytics further enabling the simulation and estimation of missing noise values. However, assimilation techniques are usually restricted to static sensing with predetermined locations and sensing times. This approach limits the capacity of assimilation models to provide estimates with high accuracy.

A solution to the above issues is through mobile participatory sensing, where noise monitoring is no longer restricted to a few expensive sensors. Participatory sensed data can be then leveraged, along with data provided from static sensors, by the assimilation techniques to further reduce the errors in the simulated maps. Toward that goal, we have been building the Urban Civics middleware, which we have further customized for noise monitoring [20]. The refined Urban Civics comprises middleware solutions for noise sensing, crowd-sourcing and data assimilation with the data assimilation component being more specifically developed by the Inria CLIME team. The noise-sensing itself is performed through existing dedicated applications, integrated with our middleware. Such approach enables us to alleviate the burden of domain-specific development and exploit the knowledge of domain experts.

SoundCity and supporting Urban Civics middleware are developed in collaboration with the Inria CLIME team, Ambientic (FR) and the Civic Engine at Berkeley (USA) in the context of CityLab@Inria and Inria@SiliconValley.

6.4. AppCivist-PB: A Platform for Democratic Assembly Customized for Participatory Budgeting

Participants: Valérie Issarny [contact], Cristhian Parra Trepowski, Animesh Pathak.

Participatory budgeting processes are among the most illustrative, real-life experiences of participatory democracy. Participatory Budgeting (PB) has its beginnings in the late 1980s, when some Brazilian cities started to experiment with processes of citizen participation in decisions about how to better allocate part of the city's budget. Although PB takes different forms, they can all be considered as refining the following base process: residents of a city propose spending ideas, volunteers or delegates develop those ideas into proposals, residents then vote on the proposals, and the government finally implements the winning projects. Since the 1980s, PB processes have spread around the world as a set of administrative reforms and, more recently, as a "best practice" in mainstream international development.

Although a large array of ICT tools exist to support citizens' engagement, their use in PB is still limited and scattered. Mostly, ICT have been leveraged for communication for promotion purposes (through multiple channels such as TV, radio and social media) and for facilitating voting for citizens (usually, with custom-made web sites or SMS).

With AppCivist-PB, we want to enable city governments to configure the software assemblies that best match the requirements of the kind of PB campaign they want to support, while leveraging existing software services and components. However, from the overall perspective of participatory democracy, our goal is primarily to facilitate the elaboration of proposals by citizen assemblies that form according to the citizen interests. In other words, we want to support a process that emphasizes collaborative contribution making at all stages of the elaboration of proposals by diverse citizen assemblies, which are primarily created by and for citizens. The collaborative process must in particular facilitate the assembly of groups (or sub-assemblies) on the basis of commonalities among the proposals, which is essential if one wants to sustain city-scale participation and be inclusive of citizen contributions.

AppCivist-PB helps users assemble proposal making and selection workflows, using service-oriented architecture (SOA) principles. The composition principles of SOA allow for various implementations and instances of these workflows, including the possibility of integrating and linking different workflows for the same PB campaign. For example, a city might create and manage its own workflow to receive proposals and facilitate deliberation and voting by registered residents; at the same time, citizen groups (typically activists) can create their own, independent, workflows to co-create, develop, and promote proposals for the city, following their own collaboration practices. Compared to traditional SOA, AppCivist-PB distinguishes itself by enabling the assembly of software services dedicated to the support of online-facilitated participatory democracy by and for relevant citizen assemblies.

The AppCivist-PB platform is developed in collaboration with the Social Apps Labs at CITRIS at University of California Berkeley (USA) in the context of CityLab@Inria and Inria@SiliconValley.

MINT Project-Team

5. New Software and Platforms

5.1. Revil

SCIENTIFIC DESCRIPTION

Revil is an application for building and manipulating 3D SceneGraphs for Mixed-Reality Artistic Performances.It relies on the approach of revealing virtual content in the physical space by intersecting it with performers and spectator's bodies and props.

FUNCTIONAL DESCRIPTION

It provides a GUI for setting up the projectors, depth cameras and scene objects. It is based on OpenSceneGraph, OpenNI2 and is entirely controllable via OpenSoundControl messages so that it can be connected to Digital Musical Instruments and other interactive systems.

- Participants: Florent Berthaut, Cagan Arslan
- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/Revil

5.2. libgina

FUNCTIONAL DESCRIPTION

LibGINA is a library for fast prototyping of gestural interaction.
In 2015, new features were added in the context of Nicolas Bremard's thesis. The software was used in various projects.

- Participants: Nicolas Bremard and Laurent Grisoni
- Contact: Laurent Grisoni

5.3. SmartInteraction

FUNCTIONAL DESCRIPTION

SmartInteraction is a library, result from the FUI SmartStore project. It allows mobile services to be activated easily through automatic connection to interaction public spots, without specific user action.

- Participants: Samuel Degrande, Laurent Grisoni
- Contact: Samuel Degrande

MISTIS Project-Team

6. New Software and Platforms

6.1. MMST

Mixtures of Multiple Scaled Student T distributions
KEYWORDS: Health - Statistics - Brain MRI - Medical imaging - Robust clustering
FUNCTIONAL DESCRIPTION

The package implements mixtures of so-called multiple scaled Student distributions, which are generalisation of multivariate Student T distribution allowing different tails in each dimension. Typical applications include Robust clustering to analyse data with possible outliers. In this context, the model and package have been used on large data sets of brain MRI to segment and identify brain tumors.

- Participants: Alexis Arnaud, Florence Forbes and Darren Wraith
- Contact: Florence Forbes
- URL: http://mistis.inrialpes.fr/realisations.html

6.2. P-LOCUS

KEYWORDS: Health - Neuroimaging - Cancer - Brain MRI - Medical imaging
FUNCTIONAL DESCRIPTION

The Locus software was extended to address the delineation of lesions in pathological brains. Its extension P-LOCUS software analyses, in few minutes, a 3D MR brain scan and performs fully automatic brain lesion delineation using a combined dataset of various 3D MRI sequences.

- Participants: Senan Doyle, Florence Forbes, Michel Dojat and Pascal Rubini
- Partner: INSERM
- Contact: Florence Forbes
- URL: http://p-locus.com/

6.3. PyHRF

KEYWORDS: FMRI - Statistic analysis - Neurosciences - IRM - Brain - Health - Medical imaging
FUNCTIONAL DESCRIPTION

As part of fMRI data analysis, PyHRF provides a set of tools for addressing the two main issues involved in intra-subject fMRI data analysis : (i) the localization of cerebral regions that elicit evoked activity and (ii) the estimation of the activation dynamics also referenced to as the recovery of the Hemodynamic Response Function (HRF). To tackle these two problems, PyHRF implements the Joint Detection-Estimation framework (JDE) which recovers parcel-level HRFs and embeds an adaptive spatio-temporal regularization scheme of activation maps.

- Participants: Thomas Vincent, Solveig Badillo, Lotfi Chaari, Christine Bakhous, Florence Forbes, Philippe Ciuciu, Laurent Risser, Thomas Perret and Aina Frau Pascual
- Partners: CEA - NeuroSpin
- Contact: Florence Forbes
- URL: http://pyhrf.org

Mjolnir Team

6. New Software and Platforms

6.1. Introduction

Each software listed below is characterized according to the *criteria for software self-assessment* proposed by Inria's Evaluation Committee. Note that the only software mentioned here are those that were created or significantly modified during the year.

6.2. Libpointing

Participants: Géry Casiez [correspondent], Nicolas Roussel, Izzatbek Mukhanov, Sébastien Poulmane.

Libpointing is a software toolkit that provides direct access to HID pointing devices and supports the design and evaluation of pointing transfer functions [3]. The toolkit provides resolution and frequency information for the available pointing and display devices and makes it easy to choose between them at run-time through the use of URIs. It allows to bypass the system's transfer functions to receive raw asynchronous events from one or more pointing devices. It replicates as faithfully as possible the transfer functions used by Microsoft Windows, Apple OS X and Xorg (the X.Org Foundation server). Running on these three platforms, it makes it possible to compare the replicated functions to the genuine ones as well as custom ones. The toolkit is written in C++ with Python, Java and Node.js bindings available (about 49,000 lines of code in total). It is publicly available under the GPLv2 license.

The library has been thoroughly improved in 2015. Notable changes concern the management of pointing devices and displays, the standardization of URIs on all platforms, HID reports parsing on Linux and OS X, the integration of floating pixel coordinates and subpixel interaction [34], the improvement of existing bindings and the addition of Node.js ones, and support for Web browser integration.

Web site: http://libpointing.org/

Software characterization: [A-3] [SO-3] [SM-2] [EM-2↑] [SDL-5]

6.3. Liblag

Participants: Géry Casiez [correspondent], Matthieu Falce, Nicolas Roussel.

Liblag is a software toolkit designed to support the comparison of latency compensation techniques. The toolkit notably includes a playground application that allows to compare different trajectory prediction algorithms on desktop (OS X and Ubuntu) and mobile (iOS and Android) systems. The source code for this toolkit (about 8,500 lines of code) is only available to Turbotouch partners for now.

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

6.4. Mouse-based lagmeter

Participants: Géry Casiez [correspondent], Stéphane Huot, Matthieu Falce, Nicolas Roussel.

As part of the work reported in [18], we implemented our mouse-based method for measuring end-to-end latency using Java/Swing, C++/GLUT, C++/Qt and JavaScript/HTML5. We also wrote Python scripts to parse the logs generated by these implementations in order to compare them. This software (about 2,500 lines of code) should be made available in 2016.

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

MNEMOSYNE Project-Team

6. New Software and Platforms

6.1. Positioning

Our previous works in the domain of well-defined distributed asynchronous adaptive computations [62], [59], [64] have already made us define a library (DANA [58]), closely related to both the notion of artificial neural networks and cellular automata. From a conceptual point of view, the computational paradigm supporting the library is grounded on the notion of a unit that is essentially a (vector of) potential that can vary along time under the influence of other units and learning. Those units can be organized into layers, maps and networks.

We will also have to interact with the High Performance Computing (HPC) community, since having large scale simulations at that mesoscopic level is an important challenge in our systemic view of computational neuroscience. Our approach implies to emulate the dynamics of thousands, or even millions, of integrated computational units, each of them playing the role of a whole elementary neural circuit (e.g. the microcolumn for the cortex). Mesoscopic models are considered in such an integrative approach, in order to exhibit global dynamical effect that would be hardly reachable by compartment models involving membrane equations or even spiking neuron networks.

The vast majority of high performance computing softwares for computational neuroscience addresses sub-neural or neural models [48], but coarser grained population models are also demanding for large scale simulations, with fully distributed computations, without global memory or time reference, as it is specified in (*cf.* § 3.2).

6.2. DANA

Distributed Asynchronous Numerical & Adaptive computing framework
FUNCTIONAL DESCRIPTION

DANA is a python framework whose computational paradigm is grounded on the notion of a unit that is essentially a set of time dependent values varying under the influence of other units via adaptive weighted connections. The evolutions of a unit's value are defined by a set of differential equations expressed in standard mathematical notation which greatly ease their definition. The units are organized into groups that form a model. Each unit can be connected to any other unit (including itself) using a weighted connection. The DANA framework offers a set of core objects needed to design and run such models. The modeler only has to define the equations of a unit as well as the equations governing the training of the connections. The simulation is completely transparent to the modeler and is handled by DANA. This allows DANA to be used for a wide range of numerical and distributed models as long as they fit the proposed framework (e.g. cellular automata, reaction-diffusion system, decentralized neural networks, recurrent neural networks, kernel-based image processing, etc.).

- Participant: Nicolas Rougier
- Contact: Nicolas Rougier
- URL: http://dana.loria.fr/

6.3. Virtual Enaction

KEYWORDS: Neurosciences - Simulation - Health
FUNCTIONAL DESCRIPTION

VirtualEnaction: A Platform for Systemic Neuroscience Simulation. The computational models studied in this project have applications that extend far beyond what is possible to experiment yet in human or non-human primate subjects. Real robotics experimentations are also impaired by rather heavy technological constraints, for instance, it is not easy to dismantle a given embedded system in the course of emerging ideas. The only versatile environment in which such complex behaviors can be studied both globally and at the level of details of the available modeling is a virtual environment, as in video games, Such a system can be implemented as “brainy-bot” (a programmed player based on our knowledge of the brain architecture) which goal is to survive in a complete manipulable environment.

In order to attain this rather ambitious objective we both (i) deploy an existing open-source video game middleware in order to be able to shape the survival situation to be studied and (ii) revisit the existing models in order to be able to integrate them as an effective brainy-bot. It consists of a platform associated to a scenario that is the closest possible to a survival situation (foraging, predator-prey relationship, partner approach to reproduction) and in which it is easy to integrate an artificial agent with sensory inputs (visual, touch and smell), emotional and somatosensory cues (hunger, thirst, fear, ..) and motor outputs (movement, gesture, ..) connected to a "brain" whose architecture will correspond to the major anatomical regions involved in the issues of learning and action selection (cortex areas detailed here, basal ganglia, hippocampus, and areas dedicated to sensorimotor processes). The internal game clock can be slowed down enough to be able to run non trivial brainy-bot implementations. This platform has already being used by two students of the team and is now a new deliverable of the KEOpS project.

- Participants: André Garenne, Frédéric Alexandre, Nicolas Rougier and Thierry Viéville
- Contact: Frédéric Alexandre
- URL: http://virtualenaction.gforge.inria.fr/

MOAIS Project-Team

4. New Software and Platforms

4.1. FlowVR

FUNCTIONAL DESCRIPTION

The goal of the FlowVR library is to provide users with the necessary tools to develop and run high performance interactive applications on PC clusters and Grids. The main target applications include virtual reality, scientific visualization and Web3D. FlowVR enforces a modular programming that leverages software engineering issues while enabling high performance executions on distributed and parallel architectures.

- Participants: Jérémie Allard, Valérie Gourantou, Jean Denis Lesage, Sébastien Limet, Emmanuel Melin, Clément Ménier, Bruno Raffin, Sophie Robert, Matthieu Dreher and Jérémy Jaussaud
- Contact: Bruno Raffin
- URL: http://flowvr.sf.net

4.2. K'Star

K'Star Action

KEYWORDS: Parallel computing - Task-based algorithm - Runtime system - Task scheduling - OpenMP - Source-to-source compiler - Data parallelism

FUNCTIONAL DESCRIPTION

The K'Star action supports the development of Klang-Omp, a source-to-source compiler that turns C and C++ programs with OpenMP pragmas to C programs with calls to either the StarPU or the XKaapi runtime system, as well as the development of the KaStORS benchmarks suite for experimenting with OpenMP dependent tasks.

- Participants: Philippe Virouleau, Pierrick Brunet, Thierry Gautier, Olivier Aumage, Samuel Thibault, Nathalie Furmento, Samuel Pitoiset and François Broquedis
- Contact: Thierry Gautier
- URL: http://kstar.gforge.inria.fr/

4.3. KAAPI

KAAPI – *Kernel for Adaptative, Asynchronous Parallel and Interactive programming* – is a C library that allows to execute fine/medium grain multithreaded computation with dynamic data flow synchronizations.

FUNCTIONAL DESCRIPTION

KAAPI means Kernel for Adaptative, Asynchronous Parallel and Interactive programming. It is a C library that allows to execute multithreaded computation with data flow synchronization between threads. The library is able to schedule fine/medium size grain programs on a multicore machine with several GPUs. The data flow graph is unfold at runtime.

- Contact: Thierry Gautier
- URL: http://kaapi.gforge.inria.fr

4.4. KaStORS

The KaStORS OpenMP Benchmark Suite

KEYWORDS: Benchmarking - HPC - Task-based algorithm - Task scheduling - OpenMP - Data parallelism

FUNCTIONAL DESCRIPTION

The KaStORS benchmarks suite has been designed to evaluate implementations of the OpenMP dependent task paradigm, introduced as part of the OpenMP 4.0 specification.

- Participants: Olivier Aumage, François Broquedis, Pierrick Brunet, Nathalie Furmento, Thierry Gautier, Samuel Thibault and Philippe Virouleau
- Contact: Thierry Gautier
- URL: http://kastors.gforge.inria.fr/

4.5. LinBox

FUNCTIONAL DESCRIPTION

LinBox is an open-source C++ template library for exact, high-performance linear algebra computations. It is considered as the reference library for numerous computations (such as linear system solving, rank, characteristic polynomial, Smith normal forms,...) over finite fields and integers with dense, sparse, and structured matrices.

- Participants: Clément Pernet and Thierry Gautier
- Contact: Clément Pernet
- URL: http://linalg.org/

4.6. OAR

KEYWORDS: HPC - Cloud - Clusters - Resource manager - Light grid

SCIENTIFIC DESCRIPTION

This batch system is based on a database (PostgreSQL (preferred) or MySQL), a script language (Perl) and an optional scalable administrative tool (e.g. Taktuk). It is composed of modules which interact mainly via the database and are executed as independent programs. Therefore, formally, there is no API, the system interaction is completely defined by the database schema. This approach eases the development of specific modules. Indeed, each module (such as schedulers) may be developed in any language having a database access library.

FUNCTIONAL DESCRIPTION

OAR is a versatile resource and task manager (also called a batch scheduler) for HPC clusters, and other computing infrastructures (like distributed computing experimental testbeds where versatility is a key).

- Participants: Olivier Richard, Pierre Neyron, Salem Harrache and Bruno Bzeznik
- Partners: LIG - CNRS - Grid'5000 - CIMENT
- Contact: Olivier Richard
- URL: http://oar.imag.fr

4.7. QuickCSG

KEYWORDS: 3D modeling - CAD - 3D reconstruction - Geometric algorithms

FUNCTIONAL DESCRIPTION

QuickCSG is a library and command-line application that computes boolean operations between polyhedra.

- Participants: Matthys Douze, Jean-Sébastien Franco and Bruno Raffin
- Partner: Grenoble-INP
- Contact: Matthys Douze
- URL: http://pascal.inrialpes.fr/data2/douze/QuickCSG

4.8. Triva

FUNCTIONAL DESCRIPTION

Triva is an open-source tool used to analyze traces (in the pajé format) registered during the execution of parallel applications. The tool serves also as a sandbox to the development of new visualization techniques.

- Participant: Guillaume Huard
- Contact: Guillaume Huard
- URL: http://triva.gforge.inria.fr/

4.9. XKaapi

FUNCTIONAL DESCRIPTION

XKaapi is a library for high performance applications running on multi-cores/multi- processors with support for multi-GPUs. XKaapi provides ABI compliant implementations of libGOMP (GCC runtime for OpenMP) and was one of the target runtime of the K'Star compiler,

- Contact: Thierry Gautier
- URL: http://kaapi.gforge.inria.fr

4.10. TakTuk

TakTuk: Adaptive large scale remote executions deployment
KEYWORD: Deployment
FUNCTIONAL DESCRIPTION

TakTuk is a tool for deploying parallel remote executions of commands to a potentially large set of remote nodes. It spreads itself using an adaptive algorithm and sets up an interconnection network to transport commands and perform I/Os multiplexing/demultiplexing. The TakTuk mechanics dynamically adapt to environment (machine performance and current load, network contention) by using a reactive work-stealing algorithm that mixes local parallelization and work distribution.

- Participants: Guillaume Huard, Pierre Neyron, Benoît Claudel, Johann Bourcier and Olivier Richard
- Partner: LIG
- Contact: Guillaume Huard
- URL: http://taktuk.gforge.inria.fr/

4.11. Platforms

4.11.1. Multi-camera Platforms Grimage and Kinovis

MOAIS has managed with the LJK-Inria Morpheo team the Grimage platfrom (http://grimage.inrialpes.fr) dedicated to off-line and on-line 3D modeling from multiple cameras and telepresence. In 2012, we received an Equipex funding, Kinovis (http://kinovis.inrialpes.fr), to renew this platform with an installation which consists of a significantly larger acquisition space with 68 cameras connected to a new computation cluster. Moais participated to the installation and setup of the new platform (in charge of the network, compute and storage infrastructures) which is operational since summer 2015. FlowVR is the software backbone of both platforms for live processing. MOAIS is participating to the FP7 infrastructure project Visionair to enable European research teams to experiment on both platforms.

4.11.2. HPC experimentation platforms: Digitalis, Grid'5000 and Ciment

MOAIS (with MESCAL) develops and operates the Digitalis experimental platform (http://digitalis.inria.fr) which hosts local experimental HPC machines as well as a site of the Grid'5000 national testbed and nodes of the CIMENT regional HPC center (mesocentre of the University of Grenoble). MOAIS with the Mescal and LIG-Erods team obtained in 2014 a grant (FAIRE from Grenoble-INP and LIG) to acquire new experimental machines. 2 ARM64 development boards and one last generation 4 CPU machine which can hosts up to 4 accelerators are now part of the platform.

MODAL Project-Team

6. New Software and Platforms

6.1. BlockCluster

SCIENTIFIC DESCRIPTION

Simultaneous clustering of rows and columns, usually designated by biclustering, co-clustering or block clustering, is an important technique in two way data analysis. It consists of estimating a mixture model which takes into account the block clustering problem on both the individual and variables sets. The blockcluster package provides a bridge between the C++ core library and the R statistical computing environment. This package allows to co-cluster binary, contingency, continuous and categorical data-sets. It also provides utility functions to visualize the results. This package may be useful for various applications in fields of Data mining, Information retrieval, Biology, computer vision and many more.

FUNCTIONAL DESCRIPTION

BlockCluster is an R package for co-clustering of binary, contingency and continuous data based on mixture models.

- Participants: Parmeet Bhatia, Serge Iovleff, Vincent Brault, Christophe Biernacki, Gilles Celeux and Vincent Kubicki
- Partner: Université de Technologie de Compiègne
- Contact: Serge Iovleff
- URL: http://cran.r-project.org/web/packages/blockcluster/index.html

6.2. Clustericat

FUNCTIONAL DESCRIPTION

Clustericat is an R package for model-based clustering of categorical data. In this package, the Conditional Correlated Model (CCM), published in 2014, takes into account the main conditional dependencies between variables through extreme dependence situations (independence and deterministic dependence). Clustericat performs the model selection and provides the best model according to the BIC criterion and the maximum likelihood estimates.

- Participants: Matthieu Marbac-Lourdelle, Vincent Vandewalle and Christophe Biernacki
- Contact: Matthieu Marbac-Lourdelle
- URL: https://r-forge.r-project.org/R/?group_id=1803

6.3. CoModes

FUNCTIONAL DESCRIPTION

CoModes is another R package for model-based clustering of categorical data. In this package, the Conditional Modes Model (CMM), submitted for publication in 2014, takes into account the main conditional dependencies between variables through particular modality crossings (so-called modes). CoModes performs the model selection and provides the best model according to the exact integrated likelihood criterion and the maximum likelihood estimates.

- Participants: Matthieu Marbac-Lourdelle, Vincent Vandewalle and Christophe Biernacki
- Contact: Christophe Biernacki
- URL: https://r-forge.r-project.org/R/?group_id=1809

6.4. CorReg

FUNCTIONAL DESCRIPTION

The main idea of the CorReg package is to consider some form of sub-regression models, some variables defining others. We can then remove temporarily some of the variables to overcome ill-conditioned matrices inherent in linear regression and then reinject the deleted information, based on the structure that links the variables. The final model therefore takes into account all the variables but without suffering from the consequences of correlations between variables or high dimension.

- Participants: Clément Thery and Christophe Biernacki
- Contact: Clément Thery
- URL: https://cran.r-project.org/web/packages/CorReg/index.html

6.5. FunFEM

FUNCTIONAL DESCRIPTION

FunFEM package for R proposes a clustering tool for functional data. The model-based algorithm clusters the functional data into discriminative subspaces.

- Participants: Charles Bouveyron and Julien Jacques
- Contact: Charles Bouveyron
- URL: https://cran.r-project.org/web/packages/funFEM/index.html

6.6. FunHDDC

FUNCTIONAL DESCRIPTION

FunHDDC package for R proposes a clustering tool for functional data. The model-based clustering algorithm considers that functional data live in cluster-specific subspaces.

- Participants: Charles Bouveyron and Julien Jacques
- Contact: Charles Bouveyron
- URL: https://cran.r-project.org/web/packages/funHDDC/index.html

6.7. Galaxy - MPAgenomics

FUNCTIONAL DESCRIPTION

Galaxy is an open, web-based platform for data intensive biomedical research. Galaxy features user friendly interface, workflow management, sharing functionalities and is widely used in the biologist community. The MPAgenomics R package developped by Modal has been integrated into Galaxy, and the Galaxy-Modal instance has been publicly deployed thanks to the IFB-cloud infrastructure.

- Participants: Guillemette Marot and Samuel Blanck
- Contact: Guillemette Marot
- URL: https://cloud.france-bioinformatique.fr/accounts/login/

6.8. HDPenReg

FUNCTIONAL DESCRIPTION

HDPenReg (High-Dimensional Penalized Regression) is an R-package based on a C++ code dedicated to the estimation of regression model with l1-penalization.

- Participants: Quentin Grimonprez and Serge Iovleff
- Contact: Quentin Grimonprez
- URL: https://cran.r-project.org/web/packages/HDPenReg/index.html

6.9. MPAGenomics

KEYWORDS: Segmentation - Genomics - Marker selection - Biostatistics

SCIENTIFIC DESCRIPTION

MPAgenomics (Multi-Patient Analysis of Genomic markers) is an R package for multi-patients analysis of genomics markers. It enables to study several copy number and SNP data profiles at the same time. It offers wrappers from commonly used packages to offer a pipeline for beginners in R. It also proposes a special way of choosing some crucial parameters to change some default values which were not adapted in the original packages. For multi-patients analysis, it wraps some penalized regression methods implemented in HDPenReg.

FUNCTIONAL DESCRIPTION

MPAgenomics provides functions to preprocess and analyze genomic data. It is devoted to: (i) efficient segmentation and (ii) genomic marker selection from multi-patient copy number and SNP data profiles.

- Participants: Quentin Grimonprez, Guillemette Marot and Samuel Blanck
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/MPAgenomics/index.html

6.10. MetaMA

FUNCTIONAL DESCRIPTION

MetaMA (Meta-analysis for MicroArrays) is a specialised software for microarrays. It is an R package which combines either p-values or modified effect sizes from different studies to find differentially expressed genes. The main competitor of metaMA is geneMeta. Compared to geneMeta, metaMA offers an improvement for small sample size datasets since the corresponding modelling is based on shrinkage approaches.

- Participant: Guillemette Marot
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/metaMA/index.html

6.11. MetaRNASeq

FUNCTIONAL DESCRIPTION

This is joint work with Andrea Rau (INRA, Jouy-en-Josas). MetaRNASeq is a specialised software for RNA-seq experiments. It is an R package which is an adaptation of the MetaMA package presented previously. Both implement the same kind of methods but specificities of the two types of technologies require some adaptations to each one.

- Participants: Guillemette Marot and Andrea Rau
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/metaRNASeq/index.html

6.12. MixAll

FUNCTIONAL DESCRIPTION

MixAll (Clustering using Mixture Models) is a model-based clustering package for modelling mixed data sets. It has been engineered around the idea of easy and quick integration of any kind of mixture models for any kind of data, under the conditional independence assumption. Currently five models (Gaussian mixtures, categorical mixtures, Poisson mixtures, Gamma mixtures and kernel mixtures) are implemented. MixAll has the ability to natively manage completely missing values when assumed as random. MixAll is used as an R package, but its internals are coded in C++ as part of the STK++ library (www.stkpp.org) for faster computation.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/MixAll/

6.13. MixCluster

FUNCTIONAL DESCRIPTION

MixCluster is an R package for model-based clustering of mixed data (continuous, binary, integer). In this package, the model, submitted for publication in 2014, takes into account the main conditional dependencies between variables through Gaussian copula. Mixcluster performs the model selection and provides the best model according to Bayesian approaches.

- Participants: Matthieu Marbac-Lourdelle, Christophe Biernacki and Vincent Vandewalle
- Contact: Christophe Biernacki
- URL: https://r-forge.r-project.org/R/?group_id=1939

6.14. Mixmod

FUNCTIONAL DESCRIPTION

Mixmod is a free toolbox for data mining and statistical learning designed for large and highdimensional data sets. Mixmod provides reliable estimation algorithms and relevant model selection criteria.

It has been successfully applied to marketing, credit scoring, epidemiology, genomics and reliability among other domains. Its particularity is to propose a model-based approach leading to a lot of methods for classification and clustering.

Mixmod allows to assess the stability of the results with simple and thorough scores. It provides an easy-to-use graphical user interface (mixmodGUI) and functions for the R (Rmixmod) and Matlab (mixmodForMatlab) environments.

- Participants: Christophe Biernacki, Gilles Celeux, Gérard Govaert, Florent Langrognet, Serge Iovleff, Remi Lebret and Benjamin Auder
- Partners: CNRS - Université Lille 1 - LIFL - Laboratoire Paul Painlevé - HEUDIASYC - LMB
- Contact: Christophe Biernacki
- URL: http://www.mixmod.org

6.15. MixtComp

FUNCTIONAL DESCRIPTION

MixtComp (Mixture Computation) is a model-based clustering package for mixed data originating from the Modal team (Inria Lille). It has been engineered around the idea of easy and quick integration of all new univariate models, under the conditional independence assumption. New models will eventually be available from researches, carried out by the Modal team or by other teams. Currently, central architecture of MixtComp is built and functionality has been field-tested through industry partnerships. Three basic models (Gaussian, multinomial, Poisson) are implemented, as well as two advanced models (Ordinal and Rank). MixtComp has the ability to natively manage missing data (completely or by interval). MixtComp is used as an R package, but its internals are coded in C++ using state of the art libraries for faster computation.

- Participants: Vincent Kubicki, Christophe Biernacki and Serge Iovleff
- Contact: Christophe Biernacki
- URL: https://modal-research.lille.inria.fr/BigStat

6.16. RankCluster

FUNCTIONAL DESCRIPTION

Rankcluster package for R proposes a clustering tool for ranking data. Multivariate and partial rankings can be also taken into account. Rankcluster now supports tied ranking data.

- Participants: Christophe Biernacki, Julien Jacques and Quentin Grimonprez
- Contact: Quentin Grimonprez
- URL: https://cran.r-project.org/web/packages/Rankcluster/index.html

6.17. STK++

FUNCTIONAL DESCRIPTION

STK++ (C++ Statistical ToolKit) is a versatile, fast, reliable and elegant collection of C++ classes for statistics, clustering, linear algebra, arrays (with an API Eigen-like), regression, dimension reduction, etc. The library is interfaced with lapack for many linear algebra usual methods. Some functionalities provided by the library are available in the R environment using rtkpp and rtkore.

STK++ is suitable for projects ranging from small one-off projects to complete data mining application suites.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: http://www.stkpp.org

6.18. clere

FUNCTIONAL DESCRIPTION

The clere package for R proposes variable clustering in high dimensional linear regression. Available on CRAN and now submitted to an international journal dedicated to software.

- Participants: Loïc Yengo, Christophe Biernacki and Julien Jacques
- Contact: Loïc Yengo
- URL: https://cran.r-project.org/web/packages/clere/index.html

6.19. rtkore

FUNCTIONAL DESCRIPTION

STK++ (http://www.stkpp.org) is a collection of C++ classes for statistics, clustering, linear algebra, arrays (with an Eigen-like API), regression, dimension reduction, etc. The integration of the library to R is using Rcpp. The rtkore (STK++ core library integration to R using Rcpp) package includes the header files from the STK++ core library. All files contain only templated classes or inlined functions. STK++ is licensed under the GNU LGPL version 2 or later. rtkore (the stkpp integration into R) is licensed under the GNU GPL version 2 or later. See file LICENSE.note for details.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/rtkore/index.html

MODEMIC Project-Team

6. New Software and Platforms

6.1. Landfill Recirculation Management Simulator

FUNCTIONAL DESCRIPTION

Following the first works on modeling and control of landfills performed in the framework of the associated team DYMECOS with Chile, that have proposed an optimal feedback strategy for the leachate recirculation under the assumption of a perfectly mixed medium [40], a first mock-up software has been conceived in view of studying the effects of inhomogeneity along with identification procedures of spatial network structures on data (interconnection of bioreactors as in VITELBIO project). The development of the software is in progress.

- Participants: Andres Donoso-Bravo (PUCV, Chile), J.R. de Dreuzy (GéoSciences Rennes), Alain Rapaport, Hector Ramirez, Alejandro Rojas Palma
- Contact: Alain Rapaport
- URL: https://sites.google.com/site/eadymecos/resultats

6.2. Action Dépollution

FUNCTIONAL DESCRIPTION

Action Dépollution is a serious game made for learning how to purify fast and well a water reservoir, such as lakes. In the scope of the international initiative Mathematics of Planet Earth, this game shows an application of mathematics related to environmental education and sustainable development. The player can act as a researcher, that compares different strategies and looks for the best solution.

- Participants: Alain Rapaport, Antoine Rousseau (EPI LEMON)
- Contact: Antoine Rousseau
- URL: https://depollution.inria.fr/

6.3. VITELBIO (VIrtual TELluric BIOreactors)

FUNCTIONAL DESCRIPTION

Vitelbio is a simulator of the microbial activity in soils, for which the spatialization is represented as a network of interconnected reservoirs. The software allows to draw an interconnections graph, that respects the constraint of the maximum flow, and to choose the biological characteristics of various bacterial species in competition for a single nutrient. The simulator computes the time evaluations of the different populations in each compartment, and compares the overall yielding of the ecosystem in terms of bio-conversion of the substrate. This software has been developed in the framework of the INRA/Inria project VITELBIO (VIrtual TELluric BIOreactors), with the help of the company ITK. It is today mainly used for educational purposes (in MSC and PhD lectures).

- Participants: Jérôme Harmand, Alain Rapaport
- Contact: Alain Rapaport
- URL: http://vitelbio.itkweb.fr/vitelbio/

MOKAPLAN Project-Team

6. New Software and Platforms

6.1. ALG2

FUNCTIONAL DESCRIPTION

ALG2 for Monge Mean-Field Games, Monge problem and Variational problems under divergence constraint. A generalisation of the ALG2 algorithm has been implemented in FreeFem++.

- Contact: Jean-David Benamou
- URL: https://team.inria.fr/mokaplan/augmented-lagrangian-simulations/

6.2. Mokabajour

FUNCTIONAL DESCRIPTION

We design a software resolving the following inverse problem: define the shape of a mirror which reflects the light from a source to a defined target, distribution and support of densities being prescribed. Classical applications include the conception of solar oven, public lightning, car headlights...Mathematical modeling of this problem, related to the optimal transport theory, takes the form of a nonlinear Monge-Ampere type PDE. The numerical resolution of these models remained until recently a largely open problem. MOKABAJOUR project aims to develop, using algorithms invented especially at Inria and LJK, a reflector design software more efficient than geometrical methods used so far.

- Participants: Jean-David Benamou, Vincent Duval, Simon Legrand, Quentin Mérigot and Boris Thibert
- Contact: Jean-David Benamou
- URL: https://project.inria.fr/mokabajour/

6.3. Entropic OT

FUNCTIONAL DESCRIPTION

We design a software to compute fast approximation of optimal transport (and related problems such as barycenters) on geometric domains (either regular Euclidean grid or triangulated meshes). This numerical scheme relies on two key ideas: entropic regularization of the initial linear problem [3] and fast approximate convolution on geometric domains [22] This algorithm is both extremely fast and highly parallelizable, being able to take advantage of GPU computational architectures.

- Gabriel Peyré, Jean-David Benamou, Guillaume Carlier, Marco Cuturi (Kyoto), Justin Solomon.
- Contact: Gabriel Peyré
- URL: https://github.com/gpeyre/2015-SIGGRAPH-convolutional-ot

6.4. Jupyter Notebook

FUNCTIONAL DESCRIPTION

Several codes deevlloped by the team are available on an online Jupyter Notebook (Julia and Python) In particular the Semi Discrete Principal Agent Code and also a new Monge-Amère second boundary value problem Finite Difference code.

- Simon Legrand, Xavier Dupuis, Vincent Duval, Jean-David Benamou.
- Contact: Simon Legrand
- URL: https://mathmarx.paris.inria.fr:8080

Monc Team

6. New Software and Platforms

6.1. CADMOS

KEYWORDS: Health - Cancer - Partial differential equation - Cartesian grid

- Participants: Olivier Saut and Julien Jouganous
- Partners: Université de Bordeaux - CNRS - INP Bordeaux
- Contact: Olivier Saut

6.2. Carcinom (Computer-Assisted Research about Cancer growth and INsights on Oncological Mechanisms)

KEYWORDS: Cancer - Data modeling - Regression

- Participants: Sébastien Benzekry
- Contact: Sébastien Benzekry
- FUNCTIONAL DESCRIPTION A software for nonlinear regression of tumor growth and therapy models and statistical inference. This software is primarily designed to perform a modeling analysis of tumor growth kinetics. Given a data set of longitudinal measurements of tumor size in a population, it fits several models of tumor growth, computes several goodness-of-fit statistical metrics, identifies the parameters of the models and estimates the uncertainty associated to their determination. It provides several graphical and numerical outputs (in the form of LaTeX tables).

6.3. ELMO (Numerical Simulation of cell electroporation)

KEYWORDS: Bioinformatics - Biology - Numerical electroporation - Finite difference method in 2D-3D

- Participants: Clair Poignard and Michael Leguebe
- Partners: Université de Bordeaux - CNRS - INP Bordeaux
- Contact: Michael Leguebe
- URL: http://www.math.u-bordeaux1.fr/~mleguebe/phd_fr.html
- SCIENTIFIC DESCRIPTION 2D-3D code of finite difference method in C++ to compute the electroquasistatic field in a biological cell, with non-linear model of membrane conductance and lateral diffusion of lipids.
- FUNCTIONAL DESCRIPTION Compute the electroquasistatic field and the porated region of the cell membrane. The aim is to provide a user-friendly code for applied mathematicians and biophysicists.

6.4. Meta-poumon

KEYWORDS: Health - Evolution - Cancer - Medical imaging

- Participants: Olivier Saut, Thierry Colin, Marie Martin and Julien Jouganous
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: Olivier Saut
- FUNCTIONAL DESCRIPTION The software evaluates the aggressiveness of pulmonary metastasis or response to treatment for predictive goal. To do this, we use a mathematical model based on a set of equations to nonlinear partial differential equations. This model is calibrated to the patient data using a longitudinal sequence of CT or MRI of the patient.

6.5. Nenuphar

KEYWORDS: Modeling - Oncologie - Cancer - Partial differential equation - Medical - Medical imaging

- Partners: CNRS - INP Bordeaux - Université Bordeaux 1
- Contact: Marie Martin
- FUNCTIONAL DESCRIPTION The goal of project is to evaluate the aggressiveness of a tumor or its response to therapy. For that purpose, we use a mathematical model based on a set of nonlinear partial differential equations. This model is calibrated on patient data using a longitudinal sequence of CT Scan or MRI of the patient. This approach has been validated on about 35 clinical cases of lung metastases from various primary tumors (kidney, bladder, thyroid). Using two initial images showing the targeted lesion, we recover the patient-specific parameters of the model. The evolution of the disease is then predicted by letting the model run for later times with these parameters.

6.6. SESAR (Monitor of the effect of RT on Retroperitoneal Sarcoma)

KEYWORDS: Segmentation - Health - DICOM - Cancer - Medical imaging

- Partner: Institut Bergonié
- Contact: Olivier Saut

6.7. SegmentIt

KEYWORDS: Health - Signal - Registration of 2D and 3D multimodal images - 3D - Image analysis - Image - Processing - Medical imaging

- Participants: Thierry Colin, Olivier Saut, Vivien Pianet, Agathe Peretti, Marie Martin, Sébastien Benzekry, Baudoin Denis De Senneville, Cynthia Perier, Benjamin Taton, Nicolas Grenier and Christian Combe
- Contact: Benjamin Taton
- FUNCTIONAL DESCRIPTION Image processing software for anatomical and functional data. Segmentation, registration and digital filtering. Assessement of the kidney perfusion and the kidney function (to be continued).

MORPHEME Project-Team

5. New Software and Platforms

5.1. BioLib

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION

Library of image analysis for biology: object detection, tracking. This year some new developments for embedding attractive interactions in the Multiple Births and Cut algorithm have been included.

- Participants: Sylvain Prigent, Xavier Descombes, Grégoire Malandain, Étienne Delclaux, Emmanuel Soubies and Sen Wang.
- Contact: Xavier Descombes

5.2. PIB

Biological imaging platform
FUNCTIONAL DESCRIPTION

This platform, based on the DTK meta-platform, aims at gathering the team software development, and at providing a visual development tool.

- Participants: Étienne Delclaux, Grégoire Malandain and Xavier Descombes
- Contact: Xavier Descombes

5.3. Stracking

KEYWORDS: Bioinformatics - Biology - Biomedical imaging
SCIENTIFIC DESCRIPTION

Head Tracking and Flagellum Tracing for Sperm Motility Analysis : Sperm quality assessment plays an essential role in human fertility and animal breeding. Manual analysis is time-consuming and subject to intra- and inter-observer variability. To automate the analysis process, as well as to offer a means of statistical analysis that may not be achieved by visual inspection, we present a computational framework that tracks the heads and traces the tails for analyzing sperm motility, one of the most important attributes in semen quality evaluation. Our framework consists of 3 modules: head detection, head tracking, and flagellum tracing. The head detection module detects the sperm heads from the image data, and the detected heads are the inputs to the head tracking module for obtaining the head trajectories. Finally, a flagellum tracing algorithm is proposed to obtain the flagellar beat patterns.
FUNCTIONAL DESCRIPTION

This software is developed within the ANR project MOTIMO. It allows to segment and track spermatozoons from confocal microscopy image sequences.

- Participants: Huei Fang Yang, Xavier Descombes, Sylvain Prigent and Grégoire Malandain
- Contact: Xavier Descombes

MORPHEO Project-Team

6. New Software and Platforms

6.1. 4D repository

FUNCTIONAL DESCRIPTION

This website hosts dynamic mesh sequences reconstructed from images captured using a multi-camera set up. Such mesh-sequences offer a new promising vision of virtual reality, by capturing real actors and their interactions. The texture information is trivially mapped to the reconstructed geometry, by back-projecting from the images. These sequences can be seen from arbitrary viewing angles as the user navigates in 4D (3D geometry + time) . Different sequences of human / non-human interaction can be browsed and downloaded from the data section.

- Contact: Bruno Raffin
- URL: http://4drepository.inrialpes.fr/

6.2. ETHOMICE

KEYWORDS: Biology - Health - Biomechanics - Motion analysis - Ethology - Mouse
FUNCTIONAL DESCRIPTION

Ethomice is a motion analysis software to characterize motor behavior of small vertebrates such as mice or rats. From a multiple views video input, a biomechanical model of the skeleton is registered. Study on animal model is the first important step in Biology and Clinical research. In this context, the analysis of the neuro-motor behaviour is a frequent cue to test the effect of a gene or a drug. Ethomice is a platform for simulation and analysis of the small laboratory animal, such as rat or mouse. This platform links the internal skeletal structure with 3D measurements of the external appearance of the animal under study. From a stream of multiple views video, the platform aims at delivering a three dimensional analysis of the body posture and the behaviour of the animal.

- Participants: Lionel Reveret
- Partners: CNRS - Inria - Université Descartes - ICS
- Contact: Lionel Reveret
- URL: http://morpheo.inrialpes.fr/people/reveret/ethomice

6.3. Lucy Viewer

FUNCTIONAL DESCRIPTION

Lucy Viewer is an interactive viewing software for 4D models, i.e, dynamic three-dimensional scenes that evolve over time. Each 4D model is a sequence of meshes with associated texture information, in terms of images captured from multiple cameras at each frame.

- Participants: Edmond Boyer and Florent Lagaye
- Contact: Edmond Boyer
- URL: http://4drepository.inrialpes.fr/lucy_viewer/

6.4. QuickCSG

KEYWORDS: 3D modeling - CAD - 3D reconstruction - Geometric algorithms
FUNCTIONAL DESCRIPTION

QuickCSG is a library and command-line application that computes boolean operations between polyhedra. It is able to direcly compute resulting solids from an arbitrary number of inputs and for an arbitrary boolean combination function, with state of the art execution times.

- Participants: Matthys Douze, Jean-Sébastien Franco and Bruno Raffin
- Partner: INP Grenoble
- Contact: Matthys Douze
- URL: http://kinovis.inrialpes.fr/static/QuickCSG/

6.5. Shape Tracking

FUNCTIONAL DESCRIPTION

We are developing a software suite to track shapes over temporal sequences. The motivation is to provide temporally coherent 4D Models, i.e. 3D models and their evolutions over time, as required by motion related applications such as motion analysis. This software takes as input a temporal sequence of 3D models in addition to a template and estimates the template deformations over the sequence that fit the observed 3D models. This software is particularly developed in the context of the FUI project Creamove.

- Contact: Edmond Boyer

6.6. Platforms

6.6.1. Platform Kinovis

Kinovis (http://kinovis.inrialpes.fr/) is a multi-camera acquisition project that was was selected within the call for proposals ”Equipements d’Excellence” of the program “Investissement d’Avenir˝ funded by the French government. The project involves 2 institutes: the Inria Grenoble Rhône-Alpes, the université Joseph Fourier and 4 laboratories: the LJK (laboratoire Jean Kuntzmann - applied mathematics), the LIG (laboratoire d’informatique de Grenoble - Computer Science), the Gipsa lab (Signal, Speech and Image processing) and the LADAF (Grenoble Hospitals - Anatomy). The Kinovis environment is composed of 2 complementary platforms. A first platform located at Inria Grenoble with a 10mx10m acquisition surface is equipped with 68 color cameras and 20 IR motion capture (mocap) cameras. It is the evolution of the Grimage platform towards the production of better models of more complex dynamic scenes. A second platform located at Grenoble Hospitals, within the LADAF anatomy laboratory, is equipped with 10 color and 2 X-ray cameras to enable combined analysis of internal and external shape structures, typically skeleton and bodies of animals. Installation works of both platforms started in 2013 and are now finished. Both platforms have already demonstrated their potential through a range of projects lead by the team and externally. Members of Morpheo are highly involved in this project. Edmond Boyer is coordinating this project and Lionel Reveret is in charge of the LADAF platform. Thomas Pasquier, Mickaël Heudre and Julien Pansiot are managing the technical resources of both platforms.

6.6.2. Multicamera platform for video analysis of mice behavior

This project is a follow-up of the experimental set-up developed for a CNES project with Mathieu Beraneck from the CESeM laboratory (centre for the study of sensorimotor control, CNRS UMR 8194) at the Paris-Descartes University. The goal of this project was to analyze the 3D body postures of mice with various vestibular deficiencies in low gravity condition (3D posturography) during a parabolic flight campaign. The set-up has been now adapted for new experiments on motor-control disorders for other mice models. This experimental platform is currently under development for a broader deployment for high throughput phenotyping with the technology transfer project ETHOMICE. This project involves a close relationship with the CESeM laboratory and the European Mouse Clinical Institute in Strasbourg (Institut Clinique de la Souris, ICS).

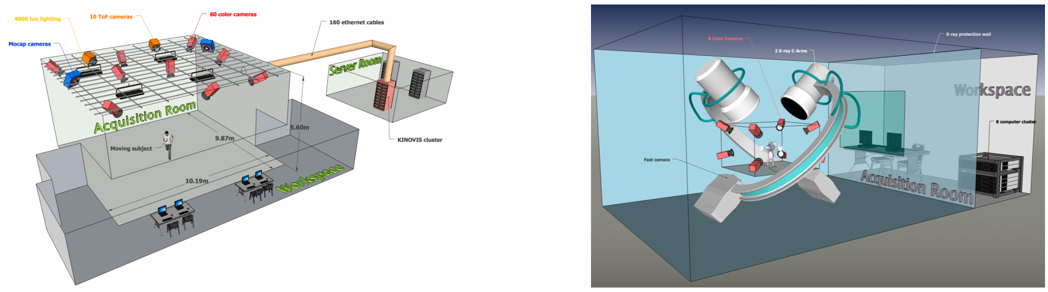


Figure 1. Kinovis platforms: on the left the Inria platform; on the right Grenoble Hospital platform.

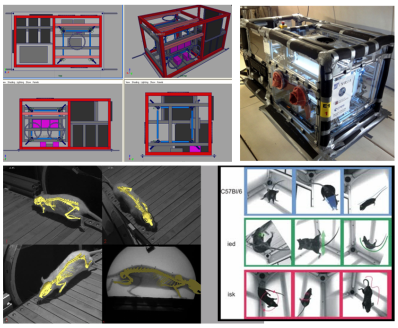


Figure 2. Ethomice: Experimental platform for video analysis of mice behavior.

MULTISPEECH Project-Team

6. New Software and Platforms

6.1. ANTS - Automatic News Transcription System

FUNCTIONAL DESCRIPTION: ANTS is a multipass system for transcribing audio data, and in particular radio or TV shows. The audio stream is first split into homogeneous segments that are decoded using the most adequate acoustic model with a large vocabulary continuous speech recognition engine (Julius, Sphinx or Kaldi). Further processing passes are run in order to apply unsupervised adaptation processes on the features and/or on the model parameters, or to use Speaker Adaptive Training based models. Latest version include DNN (Deep Neural Network) acoustic modeling.

- Participants: Dominique Fohr, Odile Mella, Irina Illina and Denis Jouvet
- Contact: Dominique Fohr

6.2. ASTALI - Automatic Speech-Text Alignment

FUNCTIONAL DESCRIPTION: ASTALI is a software for aligning a speech signal with its corresponding orthographic transcription (given in simple text file for short audio signals or in .trs files as generated by transcriber for longer speech signals). Using a phonetic lexicon and automatic grapheme-to-phoneme converters, all the potential sequences of phones corresponding to the text are generated. Then, using acoustic models, the tool finds the best phone sequence and provides the boundaries at the phone and at the word levels. The web application makes the service easy to use, without requiring any software downloading. Also, the software is currently under integration in the EQUIPEX ORTOLANG platform.

- Participants: Dominique Fohr, Odile Mella, Antoine Chemardin and Denis Jouvet
- Contact: Dominique Fohr
- URL: http://astali.loria.fr/

6.3. JCorpusRecorder

FUNCTIONAL DESCRIPTION: JCorpusRecorder is a software for the recording of audio corpora. It provides an easy tool to record with a microphone. The audio input gain is controlled during the recording. From a list of sentences, the output is a set of wav files automatically renamed according to textual information given in input (nationality, speaker language, gender, ...). An easy to use tagging allows for displaying a textual/visual/audio context for guiding the speaker, along with the text of the sentence to pronounce. Several text encodings are enabled (allowing for instance Chinese texts). The sentences can be presented in a random order. The last version can record up to 8 synchronous channels (8 channels under Linux and 2 channels under Windows). The software is developed in Java, and is currently used for the recording of sentences in several projects.

- Contact: Vincent Colotte

6.4. JSnoori

FUNCTIONAL DESCRIPTION: JSnoori is written in Java and uses signal processing algorithms developed within the WinSnoori software with the double objective of being a platform independent signal visualization and manipulation tool, and also for designing exercises for learning the prosody of a foreign language. Thus JSnoori currently focuses the calculation of F0, the forced alignment of non native English uttered by French speakers and the correction of prosody parameters (F0, rhythm and energy). Several tools have been incorporated to segment and annotate speech. A complete phonetic keyboard is available, several levels of annotation can be used (phonemes, syllables and words) and forced alignment can exploit pronunciation variants. In addition, JSnoori offers real time F0 calculation which can be useful from a pedagogical point of view. Besides the traditional graphic interface, JSnoori can now be used via scripts written in Jython.

- Participants: Yves Laprie, Slim Ouni, Julie Busset, Aghilas Sini and Ilef Ben Farhat
- Contact: Yves Laprie
- URL: http://www.loria.fr/~laprie/WinSnoori/

6.5. VisArtico - Visualization of EMA Articulatory Data

FUNCTIONAL DESCRIPTION: VisArtico is a user-friendly software which allows visualizing EMA data acquired by an articulograph (AG500, AG501 or NDI Wave). This visualization software has been designed so that it can directly use the data provided by the articulograph to display the articulatory coil trajectories, synchronized with the corresponding acoustic recordings. Moreover, VisArtico not only allows viewing the coils but also enriches the visual information by indicating clearly and graphically the data for the tongue, lips and jaw. In addition, it is possible to insert images (MRI or X-Ray, for instance) to compare the EMA data with data obtained through other acquisition techniques. The last version of VisArtico can handle multimodal data, not articulatory data only. In fact, it is possible to visualize motion capture data from Vicon or kinect-like systems (PrimeSense and RealSense). It is possible to generate video from the visualized trajectories. A derived version from VisArtico is also used in the ADT Plavis as a tool to visualize and process the audiovisual data. The software is used by more than 170 researchers around the world.

- Participants: Slim Ouni, Loïc Mangeonjean and Ilef Ben Farhat
- Contact: Slim Ouni
- URL: http://visartico.loria.fr

6.6. Xarticulators

KEYWORD: Medical imaging

FUNCTIONAL DESCRIPTION: The Xarticulators software is intended to delineate contours of speech articulators in X-ray images, construct articulatory models and synthesize speech from X-ray films. This software provides tools to track contours automatically, semi-automatically or by hand, to make the visibility of contours easier, to add anatomical landmarks to speech articulators and to synchronize images with the sound. In addition we also added the possibility of processing digitized manual delineation results made on sheets of papers. Xarticulators also enables the construction of adaptable linear articulatory models from the X-ray images and incorporates acoustic simulation tools to synthesize speech signals from the vocal tract shape. Recent work was on the possibility of constructing a velum model and incorporating it into the area functions.

- Contact: Yves Laprie

6.7. Platform EMA - Electromagnetic Articulography Acquisition

FUNCTIONAL DESCRIPTION: Since the purchase of the articulograph AG500 in 2007, we have built a strong experience with respect to the acquisition technique and we have developed an acquisition protocol. The platform has been improved by acquiring the latest articulograph AG501 funded by the EQUIPEX ORTOLANG project. The AG501 allows tracking the movement of 24 sensors at reasonable high frequency (250Hz) up to a very high frequency (1250Hz). In addition, we have continued improving VisArtico (cf. 6.5), a powerful tool to visualize articulatory data acquired using an articulograph. This year we have used the system to acquire articulatory data for the tongue, jaw and lips to study stuttering speech disorder (informal collaboration with F. Hirsch, Praxiling (UMR 5267)). We have also used the EMA platform to acquire motion capture data for the lips, to be used in the context of audiovisual speech synthesis [82].

- Contact: Slim Ouni

6.8. Platform MRI - Magnetic Resonance Imaging

KEYWORDS: Health - Medical imaging

FUNCTIONAL DESCRIPTION: Magnetic Resonance Imaging (MRI) takes an increasing place in the investigation of speech production because it provides a complete geometrical information of the vocal tract. We thus initiated a cooperation with the IADI laboratory (Imagerie Adaptive Diagnostique et Interventionnelle) at Nancy Hospital, which studies in particular magnetic resonance imaging. This year the work focused on the development of compressed sensing algorithms and the reconstruction of good quality images to acquire cineMRI at a sampling rate between 25 and 60 Hz. The algorithms were implemented on the 3T GE research MRI machine of the Nancy Hospital.

- Contact: Yves Laprie

MUSE Team

5. New Software and Platforms

5.1. Fathom

Fathom - browser-based network measurement platform
KEYWORDS: Internet access - Performance measure - Network monitoring
FUNCTIONAL DESCRIPTION

Fathom is a Firefox browser extension that explores the browser as a platform for network measurement and troubleshooting. It provides a wide range of networking primitives directly to in-page JavaScript including raw TCP/UDP sockets, higher-level protocol APIs such as DNS, HTTP, and UPnP, and ready-made functionality such as pings and traceroutes.

- Participants: Anna-Kaisa Pietilainen and Stéphane Archer
- Contact: Anna-Kaisa Pietilainen
- URL: https://muse.inria.fr/fathom/

5.2. HostView

FUNCTIONAL DESCRIPTION

End-host performance monitoring and user feedback reporting

- Participants: George Rosca, Anna-Kaisa Pietilainen and Renata Cruz Teixeira
- Contact: Renata Cruz Teixeira
- URL: https://muse.inria.fr/hostview/

5.3. Online HoA

Online implementation of home and access throughput bottleneck detection algorithm ’HoA’
FUNCTIONAL DESCRIPTION

Implementation of HoA as collectd plugin for OpenWRT.

- Contact: Renata Cruz Teixeira
- URL: https://github.com/inria-muse/browserlab

5.4. SimilarityExplanation

Prototype implementation for explaining a set of similar and recommended movies.
FUNCTIONAL DESCRIPTION

In this web-based prototype for similar movies explanation, we propose two types of browsing for : personalized browsing and non personalized browsing. In the non personalized browsing we suppose that we don’t have the user profile. Similar movie sublists are ordered only according to their similarity to the selected movie. For the personalized browsing , we select users that have different profiles from our dataset. We give these users names of actors, according to the types of movies they watch. For each user, we compute the predicted ratings using the matrix factorization model. We select pairs of genres to display to each user based on the preferred genres for the user. In our prototype we identify the preferred genres per user based on the most frequent movie genre pairs that the user has already seen. We then organize the recommended movies with a high rating prediction in sublists, according to the user most preferred genre pairs. When a user selects a movie from the sublists of recommended movies, our application suggests the similar movies presented under four sublists with the added list of words. The sublists are personalized for each user by reordering the movies according to the users predicted ratings.

- Contact: Sara El Aouad
- URL: http://muse.inria.fr/tagit

5.5. UCN

User-Centric Networking

FUNCTIONAL DESCRIPTION

The User-Centric Networking (UCN) project is seeking to understand how people consume various kinds of content when using computer networks. Within this project we are undertaking a detailed user study across a range of environments in order to understand the practices involved in consuming media and other content according to context.

- Participants: Renata Cruz Teixeira and Anna-Kaisa Pietilainen
- Contact: Anna-Kaisa Pietilainen
- URL: https://muse.inria.fr/ucn

5.6. WeBrowse

FUNCTIONAL DESCRIPTION

WeBrowse is the first passive crowdsource-based content curation system. Content curation is the act of assisting users to identify relevant and interesting content in the Internet. WeBrowse requires no active user engagement to promote content. Instead, it extracts the URLs users visit from traffic traversing an ISP network to identify popular content. WeBrowse contains a set of heuristics to identify the set of URLs users visit and to select the subset that are interesting to users.

- Contact: Giuseppe Scavo
- URL: http://webrowse.polito.it/

MUTANT Project-Team

6. New Software and Platforms

6.1. Antescofo

Participants: Arshia Cont, Jean-Louis Giavitto, Philippe Cuvillier, José Echeveste.

FUNCTIONAL DESCRIPTION Antescofo is a modular polyphonic Score Following system as well as a Synchronous Programming language for musical composition. The module allows for automatic recognition of music score position and tempo from a realtime audio Stream coming from performer(s), making it possible to synchronize an instrumental performance with computer realized elements. The synchronous language within Antescofo allows flexible writing of time and interaction in computer music.

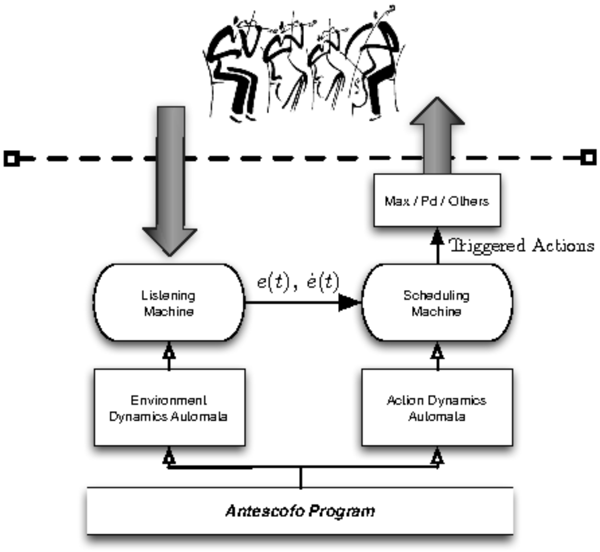


Figure 4. General scheme of Antescofo virtual machine

Antescofo v0.9 was released in November 2015. It contains major additions in the language (see Sections 7.5 and 7.6) as well as machine listning especially for singing voice and highly polyphonic instruments (See Release Notes). Antescofo Reference Guide is a collaborative document referencing the language and its usage, showcasing the software's latest developments.

- Participants: Arshia Cont, Jean-Louis Giavitto, Philippe Cuvillier and José Echeveste
- Contact: Arshia Cont
- URL: http://forumnet.ircam.fr/product/antescofo/

6.2. Ascograph

Participants: Arshia Cont, Grig Burloiu, Robert Piéchaud.

FUNCTIONAL DESCRIPTION

AscoGraph, the Antescofo graphical score editor released in 2013, provides a autonomous Integrated Development Environment (IDE) for the authoring of Antescofo scores. Antescofo listening machine, when going forward in the score during recognition, uses the message passing paradigm to perform tasks such as automatic accompaniment, spatialization, etc. The Antescofo score is a text file containing notes (chord, notes, trills, ...) to follow, synchronization strategies on how to trigger actions, and electronic actions (the reactive language). This editor shares the same score parsing routines with Antescofo core, so the validity of the score is checked on saving while editing in AscoGraph, with proper parsing errors handling. Graphically, the application is divided in two parts. On the left side, a graphical representation of the score, using a timeline with tracks view. On the right side, a text editor with syntax coloring of the score is displayed. Both views can be edited and are synchronized on saving. Special objects such as "curves", are graphically editable: they are used to provide high-level variable automation facilities like breakpoints functions (BPF) with more than 30 interpolations possible types between points, graphically editable.

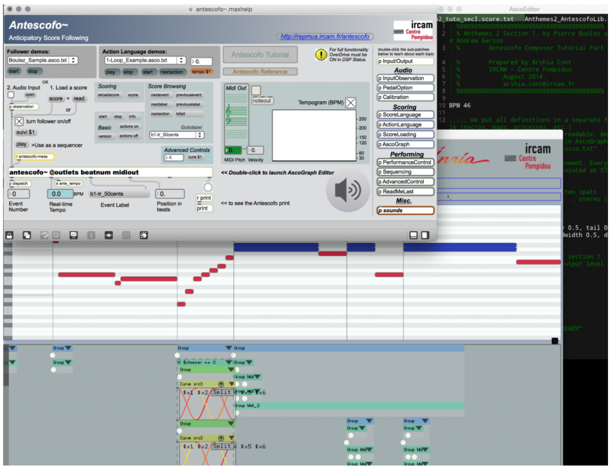


Figure 5. Antescofo and AscoGraph Screen Shorts (Nov. 2015)

In 2015, AscoGraph's User Interaction was redesigned as reported in [12], [13] and furthermore, a new Score Import procedure was developped and released in v0.25 (See Release Notes). See also 7.8 .

- Contact: Arshia Cont
- URL: http://forumnet.ircam.fr/product/antescofo/

6.3. Antescofo Timed Test Platform

Participants: Clément Poncelet, Florent Jacquemard, Pierre Donat-Bouillud.

The frequent use of Antescofo in live and public performances with human musicians implies strong requirements of temporal reliability and robustness to unforeseen errors in input. To address these requirements and help the development of the system and authoring of pieces by users, we are developing a platform for the automation of testing the behavior of Antescofo on a given score, with of focus on timed behavior. It is based on state of the art techniques and tools for *model-based testing* of embedded systems [37], and makes it possible to automate the following main tasks:

1. offline and on-the-fly generation of relevant input data for testing (i.e. fake performances of musicians, including timing values), with the sake of exhaustiveness,
2. computation of the corresponding expected output, according to a formal specification of the expected behavior of the system on a given mixed score,

3. black-box execution of the input test data on the System Under Test,
4. comparison of expected and real output and production of a test verdict.

The input and output data are timed traces (sequences of discrete events together with inter-event durations). Our method is based on formal models (specifications) in an ad hoc medium-level intermediate representation (IR). We have developed a compiler for producing automatically such IR models from Antescofo high level mixed scores.

Then, in the offline approach, the IR is passed, after conversion to Timed Automata, to the model-checker Uppaal, to which is delegated the above task (1), following coverage criteria, and the task (2), by simulation. In the online approach, tasks (1) and (2) are realized during the execution of the IR by a Virtual Machine developed on purpose. Moreover, we have implemented several tools for Tasks (3) and (4), corresponding to different boundaries for the implementation under test (black box): e.g. the interpreter of Antescofo's synchronous language alone, or with tempo detection, or the whole system.

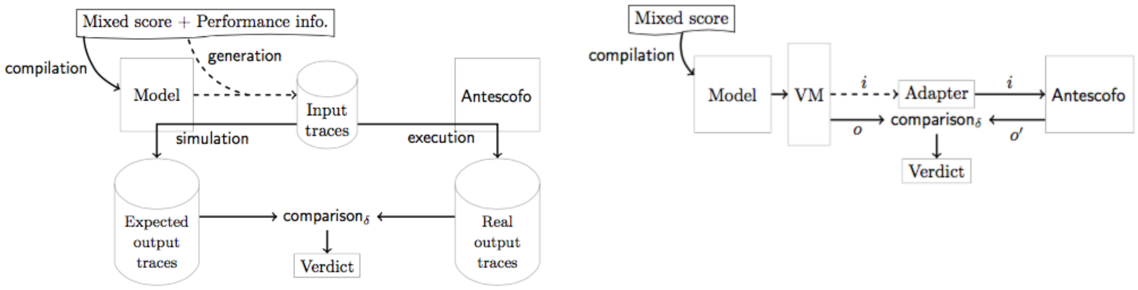


Figure 6. Offline and Online workflows for Antescofo Model Based Testing

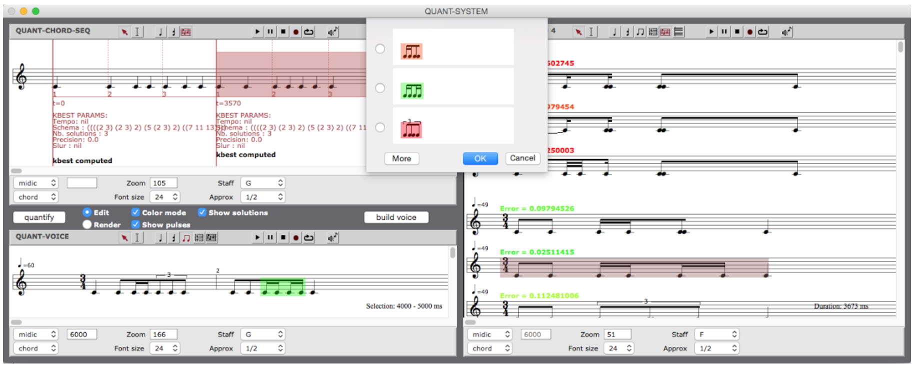
Our fully automatic framework has been applied to real mixed scores used in concerts and the results obtained have permitted to identify bugs in Antescofo.

6.4. Rhythm Quantization in Open Music

Participants: Adrien Ycart, Florent Jacquemard, Jean Bresson.

We are developing a new system for rhythm transcription, which is the conversion of sequences of timestamped discrete events into common-western music notation. The input events may e.g. come from a performance on a MIDI keyboard or may also be the result of a computation. Our system privileges the user interactions in order to search for a satisfying balances between different criteria, in particular the precision of the transcription and the readability of the music score in outcome. It is integrated in the graphical environment for computer assisted music composition OpenMusic, and and will be released publicly as a library of this system on the the Ircam's Forum.

We have developed a uniform approach for transcription, based on hierarchical representations of notation of duration as rhythm trees, and efficient algorithms for the lazy enumeration of solutions. It has been implemented via a dedicated interface making it possible the interactive exploration of the space of solutions, their visualization and their edition, with a particular focus on the processing of grace-notes and rests.



t=0

KBEST PARAMS:
Tempo: nil
Schema : ((((2 3) (2 3) 2) (5 (2 3) 2) ((7 11 13)))
Nb. solutions : 3
Precision: 0.0
Slur : nil

kbest computed

t=3570

KBEST PARAMS:
Tempo: nil
Schema : ((((2 3) (2 3) 2) (5 (2 3) 2) ((7 11
Nb. solutions : 3
Precision: 0.0
Slur : nil

kbest computed

Zoom 105, Font size 24, Staff G, Approx 1/2

Selection: 4000 - 5000 ms

6000, Zoom 166, Font size 24, Staff G, Approx 1/2

602745

979454

250003

Error = 0.09794526

Error = 0.02511415

Error = 0.112481006

Duration: 3673 ms

6000, Zoom 51, Font size 24, Staff F, Approx 1/2

Figure 7. Rhythm Quantization in Open Music

MYCENAE Project-Team (section vide)

MYRIADS Project-Team

6. New Software and Platforms

6.1. ConPaaS

Hosting complex applications in the cloud

Contact: Guillaume Pierre, `Guillaume.Pierre@irisa.fr`

URL: http://www.conpaas.eu/

Status: Version 1.5.1

License: BSD

Presentation: ConPaaS [55] is a runtime environment for hosting applications in the cloud. It aims at offering the full power of the cloud to application developers while shielding them from the associated complexity of the cloud. ConPaaS is designed to host both high-performance scientific applications and online Web applications. It automates the entire life-cycle of an application, including collaborative development, deployment, performance monitoring, and automatic scaling. This allows developers to focus their attention on application-specific concerns rather than on cloud-specific details.

New features developed in 2015 include: a “Generic” service which allows the easy deployment and execution of arbitrary applications in ConPaaS; the “ConPaaS Nutshell edition” which allows users to deploy a fully-functional ConPaaS installation within a single VirtualBox VM; and the “ConPaaS Raspberry Pi edition” which allows users to deploy ConPaaS on a set of Raspberry Pi devices, paving the way toward the development of a fully-featured mobile edge cloud.

Active contributors (from the Myriads team): Ancuta Iordache, Genc Tato, Teodor Crivat, Guillaume Pierre.

Impact: ConPaaS is recognized as one of the major open-source PaaS environments. It is being developed by teams in Rennes, Amsterdam, Berlin and Ljubljana. Technology transfer of ConPaaS technology is ongoing in the context of the MC-DATA EIT Digital project.

6.2. GinFlow

Contact: Cédric Tedeschi, `Cedric.Tedeschi@irisa.fr`

Status: Version 1.0 released in open source, and registered at APP.

License: LGPL-3

Presentation: GinFlow is a decentralized workflow engine. It relies on a set of processes deployed over a cluster. Every task of the workflow is basically encapsulated into a GinFlow worker, workers being able to coordinate with others through read and write operations of a shared space containing the status of the workflow. GinFlow provides the ability to change the workflow logic on-the-fly upon the detection of a non-desired behavior within the execution of some of the tasks of the workflow.

Users typically submit a workflow through its JSON representation (both the by-default workflow and its alternate version if adaptation is needed). It can also use the API to describe its workflow in a more *programmatic* fashion.

Active contributors (from Myriads project-team): Matthieu Simonin, Cédric Tedeschi, Javier Rojas Balderrama.

Impact: GinFlow is a tool meant to provide support for workflow-based applications needing adaptation at run time. It is also targeted at offering a platform for future development and researches around the decentralized execution of workflows. It has been used in the framework of the DALHIS [0] associate team, as a workflow template executor, integrated with the TIGRES workflow manager developed at the Lawrence Berkeley National Lab. It has been supported by the GinFlow ADT funded by Inria since 2014 (see Section 9.2.1).

---

[0] http://project.inria.fr/dalhis

6.3. Merkat

Contact: Nikolaos Parlavantzas, `Nikolaos.Parlavantzas@irisa.fr`

URL: http://www.irisa.fr/myriads/software/Merkat/

Status: Version 1.0

Presentation: Merkat is a market-based private PaaS (Platform-as-a-Service) system, supporting dynamic, fine-grained resource allocation and automatic application management [47], [46] [3]. Merkat implements a proportional-share auction that ensures maximum resource utilization while providing incentives to applications to regulate their resource usage. Merkat includes generic mechanisms for application deployment and automatic scaling. These mechanisms can be adapted to support diverse performance goals and application types, such as master-worker, MPI, or MapReduce applications. Merkat is implemented in Python and uses OpenNebula for virtual machine management. Experimental results on the Grid'5000 testbed show that using Merkat increases resource utilization and improves application performance. The development was initiated in the framework of Stefania Costache PhD's thesis.

Active contributors (from the Myriads team): Christine Morin, Nikolaos Parlavantzas.

Other contributors: Stefania Costache.

Impact: Merkat has been integrated in EDF R&D portal providing access to internal computing resources and is currently used on a testbed at EDF R&D.

6.4. Meryn

Contact: Nikolaos Parlavantzas, `Nikolaos.Parlavantzas@irisa.fr`

URL: http://www.irisa.fr/myriads/software/Meryn/

Status: Version 1.0

Presentation: Meryn is an open, SLA-driven PaaS architecture that supports cloud bursting and allows hosting an extensible set of application types. Meryn relies on a decentralized optimization policy that aims at maximizing the overall provider profit, taking into account the penalties incurred when quality guarantees are unsatisfied [49]. The current Meryn prototype was implemented using shell scripts, builds upon the Snooze VM manager software, and supports batch and MapReduce applications using respectively the Oracle Grid Engine OGE 6.2u7 and Hadoop 0.20.2 frameworks.

Active contributors (from the Myriads team): Christine Morin, Nikolaos Parlavantzas.

Other contributors: Djawida Dib.

Impact: Meryn is not yet distributed as an open source software.

6.5. Snooze

Contact: Christine Morin, `Christine.Morin@inria.fr`

URL: http://snooze.inria.fr

Status: Version 2.1.5

License: GPLv2

Presentation: Snooze [51], [50], [52] [4] is a novel Infrastructure-as-a-Service (IaaS) cloud-management system, which is designed to scale across many thousands of servers and virtual machines (VMs) while being easy to configure, highly available, and energy efficient. For scalability, Snooze performs distributed VM management based on a hierarchical architecture. To support ease of configuration and high availability Snooze implements self-configuring and self-healing features. Finally, for energy efficiency, Snooze integrates a holistic energy management approach via VM resource (i.e. CPU, memory, network) utilization monitoring, underload/overload detection and mitigation, VM consolidation (by implementing a modified version of the Sercon algorithm [54]), and power management to transition idle servers into a power saving mode. Snooze is a highly modular piece of software. It has been extensively evaluated on the Grid'5000 testbed using realistic applications.

Snooze is fully implemented from scratch in Java and currently comprises approximately 15.000 lines of maintainable abstractions-based code. In order to provide a uniform interface to the underlying hypervisors and support transparent VM monitoring and management, Snooze integrates the *libvirt* virtualization library. Cassandra (since 2.0.0) can be used as base backend, providing reliability and scalability to the database management system. At a higher level Snooze provides its own REST API as well as an EC2 compatible API (since 2.1.0). It can thus be controlled from the command line (using the legacy client or an EC2 compatible tool), or from different language libraries (libcloud, jcloud ...). Snooze also provides a web interface to control the system. In collaboration with the Northeastern University of Bostonwe built the *Checkpoint as a Service* system on top of Snooze. The service allows users to execute their computations in a cloud environment in a reliable way. Periodic checkpoints are saved making it possible to restore the computation from a previous state in the event of failures. This work is described in [16].

Active contributors (from Myriads team): Yvon Jégou, David Margery, Christine Morin, Matthieu Simonin.

Other contributors: Jiajun Cao, Gene Cooperman, Eugen Feller.

Impact: Snooze has been used by students at LIFL, IRIT in France and LBNL in the US in the framework of internships. It has also been deployed and experimented at EDF R&D. Snooze entry won the 2nd prize of the scalability challenge at CCGrid 2013. Finally, we know that it was used by external users from academia and industry as we received feed-back from them. Snooze development was supported by the Snooze ADT funded by Inria from October 2012 to September 2014.

6.6. SimGrid

Scientific Instrument for the study of Large-Scale Distributed Systems.

Contact: Martin Quinson, `Martin.Quinson@ens-rennes.fr`

URL: http://simgrid.gforge.inria.fr/

Status: Version 3.12

License: LGPL 2.1

Presentation: SimGrid is a toolkit providing core features for the simulation of distributed applications in heterogeneous distributed environments.

The simulation engine uses algorithmic and implementation techniques toward the fast simulation of large systems on a single machine. The models are theoretically grounded and experimentally validated. The results are reproducible, enabling better scientific practices.

Its models of networks, cpus and disks are adapted to (Data)Grids, P2P, Clouds, Clusters and HPC, allowing multi-domain studies. It can be used either to simulate algorithms and prototypes of applications, or to emulate real MPI applications through the virtualization of their communication, or to formally assess algorithms and applications that can run in the framework.

The formal verification module explores all possible message interleavings in the application, searching for states violating the provided properties. We recently added the ability to assess liveness properties over arbitrary and legacy codes, thanks to a system-level introspection tool that provides a finely detailed view of the running application to the model checker. This can for example be leveraged to verify both safety or liveness properties, on arbitrary MPI code written in C/C++/Fortran.

Active contributors from Myriads project-team: Martin Quinson and Anne-Cécile Orgerie.

Other active contributors: Arnaud Legrand (Mescal project-team, CNRS & Inria Rhone-Alpes), Frédéric Suter (Avalon project-team, CNRS & Inria Rhone-Alpes).

Impact: SimGrid has an active user community of more than one hundred members, mainly composed of researchers and students. In the last decade only, it grounded the experiments of 6 PhDs works, 25 journal papers, and over 100 conference papers. The community gathers every year during the SimGrid User's Days workshop.

SimGrid is also used to run the regression and performance tests and tuning of two large applications: BigDFT (a massively parallel code computing the electronic structure of chemical elements developed by the CEA) and StarPU (a Unified Runtime System for Heterogeneous Multicore Architectures developed by Inria Bordeaux). Both of these programs enjoy large user communities themselves.

NACHOS Project-Team

5. New Software and Platforms

5.1. MAXW-DGTD

- Participants: Alexandra Christophe-Argenvillier, Loula Fezoui, Stéphane Lanteri, Raphaël Léger, Jonathan Viquerat
- Contact: Stéphane Lanteri
- Keywords: Computational electromagnetics, Maxwell equations, discontinuous Galerkin, tetrahedral mesh.
- OS/Middelware: Linux
- Required library or software: MPI (Message Passing Interface), CUDA
- Programming language: Fortran 77/95

MAXW-DGTD is a software suite for the simulation of time domain electromagnetic wave propagation. It implements a solution method for the Maxwell equations in the time-domain. MAXW-DGTD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes [13]. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. This discontinuous Galerkin method combines a centered scheme for the evaluation of numerical fluxes at a face shared by two neighboring elements, with an explicit Leap-Frog time scheme. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with message passing programming using the MPI standard. Besides, a peripheral version of the software has been recently developed which is able to exploit the processing capabilities of a hybrid parallel computing system comprising muticore CPU and GPU nodes.

5.2. MAXW-DGFD

- Participants: Thomas Frachon, Stéphane Lanteri, Ludovic Moya
- Contact: Stéphane Lanteri
- Keywords: Computational electromagnetics, Maxwell equations, discontinuous Galerkin, tetrahedral mesh.
- OS/Middelware: Linux
- Required library or software: MPI (Message Passing Interface)
- Programming language: Fortran 77/95

MAXW-DGFD is a software suite for the simulation of time-harmonic electromagnetic wave propagation. It implements a solution method for the Maxwell equations in the frequency domain. MAXW-DGFD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. The resolution of the sparse, complex coefficients, linear systems resulting from the discontinuous Galerkin formulation is performed by a hybrid iterative/direct solver whose design is based on domain decomposition principles. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with a message passing programming using the MPI standard. Some recent achievements have been the implementation of non-uniform order DG method in the 2d case and of a new hybridizable discontinuous Galerkin (HDG) formulation also in the 2d and 3d cases.

5.3. SISMO-DGTD

- Participants: Nathalie Glinsky, Stéphane Lanteri
- Contact: Stéphane Lanteri

SISMO-DGTD is a software for the simulation of time-domain seismic wave propagation. It implements a solution method for the velocity-stress equations in the time-domain. SISMO-DGTD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes [2]. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. This discontinuous Galerkin method combines a centered scheme for the evaluation of numerical fluxes at a face shared by two neighboring elements, with an explicit Leap-Frog time scheme. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with a message passing programming using the MPI standard.

NANO-D Project-Team

6. New Software and Platforms

6.1. SAMSON

SAMSON (Software for Adaptive Modeling and Simulation Of Nanosystems) is a software platform for computational nanoscience. SAMSON has a modular architecture that makes it suitable for different domains of nanoscience, including material science, life science, physics, electronics, chemistry, and education.

SAMSON Elements are modules for SAMSON, developed with the SAMSON Software Development Kit (SDK). SAMSON Elements help users perform tasks in SAMSON, including building new models, performing calculations, running interactive or offline simulations, and visualizing and interpreting results.

SAMSON Elements may contain different class types, including for example:

- Apps - generic classes with a graphical user interface that extend the functions of SAMSON
- Editors - classes that receive user interaction events to provide editing functions (e.g., model generation, structure deformation, etc.)
- Models - classes that describe properties of nanosystems (see below)
- Parsers - classes that may parse files to add content to SAMSON's data graph (see below)

SAMSON Elements expose their functions to SAMSON and other Elements through an introspection mechanism, and may thus be integrated and pipelined.

SAMSON represents nanosystems using five categories of models:

- Structural models - describe geometry and topology
- Visual models - provide graphical representations
- Dynamical models - describe dynamical degrees of freedom
- Interaction models - describe energies and forces
- Property models - describe traits that do not enter in the first four model categories

Simulators (potentially interactive ones) are used to build physically-based models, and predict properties. All models and simulators are integrated into a hierarchical, layered structure that form the SAMSON data graph. SAMSON Elements interact with each other and with the data graph to perform modeling and simulation tasks. A signals and slots mechanism makes it possible for data graph nodes to send events when they are updated, which makes it possible to develop e.g., adaptive simulation algorithms.

SAMSON is developed in C++ and implements many features to ease development of SAMSON Elements, including:

- Managed memory
- Signals and slots
- Serialization
- Multilevel undo-redo
- Introspection
- Referencing
- Unit system
- SAMSON Element source code generators

SAMSON, SAMSON Elements and the SAMSON Software Development Kit are distributed via the SAMSON Connect website (http://www.samson-connect.net). The site acts as a repository for the SAMSON Elements being uploaded by developers, and users of SAMSON choose and add Elements from SAMSON Connect.

NECS Project-Team

6. New Software and Platforms

6.1. GTL – Grenoble Traffic Lab

Participants: C. Canudas de Wit [contact person], I. Bellicot, P. Bellemain, L. Leon Ojeda, D. Pisarski, A. Kibangou, H. Fourati, F. Morbidi, F. Garin, A. Ladino Lopez, P. Grandinetti, E. Lovisari, R. Singhal, A. Andreev, R. Piotaix.

The Grenoble Traffic Lab (GTL) initiative, led by the NECS team, is a real-time traffic data Center (platform) that collects traffic road infrastructure information in real-time with minimum latency and fast sampling periods. The main elements of the GTL are: a real-time data-base, a show room, and a calibrated micro-simulator of the Grenoble South Ring. Sensed information comes from a dense wireless sensor network deployed on Grenoble South Ring, providing macroscopic traffic signals such as flows, velocities, densities, and magnetic signatures. This sensor network was set in place in collaboration with Inria spin-off Karrus-ITS, local traffic authorities (DIR-CE, CG38, La Metro), and specialized traffic research centers. In addition to real data, the project also uses simulated data, in order to validate models and to test traffic control policies (ramp metering for the south-ring and optimization of urban signals); the micro-simulator is developed using AIMSUN.

More details at http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php

6.2. Senslogs – Sensors recorder for Android application

Participants: T. Michel [contact person], H. Fourati, P. Geneves, N. Layaida.

This Android application records direct and computed measurements from internal sensors (Accelerometer, gyroscope, magnetometer, calibrated gyroscope, calibrated magnetic field, game rotation vector, geomagnetic, rotation vector, gravity, linear acceleration, significant motion, step counter, step detector, ambient temperature, light, pressure, relative humidity, heart rate, proximity, GPS location, cell and wifi location, passive location, NMEA data, wifi signals, Bluetooth signals (not yet), NFC (not yet), and others available...). Data are stored in files using space-separated values. This application has been designed for post-processing projects. It will be used in pedestrian navigation and augmented reality applications. This application is available online: https://play.google.com/store/apps/details?id=fr.inria.tyrex.senslogs&hl=fr_BE

NEUROMATHCOMP Project-Team

5. New Software and Platforms

5.1. ENAS

Event Neural Assembly Simulation
KEYWORDS: Neurosciences - Health - Physiology
FUNCTIONAL DESCRIPTION Enas is a software for the analysis of spike trains either coming from neural simulators or from biological experiments. Spike trains statistical analysis is based on the estimation of a Gibbs distribution with a spatio-temporal potential optimaly characterizing the statistics of empirical spike trains by minimisation of the Kullback-Leibler divergence between the empirical measure and the Gibbs measure. From this, classical statistical indicators such as firing rate, correlations, higher order moments statistical entropy, effective connectivity graph, confidence plots and so on are obtained. Also, the form of the Gibbs potential provides essential informations on the underlying neural network and its structure. This method does not only allows us to estimate the spikes statistics but also to compare different models, thus answering such questions about the neural code as, e.g., are correlations (or time synchrony or a given set of spike patterns, etc.) significant with respect to rate coding? The software includes classical Maximum Entropy Models such as Ising model, but also more general forms of potentials with spatio-temporal interactions. It also has a functionality attempting to guess the shape of the potential from data and a procedure fitting an Integrate and Fire Neural Network reproducing the empirical rasters statistics. Finally, it allows to generate artificial rasters having a given distribution (e.g. corresponding to biological spike trains).

- Participants: Bruno Cessac, Sélim Kraria, Hassan Nasser, Thierry Viéville, Rodrigo Cofre Torres, Audric Drogoul, Geoffrey Portelli, Pierre Kornprobst, Theodora Karvouniari and Daniela Pamplona
- Contact: Bruno Cessac
- URL: https://enas.inria.fr

5.2. Virtual Retina

KEYWORDS: Neurosciences - Simulation - Biology
FUNCTIONAL DESCRIPTION Virtual Retina [14] allows large-scale simulations of biologically-plausible retinas, with customizable parameters. Virtual Retina has been shown to reproduce a wide range of experimental data from salamander, cat and primate retinas [14], and has been used in several theoretical studies [79], [82], [83], [56]. It has recently been shown to predict spikes in a mouse retina more accurately than linear-nonlinear (LN) models [93]. The underlying model includes a non-separable spatio-temporal linear model of filtering in the Outer Plexiform Layer, a shunting feedback at the level of bipolar cells, and a spike generation process using noisy leaky integrate-and-fire neurons to model retinal ganglion cells (RGCs). All parameters for the different stages of the model are customizable so that the visual field can be paved with different RGC types.

- Participants: Bruno Cessac, Maria-Jose Escobar, Pierre Kornprobst, Adrien Wohrer and Thierry Viéville
- Contact: Pierre Kornprobst
- URL: http://www-sop.inria.fr/neuromathcomp/public/software/virtualretina/

NEUROSYS Project-Team

6. New Software and Platforms

6.1. AnaesthesiaSimulator

KEYWORDS: General anaesthesia - Spiking neural networks - Health
FUNCTIONAL DESCRIPTION

AnaesthesiaSimulator simulates the activity of networks of spiking neurons subject to specific receptor dynamics. The tool is a platform to test effects of anaesthetics on neural activity and is still in its first stage of development. The neural activity can be visualized in a 2D and 3D-plot evolving in time. It is written in Python, open-source and involves heavily the simulation package BRIAN [0].

- Participants: Axel Hutt and Laure Buhry
- Partner: University of Auckland
- Contact: Axel Hutt
- URL: https://gforge.inria.fr/projects/anasim/

6.2. NeuralFieldSimulator

NeuralFieldSimulator
KEYWORDS: Neurosciences - Simulation - Health
FUNCTIONAL DESCRIPTION

The NeuralFieldSimulator computes numerically activity in two-dimensional neural fields by solving integral-differential equations involving transmission delays and visualizes the spatio-temporal activity. The tool includes a GUI that allows the user to choose field parameters. It is written in Python, open-source and is aimed to be promoted to become a major graphical visualization tool in the domain of neural field theory. We aim to establish this simulation software as the first open-source standard simulator for the neural field research community.

- Participants: Axel Hutt and Eric Nichols
- Partner: Kevin Green, University of Ontario, Canada
- Contact: Axel Hutt
- URL: https://gforge.inria.fr/projects/nfsimulator/

6.3. OpenVIBE

KEYWORDS: Neurosciences - Interaction - Virtual reality - Health - Real time - Neurofeedback - Brain-Computer Interface - EEG - 3D interaction
FUNCTIONAL DESCRIPTION

OpenViBE is a software platform for real-time neurosciences (that is, for real-time processing of brain signals). It can be used to acquire, filter, process, classify and visualize brain signals in real time from various signal sources. OpenViBE is free and open source software. It works on Windows and Linux operating systems.

---

[0] http://briansimulator.org/

This year, Neurosys was in charge of the linux release. the main development efforts concern machine learning: Multi-layer perceptrons have been added as classification methods and evaluation plugins allow to get standalone visualization for Kappa coefficient, Receiving Operative Curve (ROC) curve and general statistics.

- Participants: Yann Renard, Anatole Lécuyer, Fabien Lotte, Bruno Renier, Vincent Delannoy, Laurent Bonnet, Baptiste Payan, Jozef Legény, Jussi Tapio Lindgren, Alison Cellard, Loïc Mahé, Guillaume Serrière, Marsel Mano, Maureen Clerc Gallagher, Théodore Papadopoulo, Laurent Bougrain, Jérémy Frey and Nathanaël Foy
- Partners: INSERM - CEA-List - GIPSA-Lab
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

6.4. BRIAN Contributions

KEYWORDS: Spiking neurons models - Neurosciences - BRIAN
FUNCTIONAL DESCRIPTION

6.4.1. Spiking Neuron Templates

BRIAN-compatible libraries has been developed by the team for various ionic currents to be assembled together to create template neurons. The purpose of these is to speed up simulation set-up time and reduce code duplication across simulation scripts. Template neurons are defined by the ionic currents that flow through their membrane. Implemented templates include:

- Hodgkin-Huxley pyramidal neuron (leak, sodium and potassium)
- Hodgkin-Huxley pyramidal neuron with calcium-activated non-specific (CAN) receptors (leak, sodium, potassium, m-current, calcium, CAN)
- Hodgkin-Huxley fast-spiking inhibitory hippocampal (leak, sodium, potassium, m-current)

Implemented ionic current libraries include:

- Traub and Miles Hodgkin-Huxley (I_{Leak}, I_K, I_{Na}) implementation;
- M-Current (I_M) implementation;
- Calcium current (I_L) implementation;
- Calcium pump mechanisms ($\frac{\mathrm{d}Ca}{\mathrm{d}t}$) implementation;
- Calcium-activated non-selective current (I_{CAN}) implementation;
- Wang and Buszáki inhibitory Hodgkin-Huxley (I_{Leak}, I_K, I_{Na}) implementation;

The current library is easily extensible by third-party users due to its hierarchical design. The template neurons and their currents are defined as YAML [0] files, which are conveniently parsed by a Python library which acts as an interface to the BRIAN simulator API's.

6.4.2. BRIAN Simulation Parameters

A python library which acts as a wrapper for BRIAN simulations, allowing the user to define simulation parameters in external YAML files, which are then parsed and forwarded to the BRIAN simulator. In addition, simulation parameters can be overridden via the command-line when invoking the python script containing the simulation.

- Participants: Francesco Giovannini
- Contact: Francesco Giovannini
- URL: http://www.briansimulator.org

---

[0] http://www.yaml.org/

NON-A Project-Team

5. New Software and Platforms

5.1. Blimp

FUNCTIONAL DESCRIPTION

Scientific research and development on the control of autonomous airships have shown a significant growth in recent years. New applications appear in the areas such as freight carrier, advertising, monitoring, surveillance, transportation, military and scientific research. The control of autonomous airships is a very important problem for the aerial robots research.

The development of Blimp by Non-A is used for experimentation and demonstration of controlling algorithms. The blimp is required to provide some environment information and status of itself, such as surveillance video of surrounding environment, gesture of blimp, altitude of blimp. With these basic information, one could localize blimp with certain algorithm (visual SLAM for example) or implement one controller in order to improve the stability and maneuverability of blimp.

- Contact: Jean-Pierre Richard

5.2. SLIM

FUNCTIONAL DESCRIPTION

Multi-robots cooperation can be found as an application in many domains of science and technology: manufacturing, medical robotics, personal assistance, military/security and spatial robots. The market of robots is quickly developing and its capacity is continuously growing. Concerning cooperation of mobile multi-robots, 3 key issues have to be studied: Localization, path planning and robust control, for which Non-A team has worked and proposed new algorithms. Due to the ADT SLIM, we implement our algorithms (localization, path planning and robust control) and integrate them into ROS (Robotic Operating System) as a package, named SLIM.

- Contact: Jean-Pierre Richard

NUMED Project-Team

4. New Software and Platforms

4.1. Bingham flows

FUNCTIONAL DESCRIPTION

A 1D and 2D code with a new method for the computation of viscoplatic flows with free-surface. It essentially couples Optimization methods and Well-Balanced Finite-Volumes schemes for viscous shallow-water equations (induced by the viscoplastic nature of the fluid). Currently applied to avalanches of dense snow, it is a private code currently actively developed (in C++). One of the key feature is that its well-balanced property allows to obtained the stationary states which are linked to the stopping of the snow avalanche for this highly non-linear type of fluid.

- Contact: Paul Vigneaux

4.2. OptimChemo

FUNCTIONAL DESCRIPTION

OptimChemo is a userfriendly software designed to study numerically the effect of multiple chemotherapies on simple models of tumour growth and to optimize chemotherapy schedules.

- Participants: Emmanuel Grenier, Violaine Louvet, Paul Vigneaux and Ehouarn Maguet
- Contact: Emmanuel Grenier

4.3. SETIS

KEYWORDS: Health - DICOM - Medical imaging - Drug development

FUNCTIONAL DESCRIPTION

SETIS software is a GUI allowing to treat DICOM medical images to extract pathological data. These data can then be exported and used in a SAEM software (including Monolix (Inria and Lixoft)) for the parameters' estimation of models in the context of population approaches. As an example SETIS can be used to segment and compute the tumor size of a patients from MRI scans taken at different times. The software is sufficiently general to be used in various situations by clinicians (already done by colleagues in Lyon Hospital). SETIS is filed under APP number IDDN.FR.001.150013.000.S.A.2014.000.21000.

- Participants: Paul Vigneaux and Ehouarn Maguet
- Partner: ENS Lyon
- Contact: Paul Vigneaux

4.4. SIMPHYT

KEYWORDS: Bioinformatics - Cancer - Drug development

FUNCTIONAL DESCRIPTION

SimPHyt is an implementation in Python of the low grad glioma model. The aim is to predict the evolution of the glioma size of patients.

- Participant: Benjamin Ribba
- Contact: Benjamin Ribba

4.5. VAXSIMSTAB

KEYWORDS: Bioinformatics - Health - Drug development

FUNCTIONAL DESCRIPTION

VAXSIMSTAB is a modeler stability prediction of vaccine software, property of Sanofi Pasteur.

- Participants: Benjamin Ribba, Emmanuel Grenier and Vincent Calvez
- Contact: Emmanuel Grenier

OAK Project-Team

6. New Software and Platforms

6.1. Amada

FUNCTIONAL DESCRIPTION

AMADA is a platform for storing Web data (in particular, XML documents and RDF graphs) based on the Amazon Web Services (AWS) cloud infrastructure. AMADA operates in a Software as a Service (SaaS) approach, allowing users to upload, index, store, and query large volumes of Web data.

- Participants: Jesùs Camacho-Rodriguez, Manolescu Ioana, Dario Colazzo and François Goasdoué
- Contact: Ioana Manolescu
- URL: https://team.inria.fr/oak/projects/amada/

6.2. Clique Square

RDF data management platform based on Hadoop architecture
KEYWORDS: Map-Reduce - Hadoop - RDF - Big data
SCIENTIFIC DESCRIPTION

CliqueSquare is a system for storing and querying large RDF graphs relying on Hadoop's distributed file system (HDFS) and Hadoop's MapReduce open-source implementation. CliqueSquare is equipped with a unique optimization algorithm capable of generating highly parallelizable flat query plans relying on n-ary equality joins. In addition, it provides a novel partitioning and storage scheme that permits first-level joins to be evaluated locally using efficient map-only joins.
FUNCTIONAL DESCRIPTION

RDF (Ressource Description Framework) is the data format for the semantic web. CliqueSquare allows storing and querying very large volumes of RDF data in a massively parralel fashion in a Hadoop cluster. The system uses its own partitioning and storage model for the RDF triples in the cluster.

CliqueSquare evaluates queries expressed in a dialect of the SPARQL query language. It is particularly efficient when processing complex queries, because it is capable of translating them into MapReduce programs guaranteed to have the minimum number of successive jobs. Given the high overhead of a MapReduce job, this advantage is considerable.

- Participants: Ioana Manolescu, Benjamin Djahandideh, Stamatios Zampetakis, Zoi Kaoudi, François Goasdoué and Jorge Arnulfo Quiane Ruiz
- Partners: Université de Rennes 1 - Qatar Computing Research Institute
- Contact: Ioana Manolescu
- URL: https://team.inria.fr/oak/projects/cliquesquare/

6.3. FactMinder

KEYWORDS: Web - Fact-checking - Data Journalism - Open data
FUNCTIONAL DESCRIPTION

FactMinder is a browser extension targeted at online fact checkers and data journalists. It enables users to analyze web pages with entity extractors and create, in a separate panel, views to cross these annotations with background knowledge from trusted XML or RDF sources such as data sets from the Linked Open Data or governmental agencies.

FactMinder is the basis of the ANR project ContentCheck and was awarded a Google Computational Journalism Research Award in June 2015.

- Participants: Ioana Manolescu, Stamatios Zampetakis and François Goasdoué
- Partner: Université Paris-Sud
- Contact: Ioana Manolescu
- URL: https://team.inria.fr/oak/projects/xr-an-xml-rdf-hybrid-model-for-annotated-documents/

6.4. PAXQuery

FUNCTIONAL DESCRIPTION

The PAXQuery engine seamlessly parallelizes the execution of XQuery queries. By applying on-the-fly translation and optimization procedures, PAXQuery runs user queries over massive collections of XML documents in a distributed fashion. PAXQuery runs on top of Apache Flink, a distributed execution platform that relies on the PACT model.

- Participants: Jesùs Camacho-Rodriguez, Ioana Manolescu, Dario Colazzo and Juan Alvaro Munoz Naranjo
- Contact: Ioana Manolescu
- URL: https://team.inria.fr/oak/projects/paxquery/

6.5. RDFSummary

RDF Summary
FUNCTIONAL DESCRIPTION

RDF Summary is a standalone Java software capable of building summaries of RDF graphs. Summaries are compact graphs (typically several orders of magnitude smaller than the original graph), which can be used to get acquainted quickly with a given graph, they can also be used to perform static query analysis, infer certain things about the answer of a query on a graph, just by considering the query and the summary.

- Contact: Sejla Cebiric
- URL: https://team.inria.fr/oak/projects/rdfsummary/

6.6. WaRG

Warehousing RDF Graphs
KEYWORDS: Data mining - Semantic Web - Data management - Decision - Big data
SCIENTIFIC DESCRIPTION

WaRG is a warehouse-style analytics platform on RDF graphs. The tool stores data in kdb+ with a Java frontend based on the Prefuse Visualization toolkit. The novelty of WaRG is to redesign the full stack of Data Warehouse abstractions and tools for heterogeneous, semantics-rich RDF data, this enables a WaRG RDF DW to be an RDF graph itself, heterogeneous and semantics-rich in its turn. Thus, WaRG benefits both from powerful analytics and the rich interoperability and semantic features of Semantic Web databases.

FUNCTIONAL DESCRIPTION

WaRG (Warehousing RDF graph) is an analytical platform specially designed for the analysis of RDF data.

WaRG allows defining RDF analytical schemas, comprising classes and properties interesting for the analysis. The analytical schema can then be materialized, leading to an instance (RDF graph) refined for the needs of the analysis.

The analytical schema can also be automatically built from the input RDF instance. Finally, RDF analytical queries can be specified and lead to RDF analysis cubes.

- Participants: Roatis Alexandra, Ioana Manolescu, Sejla Cebiric and François Goasdoué
- Partners: Université de Rennes 1 - Université Paris-Sud
- Contact: Ioana Manolescu
- URL: https://team.inria.fr/oak/projects/warg/

ORPAILLEUR Project-Team

6. New Software and Platforms

6.1. Symbolic KDD Systems

6.1.1. The Coron Platform

- Contact: Amedeo Napoli
- URL: http://coron.loria.fr/site/index.php
- KEYWORDS: Data mining, Closed itemset, Frequent itemset, Generator, Association rule, Rare itemset

FUNCTIONAL DESCRIPTION.

The Coron platform [102], [96] is a KDD toolkit organized around three main components: (1) Coron-base, (2) AssRuleX, and (3) pre- and post-processing modules. The software was registered at the "Agence pour la Protection des Programmes" (APP) and is freely available (see http://coron.loria.fr).

The Coron-base component includes a complete collection of data mining algorithms for extracting itemsets such as frequent itemsets, closed itemsets, generators and rare itemsets. In this collection we can find APriori, Close, Pascal, Eclat, Charm, and, as well, original algorithms such as ZART, Snow, Touch, and Talky-G [103]. AssRuleX generates different sets of association rules (from itemsets), such as minimal non-redundant association rules, generic basis, and informative basis. In addition, the Coron system supports the whole life-cycle of a data mining task and proposes modules for cleaning the input dataset, and for reducing its size if necessary.

The Coron toolkit is developed in Java, is operational, and was already used in several research projects.

6.1.2. Orion: Skycube Computation Software

- Contact: Chedy Raissi
- URL: https://github.com/leander256/Orion
- KEYWORDS: Skyline, skycube.

FUNCTIONAL DESCRIPTION.

This program implements the algorithms described in a research paper published at VLDB 2010 [100]. The software provides a list of four algorithms discussed in the paper in order to compute skycubes. This is the most efficient –in term of space usage and runtime– implementation for skycube computation.

6.1.3. OrphaMine – Data mining platform for orphan diseases

- Partners: INSERM - MoDYCo CNRS - Délégation régionale Ile-de-France, secteur ouest et nord - Greyc Université de Caen - Basse-Normandie
- Contact: Chedy Raissi
- URL: http://webloria.loria.fr/~mosmuk/orphamine/
- KEYWORDS: Bioinformatics, data mining, biology, health, data visualization, drug development.

FUNCTIONAL DESCRIPTION.

The OrphaMine platform, developed as part of the ANR Hybrid project, enables visualization, data integration and in-depth analytics. The data at the heart of the platform is about orphan diseases and is extracted from the OrphaData ontology (http://www.orpha.net).

We aim to build a true collaborative portal that will serve the different actors of the Hybrid project: (i) A general visualization of OrphaData data for physicians working, maintaining and developing this knowledge database about orphan diseases. (ii) The integration of analytics (data mining) algorithms developed by the different academic actors. (iii) The use of these algorithms to improve our general knowledge of rare diseases.

6.1.4. PoQeMON Analytics: Platform for Quality Evaluation of Mobile Netwoks

- Partners: Altran, DataPublica, GenyMobile, HEC, Inria Nancy-Grand Est, IP-Label, Next Interactive Media, Orange, Université Paris-Est Créteil
- Contact: Chedy Raissi
- URL: https://members.loria.fr/poqemon/
- KEYWORDS: Data mining, data visualization.

FUNCTIONAL DESCRIPTION.

PoQEMoN is a quality evaluation platform for mobile phone networks. The quality measures include the coverage, availability and network performances. Multiple methods are implemented in this platform, either in visualization or in data anonymization to make on-line analytics as simple as possible.

6.2. Stochastic systems for knowledge discovery and simulation

6.2.1. The CarottAge System

- Contact: Jean-François Mari
- URL: http://www.loria.fr/~jfmari/App/index_in_english.html
- KEYWORDS: Stochastic process, Hidden Markov Models.

FUNCTIONAL DESCRIPTION.

The system CarottAge is based on Hidden Markov Models of second order and provides a non supervised temporal clustering algorithm for data mining and a synthetic representation of temporal and spatial data [97]. CarottAge is currently used by INRA researchers interested in mining the changes in territories related to the loss of biodiversity (projects ANR BiodivAgrim and ACI Ecoger) and/or water contamination. CarottAge is also used for mining hydromorphological data proved to give very interesting results for that purpose.

CarottAge is freely available under GPL license (see http://www.loria.fr/~jfmari/App/). A special effort is currently aimed at designing interactive visualization tools to provide the expert a user-friendly interface.

6.2.2. The ARPEnTAge System

- Contact: Jean-François Mari
- URL: http://www.loria.fr/~jfmari/App/index_in_english.html
- KEYWORDS: Stochastic process, Hidden Markov Models.

FUNCTIONAL DESCRIPTION.

ARPEnTAge, for “*Analyse de Régularités dans les Paysages : Environnement, Territoires, Agronomie*” (http://www.loria.fr/~jfmari/App/) is a software based on stochastic models (HMM2 and Markov Field) for analyzing spatio-temporal data-bases [98]. ARPEnTAge is built on top of the CarottAge system to fully take into account the spatial dimension of input sequences. It takes as input an array of discrete data in which the columns contain the annual land-uses and the rows are regularly spaced locations of the studied landscape. It performs a Time-Space clustering of a landscape based on its time dynamic Land Uses (LUS). Displaying tools and the generation of Time-dominant shape files have also been defined.

ARPEnTAge is freely available (GPL license) and is currently used by INRA researchers interested in mining the changes in territories related to the loss of biodiversity (projects ANR BiodivAgrim and ACI Ecoger) and/or water contamination. In these practical applications, CarottAge and ARPEnTAge aim at building a partition –called the hidden partition– in which the inherent noise of the data is withdrawn as much as possible. The estimation of the model parameters is performed by training algorithms based on the Expectation Maximization and Mean Field theories. The ARPEnTAge system takes into account: (i) the various shapes of the territories that are not represented by square matrices of pixels, (ii) the use of pixels of different size with composite attributes representing the agricultural pieces and their attributes, (iii) the irregular neighborhood relation between those pixels, (iv) the use of shape files to facilitate the interaction with GIS (geographical information system).

ARPEnTAge and CarottAge were used for mining decision rules in a territory showing environmental issues. They provide a way of visualizing the impact of farmers decision rules in the landscape and revealing new extra hidden decision rules.

6.2.3. The GenExp System

- Contact: Florence Le Ber
- URL: http://orpailleur.loria.fr/index.php/GenExp-LandSiTes:_KDD_and_simulation
- KEYWORDS: Simulation, Hidden Markov Models.

FUNCTIONAL DESCRIPTION.

In the framework of the project “Impact des OGM” initiated by the French Ministry of Research, we have developed a software called GenExp-LandSiTes for simulating bidimensional random landscapes, and then studying the dissemination of vegetable transgenes. The GenExp-LandSiTes system is linked to the CarottAge system, and is based on computational geometry and spatial statistics. The simulated landscapes are given as input for programs such as “Mapod-Maïs” or “GeneSys-Colza” for studying the transgene diffusion. Other landscape models based on tessellation methods are under studies. The last version of GenExp allows an interaction with R and deals with several geographical data formats.

6.3. KDD systems in Biology

6.3.1. IntelliGO Online

- Contact: Malika Smaïl-Tabbone
- URL: http://plateforme-mbi.loria.fr/intelligo/
- KEYWORDS: Bioinformatics, genomics.

FUNCTIONAL DESCRIPTION.

The IntelliGO measure computes semantic similarity between terms from a structured vocabulary (Gene Ontology: GO) and uses these values for computing functional similarity between genes annotated by sets of GO terms [82]. The IntelliGO measure is available on line (http://plateforme-mbi.loria.fr/intelligo/) to be used for evaluation purposes. It is possible to compute the functional similarity between two genes, the intra-set similarity value in a given set of genes, and the inter-set similarity value for two given sets of genes.

6.3.2. WAFOBI: KNIME Nodes for Relational Mining of Biological Data

- Contact: Malika Smaïl-Tabbone
- KEYWORDS: Bioinformatics, genomics.

FUNCTIONAL DESCRIPTION.

KNIME (for “Konstanz Information Miner”) is an open-source visual programming environment for data integration, processing, and analysis. The KNIME platform aims at facilitating the data mining experiment settings as many tests are required for tuning the mining algorithms. Various KNIME nodes were developed for supporting relational data mining using the ALEPH program (http://www.comlab.ox.ac.uk/oucl/research/areas/machlearn/Aleph/aleph.pl). These nodes include a data preparation node for defining a set of first-order predicates from a set of relation schemes and then a set of facts from the corresponding data tables (learning set). A specific node allows to configure and run the ALEPH program to build a set of rules. Subsequent nodes allow to test the first-order rules on a test set and to perform configurable cross validations.

6.3.3. MODIM: MOdel-driven Data Integration for Mining

- Contact: Malika Smaïl-Tabbone
- URL: https://gforge.inria.fr/projects/modim/
- KEYWORDS: Data integration, workflow, data modeling.

FUNCTIONAL DESCRIPTION.

The MODIM software (MOdel-driven Data Integration for Mining) is a user-friendly data integration tool which can be summarized along three functions: (i) building a data model taking into account mining requirements and existing resources; (ii) specifying a workflow for collecting data, leading to the specification of wrappers for populating a target database; (iii) defining views on the data model for identified mining scenarios.

Although MODIM is domain independent, it was used so far for biological data integration in various internal research studies and for organizing data about non ribosomal peptide syntheses.

6.4. Knowledge Systems in Health and Cooking

6.4.1. The Kasimir System for Decision Knowledge Management

- Contact: Jean Lieber
- KEYWORDS: Classification-based reasoning, case-based reasoning, decision knowledge management, knowledge edition, knowledge base maintenance, semantic portal

FUNCTIONAL DESCRIPTION.

The objective of the Kasimir system is decision support and knowledge management for the treatment of cancer. A number of modules have been developed within the Kasimir system for editing treatment protocols, visualization, and maintenance. Kasimir is developed within a semantic portal, based on OWL. KatexOWL (Kasimir Toolkit for Exploiting OWL Ontologies, http://katexowl.loria.fr) was developed in a generic way and is applied to Kasimir. In particular, the user interface EdHibou of KatexOWL is used for querying the protocols represented within the Kasimir system. In [86], this research is presented, together with an extension of Kasimir for multi-viewpoint case-based reasoning.

CabamakA (case base mining for adaptation knowledge acquisition) is a module of the Kasimir system. This system performs case base mining for adaptation knowledge acquisition and provides information units to be used for building adaptation rules. Actually, the mining process in CabamakA is based on a frequent close itemset extraction module from the Coron platform (see §6.1.1).

The Oncologik system is a collaborative editing tool aiming at facilitating the management of medical guidelines. Based on a semantic wiki, it allows the acquisition of formalized decision knowledge also includes a graphical decision tree editor called KcatoS. A version of Oncologik was released in 2012 (http://www.oncologik.fr/).

6.4.2. Taaable: a System for Retrieving and Creating New Cooking Recipes by Adaptation

- Contact: Emmanuel Nauer
- URL: http://intoweb.loria.fr/taaable3ccc/
- KEYWORDS: Knowledge acquisition, ontology engineering, semantic annotation, case-based reasoning, hierarchical classification, text mining.

FUNCTIONAL DESCRIPTION.

The objectives of the Taaable system are to retrieve textual cooking recipes and to adapt these retrieved recipes whenever needed [84]. Suppose that someone is looking for a “leek pie” but has only an “onion pie” recipe: how can the onion pie recipe be adapted?

The Taaable system combines principles, methods, and technologies such as case-based reasoning (CBR), ontology engineering, text mining, text annotation, knowledge representation, and hierarchical classification. Ontologies for representing knowledge about the cooking domain, and a terminological base for binding texts and ontology concepts, were built from textual web resources. These resources are used by an annotation process for building a formal representation of textual recipes. A CBR engine considers each recipe as a case, and uses domain knowledge for reasoning, especially for adapting an existing recipe w.r.t. constraints provided by the user, holding on ingredients and dish types.

The Taaable system is available on line since 2008 at http://intoweb.loria.fr/taaable3ccc/, and is constantly evolving. Since 2014, Taaable is based on Tuuurbine, a generic ontology guided CBR engine over RDFS, and Revisor, an adaptation engine implementing various revision operators. This year, new features have been added to the Taaable system in order to address the new challenges of the 8th Computer Cooking Contest at ICCBR 2015. Firstly, FCA was used to improve the ingredient substitution, by taking into account ingredient combinations in a large set of recipes. Secondly, an approach based on mixed linear optimization has been used to adapt ingredient quantities, in order to be more realistic with a real cooking setting.

6.4.3. Tuuurbine: a Generic Ontology Guided Case-Based Inference Engine

- Contact: Emmanuel Nauer
- URL: http://tuuurbine.loria.fr/
- KEYWORDS: case-based reasoning, inference engine, knowledge representation, ontology engineering, semantic web

FUNCTIONAL DESCRIPTION.

The experience acquired since 5 years with the Taaable system conducted to the creation of a generic cased-based reasoning system, whose reasoning procedure is based on a domain ontology [91]. This new system, called Tuuurbine (http://tuuurbine.loria.fr/), takes into account the retrieval step, the case base organization, and also an adaptation procedure which is not addressed by other generic case-based reasoning tools. Moreover, Tuuurbine is built over semantic web standards that will ensure facilities for being plugged over data available on the web. The domain knowledge is represented in an RDF store, which can be interfaced with a semantic wiki, for collaborative edition and management of the knowledge involved in the reasoning system (cases, ontology, adaptation rules). The development of Tuuurbine was supported by an Inria ADT funding until October 2013.

6.4.4. BeGoood: a Generic System for Managing Non-Regression Tests on Knowledge Bases

- Contact: Emmanuel Nauer
- URL: https://github.com/kolflow/begoood
- KEYWORDS: Tests, non-regression, knowledge evolution.

FUNCTIONAL DESCRIPTION.

BeGoood is a system allowing to define test plans, independent of any application domain, and usable for testing any system answering queries by providing results in the form of sets of strings. BeGoood provides all the features usually found in test systems, such as tests, associated queries, assertions, and expected result sets, test plans (sets of tests) and test reports. The system is able to evaluate the impact of a system modification by running again test plans and by evaluating the assertions which define whether a test fails or succeeds. BeGoood is used by the Taaable system for managing the evolution of the knowledge base used by the CBR system.

6.4.5. Revisor: a Library of Revision Operators and Revision-Based Adaptation Operators

- Contact: Jean Lieber
- URL: http://revisor.loria.fr/
- KEYWORDS: Belief revision, adaptation, revision-based adaptation, case-based reasoning, inference engines, knowledge representation.

FUNCTIONAL DESCRIPTION.

Revisor is a library of inference engines dedicated to belief revision and to revision-based adaptation for case-based reasoning. It is open source, under a GPL license and available on the web (http://revisor.loria.fr/). It gathers several engines developed during the previous years for various knowledge representation formalisms (propositional logic, with or without the use of adaptation knowledge, conjunction of linear constraints, and qualitative algebras [89]). Some of these engines are already used in the Taaable system. Current developments on Revisor aim at defining new engines in other formalisms. In particular, a study on a revision operator in the propositional closure of linear constraints (with integer and real number variables) has been carried out [70]: definition, properties and algorithm.

PANAMA Project-Team

6. New Software and Platforms

6.1. FASST2

Flexible Audio Source Separation Toolbox
KEYWORDS: Audio - Source Separation
SCIENTIFIC DESCRIPTION

Only source separation software publicly availble allowing to use both spacial and spectral source properties with a generalised EM algorithm (expectation - maximisation). Fast specification of each use case by the choice of suitable constraints in constraint libraries.

FUNCTIONAL DESCRIPTION

Toolbox for the fast design of audio source separation adapted to any use case.

- Participants: Emmanuel Vincent and Yann Salaun
- Contact: Emmanuel Vincent
- URL: http://fasst.gforge.inria.fr

6.2. Multi-channel BSS Locate Basic

KEYWORDS: Audio - Localization - Signal processing - Multichannel signal
SCIENTIFIC DESCRIPTION

Multi-Channel BSS Locate is a Matlab toolbox to estimate Direction Of Arrival (expressed both in azimuth and elevation) of multiple sources in a multi-channel audio signal recorded by an array of microphones. This toolbox implements the previous 8 angular spectrum methods presented in BSS Locate (GCC-PHAT, GCC-NONLIN, MUSIC and several SNR-based spectra).

- Authors: Emmanuel Vincent, Charles Blandin, Alexey Ozerov, Ewen Camberlein, Romain Lebarbenchon, Frédéric Bimbot and Nancy Bertin
- Contact: Emmanuel Vincent
- URL: http://bass-db.gforge.inria.fr/bss_locate/

6.3. SPADE

Sparse Audio Declipper
KEYWORDS: Audio - Sparse regularization - Declipping
FUNCTIONAL DESCRIPTION

Matlab routines to reproduce audio declipping experiments from the papers:

- Srdan Kitic, Nancy Bertin, Remi Gribonval. Audio Declipping by Cosparse Hard Thresholding. iTwist - 2nd international - Traveling Workshop on Interactions between Sparse models and Technology, Aug 2014, Namur, Belgium. [95]
- Srdan Kitic, Nancy Bertin, Remi Gribonval. Sparsity and cosparsity for audio declipping: a flexible non-convex approach. LVA/ICA 2015 - The 12th International Conference on Latent Variable Analysis and Signal Separation, Aug 2015, Liberec, Czech Republic. pp.8. [31]
- Participants: Srdan Kitic, Nancy Bertin and Rémi Gribonval
- Contact: Rémi Gribonval
- URL: http://xspaad.gforge.inria.fr/

PARIETAL Project-Team

6. New Software and Platforms

6.1. Scikit-learn

KEYWORDS: Classification - Learning - Clustering - Regession - Medical imaging

SCIENTIFIC DESCRIPTION

Scikit-learn is a Python module integrating classic machine learning algorithms in the tightly-knit scientific Python world. It aims to provide simple and efficient solutions to learning problems, accessible to everybody and reusable in various contexts: machine-learning as a versatile tool for science and engineering.

FUNCTIONAL DESCRIPTION

Scikit-learn can be used as a middleware for prediction tasks. For example, many web startups adapt Scikitlearn to predict buying behavior of users, provide product recommendations, detect trends or abusive behavior (fraud, spam). Scikit-learn is used to extract the structure of complex data (text, images) and classify such data with techniques relevant to the state of the art.

Easy to use, efficient and accessible to non datascience experts, Scikit-learn is an increasingly popular machine learning library in Python. In a data exploration step, the user can enter a few lines on an interactive (but non-graphical) interface and immediately sees the results of his request. Scikitlearn is a prediction engine . Scikit-learn is developed in open source, and available under the BSD license.

- Participants: Olivier Grisel, Gaël Varoquaux, Bertrand Thirion, Michael Eickenberg, Loïc Estève, Alexandre Gramfort and Fabian Pedregosa Izquierdo
- Partners: CEA - Logilab - Nuxeo - Saint Gobain - Tinyclues - Telecom Paris
- Contact: Olivier Grisel
- URL: http://scikit-learn.org

6.2. Nilearn

KEYWORDS: Health - Neuroimaging - Medical imaging

FUNCTIONAL DESCRIPTION

NiLearn is the neuroimaging library that adapts the concepts and tools of scikit-learn to neuroimaging problems. As a pure Python library, it depends on scikit-learn and nibabel, the main Python library for neuroimaging I/O. It is an open-source project, available under BSD license. The two key components of NiLearn are i) the analysis of functional connectivity (spatial decompositions and covariance learning) and ii) the most common tools for multivariate pattern analysis. A great deal of efforts has been put on the efficiency of the procedures both in terms of memory cost and computation time.

- Participants: Gaël Varoquaux, Bertrand Thirion, Loïc Estève, Alexandre Abraham, Michael Eickenberg, Alexandre Gramfort, Fabian Pedregosa Izquierdo, Elvis Dohmatob.
- Contact: Bertrand Thirion
- URL: http://nilearn.github.io

6.3. Mayavi

FUNCTIONAL DESCRIPTION

Mayavi is the most used scientific 3D visualization Python software. Mayavi can be used as a visualization tool, through interactive command line or as a library. It is distributed under Linux through Ubuntu, Debian, Fedora and Mandriva, as well as in PythonXY and EPD Python scientific distributions. Mayavi is used by several software platforms, such as PDE solvers (fipy, sfepy), molecule visualization tools and brain connectivity analysis tools (connectomeViewer).

- Contact: Gaël Varoquaux
- URL: http://mayavi.sourceforge.net/

6.4. PyHRF

KEYWORDS: FMRI - Statistic analysis - Neurosciences - IRM - Brain - Health - Medical imaging

FUNCTIONAL DESCRIPTION

As part of fMRI data analysis, PyHRF provides a set of tools for addressing the two main issues involved in intra-subject fMRI data analysis : (i) the localization of cerebral regions that elicit evoked activity and (ii) the estimation of the activation dynamics also referenced to as the recovery of the Hemodynamic Response Function (HRF). To tackle these two problems, PyHRF implements the Joint Detection-Estimation framework (JDE) which recovers parcel-level HRFs and embeds an adaptive spatio-temporal regularization scheme of activation maps.

- Participants: Thomas Vincent, Solveig Badillo, Lotfi Chaari, Christine Bakhous, Florence Forbes, Philippe Ciuciu, Laurent Risser, Thomas Perret, Aina Frau Pascual and Lotfi Chaari
- Partners: CEA - NeuroSpin
- Contact: Florence Forbes
- URL: http://pyhrf.org

PARKAS Project-Team

5. New Software and Platforms

5.1. Cmmtest: a tool for hunting concurrency compiler bugs

Participant: Francesco Zappa Nardelli [contact].

Languages, concurrency, memory models, C11/C++11, compiler, bugs.

The Cmmtest tool performs random testing of C and C++ compilers against the C11/C++11 memory model. A test case is any well-defined, sequential C program; for each test case, cmmtest:

1. compiles the program using the compiler and compiler optimisations that are being tested;
2. runs the compiled program in an instrumented execution environment that logs all memory accesses to global variables and synchronisations;
3. compares the recorded trace with a reference trace for the same program, checking if the recorded trace can be obtained from the reference trace by valid eliminations, reorderings and introductions.

Cmmtest identified several mistaken write introductions and other unexpected behaviours in the latest release of the gcc compiler. These have been promptly fixed by the gcc developers.

Cmmtest is available from http://www.di.ens.fr/~zappa/projects/cmmtest/ and a list of bugs reported thanks to cmmtest is available from http://www.di.ens.fr/~zappa/projects/cmmtest/gcc-bugs.html.

5.2. GCC

KEYWORDS: Compilation - Polyhedral compilation
FUNCTIONAL DESCRIPTION

The GNU Compiler Collection includes front ends for C, C++, Objective-C, Fortran, Java, Ada, and Go, as well as libraries for these languages (libstdc++, libgcj,...). GCC was originally written as the compiler for the GNU operating system. The GNU system was developed to be 100% free software, free in the sense that it respects the user's freedom.

The emphasis as now moved towards LLVM and its Polly framework for polyhedral compilation.

- Participants: Albert Cohen, Riyadh Baghdadi, Mircea Namolaru and Nhat Minh Le
- Contact: Albert Cohen
- URL: http://gcc.gnu.org/

5.3. Heptagon

FUNCTIONAL DESCRIPTION

Heptagon is an experimental language for the implementation of embedded real-time reactive systems. It is developed inside the Synchronics large-scale initiative, in collaboration with Inria Rhones-Alpes. It is essentially a subset of Lucid Synchrone, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

- Participants: Adrien Guatto, Marc Pouzet, Cédric Pasteur, Léonard Gérard, Brice Gelineau, Gwenaël Delaval and Eric Rutten
- Contact: Marc Pouzet
- URL: http://heptagon.gforge.inria.fr

5.4. Ott and Lem

lightweight executable mathematics

FUNCTIONAL DESCRIPTION

Ott and Lem are lightweight tools for writing, managing, and publishing large scale semantic definitions, where the scale makes it hard to keep a definition internally consistent, and to keep a tight correspondence between a definition and implementations.

The two tools are complementary. Ott focuses on higher-level programming language semantics. Lem is domain-specific language that resembles a pure subset of Objective Caml, supporting typical functional programming constructs and common logical mechanisms. Both tools can generate OCaml, HOL4, Coq, and Isabelle code. They also generate LaTeX code for inclusion of the language definition in scientific documents. Ott also supports a Lem backend for a tight integration between the two tools.

- Participants: Francesco Zappa Nardelli, Scott Owens, Peter Sewell
- Contact: Francesco Zappa Nardelli
- URL: http://www.cl.cam.ac.uk/~pes20/ott/ and http://www.cl.cam.ac.uk/~pes20/lem/

5.5. Lucid Synchrone

FUNCTIONAL DESCRIPTION

Lucid Synchrone is a language for the implementation of reactive systems. It is based on the synchronous model of time as provided by Lustre combined with features from ML languages. It provides powerful extensions such as type and clock inference, type-based causality and initialization analysis and allows to arbitrarily mix data-flow systems and hierarchical automata or flows and valued signals.

- Contact: Marc Pouzet
- URL: http://www.di.ens.fr/~pouzet/lucid-synchrone/

5.6. Lucy-n

Lucy-n: an n-synchronous data-flow programming language

FUNCTIONAL DESCRIPTION

Lucy-n is a language to program in the n-synchronous model. The language is similar to Lustre with a buffer construct. The Lucy-n compiler ensures that programs can be executed in bounded memory and automatically computes buffer sizes. Hence this language allows to program Kahn networks, the compiler being able to statically compute bounds for all FIFOs in the program.

- Participants: Albert Cohen, Adrien Guatto, Marc Pouzet and Louis Mandel
- Contact: Albert Cohen
- URL: https://www.lri.fr/~mandel/lucy-n/

5.7. PPCG

FUNCTIONAL DESCRIPTION

PPCG is our source-to-source research tool for automatic parallelization in the polyhedral model. It serves as a test bed for many compilation algorithms and heuristics published by our group, and is currently the best automatic parallelizer for CUDA and OpenCL (on the Polybench suite).

- Participants: Sven Verdoolaege, Tobias Grosser, Michael Kruse, Chandan Reddy, Riyadh Baghdadi and Albert Cohen
- Contact: Sven Verdoolaege
- URL: http://repo.or.cz/w/ppcg.git

5.8. ReactiveML

FUNCTIONAL DESCRIPTION

ReactiveML is a programming language dedicated to the implementation of interactive systems as found in graphical user interfaces, video games or simulation problems. ReactiveML is based on the synchronous reactive model due to Boussinot, embedded in an ML language (OCaml).

The Synchronous reactive model provides synchronous parallel composition and dynamic features like the dynamic creation of processes. In ReactiveML, the reactive model is integrated at the language level (not as a library) which leads to a safer and a more natural programming paradigm.

- Participants: Guillaume Baudart, in collaboration with Louis Mandel now at IBM Research
- Contact: Guillaume Baudart
- URL: http://rml.lri.fr

5.9. SundialsML

Sundials/ML
KEYWORDS: Simulation - Mathematics - Numerical simulations
FUNCTIONAL DESCRIPTION

Sundials/ML is a comprehensive OCaml interface to the Sundials suite of numerical solvers (CVODE, CVODES, IDA, IDAS, KINSOL, ARKODE). Its structure mostly follows that of the Sundials library, both for ease of reading the existing documentation and for adapting existing source code, but several changes have been made for programming convenience and to increase safety, namely:

- solver sessions are mostly configured via algebraic data types rather than multiple function calls;
- errors are signalled by exceptions not return codes (also from user-supplied callback routines);
- user data is shared between callback routines via closures (partial applications of functions);
- vectors are checked for compatibility (using a combination of static and dynamic checks); and
- explicit free commands are not necessary since OCaml is a garbage-collected language.

OCaml versions of the standard examples usually have an overhead of about 50% compared to the original C versions, and almost never more than 100%.

NEW PROGRESS

The current version of Sundials/ML comprises about 37,000 lines of OCaml (plus 15,000 lines of api documentation) and 16,000 lines of C (plus 1600 lines of commentary). This year we worked on updating the interface to support Sundials 2.6.x. This involved adding support for a new solver (ARKODE), new modules for sparse matrices (SuperLU_MT and KLU), new nvectors (pthreads and OpenMP), and new linear solvers (SPFGMR and PCG), as well as treating several other new or modified features. This work is almost complete and will be released early in 2016. The technical developments required to interface OCaml with this library are explained in a report which has been sumitted as a deliverable in the MODRIO project: “D.4.2.16—OCaml interface to the Sundials suite of numerical solvers”. This text will be developed and submitted for journal publication in early 2016.

- Participants: Marc Pouzet and Timothy Bourke
- Partner: UPMC, AIST (Jun Inoue)
- Contact: Timothy Bourke
- URL: http://inria-parkas.github.io/sundialsml/

5.10. Zelus

SCIENTIFIC DESCRIPTION

The Zélus implementation has two main parts: a compiler that transforms Zélus programs into OCaml programs and a runtime library that orchestrates compiled programs and numeric solvers. The runtime can use the Sundials numeric solver, or custom implementations of well-known algorithms for numerically approximating continuous dynamics.

FUNCTIONAL DESCRIPTION

Zélus is a new programming language for hybrid system modeling. It is based on a synchronous language but extends it with Ordinary Differential Equations (ODEs) to model continuous-time behaviors. It allows for combining arbitrarily data-flow equations, hierarchical automata and ODEs. The language keeps all the fundamental features of synchronous languages: the compiler statically ensure the absence of deadlocks and critical races, it is able to generate statically scheduled code running in bounded time and space and a type-system is used to distinguish discrete and logical-time signals from continuous-time ones. The ability to combines those features with ODEs made the language usable both for programming discrete controllers and their physical environment.

NEW PROGRESS

- Development and release of a comprehensive manual: http://zelus.di.ens.fr/man/
- Progress on the interaction of multiple numeric solvers (masters internship of V. Andreani).
- New causality analysis (detection of algebraic loops).
- Participants: Marc Pouzet and Timothy Bourke
- Contact: Marc Pouzet
- http://zelus.di.ens.fr

5.11. isl

FUNCTIONAL DESCRIPTION

isl is a library for manipulating sets and relations of integer points bounded by linear constraints. Supported operations on sets include intersection, union, set difference, emptiness check, convex hull, (integer) affine hull, integer projection, transitive closure (and over-approximation), computing the lexicographic minimum using parametric integer programming. It includes an ILP solver based on generalized basis reduction, and a new polyhedral code generator. isl also supports affine transformations for polyhedral compilation, and increasingly abstract representations to model source and intermediate code in a polyhedral framework.

- Participants: Sven Verdoolaege, Michael Kruse and Albert Cohen
- Contact: Sven Verdoolaege
- URL: http://repo.or.cz/w/isl.git

5.12. LaTeX package: Checklistings

FUNCTIONAL DESCRIPTION

User manuals and papers about programming languages usually contain many code samples, often with accompanying compiler messages giving the types of declarations or error messages explaining why certain declarations are invalid.

The checklistings package augments the fancyvrb and listings packages for including source code in LaTeX documents with a way to pass the source code through a compiler and also include the resulting messages in the document. It also integrates with the HeVeA tool developed in the Gallium team: http://hevea.inria.fr.

The motivation is to check the code samples in a document for syntax and typing errors and to facilitate the inclusion of inferred types and compiler warnings or errors in a text. This package is intentionally very lightweight and unlike packages like python it is not intended for interacting with an interpretor or including the execution traces of code. While checklistings does not focus on a specific programming language, it is designed to work well with ML-like languages.

We developed this package to improve the quality of our papers and presentations on the Zélus programming language, but it is designed to be general purpose and also works, for instance, with OCaml programs.

- Participants: Timothy Bourke and Marc Pouzet
- Contact: Timothy Bourke
- URL: http://www.ctan.org/pkg/checklistings

PARSIFAL Project-Team

6. New Software and Platforms

6.1. Abella

FUNCTIONAL DESCRIPTION

Abella is an interactive theorem prover for reasoning about computations given as relational specifications. Abella is particuarly well suited for reasoning about binding constructs.

In 2015, Abella has been extended with

- support for polymorphic definitions and theorems;
- schemas and automatically derived theorems about them;
- the ability to record and replay automated search;
- a number of new examples from process calculi, including a contributed example from Horace Blanc about relating the π-calculus and the λ-calculus.

One further development is that Abella can now be compiled into JavaScript and run completely inside any modern browser, thanks to the `js_of_ocaml` compiler from OCaml bytecode to JavaScript. We expect this to become rather crucial in popularization of Abella, particularly in a pedagogical context, since it does not require any local software installation—just a modern web browser.

- Participants: Dale Miller, Kaustuv Chaudhuri, Horace Blanc
- Partner: Department of Computer Science and Engineering, University of Minnesota
- Contact: Kaustuv Chaudhuri
- URL: http://abella-prover.org/
- Online version: http://abella-prover.org/tutorial/try

6.2. Bedwyr

Bedwyr - A proof search approach to model checking

FUNCTIONAL DESCRIPTION

Bedwyr is a generalization of logic programming that allows model checking directly on syntactic expression possibly containing bindings. This system, written in OCaml, is a direct implementation of two recent advances in the theory of proof search.

It is possible to capture both finite success and finite failure in a sequent calculus. Proof search in such a proof system can capture both “may” and “must” behavior in operational semantics. Higher-order abstract syntax is directly supported using term-level lambda-binders, the nabla quantifier, higher-order pattern unification, and explicit substitutions. These features allow reasoning directly on expressions containing bound variables.

The distributed system comes with several example applications, including the finite pi-calculus (operational semantics, bisimulation, trace analyses, and modal logics), the spi-calculus (operational semantics), value-passing CCS, the lambda-calculus, winning strategies for games, and various other model checking problems.

- Participant: Roberto Blanco Martinez
- Contact: Quentin Heath
- URL: http://slimmer.gforge.inria.fr/bedwyr/

6.3. Checkers

Checkers - A proof verifier

KEYWORDS: Proof - Certification - Verification

FUNCTIONAL DESCRIPTION

Checkers is a tool in Lambda-prolog for the certification of proofs. Checkers consists of a kernel which is based on LKF and is based on the notion of ProofCert.

- Participants: Tomer Libal and Giselle Reis
- Contact: Tomer Libal
- URL: https://github.com/proofcert/checkers

6.4. Mætning

KEYWORDS: Automated Theorem Proving - Intuitionistic Logic

FUNCTIONAL DESCRIPTION

Mætning is an automated theorem prover for first-order intuitionistic logic that is particularly suited for efficiently finding *disproofs*, i.e., for establishing that a given goal query is not provable. It is based on the focused inverse method [54] [74], but augmented by a mechanism for building finite approximations for infinite search spaces that nevertheless guarantee soundness of a disproof.

Mætning has been released under the terms of the MIT license.

- Participants: Taus Brock-Nannestad, Kaustuv Chaudhuri
- Contact: Kaustuv Chaudhuri
- URL: https://github.com/chaudhuri/maetning

6.5. Psyche

KEYWORDS: Proof-search - Correct-by-construction approach - Programmable Theorem Proving

FUNCTIONAL DESCRIPTION

Psyche is a modular platform for automated or interactive theorem proving, programmed in OCaml and built on an architecture (similar to LCF) where a small kernel interacts with plugins and decision procedures. The major effort in 2015 was a complete redesign of its architecture to allow the safe cooperation of various procedures (for e.g. different theories).

- Participants: Assia Mahboubi, Jean-Marc Notin and Stéphane Graham-Lengrand
- Contact: Assia Mahboubi and Stéphane Graham-Lengrand
- URL: http://www.lix.polytechnique.fr/~lengrand/Psyche/

PERCEPTION Project-Team

5. New Software and Platforms

5.1. Associations of Audio Cues with 3D Locations Library

FUNCTIONAL DESCRIPTION

Library to associate some auditory cues with 3D locations (points). It provides an estimation of the emitting state of each of the input locations. There are two main assumptions:

1. The 3D locations are valid during the acquisition interval related to the audio cues
2. The 3D locations are the only possible locations for the sound sources, no new locations will be created in this module

The software provides also a multimodal fusion library.

- Participants: Xavier Alameda-Pineda, Antoine Deleforge, Jordi Sanchez-Riera and Radu Horaud
- Contact: Radu Horaud

5.2. Supervised Binaural Mapping Software

FUNCTIONAL DESCRIPTION

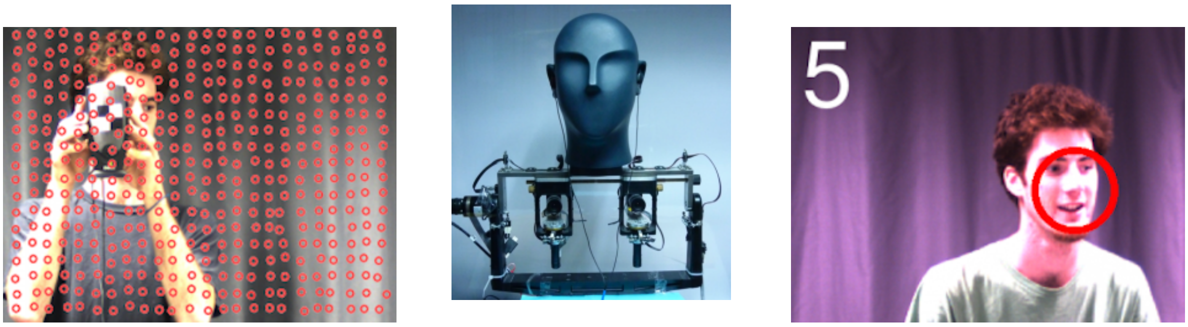


Figure 2. An audio-visual sound source (left) that emits white noise is moved in front of the POPEYE robot (middle). These input-output observation pairs are used to estimate a regression function that is then used to predict the location of a sound (right).

The SBM Matlab toolbox for “Supervised Binaural Mapping", contains a set of functions and scripts for supervised binaural sound source separation and localization. The approach consists in learning the acoustic space of a system using a set of white-noise measurements. Once the acoustic space is learned, it can be used to efficiently localize one or several natural sound sources such as speech, and to separate their signals.

- Participants: Antoine Deleforge, Soraya Arias and Radu Horaud
- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/supervised-binaural-mapping/

5.3. Audiovisual Robotic Heads

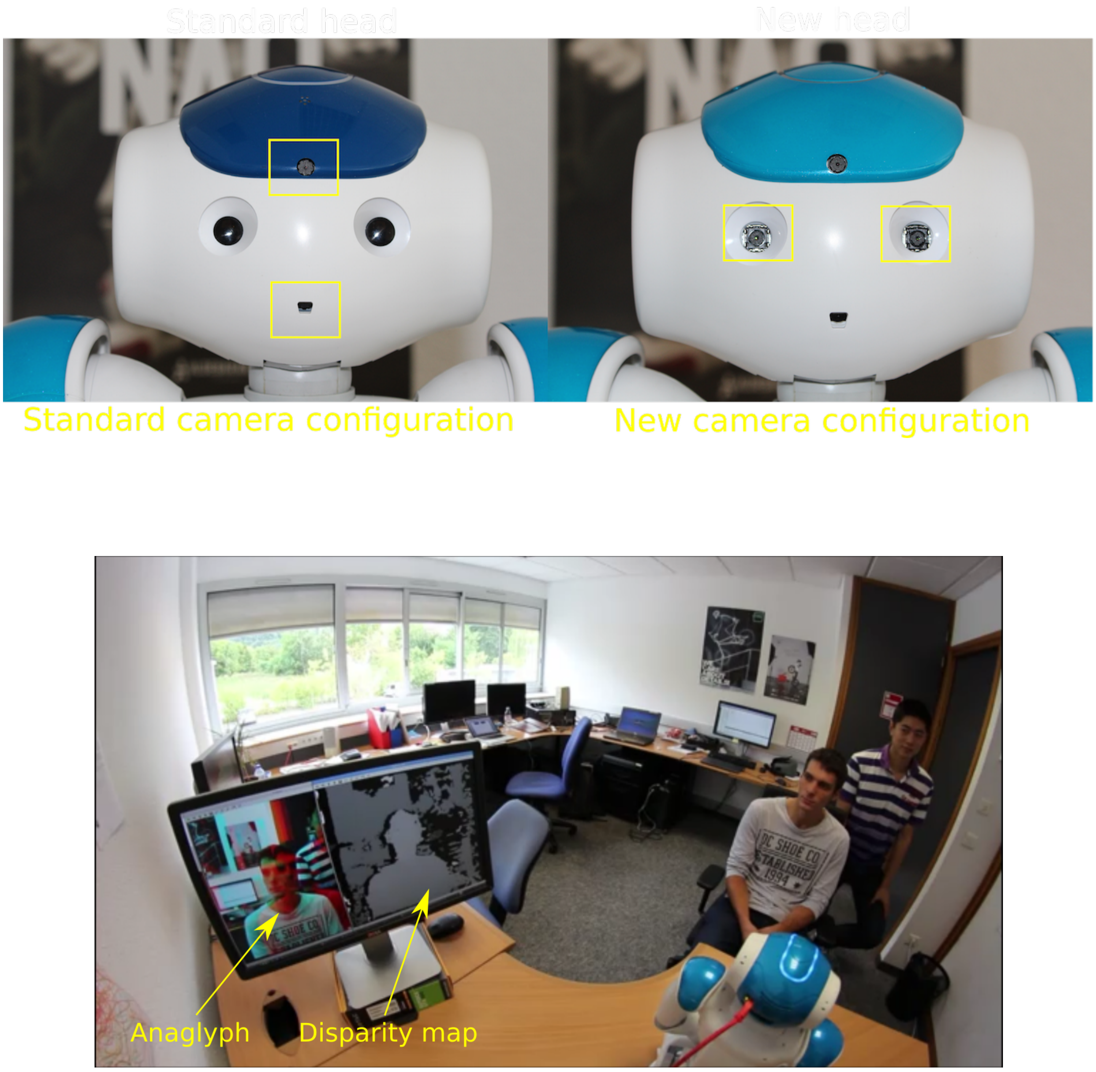


Figure 3. In collaboration with Aldebaran Robotics the team has developed a stereoscopic head for the humanoid robot NAO. Unlike the standard head that has a vertical pair of unsynchronized cameras (top-left), the new head has a horizontal pair of synchronized cameras (top-right). The latest prototype delivers VGA image pairs at 15 FPS. Based on the NAOLab library, we developed a stereo reconstruction method that delivers depth maps at 5 FPS (bottom).

FUNCTIONAL DESCRIPTION

The team has developed two audiovisual (AV) robot heads: the POPEYE head and the NAO stereo head. Both are equipped with a binocular vision system and with four microphones. The software modules comprise stereo matching and reconstruction, sound-source localization and audio-visual fusion. POPEYE has been developed within the European project POP in collaboration with the project-team MISTIS and with two other POP partners: the Speech and Hearing group of the University of Sheffield and the Institute for Systems and Robotics of the University of Coimbra. The NAO stereo head was developed under the European project HUMAVIPS in collaboration with Aldebaran Robotics (which manufactures the humanoid robot NAO) and with the University of Bielefeld, the Czech Technical Institute, and IDIAP. The software modules that we develop are compatible with both these robot heads.

- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/popeye/

5.4. MIXCAM Platform

Figure 4. MIXCAM is a multiple-camera multiple-PC hardware/software platform that combines high-resolution color (RGB) cameras with low-resolution time-of-flight (TOF) cameras. The cameras are arranged in TOF-stereo "units", where each unit is composed of two RGB cameras and one TOF camera. Currently the system is composed of four such units, or a total of eight RGB and four TOF cameras. In 2015 we completed algorithms and software packages for the calibration if individual TOF cameras [3] and of the while system composed of four units, e.g. left image, [24]. The system allows high-resolution reconstruction of people, e.g. right image, [23].

FUNCTIONAL DESCRIPTION

We developed a multiple camera platform composed of both high-definition color cameras and low-resolution depth cameras. This platform combines the advantages of the two camera types. On one side, depth (time-of-flight) cameras provide coarse low-resolution 3D scene information. On the other side, depth and color cameras can be combined such as to provide high-resolution 3D scene reconstruction and high-quality rendering of textured surfaces. The software package developed during the period 2011-2015 contains the calibration of TOF cameras, alignment between TOF and color cameras, TOF-stereo fusion, and image-based rendering. These software developments were performed in collaboration with the Samsung Advanced Institute of Technology, Seoul, Korea. The multi-camera platform and the basic software modules are products of 4D Views Solutions SAS, a start-up company issued from the PERCEPTION group.

- Participants: Quentin Pelorson, Georgios Evangelidis, Soraya Arias, Radu Horaud.

- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/mixcam-project/

5.5. NaoLAB

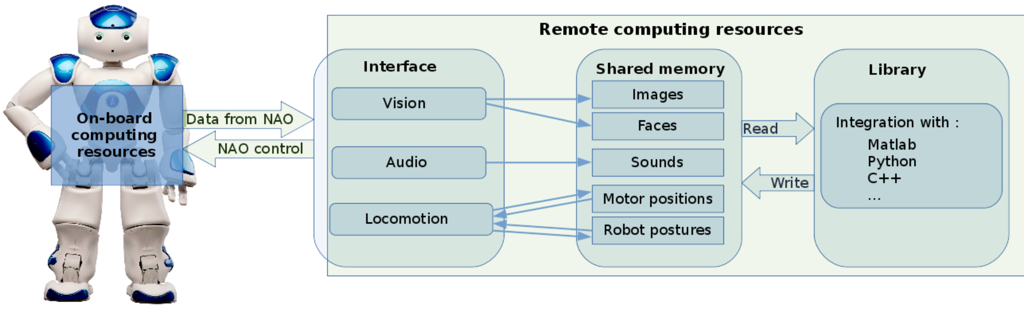


Figure 5. Overview of the proposed distributed architecture that allows fast development of interactive applications using the humanoid robot NAO.

FUNCTIONAL DESCRIPTION

NAOLab [27] is a middleware for the development of robotic applications in C, C++, Python and Matlab, using the humanoid robot NAO networked with a PC. NAOLab enables the joint use of NAO's on-board computing resources and external resources. More precisely, it allows the development of applications that combine embedded libraries, e.g. motion control, image/sound acquisition and transmission, etc., with external toolboxes, e.g. OpenCV, Matlab toolboxes, etc. The NAOLab toolbox has the following characteristic. The middleware complexity is transparent to the users. An user-friendly interface is provided through C++ and Python libraries extended with mex functions for Matlab. This enables the development of sophisticated audio and visual processing algorithms without the stringent constraints of the NAOqi SDK. NAOLab and NAOqi share the same modular approach, namely there are three categories of modules: vision, audio and motion. An interface (vision, audio, motion) is associated with each NAOqi module. Each interface deals with sensor-data access and actuator control. The role of these interfaces is twofold: (i) to feed the sensor data into a memory space that is subsequently shared with existing software or with software under development, and (ii) to send to the robot commands generated by the external modules.

- Participants: Fabien Badeig, Quentin Pelorson, Soraya Arias, Radu Horaud.
- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/research/naolab/

PHOENIX Project-Team

6. New Software and Platforms

6.1. DiaSuite: a Development Environment for Sense/Compute/Control Applications

Participants: Charles Consel [correspondent], Julien Durand, Milan Kabac, Paul Van Der Walt, Adrien Carteron.

Despite much progress, developing a pervasive computing application remains a challenge because of a lack of conceptual frameworks and supporting tools. This challenge involves coping with heterogeneous devices, overcoming the intricacies of distributed systems technologies, working out an architecture for the application, encoding it in a program, writing specific code to test the application, and finally deploying it.

DIASUITE is a suite of tools covering the development life-cycle of a pervasive computing application.
Defining an application area. First, an expert defines a catalog of entities, whether hardware or software, that are specific to a target area. These entities serve as building blocks to develop applications in this area. They are gathered in a taxonomy definition, written in the taxonomy layer of the DIASPEC language.
Designing an application. Given a taxonomy, the architect can design and structure applications. To do so, the DIASPEC language provides an application design layer [39]. This layer is dedicated to an architectural pattern commonly used in the pervasive computing domain [35]. Describing the architecture application allows to further model a pervasive computing system, making explicit its functional decomposition.
Implementing an application. We leverage the taxonomy definition and the architecture description to provide dedicated support to both the entity and the application developers. This support takes the form of a Java programming framework, generated by the DIAGEN compiler. The generated programming framework precisely guides the developer with respect to the taxonomy definition and the architecture description. It consists of high-level operations to discover entities and interact with both entities and application components. In doing so, it abstracts away from the underlying distributed technologies, providing further separation of concerns.
Testing an application.DIAGEN generates a simulation support to test pervasive computing applications before their actual deployment. An application is simulated in the DIASIM tool, without requiring any code modification. DIASIM provides an editor to define simulation scenarios and a 2D-renderer to monitor the simulated application. Furthermore, simulated and actual entities can be mixed. This hybrid simulation enables an application to migrate incrementally to an actual environment.
Deploying a system. Finally, the system administrator deploys the pervasive computing system. To this end, a distributed systems technology is selected. We have developed a back-end that currently targets the following technologies: Web Services, RMI, SIP and OSGI. This targeting is transparent for the application code. The variety of these target technologies demonstrates that our development approach separates concerns into well-defined layers.

This development cycle is summarized in the Figure 2 .

See also the web page http://diasuite.inria.fr.

6.1.1. DiaSpec: a Domain-Specific Language for Networked Entities

The core of the DIASUITE development environment is the domain specific language called DIASPEC and its compiler DIAGEN.

DIASPEC It is composed of two layers.

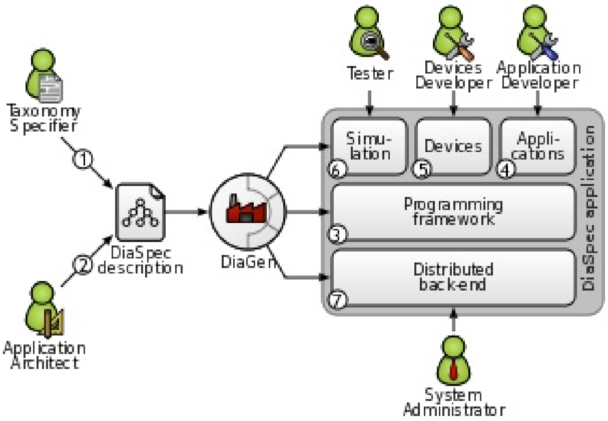


Figure 2. DIASUITE *Development Cycle*

The Taxonomy Layer. It allows the declaration of entities that are relevant to the target application area. An entity consists of sensing capabilities, producing data, and actuating capabilities, providing actions. Accordingly, an entity description declares a data source for each one of its sensing capabilities. As well, an actuating capability corresponds to a set of method declarations. An entity declaration also includes attributes, characterizing properties of entity instances. Entity declarations are organized hierarchically allowing entity classes to inherit attributes, sources and actions. A taxonomy allows separation of concerns in that the expert can focus on the concerns of cataloging area-specific entities. The entity developer is concerned about mapping a taxonomical description into an actual entity, and the application developer concentrates on the application logic.

The Architecture Layer. It is based on an architectural pattern commonly used in the pervasive computing domain [35]. It consists of context components fueled by sensing entities. These components process gathered data to make them amenable to the application needs. Context data are then passed to controller components that trigger actions on entities. Using an architecture description enables the key components of an application to be identified, allowing their implementation to evolve with the requirements (*e.g.,* varying light management implementations in a controller component to optimize energy consumption).

DIAGEN. It is the DIASPEC compiler that performs both static and runtime verifications over DIASPEC declarations and produces a dedicated programming framework that guides and eases the implementation of components. The generated framework is independent of the underlying distributed technology. As of today, DIAGEN supports multiple targets: Local, RMI, SIP, Web Services and OSGI.

6.2. DiaSuiteBox: an Open Orchestration Platform

Participants: Charles Consel, Julien Durand, Adrien Carteron, Milan Kabac.

The DiaSuiteBox platform runs an open-ended set of applications leveraging a range of appliances and web services. Our solution consists of a dedicated development environment, a certifying application store, and a lightweight runtime platform. This solution is based on the DIASUITE project.

The DiaSuiteBox platform can be embedded in a small plug-computer or deployed in the cloud. Thanks to the application store and the developer community, the platform is fed by a full offer of new innovative applications. During the submission process, an application is automatically analyzed and checked in order to be certified. The user is ensured the behavior of its applications are innocuous and correct with respect to the provided information. Finally, DiaSuiteBox provides an extensible software architecture. This allows the easily connect new device technologies to the platform. For example, the support for new wireless communication technologies such as Zigbee, Z-Wave or Sigfox can be easily added to the DiaSuiteBox platform.

More details can be found on the web page http://diasuitebox.inria.fr.

The iQSpot startup uses DiaSuiteBox as a software platform to ease the management of Smart Buildings. In this project, the DiaSuiteBox platform is first used to host building management functionalities such as lighting management, heating/ventilating/air conditioning management, energy efficiency monitoring. It is also used to host software drivers that allow the building management functionalities to interact with the connected devices deployed in buildings. These devices can use wired communication technologies such LonWorks, BACNet or KNX, as well as wireless communication technologies such as Z-Wave or Zigbee.

6.3. DiaSwarm: Orchestrating masses of objects

Participants: Charles Consel [correspondent], Milan Kabac, Eugène Volanschi.

DiaSwarm provides a design language dedicated to the domain of orchestrating masses of objects. The language provides high-level, declarative constructs that allow a developer to deal with masses of objects at design time, prior to programming the application. The DiaSwarm compiler generates programming frameworks, which provide high-level support to the developer, while ensuring that programming is driven by design.

DiaSwarm consists of two main components.

- DiaSwarm Studio. It is available as an Eclipse plugin. The tool provides of a domain-specific language and a compiler dedicated to the domain of orchestrating masses of sensors.
- Runtime environment. This is a library allowing you to execute DiaSwarm applications locally. The runtime environment comprises the Apache Hadoop framework v. 1.2.1 allowing you to run MapReduce jobs locally without the need to install the framework separately.

More details can be found on a dedicated web page http://phoenix.inria.fr/software/diaswarm. In particular, an example application is provided: it is dedicated to the management of parking lots in a city. It uses presence sensors to monitor the availability of parking spaces through magnetic field variations. The application defines a few context components, which transform sensed data to determine the availability of parking lots and average occupancy of parking lots in 24 hr. Furthermore, the application suggests parking lots to drivers entering the city. Please note that the availability of parking places is computed every 30 seconds. The average occupancy of parking lots is computed every 2 minutes.

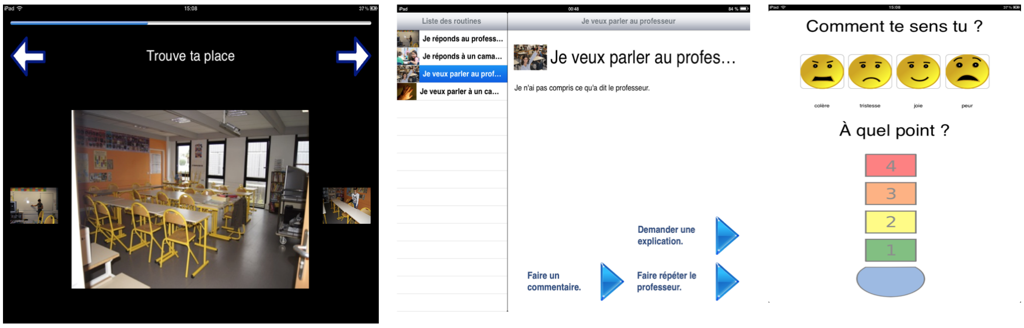
6.4. School+ Apps: Assistive tablet applications for school Inclusion

Participants: Charles Consel [correspondent], Hélène Sauzéon, Charles Fage.

School+ is a package of 7 applications. Three applications are assistive applications, guiding the child doing specific tasks. Three others are training applications made as serious games, addressing specific skills. The last application is a meta-application, comprising a link to the three training applications, with an access to statistics of their usage. For each application, data are separated from the design, meaning that every element of each application (pictures, texts, settings, etc.) can be changed at any time. Each application records a log file containing all the interactions performed by the child.

6.4.1. Assistive applications

Routines application. This application shows a list of tasks, with a short description. After clicking the starting button, a specific slideshow is shown; it decomposes a task into steps. For each step, a text and a picture can be displayed. Thumbnail of previous and next steps are also displayed. This application guides the child through classroom situations: entering classroom, taking school materials out of a backpack, writing notes, handling agenda, leaving the classroom.



Je n'ai pas compris ce qu'a dit le professeur.

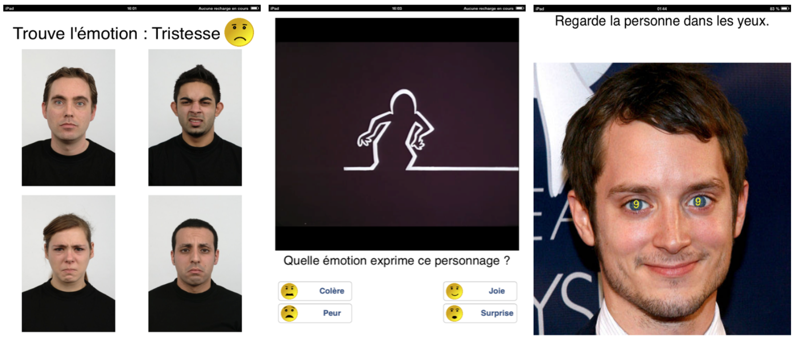
Figure 3. Assistive applications

Communication application. With the same design, the assistance provided by this application targets to communicating situations inside the classroom. The application covers four scenarios addressing two interaction situations (initiating and answering the interaction) and two types of interlocutors (professor and classmate). For each scenario, different slideshows guide the child, depending on the goal of the interaction.

Emotion Regulation application. This application aims to assist the child to self-regulate his/her emotions. Four simplified emoticons are proposed to the child to choose from: anger, sadness, joy and fear. Then, (s)he selects a level of intensity via a thermometer with a scale from 1 to 4. In response, the application delivers different multimedia contents according to the level selected to help the child regulate his/her emotions. Typically, a text (breathing instructions) are shown at level 1, pictures at level 2, a video at level 3 and another text at level 4.

6.4.2. Training applications

These three applications are serious games with increasing levels of difficulties, reachable after a ratio of good answers has been attained.



Quelle émotion exprime ce personnage ?

Regarde la personne dans les yeux.

Figure 4. Training applications

Emotion Recognition application with pictures. In this application, the child is instructed to identify a specific emotion among 4 pictures showing different people exhibiting an emotion. Seven emotions are involved in this application: joy, sadness, fear, anger, surprise, disgust and neutral. The emotion to be recognized is displayed together with its simplified emoticon. The type of pictures changes with the difficulty level: level 1 contains pictures of unfamiliar people and level 2 contains pictures of friends and relatives of the child.

Emotion Recognition application with videos. In this application, the child is presented with a fragment of an animated cartoon. At some point, the video stops and the child is asked to identify the emotion of the character. Four emotions are involved in this application: joy, sadness, fear and anger. Videos are slowed down, with a speed percentage that can be changed at each level. Videos change with difficulty level: level 1 contains videos of a very basic cartoon (only one cartoon character drawn by basic form un-textured), level 2 contains a video of more sophisticated cartoons and level 3 contains movies with actors.

Attention Training. In this application, the child is presented a picture of a face and asked to make eye contact with it. Second, a symbol appears briefly in the eyes of the character. Third, the child is asked to identify the symbol shown in the previously displayed picture, to make sure he kept eye contact. The speed at which the symbol appears and disappears is changed according to the difficulty level. Types of pictures also change with the level : level 1 contains pictures of faces and level 2 contains pictures of classroom situations.

6.5. HomeAssist: A Platform for Assistive Living

Participants: Charles Consel [correspondent], Adrien Carteron, Julien Durand, Lucile Dupuy, Hélène Sauzéon.

The HomeAssist platform proposes a systemic approach to introducing an assistive technological platform for older people. To do so, we formed a trans-disciplinary team that allows (1) to identify the user needs from a gerontological and psychological viewpoint; (2) to propose assistive applications designed by human factors and HCI experts, in collaboration with caregivers and users; (3) to develop and test applications by software engineers; (4) to conduct a field study for assessing the benefits of the platform and assistive applications, in collaboration with caregivers, by deploying the system at the actual home of older adults.

The HomeAssist platform is implemented on top of the DiaSuiteBox platform, using a suite of tools, namely DiaSuite, that have been designed, developed and tested by our research group at Inria. The DiaSuite tools include a dedicated integrated development environment that enables applications to be developed quickly and safely. This technology has been successfully applied to a variety of domains where environments consist of networked objects that need to be orchestrated.

6.5.1. Applications

HomeAssist offers an online catalog of applications. Using this catalog, the user and the caregiver determine what and how activities should be assisted by selecting the appropriate assistive applications and configuring them with respect to the user's requirements and preferences. The resulting set of applications forms a personalized assistive support. Additionally, to respond to evolving needs, our platform allows to stop/remove applications easily and to install new ones from the online catalog.

This platform proposes many applications in three domains of everyday life.

- Daily activities: including activity monitoring, light path, and a reminder.
- Home or personal safety: including entrance monitoring, stove monitoring, and warning if no movements are detected after a certain amount of time.
- Communications and social activities: including collaborative games, videoconference, information about local events, TV programming, *etc*.

For video presentations of HomeAssist, see the following:

- http://videotheque.inria.fr/videotheque/media/23705. Title: “DiaSuiteBox”, 2013.
- http://videotheque.inria.fr/videotheque/media/29998. Title: “DomAssist : L'assistance numérique à la personne”, 2014.

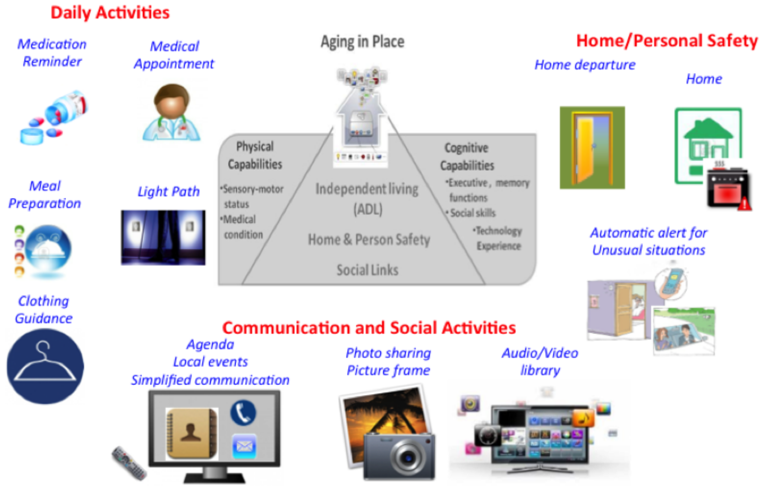


Figure 5. The HomeAssist platform and applications

6.5.2. Devices

Several entities have been identified to deliver an assistive support. These entities include (1) technological devices: wireless sensors (motion detectors, contact sensors and smart electric switches), and two tablets, and (2) software services (agenda, address book, mail agent, and photo agent) to monitor everyday activities and propose assistive applications. Sensors are placed in relevant rooms in the house: kitchen, bedroom, bathroom, and around the entrance.

Figure 6. HomeAssist devices

6.5.3. Experimental validation

A field study is currently being conducted with elderly people. The major purpose of this study is to identify the benefits of using HomeAssist for this population in an ecological framework. We selected 24 elderly people with different levels of autonomy (GIR scores). The HomeAssist technology has been installed in their house during 9 months. Twenty-four non-equipped older adults were also selected to participate to the study, as control participants.

The expected impact of HomeAssist reflects the trans-disciplinary nature of the project. We aim to deliver results in the domain of (1) elderly care, (2) ergonomics and human factors, and (3) pervasive computing.

The major expected results are that HomeAssist (1) prolongs ageing in place, improves well-being of the users, and improves the efficiency of the caregiving environment; (2) is a cognitively low-cost assistive technology, and is well accepted and perceived as useful and usable by the users; (3) is technologically robust, and is a validated assistive platform.

The preliminary results of this field study show that the platform is well adopted (highly accessible and usable) by the older users and their families or caregivers.

Additionally, these results support our claim that DiaSuiteBox is effective in terms of:

1. autonomy and well-being of older adults, comparing pre- vs. post-deployment, as well as not-equipped, control participants;
2. gains pre- vs. post deployment in management and load of caregiving tasks, and
3. longitudinal efficacy (gains unchanged at 6 vs. 9 months of use).

Most notably, this pilot project also uses a systemic approach to assistive living as illustrated by (1) its funding sources involving key stakeholders of the caregiving domain, including a territorial agency of Gironde dedicated to ageing, as well as the regional branch of the national public retirement organization (*i.e.,* CARSAT of Aquitaine), (2) their partners operating caregiving services (UDCCAS Gironde), and (3) The regional Chamber of Trades and Crafts to assist the older adults in installing and positioning the devices.

Final results are expected in March 2016.

6.5.4. External Partners

The HomeAssist platform is being developed with support from the following partners:

- Équipe “Handicap et Système Nerveux” (EA 4136), Bordeaux University
- Chaire TSA, Université du Québec Trois-Rivières
- CRIUGM, Université de Montréal
- UDCCAS Gironde
- CARSAT Aquitaine
- Conseil Général 33
- Conseil Régional d’Aquitaine

PI.R2 Project-Team

5. New Software and Platforms

5.1. Coq

KEYWORDS: Proof - Certification - Formalisation
FUNCTIONAL DESCRIPTION

Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

- Participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Dénès, Stéphane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pédrot, Loïc Pottier, Matthias Puech, Yann Régis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliâtre
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Hugo Herbelin
- URL: http://coq.inria.fr/

5.1.1. Version 8.5

Cf. Highlights section. Version 8.5 includes as well a number of miscellaneous changes, at the level of tactics, of the specification language, of the Coq tools, of the standard library, altogether amounting to about 150 items in the change log of the version. In particular, Pierre-Marie Pédrot has been working on the overall optimisation of Coq, by tracking hotspots in the code. Coq v8.5 is currently much more efficient than its v8.4 counterpart, and is about as quick as v8.3, while having been expanded with a lot of additional features.

As a counterpart, the complexity of this new version induced a long phase of experimentation which included 3 different beta versions spanned over the whole 2015 year, with the final version being eventually released for the CoqPL workshop in January 2016.

5.1.2. Universes

Matthieu Sozeau followed up his work on universe polymorphism and uncovered important theoretical and practical problems regarding conversion and unification of universe polymorphic definitions in the presence of cumulativity and the Prop $\leq$ Type rule, as well as the invariants of the consistency checker. He also collaborated with Maxime Dénès and Benjamin Grégoire (Gallium and Marelle) on adapting the efficient conversion tests to universe polymorphism and with Enrico Tassi (Marelle) on the integration with the asynchronous proof development infrastructure. The universe polymorphic system is part of the 8.5 release.

5.1.3. The Equations plugin

Matthieu Sozeau continued work on the Equations plugin and fixed the remaining bugs preventing full automation of a middle-size example of formalisation – the normalisation proof of a predicate version of System F – together with Cyprien Mangin, during his master's internship. This involved finding a new termination proof for the calculus and making the dependent pattern-matching compilation more robust and axiom-free, using a different encoding of pattern-matching problems. This work was presented at LFMTP'15 in Berlin [29]. Since then, the system has been adapted to work with universe polymorphism and the new features of Coq 8.5.

5.1.4. Proof development in Coq

Pierre Letouzey developed a few new results about some Hofstadter sequences (see https://oeis.org/A005206 and https://oeis.org/A123070). These results have been proved in Coq, and they are presented in the technical report [39].

5.1.5. Proofs of algorithms on graphs

Chen Ran (ISCAS/SKLCS, Beijing) and Jean-Jacques Lévy pursued their work about producing readable formal proofs of graph algorithms. This work is performed in Why3 and partly in Coq. Graph algorithms are a good testbed for experimenting correctness proofs of programs with shared structures. We considered basic algorithms such as depth-first-search, random walk, acyclicity test, articulation points, strongly connected components, minimum spanning trees. In each case, the goal is to provide a simple proof as abstract as possible, although checked by computer. A longer term objective is to give formal proofs which could be inserted in algorithms textbooks. A progress work paper is under submission [41].

5.1.6. Development of programs for parallel and cloud computing

Frédéric Loulergue continued his work on the SyDPaCC framework. The goal of this framework is to ease the systematic development of correct parallel programs, in particular large-scale data-intensive applications. The parallel versions of the programs are written with a Coq axiomatisation of Bulk Synchronous Parallel ML (BSML) primitives. New results about SyDPaCC include the design and implementation of a new version of the core of the framework [21]. This new version has been used in a course of École des Jeunes Chercheur/se/s en Informatique Mathématique (EJCIM 2015) [38].

As the SyDPaCC framework currently mixes certified code extracted from Coq and unverified code, Frédéric Loulergue and Pierre Letouzey have worked on an extended extraction that generates, when possible, OCaml conditions for preconditions on function arguments. This part is still on-going work.

Frédéric Loulergue collaborated with Frédéric Dabrowski and Thomas Pinsard (Univ. Orléans) on the semantics and compilation of languages with nested atomic sections and thread escape. In [18], the focus is on the semantics of programming languages providing these features. The main contribution is the precise definition of atomicity, well-synchronisation and the proof that the latter implies the strong form of the former. A formalisation of the results in the Coq proof assistant is described.

In [27], the compilation of a language with nested atomic sections and thread escape towards a language with threads and locks is addressed. The design decisions of this compilation pass and of the target language were made with respect to the ultimate goal of a mechanised proof of semantic preservation.

Frédéric Loulergue collaborated with Allan Blanchard, Nikolai Kosmatov and Matthieu Lemerre (CEA LIST) on the verification of a critical component of a hypervisor. In [23], they present a case study on formal verification of the virtual memory system of the cloud hypervisor Anaxagoros, a microkernel designed for resource isolation and protection. The code under verification is specified and proven in the software verification framework, mostly using automatic theorem proving. The remaining properties are interactively proven with the Coq proof assistant.

Frédéric Loulergue collaborated with Asma Guesmi, Pascal Berthomé and Patrice Clemente (INSA Centre Val de Loire) on resources placement in the Cloud taking into account security requirements [28].

5.2. Other software developments

In collaboration with François Pottier (Inria Gallium), Yann Régis-Gianas maintained Menhir, an LR parser generator for OCaml. Yann Régis-Gianas develops the “Hacking Dojo”, a web platform to automatically grade programming exercises. The platform is now used in several courses of the University Paris Diderot. He gets help from the internship of Alexandre Ly, a master student of the Paris Diderot University. In collaboration with Beta Ziliani (LIIS, Cordoba, Argentine), Yann Régis-Gianas, Béatrice Carré and Jacques-Pascal Deplaix develop MetaCoq, an extension of Coq to use Coq as a metalanguage for itself.

PLEIADE Team

5. New Software and Platforms

5.1. Magus

KEYWORDS: Bioinformatics - Genomic sequence - Knowledge database
SCIENTIFIC DESCRIPTION

MAGUS can be used on small installations with a web server and a relational database on a single machine, or scaled out in clusters or elastic clouds using Apache Cassandra for NoSQL data storage and Apache Hadoop for Map-Reduce.
FUNCTIONAL DESCRIPTION

The MAGUS genome annotation system integrates genome sequences and sequences features, in silico analyses, and views of external data resources into a familiar user interface requiring only a Web navigator. MAGUS implements annotation workflows and enforces curation standards to guarantee consistency and integrity. As a novel feature the system provides a workflow for simultaneous annotation of related genomes through the use of protein families identified by in silico analyses this has resulted in a three-fold increase in curation speed, compared to one-at-a-time curation of individual genes. This allows us to maintain standards of high-quality manual annotation while efficiently using the time of volunteer curators.

- Participants: Florian Lajus, David Sherman, Natalia Golenetskaya, Pascal Durrens and Xavier Calcas
- Partners: Université de Bordeaux - CNRS - INRA
- Contact: David James Sherman
- URL: http://magus.gforge.inria.fr

5.2. Mimoza

KEYWORDS: Systems Biology - Bioinformatics - Biotechnology
FUNCTIONAL DESCRIPTION

Mimoza uses metabolic model generalization and cartographic paradigms to allow human experts to explore a metabolic model in a hierarchical manner. The software creates an zoomable representation of a model submitted by the user in SBML format. The most general view represents the compartments of the model, the next view shows the visualization of generalized versions of reactions and metabolites in each compartment , and the most detailed view visualizes the initial model with the generalization-based layout (where similar metabolites and reactions are placed next to each other). The zoomable representation is implemented using the Leaflet JavaScript library for mobile-friendly interactive maps. Users can click on reactions and compounds to see the information about their annotations. The resulting map can be explored on-line, or downloaded in a COMBINE archive.

- Participants: Anna Zhukova and David James Sherman
- Contact: David James Sherman
- URL: http://mimoza.bordeaux.inria.fr/

5.3. Pantograph

KEYWORDS: Systems Biology - Bioinformatics - Genomics - Gene regulatory networks
FUNCTIONAL DESCRIPTION

Pantograph is a software toolbox to reconstruct, curate and validate genome-scale metabolic models. It uses existing metabolic models as templates, to start its reconstructions process, to which new, species-specific reactions are added. Pantograph uses an iterative approach to improve reconstructed models, facilitating manual curation and comparisons between reconstructed model's predictions and experimental evidence.

Pantograph uses a consensus procedure to infer relationships between metabolic models, based on several sources of orthology between genomes. This allows for a very detailed rewriting of reaction's genome associations between template models and the model you want to reconstruct.

- Participants: Nicolas Loira, Anna Zhukova, David James Sherman and Pascal Durrens
- Partner: University of Chile
- Contact: Nicolas Loira
- URL: http://pathtastic.gforge.inria.fr/

5.4. biorica

KEYWORDS: Systems Biology - Bioinformatics - Hierarchical models - Hybrid models - Stochastic models
FUNCTIONAL DESCRIPTION

BioRica is used to mathematically describe the behavior of complex biological systems.

It is a software platform that permits simulation of biological systems on the basis of their description. It allows one to reuse existing biological models and to combine them into more complex models.

- Partner: University of Chile
- Contact: David Sherman
- URL: http://biorica.gforge.inria.fr/

5.5. Platforms

5.5.1. Plafrim

Plafrim (http://plafrim.fr) is an essential instrument for PLEIADE. We use it for developing software data analysis methods and evaluating them at real world scale. The platform combines considerable computing power with excellent support, both in terms of the quality of the interactions with the local staff and of the ease of large-scale data transfer between Plafrim and PLEIADE's data storage infrastructure. Plafrim facilitates collaboration between team members who are not in the Bordeaux Sud-Ouest building, and furthermore allows us to share best practices and tools with other teams from the Center.

5.5.2. Inria forge and Inria continuous integration

The Inria forge (http://gforge.inria.fr) provides a secure collaboration platform for software project administration and source code management, and Inria's continuous integration platform (http://ci.inria.fr) provides a cloud-based service for automatic compilation and testing of software systems. PLEIADE uses these two services extensively for agile software development. The continuous integration platform allows us to verify the correct operation of our methods in different operating system and deployment environments.

POEMS Project-Team

5. New Software and Platforms

5.1. COFFEE

FUNCTIONAL DESCRIPTION

COFFEE is a 3D solver for linear elastodynamics based on fast BEMs (full implementation in Fortran 90). The 3-D elastodynamic equations are solved with the boundary element method accelerated by the multi-level fast multipole method or H-matrix based solvers. The fundamental solutions for the infinite or half-space are used. A boundary element-boundary element coupling strategy is also implemented so multi-region problems (strata inside a valley for example) can be solved.

- Contact: Stéphanie Chaillat
- URL: http://perso.ensta-paristech.fr/ chaillat/index.php?page=softwares

5.2. XLiFE++

FUNCTIONAL DESCRIPTION

XLiFE++ is a Finite Element library written in C++ based on a variational approach and standard finite element methods, boundary element methods, spectral approximations. It allows to mix these different methods in a easy way to deal with complex models. A new version (v1.3) has been released in December 2015 but it is still in progress. This year, the main new features are: finite elements at any order (before, they were available up to order 6), some edge elements at any order (Raviart-Thomas, Nedelec), more stable boundary element methods. The performance was highly improved and first tests with multithreading (using OpenMP) have been done. At last, a lot of work to improve and stabilize user interface was done about mesh integrated tools, solvers, and external libraries installation. To make further progress in BEM methods (FMM, H Matrix, SCSD), a DGA project started in October 2015 in collaboration with MyBEM software team at CMAP (François Allouges, Matthieu Aussal, ...). Nicolas Salles has been recruited to enhance the BEM part of XLiFE++.

- Contact: Eric Lunéville
- URL: http://uma.ensta-paristech.fr/soft/XLiFE++/

POLSYS Project-Team

5. New Software and Platforms

5.1. FGb

FUNCTIONAL DESCRIPTION

FGb is a powerful software for computing Groebner bases.It includes the new generation of algorihms for computing Gröbner bases polynomial systems (mainly the F4,F5 and FGLM algorithms).It is implemented in C/C++ (approximately 250000 lines), standalone servers are available on demand. Since 2006, FGb is dynamically linked with Maple software (version 11 and higher) and is part of the official distribution of this software.

- Participant: Jean-Charles Faugère
- Contact: Jean-Charles Faugère
- URL: http://polsys.lip6.fr/~jcf/Software/FGb/index.html

5.2. FGb Light

- Participant: Jean-Charles Faugère
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/Software/FGb/

5.3. GBLA

FUNCTIONAL DESCRIPTION

GBLA is an open source C library for linear algebra specialized for eliminating matrices generated during Gröbner basis computations in algorithms like F4 or F5.

- Contact: Brice Boyer
- URL: http://www-polsys.lip6.fr/~jcf/Software/index.html

5.4. RAGlib

FUNCTIONAL DESCRIPTION

RAGLib is a Maple library for solving over the reals polynomial systems and computing sample points in semi-algebraic sets.

- Contact: Mohab Safey El Din
- URL: http://www-polsys.lip6.fr/~safey/RAGLib

5.5. SLV

FUNCTIONAL DESCRIPTION

SLV is a software package in C that provides routines for isolating (and subsequently refine) the real roots of univariate polynomials with integer or rational coefficients based on subdivision algorithms and on the continued fraction expansion of real numbers. Special attention is given so that the package can handle polynomials that have degree several thousands and size of coefficients hundrends of Megabytes. Currently the code consists of $\sim 5\,000$ lines.

- Contact: Elias Tsigaridas
- URL: http://www-polsys.lip6.fr/~elias/soft.html

POPIX Team

6. New Software and Platforms

6.1. Clinical Trial Simulator

KEYWORDS: Statistics - Bioinformatics - Drug development
FUNCTIONAL DESCRIPTION

A clinical trial simulator (CTS) enables effective implementation of the learn-and-confirm paradigm in drug development. Through simulations the anticipated success rate of a future trial can be estimated. For various reasons industry has not embraced currently available software for trial simulation. A new tool is essential for Model Based Drug Development (MBDD).

POPIX is developing the mlxR R package for the model based simulation of clinical trials.

- Participants: Marc Lavielle
- URL: http://simulx.webpopix.org

6.2. Monolix

KEYWORDS: Statistics - Bioinformatics - Health - Drug development
FUNCTIONAL DESCRIPTION

MONOLIX is an easy, fast and powerful tool for parameter estimation in nonlinear mixed-effect models, model diagnosis and assessment, and advanced graphical representation. It is a platform of reference for model-based drug development. Pharmacometricians and biostatisticians can rely on MONOLIX for population analysis and to model PK/PD and other complex biochemical and physiological processes.

MONOLIX was developed by Inria until June 2011. The start-up Lixoft now develops and supports MONOLIX. POPIX collaborates closely with Lixoft to convert research results into new user features available in MONOLIX.

A first extension of MONOLIX for partial differential equations (PDEs) based models was developed by POPIX in 2015.

- Participants: Marc Lavielle, Raphael Kuate

6.3. MLXtran

KEYWORDS: Statistics - Bioinformatics - Health - Drug development
FUNCTIONAL DESCRIPTION

Monolix is associated with MLXtran, a powerful and immediately readable declarative language for describing complex pharmacometric and statistical models. MLXtran can be used and interfaced with various environments, e.g., R, Matlab, etc.

POPIX collaborates closely with Lixoft on the definition of the specifications and the syntax of MLXtran. Implementation is then ensured by Lixoft.

- Participants: Marc Lavielle

POSET Team

6. New Software and Platforms

6.1. i-score

The *i-score* software, whose first definition dates back to 2005 [1], [6], aims at offering graphical views, aka *scores*, of interactive system. It has already been used to experiment various graphical user interface proposals to define time constraints between processes. It has been the subject of Jaime Arias's PhD [11]. Several formalizations of its semantics have been proposed [36], [20], [21], [19]. In 2016, especially within the ADT project "Tuilage", *i-score* independent modules should be identified and integrated as possible GUIs for the *T-calculus*.

6.2. T-calculus

Sketched in [9], the *T-calculus* is a Domain Specific Language [0] to provide simple and robust high-level description mechanisms of reactive systems. It will offer a programmatic view of the tile modeling paradigm [3], [8]. Its definition has been refined a number of times (see e.g. [9], [7] and [30], [18]). A prototype implementation of its reactive kernel has eventually been achieved in Haskell on top of the Euterpea libraries by the end of 2015. Its consolidation and further developments are now scheduled for 2016, especially within the ADT project "Tuilage". Graphical representation of tiles should give rise to a robust correspondance between programmatic and graphical representations of reactive systems.

---

[0] See [40] for an early note by Hudak about the notion of Domain Specific Language, and see [39], [42] for application of this notion is computer music.

POSTALE Team

5. New Software and Platforms

5.1. Boost.SIMD

FUNCTIONAL DESCRIPTION

Boost.SIMD provides a portable way to vectorize computation on Altivec, SSE or AVX while providing a generic way to extend the set of supported functions and hardwares.

- Contact: Joël Falcou
- URL: http://www.github.com/MetaScale/nt2

5.2. CovTrack

FUNCTIONAL DESCRIPTION

CovTrack: agile realtime multi-target tracking algorithm.

- Contact: Lionel Lacassagne

5.3. Dohko

FUNCTIONAL DESCRIPTION

Dohko is a goal-oriented cloud architecture that aims to simplify the cloud for the users through a declarative strategy. It implements the autonomic properties: self-configuration, self-healing, and context-awareness. In Dohko, the users specify the applications and the requirements (e.g., number of CPU cores, maximal financial cost per hour, among others), and the system automatically (a) selects the resources (i.e., VMs) that meet the constraints, (b) configures and installs the applications in the clouds, (c) handles resource failures, and (d) executes the applications.

- Contact: Alessandro Ferreira Leite
- URL: http://dohko.io/

5.4. Molly

FUNCTIONAL DESCRIPTION

Using Polly extension, the LLVM compiler framework is able to automatically parallelize general programs for shared memory threading for by exploiting the powerful analysis and transformations of the polyhedral model.

Molly adds the ability to manage distributed memory using the polyhedral model and is therefore able to automatically parallelize even for the largest of today's supercomputer. Once the distribution of data between the computer's nodes is known, Molly determines the values that are required to be transferred between the nodes and chunks them into as few messages as possible. It also keeps tracks of the buffers required by the MPI interface. Transfers are asynchronous such that further computations take place while the data is being transferred.

- Contact: Michael Kruse

5.5. MyNRC

FUNCTIONAL DESCRIPTION

MyNRC is multi-plateform library that can handle SSE, AVX, Neon and ST VECx registers.

- Contact: Lionel Lacassagne

5.6. NT2

Numerical Template Toolbox

FUNCTIONAL DESCRIPTION

The Numerical Template Toolbox (NT2) is an Open Source C++ library aimed at simplifying the development, debugging and optimization of high-performance computing applications by providing a Matlab like syntax that eases the transition between prototype and actual application.

- Participants: Joël Falcou, Pierre Estérie and Ian Masliah
- Contact: Joël Falcou
- URL: https://github.com/jfalcou/nt2

POTIOC Project-Team

6. New Software and Platforms

6.1. OpenVIBE

KEYWORDS: Neurosciences - Interaction - Virtual reality - Health - Real time - Neurofeedback - Brain-Computer Interface - EEG - 3D interaction

FUNCTIONAL DESCRIPTION

OpenViBE is a software platform for real-time neurosciences (that is, for real-time processing of brain signals). It can be used to acquire, filter, process, classify and visualize brain signals in real time from various signal sources. OpenViBE is free and open source software. It works on Windows and Linux operating systems.

- Participants: Yann Renard, Anatole Lécuyer, Fabien Lotte, Bruno Renier, Vincent Delannoy, Laurent Bonnet, Baptiste Payan, Jozef Legény, Jussi Tapio Lindgren, Alison Cellard, Loïc Mahé, Guillaume Serriere, Marsel Mano, Maureen Clerc Gallagher, Théodore Papadopoulo, Laurent Bougrain, Jérémy Frey, Nathanael Foy
- Partners: INSERM - CEA-List - GIPSA-Lab
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

In 2015, the first stable version of the OpenViBE software, OpenViBE version 1.0.0, was released. OpenViBE 1.0.0 features lots of fixes for stability and usability. There has been a significant effort in cleanup and removal of unused components and dead code. This version introduces more tools for communicating with other software, added support for some new, emerging acquisition systems, such as OpenBCI and new signal processing algorithms such as Wavelet decomposition and artifact removal boxes. Link: http://openvibe.inria.fr/openvibe-1-0-0-has-been-released/

6.2. Platforms

6.2.1. AMI

Augmented Michelson Interferometer

SCIENTIFIC DESCRIPTION

We have developed a hybrid plateform that merges physical and virtual elements for teaching optics. This work is described in more details in Section 7.6

- Participants: David Furio, Martin Hachet, Patrick Reuter and Bruno Bousquet
- Partners: Université de Bordeaux - LaBRI
- Contact: Martin Hachet
- URL: https://team.inria.fr/potioc/fr/2015/06/30/hobit-hybrid-optical-bench-for-innovative-teaching

PRIMA Project-Team

5. New Software and Platforms

5.1. OMiSCID

An Object Oriented Open-Source Middleware for Service Communication Inspection and Discovery

- Participants: Patrick Reignier, Dominique Vaufreydaz, Amaury Negre,
- Contact: Dominique Vaufreydaz
- URL: http://omiscid.gforge.inria.fr/

KEYWORDS: Middleware - Pervasive computing - Service Oriented Software (SOA)
FUNCTIONAL DESCRIPTION

OMiSCID is lightweight middleware for dynamic integration of perceptual services in interactive environments. This middleware abstracts network communications and provides service introspection and discovery using DNS-SD (DNS-based Service Discovery). Services can declare simplex or duplex communication channels and variables. The middleware supports the low-latency, high-bandwidth communications required in interactive perceptual applications. It is designed to allow independently developed perceptual components to be integrated to construct user services. Thus our system has been designed to be cross-language, cross-platform, and easy to learn. It provides low latency communications suitable for audio and visual perception for interactive services.

5.2. AppsGate

FUNCTIONAL DESCRIPTION

The AppsGate architecture is based on the HMI Middleware developed in cooperation with the IIHM and Adele groups of the UMR Laboratoire Informatique de Grenoble (LIG). The HMI Middleware is designed to facilitate the development of end-user applications on top of the core software components described in the sections above, while ensuring service continuity and usability. The key features of the HMI Middleware include:

Integration of sensors and actuators managed by a variety of protocols, and provision of a uniform abstraction for these devices as component-oriented-services,

Integration of Web services made available on the cloud by a variety of web service providers, and provision of a uniform abstraction for these services as component-oriented-services,

Communication between the HMI middleware and client applications - typically, user interfaces for controlling and programming the smart home, that run on high-end devices such as smartphones, tablets, and TVs.

- Participants: Alexandre Demeure, James Crowley, Eméric Grange, Cédric Gérard, Camille Lenoir and Kouzma Petoukhov
- Contact: James Crowley, Alexandre Demeure
- http://iihm.imag.fr/demos/appsgate/appsgate2013.mp4
- http://www.catrene.org/web/downloads/profiles_catrene/CATRENE PP-CA110_AppsGate.pdf

5.3. SPOK

SPOK: Simple Programming Kit pour Smart Homes
KEYWORDS: End User Development - Smart Home

- Contact: James Crowley, Alexandre Demeurre

SPOK is an End-User Development Environment that permits people to monitor, control, and configure smart home services and devices. SPOK provides the end-user with the following services: (1) A syntax-oriented program editor that enforces the construction of syntactically-correct programs (see sidebar on next page). (2) A program interpreter and a clock simulator to test program execution in “simulated time”. (3) Debugging aids to support the detection and correction of programming errors or system malfunctions along with a Trace Manager. (4) A dashboard to remotely control devices and programs in a centralized and uniform manner.

Compared to the state-of-the art, the key features of SPOK are thee-fold: Expressive power of the SPOK language along with a pseudo-natural concrete syntax, dynamic adaptation to the arrival/departure of devices and services, and debugging aids.

SPOK was developed as part of the EU CATRENE APPSGATE project (CA 110) and is supported by the EquipEx AmiQual4Home, ANR-11-EQPX-00.

5.4. DomiCube

- Participant: Remi Pincent
- Contact: Remi Pincent
- https://amiqual4home.inria.fr/domicube/

The DomiCube is a home-made device designed by 5 retired seniors as the result of a 3 hour focus group. It contains an accelerometer and a gyroscope, and is Bluetooth enabled. It sends events when its state changes (e.g., new orientation, top face, and battery level). The DomiCube was built in the Creativity Lab of the EquipEx AmiQual4Home, ANR-11-EQPX-00.

5.5. EmoPRAMAD

KEYWORDS: Health - Home care

- Contact: Dominique Vaufreydaz
- https://pramad.inria.fr

FUNCTIONAL DESCRIPTION

Within the Pramad project, we want to offer a full affective loop between the companion robot and the elderly people at home. This affective loop is necessary within the context of everyday interaction of elderly and the companion robot. A part of this loop is to make the robot express emotions in response to the emotional state of the user. To do that, we need to test our working hypothesis about the visual representation of emotions with the 3D face of robot. EmoPRAMAD is an evaluation tool designed to conduct comparative studies between human faces and the 3D faces expressing a defined set of emotions.

The evaluation conducted though EmoPRAMAD concerns both unimodal (facial only) and bimodal conditions (facial/sound). The emotions set is composed of 4 basic emotions (joy, fear, anger, sadness) and a neutral state. While experimenting, the software collects several parameters in order to evaluate more than correctness of the answers: time to respond, length of mouse moves, etc.

5.6. MobileRGBD

KEYWORDS: Benchmark corpus - Health - Home Care

- Contact: Dominique Vaufreydaz
- http://mobilergbd.inrialpes.fr

FUNCTIONAL DESCRIPTION

MobileRGBD is corpus dedicated to low level RGB-D algorithms benchmarking on mobile platform. We reversed the usual corpus recording paradigm. Our goal is to facilitate ground truth annotation and reproducibility of records among speed, trajectory and environmental variations. As we want to get rid of unpredictable human moves, we used dummies in order to play static users in the environment (see figure). Interest of dummies resides in the fact that they do not move between two recordings. It is possible to record the same robot move in order to evaluate performance of detection algorithms varying speed. This benchmark corpus is intended for «low level» RGB-D algorithm family like 3D-SLAM, body/skeleton tracking or face tracking using a mobile robot. Using this open corpus, researchers can find a way to answer several questions: System performance under variations in operating conditions? on a mobile robot, what is the maximum linear/angular speed supported by the algorithm? which variables impact the algorithm? evaluate suitable height/angle of the mounted RGB-D sensor to reach goals: monitoring everyday live is different from searching fallen persons on the floor; finally, what is the performance on an algorithm with regards to others?

5.7. Online Movie Director

- Participants: Patrick Reignier, Dominique Vaufreydaz and James Crowley
- Contact: Dominique Vaufreydaz

Online Movie director is a network online video editing program. It can handle several video and audio streams over the network and resynchronize them to produce a video either for streaming or either for direct video production. The system can record lectures using multiple cameras and microphones. The system uses PRIMA techniques for modelling context to select the most appropriate camera and microphone, based on the current situation.

5.8. PALGate

KEYWORDS: Health - Home care - Handicap

- Contact: Dominique Vaufreydaz, Amaury Negre
- https://pal.inria.fr

A part of our efforts in the PAL project has been put toward developing a solution that would ease the integration of our multi-partners' software components.

The design of PAL Middleware responds to a requirement that within the PAL project, each partner is responsible for maintaining 1) its software heritage 2) its resources 3) its competences and fields of research and expertise; 4) current practices in terms of programming language, (c/c++, Java, Python), computing platforms (OSx, Linux, Windows, Android, etc.) and interconnect software components (OSGi, OMiSCID, MPI, PVM, etc.); and 5) its particular needs and constraints.

For it to be widely accepted, the PAL middleware must be designed to be ecologic and pragmatic. Ecologic in the sense that the solution does not perturb the ecology of each ecosystem, pragmatic in the sense that setting up this solution did not require an heavy development effort, also because PAL and is required to reuse existing software solutions.

For developing PALGate we introduced a novel concept: software gate. Unlike software components/services which can be instantiated, a software gate is only a concept, it is defined as an ecologic and hermetic interface between different ecosystems. A software gate is characterized by the subset of functionalities it exposes to other gates, where the functionalities it exposes are provided by the software components/services of its belonging ecosystem. A software gate is hermetic in the sense that only a selected subset of functionalities of an ecosystem are exposed but also because it propagates only filtered information exposed by other gates into its ecosystem. The last characteristic of a software gate is that it makes explicit to other gates the communication mechanisms it uses.

While a software gate is only conceptual, the PAL middleware is an implementation of a gate oriented middleware. The PAL Middleware uses ROS to support the basic communication between gates. Within PALGate, each ecosystem is associated to only one software gate. Practically, PAL middleware 1) is a ROS stack containing gates definition 2) is a set of conventions (e.g. stack organization, package/node/topic/service names, namespaces, etc.) 3) it provides dedicated tools to ease the integration and its usage by partners. A software gate in PAL is a ROS package containing definition of ROS types (i.e. msgs and srvs types), but also exposed ROS communication channels (i.e. topics and RPCs).

With this architecture each partner has to provide the PAL middleware with a package containing the definition of its gate. Then in order a) to expose functionalities out of their ecosystem and b) to propagate information into their ecosystem, each partner must create ROS nodes. These ROS nodes let each partner interface their ecosystem through ROS topics and ROS services without having to change anything about their architecture. For instance if a partner is using Java and OSGi, it can create nodes in ROS Java that will expose/register functionalities through ROS services, publish/subscribe information using ROS topics.

5.9. PERFECT MATCH STEREO

- Participants: Frédéric Devernay, Pau Gargallo and Sergi Pujades
- Contact: Frédéric Devernay

5.10. PrimaCV

- Participants: Rémi Barraquand, Claudine Combe, Lukas Rummelhard, Amaury Negre, Sergi Pujades-Rocamora and James Crowley
- Contact: James Crowley

FUNCTIONAL DESCRIPTION

PrimaCV is a software library for detecting, observing and tracking faces and emotions using the cameras on mobile devices. The PrimaCV library uses a scale invariant pyramid to construct receptive field descriptors for images. These are used by a coarse to fine multiscale "scanning window" face detector constructed as a cascade classifier constructed using an highly optimised version of Ada Boost. Because the system uses coarse to fine search within a scale invariant pyramid it automatically adapts to the number of pixels and scale of the imager. The coarse-to-fine search algorithm has been shown to provide a dramatic gain in performance over classic scanning window detectors. The algorithm produces a probability of a face for each possible scale and position in the image. Local maximum in probability are fed to a Bayesian face tracker.

Normalized imagettes of tracked faces can be fed to procedures for estimating face orientation, recognising identity, estimating parameters of emotions.

5.11. STEREO VIEWFINDER

FUNCTIONAL DESCRIPTION

Stereoscopy, Auto-calibration, Real-time video processing, Feature matching

- Participants: Frédéric Devernay, Loïc Lefort, Elise Mansilla and Sergi Pujades
- Contact: Frédéric Devernay

5.12. SmartEnergy

FUNCTIONAL DESCRIPTION

Inhabitants play a key role in buildings global energy consumption but it is difficult to involve them in energy management. Our objective is to make energy consumption visible by simulating inside a serious game the energy impact of inhabitants behaviours. A serious game is currently under development, coupling a 3D virtual environment and a building energy simulator. The 3D virtual environment is based on the JMonkey 3D engine. New houses can be easily imported using SweetHome 3D and Blender. The building energy simulator is EnergyPlus. The 3D engine and the energy engine are coupled using the Functional Mock-up Interface (FMI) standard. Using this standard will allow to easily switch between existing building energy simulators.

- Participant: Patrick Reignier
- Contact: Patrick Reignier

5.13. SmartServoFramework

- Participants: Dominique Vaufreydaz and Eméric Grange
- Contact: Dominique Vaufreydaz
- https://github.com/emericg/SmartServoFramework

SmartServoFramework is a C++ multiplatform framework used to drive "smart servo" devices such as Dynamixel or HerkuleX actuators. The Framework, developed by members of the PRIMA team supports Linux (and most Unix systems), Mac OS X and Windows operating systems. SmartServoFramework can run on Raspberry Pi or other similar boards. This framework can be used with any Dynamixel or HerkuleX devices. Dynamixel devices from Robotis and HerkuleX devices from Dongbu Robot are high-performance networked actuators for robots available in wide range of sizes and strengths. They have adjustable torque, speed, angle limits, and provide various feedback like position, load, voltage and temperature.

PRIVATICS Project-Team

5. New Software and Platforms

5.1. Mobilitics

FUNCTIONAL DESCRIPTION

Mobilitics is a joint project, started in 2012 between Inria and CNIL, which targets privacy issues on smartphones. The goal is to analyze the behavior of smartphones applications and their operating system regarding users private data, that is, the time they are accessed or sent to third party companies usually neither with user's awareness nor consent.

In the presence of a wide range of different smartphones available in terms of operating systems and hardware architecture, Mobilitics project focuses actually its study on the two mostly used mobile platforms, IOS (Iphone) and Android. Both versions of the Mobilitics software: (1) capture any access to private data, any modification (e.g., ciphering or hashing of private data), or transmission of data to remote locations on the Internet, (2) store these events in a local database on the phone for offline analysis, and (3) provide the ability to perform an in depth database analysis in order to identify personnal information leakage.

- Authors: Jagdish Achara, James-Douglass Lefruit, Claude Castelluccia, Vincent Roca, Gwendal Le Grand, Geoffrey Delcroix, Franck Baudot and Stéphane Petitcolas
- Contact: Claude Castelluccia
- URL: https://team.inria.fr/privatics/fr/mobilitics/

5.2. OMEN+

FUNCTIONAL DESCRIPTION

Omen+ is a password cracker following our previous work. It is used to guess possible passwords based on specific information about the target. It can also be used to check the strength of user password by effectively looking at the similarity of that password with both usual structures and information relative to the user, such as his name, birth date...

It is based on a Markov analysis of known passwords to build guesses. The previous work Omen needs to be cleaned in order to be scaled to real problems and to be distributed or transfered to the security community (maintainability): eventually it will become an open source software. The main challenge of Omen+ is to optimize the memory consumption.

- Participants: Pierre Rouveyrol and Claude Castelluccia
- Contact: Claude Castelluccia

5.3. OPENFEC

FUNCTIONAL DESCRIPTION

OpenFEC is an open-source C-language implementation of several Application-Level Forward Erasure Correction (AL-FEC) codecs, namely: 2D-parity, Reed-Solomon (RFC 5510) and LDPC-Staircase (RFC 5170) codes. The OpenFEC project also provides a complete performance evaluation tool-set, capable of automatically assessing the performance of various codecs, both in terms of erasure recovery and encoding/decoding speed or memory consumption.

- Participants: Mathieu Cunche, Jonathan Detchart, Julien Laboure, Christophe Neumann, Vincent Roca, Jérome Lacan and Kevin Chaumont
- Contact: Vincent Roca
- URL: http://openfec.org/

5.4. FECFRAME

FUNCTIONAL DESCRIPTION

FECFRAME implements IETF FECFRAME (RFC 6363). It allows to transmit multimedia streams to one or severals receivers at the same time while being robust to packet losses occurring on the network (par ex. 3G/4G or Wifi). This software is compatible with OpenFec which provides error-correcting codes.

- Participants: Vincent Roca
- Contact: Vincent Roca

5.5. WALTER

Walter experiment: "Is My Web Content Altered?". A web based tool detecting the unwanted injection of scripts and other contents in unencrypted webpages.

FUNCTIONAL DESCRIPTION

Disputable network agents, namely free Wi-Fi hotspots providers such as those found in airports or coffee shops, have been found to monetize their networks by injecting advertisements and trackers into their customers' traffic. Such adverts are served by network agents instead of website publishers. This is a relatively new approach, and we are trying to determine its usage worldwide. This website is designed to assess whether your internet connection is affected by such practices. We also detect local page alterations that come from browser extensions and programs that may run on your machine.

- Participants: Mathieu Cunche, Leo Letaro.
- Contact: Mathieu Cunche

PROSECCO Project-Team

6. New Software and Platforms

6.1. ProVerif

Participants: Bruno Blanchet [correspondant], Xavier Allamigeon [April–July 2004], Vincent Cheval [Sept. 2011–], Benjamin Smyth [Sept. 2009–Feb. 2010].

PROVERIF (http://proverif.inria.fr) is an automatic security protocol verifier in the symbolic model (so called Dolev-Yao model). In this model, cryptographic primitives are considered as black boxes. This protocol verifier is based on an abstract representation of the protocol by Horn clauses. Its main features are:

- It can handle many different cryptographic primitives, specified as rewrite rules or as equations.
- It can handle an unbounded number of sessions of the protocol (even in parallel) and an unbounded message space.

The PROVERIF verifier can prove the following properties:

- secrecy (the adversary cannot obtain the secret);
- authentication and more generally correspondence properties, of the form “if an event has been executed, then other events have been executed as well”;
- strong secrecy (the adversary does not see the difference when the value of the secret changes);
- equivalences between processes that differ only by terms.

PROVERIF is widely used by the research community on the verification of security protocols (see http://proverif.inria.fr/proverif-users.html for references).

PROVERIF is freely available on the web, at http://proverif.inria.fr, under the GPL license.

6.2. CryptoVerif

Participants: Bruno Blanchet [correspondant], David Cadé [Sept. 2009–].

CRYPTOVERIF(http://cryptoverif.inria.fr) is an automatic protocol prover sound in the computational model. In this model, messages are bitstrings and the adversary is a polynomial-time probabilistic Turing machine. CRYPTOVERIF can prove secrecy and correspondences, which include in particular authentication. It provides a generic mechanism for specifying the security assumptions on cryptographic primitives, which can handle in particular symmetric encryption, message authentication codes, public-key encryption, signatures, hash functions, and Diffie-Hellman key agreements.

The generated proofs are proofs by sequences of games, as used by cryptographers. These proofs are valid for a number of sessions polynomial in the security parameter, in the presence of an active adversary. CRYPTOVERIF can also evaluate the probability of success of an attack against the protocol as a function of the probability of breaking each cryptographic primitive and of the number of sessions (exact security).

CRYPTOVERIF has been used in particular for a study of Kerberos in the computational model, and as a back-end for verifying implementations of protocols in F# and C.

CRYPTOVERIF is freely available on the web, at http://cryptoverif.inria.fr, under the CeCILL license.

6.3. miTLS

Participants: Karthikeyan Bhargavan [correspondant], Antoine Delignat-Lavaud, Cedric Fournet [Microsoft Research], Markulf Kohlweiss [Microsoft Research], Alfredo Pironti, Pierre-Yves Strub [IMDEA], Santiago Zanella-Béguelin [Microsoft Research], Jean Karim Zinzindohoue.

miTLS is a verified reference implementation of the TLS security protocol in F#, a dialect of OCaml for the .NET platform. It supports SSL version 3.0 and TLS versions 1.0-1.2 and interoperates with mainstream web browsers and servers. miTLS has been verified for functional correctness and cryptographic security using the refinement typechecker F7.

A paper describing the miTLS library was published at IEEE S&P 2013, CRYPTO 2014, and several updates to the software were released in 2015. The software and associated research materials are available from http://mitls.org.

6.4. flexTLS

Participants: Karthikeyan Bhargavan [correspondant], Alfredo Pironti, Benjamin Beurdouche.

flexTLS is a TLS testing framework based on miTLS, and is released as part of the miTLS distribution. Unlike miTLS, flexTLS can be configured to run incorrect TLS clients and servers in order to test other TLS implementations. Using flexTLS we analyzed a series of open source TLS implementations and found important vulnerabilities like SKIP and FREAK. We also used flexTLS to build proof-of-concept demos for other attacks such as Logjam.

A paper describing flexTLS was published at Usenix WOOT 2015. The software and associated research materials are available from http://mitls.org.

6.5. F*

Participants: Nikhil Swamy [Microsoft Research], Karthikeyan Bhargavan, Antoine Delignat-Lavaud, Cedric Fournet [Microsoft Research], Catalin Hritcu, Chantal Keller, Aseem Rastogi, Pierre-Yves Strub.

F* is a new higher order, effectful programming language (like ML) designed with program verification in mind. Its type system is based on a core that resembles System Fω (hence the name), but is extended with dependent types, refined monadic effects, refinement types, and higher kinds. Together, these features allow expressing precise and compact specifications for programs, including functional correctness properties. The F* type-checker aims to prove that programs meet their specifications using an automated theorem prover (usually Z3) behind the scenes to discharge proof obligations. Programs written in F* can be translated to OCaml, F#, or JavaScript for execution.

A detailed description of F* (circa 2011) appeared in the Journal of Functional Programming [53]. F* has evolved substantially since then. The latest version of F* is written entirely in F*, and bootstraps in OCaml and F#. It is under active development at GitHub: https://github.com/FStarLang and the official webpage is at http://fstar-lang.org.

6.6. ProScript

Participants: Nadim Kobeissi [correspondant], Karthikeyan Bhargavan, Bruno Blanchet.

Defensive JavaScript (DJS) is a subset of the JavaScript language that guarantees the behaviour of trusted scripts when loaded in an untrusted web page. Code in this subset runs independently of the rest of the JavaScript environment. When propertly wrapped, DJS code can run safely on untrusted pages and keep secrets such as decryption keys. ProScript is a typed subset of JavaScript, inspired by DJS, that is focused on writing verifiable cryptographic protocol implementations. In addition to DJS typing, ProScript imposes a functional style that results in more readable and easily verifiable ProVerif models. ProScript has been used to write and verify a full implementation of the TextSecure protocol in JavaScript.

The ProScript compiler and various libraries written in ProScript will be made available from the Prosecco webpage.

QUANTIC Project-Team (section vide)

RAP Project-Team (section vide)

RAPSODI Team

6. New Software and Platforms

6.1. New Software and Platforms

We develop and freely distribute a new version of the matlab code NS2DDV-M (equipped with a graphic interface and an accurate documentation) to promote new collaborations in the domain, allow some easy comparisons with concurrent codes on the same benchmark cases, and compare alternative numerical solution methods. Contacts: Caterina Calgaro & Emmanuel Creusé.

REALOPT Project-Team

6. New Software and Platforms

6.1. BaPCod : a generic Branch-And-Price Code

KEYWORDS: Column Generation - Branch-and-Price - Branch-and-Cut - Mixed Integer Programming - Mathematical Optimization - Benders Decomposition - Dantzig-Wolfe Decomposition - Extended Formulation

FUNCTIONAL DESCRIPTION: BaPCod is a prototype code that solves Mixed Integer Programs (MIP) by application of reformulation and decomposition techniques. The reformulated problem is solved using a branch-and-price-and-cut (column generation) algorithm, Benders approaches, or network flow algorithms.

- Participants: Francois Vanderbeck, Ruslan Sadykov, Issam Tahiri, Artur Alves Pessoa, Boris Detienne, François Clautiaux, Pierre Pesneau, Eduardo Uchoa Barboza and Michael Poss
- Partners: Université de Bordeaux - CNRS - IPB - Universidade Federal Fluminense
- Contact: Francois Vanderbeck
- URL: https://realopt.bordeaux.inria.fr/?page_id=2

REGAL Project-Team

5. New Software and Platforms

5.1. Antidote

FUNCTIONAL DESCRIPTION

Antidote is the flexible cloud database platform currently under development in the SyncFree European project. Antidote aims to be both a research platform for studying replication and consistency at the large scale, and an instrument for exploiting research results. The platform supports replication of CRDTs, in and between sharded (partitioned) data centres (DCs). The current stable version supports strong transactional consistency inside a DC, and causal transactional consistency between DCs. Ongoing research includes support for explicit consistency [37], [50], for elastic version management, for adaptive replication, for partial replication, and for reconfigurable sharding.

- Participants: Tyler Crain, Marc Shapiro, Serdar Tasiran and Alejandro Tomsic
- Contact: Tyler Crain
- URL: https://github.com/SyncFree

5.2. G-DUR

FUNCTIONAL DESCRIPTION

A large family of distributed transactional protocols have a common structure, called Deferred Update Replication (DUR). DUR provides dependability by replicating data, and performance by not re-executing transactions but only applying their updates. Protocols of the DUR family differ only in behaviors of few generic functions. Based on this insight, we offer a generic DUR middleware, called G-DUR, along with a library of finely-optimized plug-in implementations of the required behaviors.

- Participants: Marc Shapiro, Alejandro Tomsic
- Contact: Marc Shapiro
- URL: https://github.com/msaeida/jessy

5.3. NumaGIC

FUNCTIONAL DESCRIPTION

NumaGiC is a version of the HotSpot garbage collector (GC) adapted to many-core computers with very large main memories. In order to maximise GC throughput, it manages the trade-off between memory locality (local scans) and parallelism (work stealing) in a self-balancing manner. Furthemore, the collector features several memory placement heuristics that improve locality.

- Participants: Lokesh Gidra, Marc Shapiro, Julien Sopena and Gaël Thomas
- Contact: Marc Shapiro
- URL: https://scm.gforge.inria.fr/anonscm/git/transgc/.

5.4. SwiftCloud

FUNCTIONAL DESCRIPTION

Client-side (e.g., mobile or in-browser) apps need local access to shared cloud data, but current technologies either do not provide fault-tolerant consistency guarantees, or do not scale to high numbers of unreliable and resource-poor clients, or both. Addressing this issue, the SwiftCloud distributed object database supports high numbers of client-side partial replicas. SwiftCloud offers fast reads and writes from a causally-consistent client-side cache. It is scalable, thanks to small and bounded metadata, and available, tolerating faults and intermittent connectivity by switching between data centres. The price to pay is a modest amount of staleness. A recent Inria Research Report (submitted for publication) presents the SwiftCloud algorithms, design, and experimental evaluation, which shows that client-side apps enjoy the same guarantees as a cloud data store, at a small cost.

- Participants: Marc Shapiro, Serdar Tasiran, Marek Zawirski and Mahsa Najafzadeh
- Contact: Marc Shapiro
- URL: git+ssh://scm.gforge.inria.fr//gitroot/swiftcloud

5.5. PUMA

FUNCTIONAL DESCRIPTION

PUMA is a system that is based on a kernel-level remote caching mechanism that provides the ability to pool VMs memory at the scale of a data center. An important property while lending memory to another VM, is the ability to quickly retrieve memory in case of need. Our approach aims at lending memory only for clean cache pages: in case of need, the VM which lent the memory can retrieve it easily. We use the system page cache to store remote pages such that: (i) if local processes allocate memory the borrowed memory can be retrieved immediately; and (ii) if they need cache the remote pages have a lower priority than the local ones.

- Participants: Maxime Lorrillere, Sébastien Monnet, Pierre Sens, Julien Sopena
- Contact: Maxime Lorrillere
- URL: https://github.com/mlorrillere/puma

REO Project-Team

6. New Software and Platforms

6.1. FELiScE

Finite Elements for Life SCiences and Engineering problems
KEYWORDS: Finite element modelling - Cardiac Electrophysiology - Cardiovascular and respiratory systems
FUNCTIONAL DESCRIPTION

FELiScE is a finite element code which the M3DISIM and REO project-teams have decided to jointly develop in order to build up on their respective experiences concerning finite element simulations. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex respiratory and cardiovascular models considered in the two teams – namely involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena. FELISCE is written in C++, and may be later released as an opensource library. FELiScE was registered in July 2014 at the Agence pour la Protection des Programmes under the Inter Deposit Digital Number IDDN.FR.001.350015.000.S.P.2014.000.10000.

- Participants: Dominique Chapelle, Miguel Angel Fernandez Varela, Jean-Frédéric Gerbeau, Philippe Moireau, Marina Vidrascu, Sébastien Gilles, Benoit Fabreges, Axel Fourmont, Mikel Landajuela Larma, Damiano Lombardi, Matteo Aletti, Irène Vignon-Clementel and Faisal Amlani
- Contact: Jean-Frédéric Gerbeau
- URL: http://felisce.gforge.inria.fr

6.2. LIFE-V

KEYWORD: Finite element modelling
FUNCTIONAL DESCRIPTION

LiFE-V is a finite element library providing implementations of state of the art mathematical and numerical methods. It serves both as a research and production library. LiFE-V is the joint collaboration between three institutions: Ecole Polytechnique Fédérale de Lausanne (CMCS) in Switzerland, Politecnico di Milano (MOX) in Italy and Inria (REO) in France. It is a free software under LGPL license.

- Participants: Jean-Frédéric Gerbeau and Miguel Angel Fernandez Varela
- Partners: EPFL - Ecole Polytechnique Fédérale de Lausanne - MOX Politecnico di Milano
- Contact: Miguel Angel Fernández Varela
- URL: http://www.lifev.org/

6.3. SHELDDON

SHELls and structural Dynamics with DOmain decomposition in Nonlinear analysis
FUNCTIONAL DESCRIPTION

SHELDDON is a finite element library based on the Modulef package which contains shell elements, nonlinear procedures and PVM subroutines used in domain decomposition or coupling methods, in particular fluid-structure interaction.

- Participants: Dominique Chapelle, Patrick Le Tallec and Marina Vidrascu
- Contact: Marina Vidrascu
- URL: https://gforge.inria.fr/projects/shelddon/

RITS Project-Team

6. New Software and Platforms

6.1. DOLAR

FUNCTIONAL DESCRIPTION

This software performs real-time obstacle detection and tracking using laser data scanned with one or several laser sensors with different geometric configurations. Obstacle detection is based on laser data segmentation while obstacle tracking uses PHD-based filtering techniques.

- Contact: Fawzi Nashashibi

6.2. MELOSYM

FUNCTIONAL DESCRIPTION

MELOSYM is the latest laser based Hierarchical ML-SLAM algorithm developed by RITS. It contains all the functions needed to perform the vehicle localization and the mapping of the environment. Windows compatible, it was initially developed under the RTMAPS platform but the version includes a standalone version.

- Participants: Fawzi Nashashibi, Benjamin Lefaudeux, Jianping Xie and Paulo Lopes Resende
- Contact: Benjamin Lefaudeux

6.3. PML-SLAM

- Participants: Zayed Alsayed and Fawzi Nashashibi
- Contact: Fawzi Nashashibi

6.4. STEREOLOC-3D

FUNCTIONAL DESCRIPTION

STEREOLOC is the package performing stereovision based localization and mapping. It performs semi-dense mapping of outdoor large environments and provides real-time estimates of the vehicle position.

- Participants: Benjamin Lefaudeux and Fawzi Nashashibi
- Contact: Fawzi Nashashibi

6.5. SODA

SOftwares for Driving Automation
KEYWORD: Environment perception
FUNCTIONAL DESCRIPTION

This software has been developed in the context of the French ABV (Automatisation Basse Vitesse) project. This package contains the functions that are necessary to automate the vehicle navigation in its secured lane.

- Participants: Paulo Lopes Resende and Fawzi Nashashibi
- Contact: Fawzi Nashashibi

6.6. AutoPathPlan

Automatic Path Planning Generation
FUNCTIONAL DESCRIPTION

Automatic method for a real time path planning generation path for automated vehicles.

- Participants: David Gonzalez Bautista, Joshué Pérez Rastelli and Vicente Milanés Montero
- Contact: Fawzi Nashashibi

6.7. FEMOT

Fuzzy Embedded MOTor

FUNCTIONAL DESCRIPTION

FEMOT is an experimental motor for implementing fuzzy logic controllers, including all the fuzzy stages (fuzzification, inference, and defuzzification). This library has been compiled in Microsoft Visual (MVS) Studio and RTMaps. The proposed library is modular and adaptable to different situations and scenarios, especially for autonomous driving applications. FEMOT allows the development of the fuzzy rules to be written as sentences in an almost natural language. It allows the user to define variables and their fuzzy rules and to join them with other variables in rules to yield crisp signals for the controllers.

This software is used for the arbitration and control for fully automated functions. The behaviour of a human driver can be emulated with this technique. First simulations are showing promising results, and the library allows an easy adaptation in decision marking situations.

- Participants: Joshué Pérez Rastelli and Vicente Milanés Montero
- Contact: Fawzi Nashashibi

6.8. Platools

KEYWORD: Telecommunications

- Participant: Marios Makassikis
- Contact: Thierry Ernst

6.9. V2Provue

Vehicle-to-Pedestrian

KEYWORD: vehicle-to-pedestrian communications

FUNCTIONAL DESCRIPTION

It is a software developed for the Vehicle-to-Pedestrian (V2P) communications, risk calculation, and alarming pedestrians of collision risk. This software is made of an Android application dedicated to pedestrians and RtMaps modules for the vehicles.

On the pedestrian side, the application is relying on GPS data to localize the user and Wi-Fi communications are used to receive messages about close vehicles and send information about the pedestrian positioning. Besides, a service has been developed to evaluate the collision risk with the vehicles near the pedestrian and an HMI based on OpenStreetMap displays all the useful information such as pedestrian and vehicles localization and, collision risk.

On the vehicle side, RtMaps modules allowing V2X communications have been developed. These modules contain features such as TCP/UDP socket transmissions, broadcast, multicast, unicast communications, routing, forwarding algorithms, and application specific modules. In the V2ProVu software, a particular application module has been implemented to create data packets containing information about the vehicle state (position, speed, yaw rate,...) and the V2X communication stack is used to broadcast these packets towards pedestrians. Moreover, the V2proVu application can also receive data from pedestrians and create objects structures that can be shared with the vehicle perception tools.

- Contact: Fawzi Nashashibi

6.10. Taxi-col

KEYWORD: Mobile Computing, Transportation

- Participant: Eugenie Lioris
- Contact: Fawzi Nashashibi

RMOD Project-Team

6. New Software and Platforms

6.1. Moose

FUNCTIONAL DESCRIPTION

Moose is an extensive platform for software and data analysis. It offers multiple services ranging from importing and parsing data, to modeling, to measuring, querying, mining, and to building interactive and visual analysis tools.

- Participants: Stéphane Ducasse, Muhammad Bhatti, Andre Cavalcante Hora, Nicolas Anquetil, Anne Etien, Guillaume Larcheveque and Alexandre Bergel
- Partners: Université de Berne - Sensus - Synectique - Pleiad - USI - Vrije Universiteit Brussel
- Contact: Stéphane Ducasse
- URL: http://www.moosetechnology.org

6.2. Pharo

KEYWORDS: Live programmation objet - Reflective system
FUNCTIONAL DESCRIPTION

The platform Pharo is an open-source Smalltalk-inspired language and environment. It provides a platform for innovative development both in industry and research. By providing a stable and small core system, excellent developer tools, and maintained releases, Pharo's goal is to be a platform to build and deploy mission critical applications, while at the same time continue to evolve.

- Participants: Marcus Denker, Damien Cassou, Christophe Demarey, Stéphane Ducasse, Esteban Lorenzano, Damien Pollet, Camille Teruel and Clément Béra
- Partners: Université de Berne - École des Mines de Douai - Uqbar foundation Argentina - Sensus - Synectique - Pleiad - Debris publishing - Yesplan - HR Works - MAD - BetaNine - Vmware
- Contact: Marcus Denker
- URL: http://www.pharo.org

6.3. Pillar

KEYWORDS: HTML - LaTeX - HTML5
FUNCTIONAL DESCRIPTION

Pillar is a markup syntax and associated tools to write and generate documentation and books. Pillar is currently used to write several books and other documentation. Two platforms have already been created on top of Pillar: PillarHub and Marina.

- Contact: Damien Cassou
- URL: http://www.smalltalkhub.com/#!/~Pier/Pillar

ROMA Project-Team

6. New Software and Platforms

6.1. MUMPS

A MUltifrontal Massively Parallel Solver
KEYWORDS: High-Performance Computing - Direct solvers - Finite element modelling
FUNCTIONAL DESCRIPTION

MUMPS is a software library to solve large sparse linear systems (AX=B) on sequential and parallel distributed memory computers. It implements a sparse direct method called the multifrontal method. It is used worldwide in academic and industrial codes, in the context numerical modeling of physical phenomena with finite elements. Its main characteristics are its numerical stability, its large number of features, its high performance and its constant evolution through research and feedback from its community of users. Examples of application fields include structural mechanics, electromagnetism, geophysics, acoustics, computational fluid dynamics. MUMPS has been developed by INPT(ENSEEIHT)-IRIT, Inria, CERFACS, University of Bordeaux, CNRS and ENS Lyon.

- Participants: Patrick Amestoy, Alfredo Buttari, Jean-Yves L'Excellent, Chiara Puglisi, Mohamed Sid-Lakhdar, Bora Uçar, Marie Durand, Abdou Guermouche, Maurice Bremond, Guillaume Joslin, Stéphane Pralet, Aurélia Fevre, Clément Weisbecker, Theo Mary, Emmanuel Agullo, Jacko Koster, Tzvetomila Slavova and François-Henry Rouet
- Partners: Université de Bordeaux - CNRS - CERFACS - ENS Lyon - INPT - IRIT - Université de Lyon - Université de Toulouse - LIP
- Contact: Jean-Yves L'Excellent
- Public releases in 2015: MUMPS 5.0.0 (February 2015), including major improvements in terms of performance and robustness, and MUMPS 5.0.1 (July 2015)
- URL: http://mumps-solver.org/

Following the creation in 2014 of a consortium for industrial users of MUMPS (http://mumps-consortium.org), some collaborations with industry (scientific exchanges, support, releases in advance) are mentioned in Section 8.1 . We pursued our work on block low-rank solvers [2] (Section 7.13), which was extended and applied to 3D frequency domain seismic modeling [19], [18] (Section 7.15) in the context of an on-going collaboration with the Seiscope consortium (https://seiscope2.obs.ujf-grenoble.fr/?lang=en?). We also worked on the parallel computation of selected entries of the inverse of a sparse matrix [3] (Section 7.14).

6.2. DCC

DPN C Compiler
KEYWORDS: Polyhedral compilation - Automatic parallelization - High-level synthesis
FUNCTIONAL DESCRIPTION

Dcc (Data-aware process network C compiler) analyzes a sequential regular program written in C and generates an equivalent architecture of parallel computer as a communicating process network (Data-aware Process Network, DPN). Internal communications (channels) and external communications (external memory) are automatically handled while fitting optimally the characteristics of the global memory (latency and throughput). The parallelism can be tuned. Dcc has been registered at the APP ("Agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria license.

- Participants: Christophe Alias and Alexandru Plesco
- Contact: Christophe Alias
- Software transferred by Inria under an exclusive license, no web page.

6.3. PoCo

Polyhedral Compilation library
KEYWORDS: Polyhedral compilation - Automatic parallelization
FUNCTIONAL DESCRIPTION

PoCo (Polyhedral Compilation library) is a compilation framework allowing to develop parallelizing compilers for regular programs. PoCo features many state-of-the-art polyhedral program analysis (dependences, affine scheduling, copde generation) and a symbolic calculator on execution traces (represented as convex polyhedra). PoCo has been registered at the APP ("agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria licence.

- Participant: Christophe Alias
- Contact: Christophe Alias
- Software transferred by Inria under an exclusive license, no web page.

6.4. Aspic

Accelerated Symbolic Polyhedral Invariant Geneneration
KEYWORDS: Abstract Interpretation - Invariant Generation
FUNCTIONAL DESCRIPTION

Aspic is an invariant generator for general counter automata. Used with C2fsm (a tool developed by P. Feautrier in COMPSYS), it can be used to derivate invariants for numerical C programs, and also to prove safety. It is also part of the WTC toolsuite (see http://compsys-tools.ens-lyon.fr/wtc/index.html), a tool chain to compute worse-case time complexity of a given sequential program.

Aspic implements the theoretical results of Laure Gonnord's PhD thesis on acceleration techniques and has been maintained since 2007.

- Participant: Laure Gonnord
- Contact: Laure Gonnord
- URL: http://laure.gonnord.org/pro/aspic/aspic.html

6.5. Termite

Termination of C programs

KEYWORDS: Abstract Interpretation - Termination
FUNCTIONAL DESCRIPTION

TERMITE is the implementation of our new algorithm "Counter-example based generation of ranking functions" (see Section 7.29). Based on LLVM and Pagai (a tool that generates invariants), the tool automatically generates a ranking function for each *head of loop*.

TERMITE represents 3000 lines of OCaml and is now available via the opam installer.

- Participants: Laure Gonnord, Gabriel Radanne (PPS, Univ Paris 7), David Monniaux (CNRS/Verimag).
- Contact: Laure Gonnord
- URL: https://termite-analyser.github.io/

6.6. Vaphor

Validation of C programs with arrays with Horn Clauses

KEYWORDS: Abstract Interpretation - Safety - Array Programs
FUNCTIONAL DESCRIPTION

VAPHOR (Validation of Programs with Horn Clauses) is the implementation of our new algorithm "An encoding of array verification problems into array-free Horn clauses" (see Section 7.30). The tool implements a traduction from a C-like imperative language into Horn clauses in the SMT-lib Format.

VAPHOR represents 2000 lines of OCaml and its development is under consolidation.

- Participants: Laure Gonnord, David Monniaux (CNRS/Verimag).
- Contact: Laure Gonnord
- Software not yet published, under consolidation.

SAGE Project-Team

6. New Software and Platforms

6.1. GENFIELD

FUNCTIONAL DESCRIPTION

GENFIELD allows the generation of log-normal correlated fields. It is based on a spectral method and uses the FFTW library. Parallelism is implemented using MPI communications. GENFIELD is used in hydrogeology to model natural fields, like hydraulic conductivity or porosity fields.

- Authors: Grégoire Lecourt, Jocelyne Erhel, Jean-Raynald De Dreuzy and Géraldine Pichot
- Contact: Jocelyne Erhel

6.2. GLiMuH

Grains with Liquid Meniscus under Heating
FUNCTIONAL DESCRIPTION

The GLiMuH code is devoted to the understanding of how heat diffuses in an assembly of solid grains separated by air and water. In the pendular regime, the quantity of water is very small, leading to liquid bridges between the grains. In the current approximation, the grains are spherical in shape, and the numerical simulation is done in a 3D axisymmetric coordinate system. The shape of the liquid/gas interface is computed by integrating a differential algebraic system of equations, with a given quantity of water per unit volume of the porous medium, and under the constraint of a given contact angle between the liquid/gas interface and the solid boundaries. The numerical results allow us to estimate the effective thermal conductivity of a real wet granular medium, which is required to establish more realistic models for the HeMaTiS code.

- Authors: Édouard Canot, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.3. GRT3D

KEYWORDS: Advection - Simulation - Scientific calculation - Dispersion - Geochemistry
APP: version 2.0, April 2014, registered

Programming language: C

Current work: refactoring

FUNCTIONAL DESCRIPTION

Reactive transport modeling has become an essential tool for understanding complex environmental problems. It is an important issue for MoMaS and C2S@EXA partners, in particular Andra. We have developed a method coupling transport and chemistry, based on a method of lines such that spatial discretization leads to a semi-discrete system of algebraic differential equations (DAE system). The main advantage is to use a complex DAE solver, which controls simultaneously the timestep and the convergence of Newton algorithm. The approach SIA uses a fixed-point method to solve the nonlinear system at each timestep, whereas the approach SNIA uses an explicit scheme.

- Authors: Yvan Crenner, Caroline De Dieuleveult, Jocelyne Erhel, Souhila Sabit, Nadir Soualem
- Partner: ANDRA
- Contact: Jocelyne Erhel

6.4. HeMaTiS

Heat and Mass Transfer in Soils
FUNCTIONAL DESCRIPTION

HeMaTiS is a set of Finite Volume programs (variants concern different geometrical configurations: 1D, 1D-radial, 2D, 3D-axisymmetric) for computing the transient heat diffusion in soils when there is a phase change of water. Currently, the soil is modelled by a heterogeneous porous medium having constant thermo-physical properties, and the porous medium is saturated with water. The phase change is treated by means of the Apparent Heat Capacity method. In the near future, we plan to use an unsaturated model (but limited to small water content), and an effective thermal conductivity which depends on the local humidity (this latter law may reveal hysteresis behaviour). The software is written in Fortran 95 and is based on the Muesli library. A Computer Algebra System (Maple or Maxima) is used to compute the Jacobian matrix.

- Authors: Édouard Canot, Mohamad Muhieddine, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.5. PALMTREE

FUNCTIONAL DESCRIPTION PALMTREE is an easy-to-use library for the parallelization of Lagrangian methods for partial differential equations and general Monte Carlo methods. The code aims at satisfying three properties:

1. Reduction of computation time by using parallel architecture,
2. Simplicity as the user just has to add the algorithm governing the behaviour of the particles,
3. Portability since one has the possibility to use the package with any compiler and OS,
4. Action-Replay which provides the ability of the package to replay a selected batch of particles.

The software also now possesses a beta version which allows to run in parallel hybrid solvers, that is solvers which use both deterministic methods (FEM, FDM, etc...) and probabilistic methods. Moreover, the engineering being this software was published in MCQMC 2014 [32].

- Authors: Lionel Lenôtre, Géraldine Pichot.
- Contact: Lionel Lenôtre.
- URL: http://people.irisa.fr/Lionel.Lenotre/software.html

6.6. SBM

Skew Brownian Motion
FUNCTIONAL DESCRIPTION

SBM is a code allowing exact or approximated simulations of the Skew Brownian Motion. This code is used for the simulation, with a Monte-Carlo approach, of a 1D diffusion process with a discontinuous diffusion coefficient. Several benchmark tests are also implemented.

- Authors: Antoine Lejay and Géraldine Pichot
- Contact: Géraldine Pichot

6.7. TPIP

Thermal Properties by Inverse Problem
FUNCTIONAL DESCRIPTION

TPIP is a program which aims at estimating the thermo-physical of a saturated porous medium after a strong heating which leads to the phase change of the water contained in the pores, knowing the experimental heating curves history at few selected points. The least-square criterion is used, in which sensitivity coefficients are the solution of a huge, complex PDE system in order to take into account the phase change of water. These equations for the sensitivity coefficients are therefore obtained via a Computer Algebra System (Maple or Maxima). In many aspects, the forward problem is similar to the HeMaTiS code, and like it, is based on Muesli. Two different minimization algorithms may be used, Damped Gauss-Newton or Levenberg-Marquardt. A special procedure has been applied in order to obtain a robust convergence, by changing some parameters of the forward problem during the iterations.

- Authors: Édouard Canot, Mohamad Muhieddine, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.8. Zohour

FUNCTIONAL DESCRIPTION

Zohour is a node-based adaptive 2D mesh algorithm, written in Fortran 2003. A basic rectangular, regular set of nodes is recursively refined. Then the cells come from the Voronoi tessellation. While the domain is currently limited to a rectangular shape, its strength is three-fold:first, computing the flux via a Finite Element or Finite Volume method is both simple and accurate because each cell-side of cells is the bisection of two nodes,

second, the transition between zones of different levels of refinement is more progressive than other methods, leading to a smaller number of nodes for the whole mesh,

third, during successive refinements when dealing with a transient problem, interpolation is needed only by the new nodes, limiting the numerical errors.

- Author: Édouard Canot
- Contact: Édouard Canot
- URL: http://people.irisa.fr/Edouard.Canot/zohour/

SCALE Team

6. New Software and Platforms

6.1. BigGrph

- Participants: Eric Madelaine, Fabrice Huet
- Contact: Luc Hogie
- The objective of "biggrph" is to provide a distributed platform for very large graphs processing. A typical data set for testing purpose is a sample of the Twitter graph : 240GB on disk, 398M vertices, 23G edges, average degree of 58 and max degree of 24,635,412.

  We started the project in 2014 with the evaluation of existing middleware (GraphX / Spark and Giraph / Hadoop). After having tested some useful algorithms (written according to the BSP model) we decided to develop our own platform.

  The development of the "biggrph" platform is now at the stage where we focus on the quality and the improvement of the code.

  In particular we have designed strong test suites and some non trivial bugs have been fixed. We have also solved problems of scalability, in particular concerning the communication layer with billions of messages exchanged between BSP steps. Moreover, we have implemented specific data structures for BSP and support for distributed debugging. This comes along with the implementation of algorithms such as BFS or strongly connected components that are run on the NEF cluster (a facility maintained at Inria Sophia Antipolis).
- This project is a joint work of the three EPs Coati, Diana and Scale and is supported by an ADT grant.
- URL : http://www.i3s.unice.fr/~hogie/software/?name=biggrph

6.2. BtrPlace

FUNCTIONAL DESCRIPTION

BtrPlace dynamically adapts the VM placement depending on pluggable expectations using a network and memory-aware migration scheduler. It currently addresses affinity constraints, resource booking, node state manipulation and hosting restrictions. BtrPlace is a complete rewrite of the reconfiguration algorithm that was inside OW2 project Entropy with a clear focus on extensibility. It embeds the constraint programming library Choco to compute solutions.

BtrPlace has been released 5 times this year. The current code amounts for 44000 lines of Java (production and test code, comments) and the online documentation amounts for around 1500 lines. BtrPlace is available from the Maven central repository. In 2015, it has been downloaded around 480 times from unique IPs and 2400 unique visitors accessed the Website.

- Contact: Fabien Hermenier
- Participants: Fabien Hermenier, Vincent Kherbache
- URL: http://www.btrplace.org/
- APP registration code: IDDN.FR.001.330025.000.S.C.2014.000.31235

6.3. EventCloud

SCIENTIFIC DESCRIPTION

The EventCloud architecture is based on a structured P2P overlay network targetting high-performance elastic data processing. Consequently it aims to be deployed on infrastructures like grids, clouds, i.e. whose nodes acquisition and relinquishment can be dynamic and subject to a pay-per-use mode. Each node participating in the overlay networks constituting EventCloud instances, is responsible for managing the storage of subsets of the events, and helps in matching potential looked up events and disseminating them in a collaborative manner. As such, each node is also potentially an event broker responsible for managing subscriptions and routing notifications. The EventCloud provides a high level publish-subscribe API where users can register their interests using SPARQL. When matching RDF data are added, subscribers are automatically notified. Recent work around the EventCloud has focused on efficient algorithms for managing subscription and notification.

FUNCTIONAL DESCRIPTION

The EventCloud is an open source middleware that aims to act as a distributed datastore for data fulfiling the W3C RDF specification (http://www.w3.org/RDF/). It allows to store and retrieve quadruples (RDF triples with context) through SPARQL but also to manage events represented as quadruples.

- Participants: Laurent Pellegrino, Fabrice Huet, Françoise Baude, Maeva Antoine and Iyad Alshabani
- Partner: CNRS
- Contact: Françoise Baude

6.4. OSA

Open Simulation Architecture

FUNCTIONAL DESCRIPTION

OSA on of new or existing contributions at every level of its architecture. The platform core supports discrete-event simulation engine(s) built on top of the ObjectWeb Consortium?s Fractal component model. In OSA, the systems to be simulated are modeled and instrumented using Fractal components. In OSA, the event handling is mostly hidden in the controller part of the components, which alleviates noticeably the modeling process, but also eases the replacement of any part of the simulation engine. Apart the simulation engine, OSA aims at integrating useful tools for modeling, developing, experimenting, and analysing simulations. OSA is also a platform for experimenting new techniques and approaches in simulation, such as aspect oriented programming, separation of concerns, innovative component architectures, and so on.

- Participant: Olivier Dalle
- Contact: Olivier Dalle
- URL: http://osa.inria.fr/

6.5. Vercors Component Editor (VCE)

VERification of models for distributed communicating COmponants, with safety and Security

FUNCTIONAL DESCRIPTION

The Vercors tools include front-ends for specifying the architecture and behaviour of components in the form of UML diagrams. We translate these high-level specifications, into behavioural models in various formats, and we also transform these models using abstractions. In a final step, abstract models are translated into the input format for various verification toolsets. Currently we mainly use the various analysis modules of the CADP toolset.

- Participants: Eric Madelaine, Antonio Cansado, Ludovic Henrio, Marcela Rivera, Oleksandra Kulankhina, Bartlomiej Szejna, Nassim Jibai and Siqi Li
- Contact: Eric Madelaine
- URL: http://team.inria.fr/scale/software/vercors/

SECRET Project-Team (section vide)

SELECT Project-Team

5. New Software and Platforms

5.1. MIXMOD software

Participants: Gilles Celeux [Correspondant], Benjamin Auder, Jonas Renault.

Mixture model, cluster analysis, discriminant analysis MIXMOD is being developed in collaboration with Christophe Biernacki, Florent Langrognet (Université de Franche-Comté) and Gérard Govaert (Université de Technologie de Compiègne). MIXMOD (MIXture MODeling) software fits mixture models to a given data set, with either a clustering or a discriminant analysis purpose. MIXMOD uses a large variety of algorithms to estimate mixture parameters, e.g., EM, Classification EM, and Stochastic EM. They can be combined to create different strategies that lead to a sensible maximum of the likelihood (or completed likelihood) function. Moreover, different information criteria for choosing a parsimonious model, e.g. the number of mixture components, some of them favoring either a cluster analysis or a discriminant analysis point of view, are included. Many Gaussian models for continuous variables and multinomial models for discrete variable are included. Written in C++, MIXMOD is interfaced with MATLAB. The software, statistical documentation, and user guide are available here: http://www.mixmod.org.

Since 2010, MIXMOD has a proper graphical user interface. A version of MIXMOD in R is now available: http://cran.r-project.org/web/packages/Rmixmod/index.html.

Benjamin Auder contributes to the software improvement of MIXMOD. He has implemented an interface to test any mathematical library (Armadillo, Eigen, etc.) to replace NEWMAT. He has contributed to the continuous integration setup using Jenkins tools, and has prepared an automated testing framework for unit and non-regression tests.

This year, MIXMOD has received the support of an ADT (MASSICCC) for three years. This ADT MASSICCC has been obtained conjointly with the MODAL team (Inria Lille). This year, an engineer, Jonas Renault, has been appointed for two years. He is in charge of developing a web version of MIXMOD.

5.2. BLOCKCLUSTER software

Participants: Gilles Celeux, Christine Keribin.

Mixture model, Block cluster analysis, Blockcluster is software devoted to model-based block clustering. It is developed in parternship with the MODAL team (Inria Lille). This year, some major bugs have been fixed, and the Bayesian point of view has been reinforced by including Gibbs sampling for binary and categorial data. This Gibbs sampler, coupled with the variational Bayes algorithm, provides solutions which are more stable and less dependent on the initial values of the algorithm. An exact expression of the ICL criterion has been provided. This non-asymptotic criterion appears to be more relevant than the BIC-like approximation of ICL.

Vincent Brault, Christine Keribin and Mahindra Mariadassou have shown the consistency and asymptotic normality of the maximum likelihood and variational estimators in stochastic or latent block models.

SEMAGRAMME Project-Team

5. New Software and Platforms

5.1. Abstract Categorial Grammar Development Toolkit (ACGtk)

The current version of the ACG development toolkit prototype focuses on providing facilities to develop grammars. To this end, the type system currently implemented is the linear core system plus the (non-linear) intuitionistic implication, and a special attention has been paid to type error management. Since 1.0b released in Feb. 2014, ACGtk allows for transformations both from abstract terms to object terms, and from object terms to abstract terms (ACG parsing). The parsing algorithm follows a method which is being implemented for second-order ACGs. It is based on a translation of ACG grammars into Datalog programs and is well-suited to fine-grained optimization.

However, since we are interested not only by recognizability (hence whether some fact is provable) but also by the parsing structure (hence the proof), the Datalog solver has been adapted to produce not only yes/no answer to queries, but also all the proofs of the answers to the queries. The next steps concern optimization and efficiency. Note however that in the general case, the decidability of translating an object term to an abstract one is still an open problem.

We also have enriched the ACG development toolkit with graphical output. The new module includes a small functional OCaml library for manipulating images which enables users to customize the rendering of formulas as pictures.

The software is implemented in OCaml and is available as OPAM [0] package. Version 1.3.0 was released on November 30th.

- Contact: Sylvain Pogodalla
- URL: http://www.loria.fr/equipes/calligramme/acg/

5.2. Grew

Grew is a Graph Rewriting tool dedicated to applications in NLP. Grew takes into account confluent and non-confluent graph rewriting and it includes several mechanisms that help to use graph rewriting in the context of NLP applications (built-in notion of feature structures, parametrization of rules with lexical information).

A online version of Grew for graph matching was presented as a demo in the TALN conference [19].

- Contact: Bruno Guillaume
- URL: http://grew.loria.fr

5.3. ZombiLingo

Crowdsourcing is nowadays a way of constructing linguistic resources which is more and more used. In the crowdsourcing area, one of the way to motivate a large amount of people to contribute to a project is to present it as a game. Games used in this particular way are called GWAPs (Game With A Purpose). ZombiLingo is a GWAP where gamers have to give linguistic information about the syntax of French natural language sentence.

At the end of 2015, 460 players are registered on the game website and they have produce 63,000 annotations.

---

[0] https://opam.ocaml.org/

In 2015, an Inria ADT started based on the prototype built in 2014. The engineer (Nicolas Lefebvre) worked on this project since October 2015. The main improvement were: migration towards a new framework (Laravel) and code refactoring, integration of new designs into the game and internationalization of the interface to prepare the game for application to other natural Languages.

- Participants: Bruno Guillaume, Karën Fort (Université Paris Sorbonne) and Nicolas Lefebvre
- Contact: Bruno Guillaume
- URL: http://zombilingo.org/

5.4. SLAMtk

A management chain of the transcriptions of interviews for the SLAM project which products of a full anonymized randomized version of the resources. Some extensions have been implemented based on Distagger (disfluencies) and MElt (POS and lemma) and propose different analyses of repartition, mainly during the Théophane De Logivière internship.

- Contact: Maxime Amblard
- URL: http://slam.loria.fr

5.5. Dep2pict

Dep2pict is a program for drawing graphical representation of dependency structures of natural language sentences.

- Contact: Bruno Guillaume
- URL: http://dep2pict.loria.fr

5.6. LEOPAR

Leopar is a parser for natural languages which is based on the formalism of Interaction Grammars. The main features of the current version of the software are: automatic parsing of a sentence or a set of sentences, dependency and parse-tree representation of sentences, interactive parsing (the user chooses the couple of nodes to merge) and visualization of grammars produced by XMG-2 or of sets of description trees associated to some word in the linguistic resources.

- Participants: Guillaume Bonfante, Bruno Guillaume and Guy Perrier
- Contact: Bruno Guillaume
- URL: http://leopar.loria.fr

SEQUEL Project-Team

6. New Software and Platforms

6.1. Function optimization

Participants: Jean-Bastien Grill, Michal Valko, Rémi Munos.

6.1.1. POO

This is a black-box function optimization toolkit that finds the global optimum of a function given a finite budget of noisy evaluations. The algorithm does not require the knowledge of the function's smoothness. It works for a larger class of functions than what was previously considered, especially for functions that are difficult to optimize, in a precise sense.

SERENA Team

6. New Software and Platforms

6.1. New Software

6.1.1. FreeFem++ a posteriori package

Participants: Martin Vohralík, Zuqi Tang.

The scientific calculation code FreeFem++ is an example of a complex software numerical simulation tool relying on traditional matching triangular meshes. It encompasses all specification of the problem, the choice and implementation of the numerical method, the choice and implementation of the linearization method (nonlinear solver), and the choice and implementation of the method of solution of the associated linear systems (linear solver). In the post-doc stay of Z. Tang, we have integrated here some recent advances of the theory of a posteriori error estimation and of adaptive algorithms. In particular, (local) adaptive stopping criteria for the linear and nonlinear solvers have been implemented.

Version 3.42

Programming language: C++

http://www.freefem.org/ff++/

https://who.rocq.inria.fr/Zuqi.Tang/freefem++.html

SERPICO Project-Team

6. New Software and Platforms

6.1. C-CRAFT

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The C-CRAFT software enables to jointly segment small particles and estimate background in 2D or 3D fluorescence microscopy image sequences. The vesicle segmentation and background estimation problem is formulated as a global energy minimization problem in the Conditional Random Field framework. A patch-based image representation is used to detect spatial irregularity in the image. An iterative scheme based on graph-cut algorithm is proposed for energy minimization.

- **Participants**: Thierry Pécot, Charles Kervrann, Patrick Bouthemy, Jean Salamero.
- **Contact:** Thierry Pécot, Charles Kervrann.
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::C-CRAFT
- **Languages:** C/C++ and JAVA (plug-in ICY: http://icy.bioimageanalysis.org/plugin/C-CRAFT)
- **Reference:** [26]

6.2. ATLAS

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The ATLAS software enables to detect spots in 2D fluoresence images. The spot size is automatically selected and the detection threshold adapts to the local image dynamics. ATLAS relies on the Laplacian of Gaussian (LoG) filter, which both reduces noise and enhances spots. A multiscale representation of the image is built to automatically select the optimal LoG variance. Local statistics of the LoG image are estimated in a Gaussian window, and the detection threshold is pointwise inferred from a probability of false alarm (PFA). The user only has to specify: i/ standard deviation of the Gaussian window; ii/ PFA value. The Gaussian window must be about the size of the background structures; increasing the PFA increases the number of detections.

- **Participants**: Antoine Basset, Patrick Bouthemy, Thierry Pécot, Charles Kervrann.
- **Contact:** Thierry Pécot, Patrick Bouthemy, Charles Kervrann.
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::ATLAS
- **Language:** C/C++
- **Reference:** [12]

6.3. Hullkground

KEYWORDS: Bioinformatics - Biomedical imaging
FUNCTIONAL DESCRIPTION: The HULLKGROUND software decomposes a fluorescence microscopy image sequence into two dynamic components: i/ an image sequence showing mobile objects, ii/ an image sequence showing the slightly moving background. Each temporal signal of the sequence is processed individually and analyzed with computational geometry tools. The convex hull is estimated automatically for each pixel and subtracted to the original signal. The method is unsupervised, requires no parameter tuning and is a simplified version of the shapes-based scale-space method.

- **Participants:** Anatole Chessel, Jean Salamero, Charles Kervrann.
- **Contact:** Charles Kervrann.
- **APP deposit number:** IDDN.FR.001.400005.000.S.P.2009.000.21000
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Hullkground
- **Free distribution:** http://serpico.rennes.inria.fr/doku.php?id=software:hullkground:hullkground
- **Language:** JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.4. Motion2D

KEYWORDS: Image sequence - Motion model - 2D
FUNCTIONAL DESCRIPTION: The MOTION2D software is a multi-platform object-oriented library to estimate 2D parametric motion models in an image sequence. It can handle several types of motion models, namely, constant (translation), affine, and quadratic models. Moreover, it includes the possibility of accounting for a global variation of illumination and more recently for temporal image intensity decay (e.g. due to photo-bleaching decay in fluorescence microscopy). The use of such motion models has been proved adequate and efficient for solving problems such as optic flow computation, motion segmentation, detection of independent moving objects, object tracking, or camera motion estimation, and in numerous application domains (video surveillance, visual servoing for robots, video coding, video indexing), including biological imaging (image stack registration, motion compensation in videomicroscopy). Motion2D is an extended and optimized implementation of the robust, multi-resolution and incremental estimation method (exploiting only the spatio-temporal derivatives of the image intensity function). Real-time processing is achievable for motion models involving up to six parameters. Motion2D can be applied to the entire image or to any pre-defined window or region in the image.

- **Participants:** Patrick Bouthemy, Jean-Marc Odobez, Fabien Spindler.
- **Contact:** Patrick Bouthemy, Fabien Spindler.
- **APP deposit number:** FR.001.520021.001.S.A.1998.000.21000 / release 1.3.11, January 2005)
- **Free academic software distribution:** http://www.irisa.fr/vista/Motion2D
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Motion2D
- **Languages:** C/C++ and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.5. ND-SAFIR

KEYWORDS: Biology - Health - Image analysis - Photonic imaging - Fluorescence microscopy - Biomedical imaging
SCIENTIFIC DESCRIPTION: The ND-SAFIR software removes additive Gaussian and non-Gaussian noise in still 2D or 3D images or in 2D or 3D image sequences (without any motion computation) [4]. The method is unsupervised and is based on a pointwise selection of small image patches of fixed size (a data-driven adapted way) in spatial or space-time neighbourhood of each pixel (or voxel). The main idea is to modify each pixel (or voxel) using the weighted sum of intensities within an adaptive 2D or 3D (or 2D or 3D + time) neighbourhood and to use image patches to take into account complex spatial interactions. The neighbourhood size is selected at each spatial or space-time position according to a bias-variance criterion. The algorithm requires no tuning of control parameters (already calibrated with statistical arguments) and no library of image patches. The method has been applied to real noisy images (old photographs, JPEG-coded images, videos, ...) and is exploited in different biomedical application domains (time-lapse fluorescence microscopy, video-microscopy, MRI imagery, X-ray imagery, ultrasound imagery, ...).

- **Participants:** Jérôme Boulanger, Charles Kervrann, Patrick Bouthemy, Jean Salamero.
- **Partners:** INRA, PiCT - CNRS - Institut Curie.
- **APP deposit number:** IDDN.FR.001.190033.002.S.A.2007.000.21000 / new release 3.0 in 2013)
- **Free academic software distribution:** Binaries of the software ND-SAFIR are freely and electronically distributed (http://serpico.rennes.inria.fr/doku.php?id=software:nd-safir:index).
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::NDSafir
- **Languages:** C/C++, MATLAB and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/). The C/C++ software has been developed under Linux using the CImg library and has been tested over several platforms such as Linux/Unix, Windows XP and Mac OS.
- **Commercial licence agreements:** Innopsys, Roper Scientfic, Photmetrics, Nikon Europe BV (2016).
- **Reference:** [4]

6.6. F2D-SAFIR

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The F2D -SAFIR software removes mixed Gaussian-Poisson noise in large 2D images, typically $10^3 \times 10^3$ pixels, in a few seconds. The method is unsupervised and is a simplified version of the method related to the ND-SAFIR software. The software dedicated to microarrays image denoising, was licensed to the INNOPSYS company which develops scanners for disease diagnosis and multiple applications (gene expression, genotyping, aCGH, ChIP-chip, microRNA, ...).

- **Participant**: Charles Kervrann.
- **Partner:** INRA.
- **Contact:** Charles Kervrann.
- **APP deposit number:** IDDN.FR.001.190033.001.S.A.2007.000.21000
- **Language:** C/C++

6.7. TubuleJ

KEYWORDS: Bioinformatics - Biomedical imaging
FUNCTIONAL DESCRIPTION: The TUBULEJ software written in java (plug-in ImageJ) is devoted to the analysis of microtubules and helical structures in 2D cryo-electron microscope images. The software straightens curved microtubule images by estimating automatically point locations on the microtubule axis. The estimation of microtubule principal axis relies on microtubule cylindrical shape analyzed in the Fourier domain. A user-friendly interface enables to filter straight fiber images by selecting manually the layer lines of interest in the Fourier domain. This software can be used to generate a set of 2D projection views from a single microtubule projection view and a few parameters of this microtubule structure.

- **Contact:** Denis Chrétien.
- **Partners:** University of Rennes 1, CNRS.
- **APP deposit number:** IDDN.FR.001.240023.000.S.P.2011.000.21000
- **On-line demo:** http://equipes.igdr.univ-rennes1.fr/en/tips/Software/TubuleJ/
- **Language:** JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

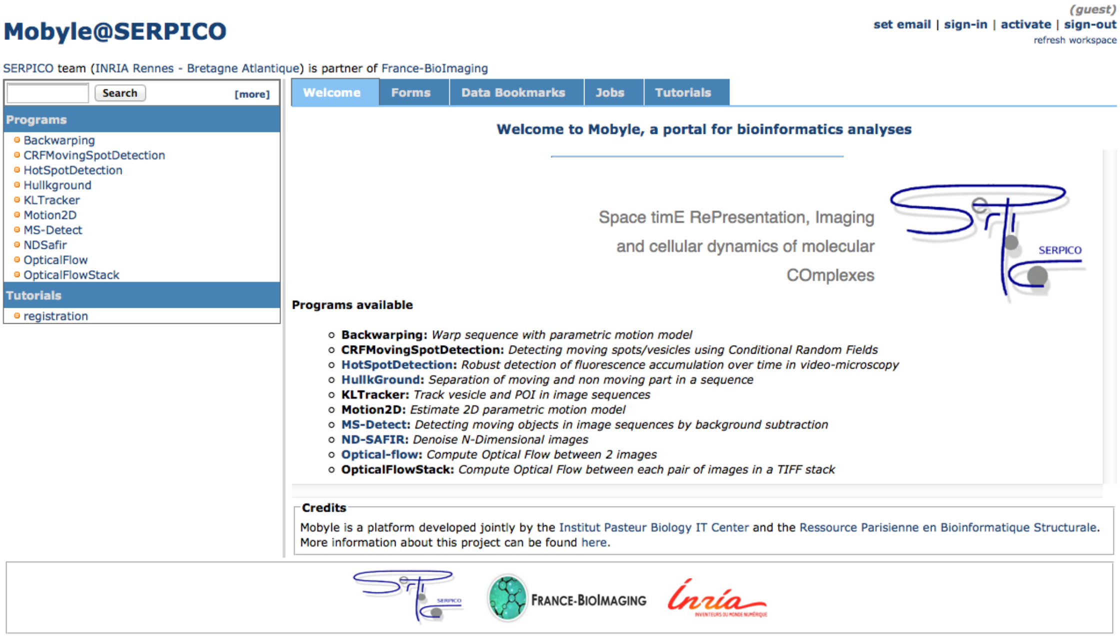
6.8. Cryo-Seg

KEYWORDS: Bioinformatics - Biomedical imaging
FUNCTIONAL DESCRIPTION: The CRYO-SEG software has been developed to detect microtubule structures and helical structures in 2D cryo-electron microscope images. Cryo-electron tomography allows 3D observation of biological specimens in their hydrated state. Segmentation is formulated as Maximum A Posteriori estimation problem and exploits image patches to take into account spatial contexts (Markov Random Fields). Because of the contrast anisotropy in the specimen thickness direction, the whole tomogram is segmented section by section, with an automatic update of reference patches. This algorithm has been evaluated on synthetic data and on cryo-electron tomograms of in vitro microtubules. On real data, this segmentation method extracts the most contrasted regions of microtubules, and 3D visualization is improved.

- **Participants:** Denis Chrétien, Charles Kervrann, Sophie Blestel.
- **Contact:** Denis Chrétien.
- **Partners:** University of Rennes 1, CNRS.
- **Languages:** C/C++ and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.9. Platforms

6.9.1. Mobyle@Serpico plateform and software distribution



SERPICO team (INRIA Rennes - Bretagne Atlantique) is partner of France-BioImaging

Welcome to Mobyle, a portal for bioinformatics analyses

Space timE RePresentation, Imaging and cellular dynamics of molecular COmplexes

Programs available

- **Backwarping:** *Warp sequence with parametric motion model*
- **CRFMovingSpotDetection:** *Detecting moving spots/vesicles using Conditional Random Fields*
- **HotSpotDetection:** *Robust detection of fluorescence accumulation over time in video-microscopy*
- **HullkGround:** *Separation of moving and non moving part in a sequence*
- **KLTracker:** *Track vesicle and POI in image sequences*
- **Motion2D:** *Estimate 2D parametric motion model*
- **MS-Detect:** *Detecting moving objects in image sequences by background subtraction*
- **ND-SAFIR:** *Denoise N-Dimensional images*
- **Optical-flow:** *Compute Optical Flow between 2 images*
- **OpticalFlowStack:** *Compute Optical Flow between each pair of images in a TIFF stack*

Credits

Mobyle is a platform developed jointly by the Institut Pasteur Biology IT Center and the Ressource Parisienne en Bioinformatique Structurale. More information about this project can be found here.

*Figure 2. Mobyle@*SERPICO *web portal.*

The objective is to disseminate the distribution of SERPICO image processing software for biologist users:
Free binaries: software packages have been compiled for the main operating systems (Linux, MacOS, Windows) using CMake (see http://www.cmake.org/). They are freely available on the team website under a proprietary license (e.g. ND-SAFIR and HULLKGROUND are distributed this way at http://serpico.rennes.inria.fr/doku.php?id=software:index).

*Mobyle@*SERPICO *web portal*: An on-line version of the image processing algorithms has been developped using the Mobyle framework (Institut Pasteur, see http://mobyle.pasteur.fr/). The main role of this web portal (see Fig. 2) is to demonstrate the performance of the programs developed by the team: C-CRAFT[26], ATLAS[12], HOTSPOTDETECTION[57], HULLKGROUND[43], KLTRACKER[55], MOTION2D[54], MS-DETECT[45], ND-SAFIR[4], OPTICALFLOW and FLUX ESTIMATION [26]. The web interface makes our image processing methods available for biologist users at Mobyle@SERPICO (http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#welcome) without any installation or configuration on their own. The size of submitted images is limited to 200 MegaBytes per user and all the results are kept 15 days. The web portal and calculations run on a server with 2 CPU x 8 cores, 64 GigaBytes of RAM (500 MegaBytes for each user / Data is saved for 3 months).

IMAGEJ *plug-ins*: IMAGEJ (see http://rsb.info.nih.gov/ij/) is a widely used image visualization and analysis software for biologist users. We have developed IMAGEJ plug-in JAVA versions of the following software: ND-SAFIR [4], HULLKGROUND [43], MOTION2D [54], HOTSPOTDETECTION [57], STLAS [12]. The C-CRAFT algorithm [26] has been developped for the image processing ICY platform (http://icy.bioimageanalysis.org/).

Institut Curie CID iManage database: The microscopy facility of Institut Curie has co-developped a commercial database system (CID iManage/Strand Avadis company). The database can be searched via meta-data and includes menu selections that enable to run remote processing from a cluster. We have integrated ND-SAFIR and HULLKGROUND in the interface environment to allow the database users to process their images easily, and store associated results and parameters used.

- **Participants:** Thierry Pécot, Charles Kervrann, Charles Deltel (Inria Rennes SED).
- **Contact:** Thierry Pécot, Charles Kervrann.

6.9.2. IGRIDA-Serpico cluster

The IGRIDA-Serpico cluster of 200 nodes is opened for end-users for large scale computing and data sets processing (200 TeraBytes).

- **Batch Scheduler:** OAR
- **File management:** Puppet / Git / Capistrano
- **OS:** Linux Debian 7
- **User connexion:** public ssh key
- **Contact:** Thierry Pécot, Charles Kervrann, Charles Deltel (Inria Rennes SED).

SIERRA Project-Team

6. New Software and Platforms

6.1. DICA: Moment Matching for Latent Dirichlet Allocation (LDA) and Discrete Independent Component Analysis (DICA)

The DICA package contains Matlab and C++ (via Matlab mex files) implementations of estimation in the LDA and closely related DICA models [21].

The implementation consists of two parts. One part contains the efficient implementation for construction of the moment/cumulant tensors, while the other part contains implementations of several so called joint diagonalization type algorithms used for matching the tensors. Any tensor type (see below) can be arbitrarily combined with one of the diagonalization algorithms (see below) leading, in total, to 6 algorithms.

Two types of tensors are considered: (a) the LDA moments and (b) the DICA cumulants. The diagonalization algorithms include: (a) the orthogonal joint diagonalization algorithm based on iterative Jacobi rotations, (b) the spectral algorithm based on two eigen decompositions, and (c) the tensor power method.

- Contact: Anastasia Podosinnikova
- URL: https://github.com/anastasia-podosinnikova/dica

6.2. LinearFW: Implementation of linearly convergent versions of Frank-Wolfe

This is the code to reproduce all the experiments in the NIPS 2015 paper: "On the Global Linear Convergence of Frank-Wolfe Optimization Variants" by Simon Lacoste-Julien and Martin Jaggi [17], which covers the global linear convergence rate of Frank-Wolfe optimization variants for problems described as in Eq. (1) in the paper. It contains the implementation of Frank-Wolfe, away-steps Frank-Wolfe and pairwise Frank-Wolfe on two applications.

- Contact: Simon Lacoste-Julien
- URL: https://github.com/Simon-Lacoste-Julien/linearFW

6.3. CNN-Head-Detection: Context-aware CNNs for person head detection

This is the code for the ICCV 2015 paper "Context-aware CNNs for person head detection" [23]. Person detection is a key problem for many computer vision tasks. While face detection has reached maturity, detecting people under a full variation of camera view-points, human poses, lighting conditions and occlusions is still a difficult challenge. In this work we focus on detecting human heads in natural scenes. Starting from the recent local R-CNN object detector, we extend it with two types of contextual cues. First, we leverage person-scene relations and propose a Global CNN model trained to predict positions and scales of heads directly from the full image. Second, we explicitly model pairwise relations among objects and train a Pairwise CNN model using a structured-output surrogate loss. The Local, Global and Pairwise models are combined into a joint CNN framework. To train and test our full model, we introduce a large dataset composed of 369,846 human heads annotated in 224,740 movie frames. We evaluate our method and demonstrate improvements of person head detection against several recent baselines in three datasets. We also show improvements of the detection speed provided by our model.

- Contact: Anton Osokin
- URL: https://github.com/aosokin/cnn_head_detection

SIROCCO Project-Team

6. New Software and Platforms

6.1. Fixation Analysis

FUNCTIONAL DESCRIPTION

From a set of fixation data and a picture, the software called Visual Fixation Analysis extracts from the input data a number of features (fixation duration, saccade length, orientation of saccade...) and computes a human saliency map. The software can also be used to assess the degree of similarity between a ground truth (eye fixation data) and a predicted saliency map. This software is dedicated to people working in cognitive science and computer vision.

- Participants: Olivier Le Meur and Thierry Baccino
- Contact: Olivier Le Meur

6.2. Salient object extraction

FUNCTIONAL DESCRIPTION

This software detects salient object in an input picture in an automatic manner. The detection is based on super-pixel segmentation and contrast of histogram. This software is dedicated to people working in image processing and post production.

- Participants: Zhi Liu and Olivier Le Meur
- Contact: Olivier Le Meur

6.3. Saccadic model

The software called Scanpath Prediction aims at predicting the visual scanpath of an observer. The visual scanpath is a set of fixation points. The computational model is based on bottom-up saliency maps, viewing tendencies (that have been learned from eye tracking datasets) and inhibition-of-return. This study is based on the following paper [20]. This software is dedicated to people working in computer science, computer vision and cognitive science. This software is being registered at the APP (Agence de Protection des Programmes).

- Participants: Olivier Le Meur
- Contact: Olivier Le Meur

6.4. Hierarchical super-resolution based inpainting

From an input binary mask and a source picture, the software performs an examplar-based inpainting. The method is based on the combination of multiple inpainting applied on a low resolution of the input picture. Once the combination has been done, a single-image super-resolution method is applied to recover the details and the high frequency in the inpainted areas. The developments have been pursued in 2014, in particular by introducing a Poisson blending step in order to improve the visual quality of the inpainted video. This software is dedicated to people working in image processing and post production. This software is being registered at the APP (Agence de Protection des Programmes).

- Participants: Olivier Le Meur
- Contact: Olivier Le Meur

6.5. Video Inpainting for Loss Concealment

KEYWORDS: Video Inpainting - Motion informations - Loss concealment - BMFI (Bilinear Motion Field Interpolation)

FUNCTIONAL DESCRIPTION

From an input binary mask and a source video, the software performs an examplar-based inpainting. The motion information of the impaired areas is first recovered with a Bilinear Motion Field Interpolation (BMFI). The texture information is then recovered using a spatio-temporal examplar-based inpainting algorithm. The method to recover the texture proceeds in two steps: it first inpaints a low resolution version using an examplar-based method. Details of the inpainted corrupted areas of the input video are then retrieved using a nearest neighbor field (NNF) based super-resolution technique. A NNF is computed between an interpolated version of the concealed LR video and the known part of the received video at native resolution. In the same vein as in single-image super-resolution, the NNF is used to recover the high frequencies of the inpainted areas of the video.

- Participants: Ronan Le Boulch
- Contact: Olivier Le Meur

6.6. Video Inpainting for Editing

KEYWORDS: Video Inpainting - Editing
FUNCTIONAL DESCRIPTION

This software performs video inpainting for both static or free-moving camera videos. The method can be used for object removal, error concealment, and background reconstruction applications. To inpaint a frame, the method starts by aligning all the frames of a group of pictures (GOP). This is achieved by a region-based homography computation method which allows us to strengthen the spatial consistency of aligned frames. Then, from the stack of aligned frames, an energy function based on both spatial and temporal coherency terms is globally minimized. This energy function is efficient enough to provide high quality results even when the number of pictures in the GoP is rather small, e.g. 20 neighboring frames. This reduces the algorithm complexity and makes the approach well suited for near real-time video editing applications as well as for loss concealment applications.

- Participants: Mounira Ebdelli
- Contact: Olivier Le Meur

SISTM Project-Team

6. New Software and Platforms

6.1. New Software

6.1.1. sgPLS

Sparse Group Partial Least Square
KEYWORD: Bioinformatics
FUNCTIONAL DESCRIPTION

The Sparse Group Partial Least Square package (sgPLS) provides sparse, group, and sparse group versions of partial least square regression models.

- Contact: Benoît Liquet
- URL: https://cran.r-project.org/web/packages/sgPLS/index.html

6.2. Upgraded Software

6.2.1. TcGSA

Time-course Gene Set Analysis
KEYWORDS: Bioinformatics - Genomics
FUNCTIONAL DESCRIPTION

An R package for the gene set analysis of longitudinal gene expression data sets. Available on the CRAN website, this package implements a Time-course Gene Set Analysis method and provides useful plotting functions facilitating the interpretation of the results.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/TcGSA/index.html

6.2.2. VSURF

Variable Selection Using Random Forests
KEYWORD: Bioinformatics
FUNCTIONAL DESCRIPTION

An R package for Variable Selection Using Random Forests. Available on CRAN, this package performs an automatic (meaning completely data-driven) variable selection procedure. Originally designed to deal with high dimensional data, it can also be applied to standard datasets.

- Contact: Robin Genuer
- URL: http://cran.r-project.org/web/packages/VSURF/index.html

SMIS Project-Team

5. New Software and Platforms

5.1. PLUG-DB ENGINE

FUNCTIONAL DESCRIPTION

PlugDB is a complete platform dedicated to a secure and ubiquitous management of personal data. It aims at providing an alternative to a systematic centralization of personal data. The PlugDB engine is a personal database server capable of storing data (tuples and documents) in tables and BLOBs, indexing them, querying them in SQL, sharing them through assertional access control policies and enforcing transactional properties (atomicity, integrity, durability). The PlugDB engine is embedded in a tamper-resistant hardware device combining the security of smartcard with the storage capacity of NAND Flash. The personal database is hosted encrypted in NAND Flash and the PlugDB engine code runs in the microcontroller. Complementary modules allow to pre-compile SQL queries for the applications, communicate with the DBMS from a remote Java program, synchronize local data with remote servers (typically used for recovering the database in the case of a broken or lost devices) and participate in distributed computation (e.g., global queries). PlugDB runs both on secure devices provided by Gemalto and on specific secure devices designed by SMIS and assembled by electronic SMEs. Mastering the hardware platform opens up new research and experiment opportunities (e.g., we have recently integrated a Bluetooth module to communicate wirelessly with PlugDB and a fingerprint module to strongly authenticate users) and allows us to engage ourselves in an open-source/open hardware initiative. Open-SW/open-HW contributes to the trust the community of users can put in any privacy preserving solution and is key to enable a diversity of solutions, hence decreasing the risk of class attacks. PlugDB engine has been registered first at APP (Agence de Protection des Programmes) in 2009 - a new version being registered every two years and the hardware datasheets in 2015. PlugDB has been experimented in the field - notably in the healthcare domain - and we recently set up an educational platform to raise students awareness of privacy protection problems and embedded programming. As a conclusion, PlugDB combines several research contributions from the team, at the crossroads of flash data management, embedded data processing and secure distributed computations. It then strongly federates all members of our team (permanent members, PhD students and engineers). It is also a vector of visibility, technological transfer and dissemination and gives us the opportunity to collaborate with researchers from other disciplines around a concrete privacy enhancing platform.

- Participants: Nicolas Anciaux, Luc Bouganim, Philippe Pucheral, Shaoyi Yin, Yanli Guo, Kevin Jacquemin, Aydogan Ersoz and Quentin Lefebvre
- Contact: Nicolas Anciaux
- URL: https://project.inria.fr/plugdb/

SOCRATE Project-Team

5. New Software and Platforms

5.1. FloPoCo

Floating-Point Cores, but not only
KEYWORD: Synthesizable VHDL generator
FUNCTIONAL DESCRIPTION

The purpose of the open-source FloPoCo project is to explore the many ways in which the flexibility of the FPGA target can be exploited in the arithmetic realm.

- Participants: Florent Dinechin, Nicolas Brunie, Matei Istoan and Antoine Martinet
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - UPVD
- Contact: Florent de Dinechin
- URL: http://flopoco.gforge.inria.fr/

5.2. Minus

KEYWORD: Experiment Handler , SDR

FUNCTIONAL DESCRIPTION

Handling and deployement of experiment on the Cognitive radio platform FIT/CorteXlab. On CorteXlab, the user does not have direct access to the SDR nodes, he has access to a server from which Minus deploys the programs on the different SDR nodes.

- Matthieu Imbert, Leonardo Sampaio Cardoso, Tanguy Risset
- Partners: Inria
- Contact: Matthieu Imbert
- URL: http://www.cortexlab.fr

5.3. FFTweb

KEYWORD: Spectrum Analyser , Data visualization , SDR

FUNCTIONAL DESCRIPTION

Visualisation tool use in CorteXlab to visualize the spectrum (or any kind vector signal) occuring in the CorteXlab room. FFTweb is a fundamental debugging and demonstration component for FIT/CorteXlab user.

- Matthieu Imbert
- Partners: Inria
- Contact: Matthieu Imbert
- URL: http://www.cortexlab.fr

5.4. WSNet

KEYWORD: Network simulator
FUNCTIONAL DESCRIPTION

The WSNet-3.0 project objective is to develop the next evolution of the WSNet simulator. It is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalabiliy, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation.

- Participants: Rodrigue Domga Komguem, Quentin Lampin, Alexandre Mouradian and Fabrice Valois
- Partner: CEA-LETI
- Contact: Fabrice Valois
- URL: https://gforge.inria.fr/projects/wsnet-3/

5.5. WiPlan

FUNCTIONAL DESCRIPTION

Wiplan is a software including an Indoor propagation engine and a wireless LAN optimization suite, which has been registered by INSA-Lyon. The heart of this software is the propagation simulation core relying on an original method, MR-FDPF (multi-resolution frequency domain ParFlow), proposed by JM Gorce in 2001 and further extended. The discrete ParFlow equations are translated in the Fourier domain providing a large linear system, solved in two steps taking advantage of a multi- resolution approach. The first step computes a cell-based tree structure referred to as the pyramid. In the second phase, a radiating source is simulated, taking advantage of the pre-processed pyramidal structure. Using of a full-space discrete simulator instead of classical ray-tracing techniques is a challenge due to the inherent high computation requests. However, we have shown that the use of a multi-resolution approach allows the main computational load to be restricted to a pre-processing phase. Extensive works have been done to make predictions more realistic.

- Contact: Jean-Marie Gorce

5.6. Platform - FIT/CortexLab

FIT(Future Internet of Things) is a french Equipex (Équipement d'excellence) which aims to develop an experimental facility, a federated and competitive infrastructure with international visibility and a broad panel of customers. FIT is be composed of four main parts: a Network Operations Center (NOC), a set of Embedded Communicating Object (ECO) test-beds, a set of wireless OneLab test-beds, and a cognitive radio test-bed (CorteXlab) deployed by the Socrate team in the Citi lab. In 2014 the construction of the room was finished see Figure 5 . SDR nodes have installed in the room, 42 industrial PCs (Aplus Nuvo-3000E/P), 22 NI radio boards (USRP) and 18 Nutaq boards (PicoSDR, 2x2 and 4X4) can be programmed from internet now.

A very successfully inauguration took place on the 28th October 2014 [0], with the noticable venue of Vincent Poor, Dean of School of Engineering and Applied Science of Princeton University. Since that date, the platform is open to public experiments.

---

[0] http://www.inria.fr/centre/grenoble/actualites/inauguration-reussie-de-la-plateforme-cortexlab-equipex-fit

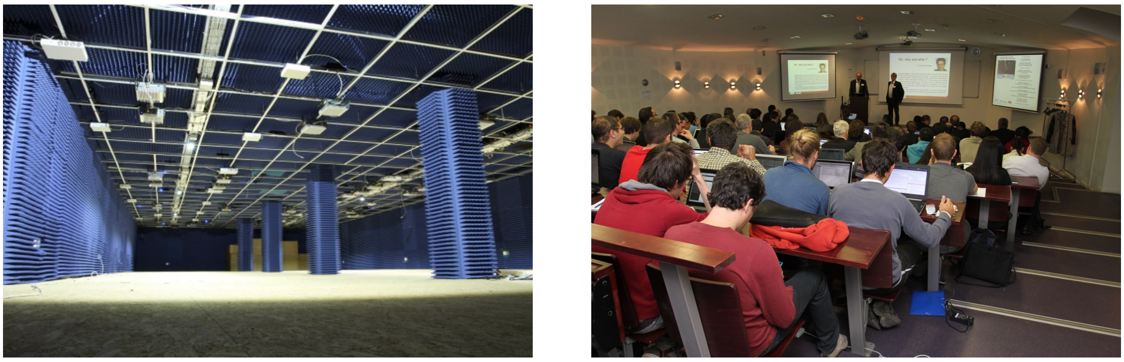


Figure 5. Photo of the FIT/CortexLab experimentation room installed and a snaptshot of the inauguration meeting

SPADES Project-Team

5. New Software and Platforms

5.1. COSYMA: Controller synthesis using multi-scale abstractions

FUNCTIONAL DESCRIPTION

CoSyMA is a tool for automatic controller synthesis for incrementally stable switched systems based on multi-scale discrete abstractions. The tool accepts as input a switched system defined by differential equations indexed by a set of modes, time and space sampling parameters used to define an approximation of the continuous state-space, and a safety or a time-bounded reachability specification. CoSyMA computes and refines discrete abstractions of the state space so as to generate a controller, if one exists, for the system that enforces the specification.

- Authors: Antoine Girard, Gregor Gössler, and Sebti Mouelhi.
- Partner: LJK.
- Contact: Gregor Gössler.

5.2. LoCa: Logical Causality Analyzer

FUNCTIONAL DESCRIPTION

Based on an execution trace, the component specifications, and a required property P, LoCA analyzes the causes of a violation of P in a component-based system. LoCA currently supports causality analysis in BIP and networks of timed automata. The core analysis engine is implemented as an abstract class, such that support for other models of computation (MoC) can be added by instantiating the class with the basic operations of the MoC.

- Authors: Lacramioara Astefanoaei, Yoann Geoffroy, and Gregor Gössler.
- Contact: Gregor Gössler.

5.3. LDDL: Coq proofs of circuit transformations for fault-tolerance

FUNCTIONAL DESCRIPTION

We have been developing a COQ-based framework to formally verify the functional and fault-tolerance properties of circuit transformations. Circuits are described at the gate level using LDDL, a Low-level Dependent Description Language inspired from μFP [87]. Our combinator language, equipped with dependent types, ensures that circuits are well-formed by construction (gates correctly plugged, no dangling wires, no combinational loops, ...). Faults like Single-Event Upsets (SEUs) (*i.e.*, bit-flips in flipflops) and SETs (*i.e.*, glitches propagating in the combinational circuit) and fault-models like *"at most 1 SEU or SET within n clock cycles"* are described in the operational semantics of LDDL. Fault-tolerance techniques are described as transformations of LDDL circuits.

The framework has been used to prove the correctness of three fault-tolerance techniques: TMR, TTR and DTR (see Section 6.3.3). The size of specifications and proofs for the common part (LDDL syntax and semantics, libraries) is 5000 lines of COQ (excluding comments and blank lines), 700 for TMR, 3500 for TTR and 7000 for DTR.

- Authors: Dmitry Burlyaev and Pascal Fradet.
- Contact: Pascal Fradet.
- URL: https://team.inria.fr/spades/fthwproofs

5.4. pyCPA_TWCA: A pyCPA plugin for computing deadline miss models

FUNCTIONAL DESCRIPTION

We are developing pyCPA_TWCA, a pyCPA plugin for Typical Worst-Case Analysis as described in Section 6.2.5 . pyCPA is an open-source Python implementation of Compositional Performance Analysis developed at TU Braunschweig, which allows in particular response-time analysis. pyCPA_TWCA is an extension of this tool that is co-developed by Sophie Quinton and Zain Hammadeh (TU Braunschweig). It allows in particular the computation of weakly-hard guarantees for real-time tasks, *i.e.*, the number of deadline misses out of a sequence of executions. So far, pyCPA_TWCA is restricted to uniprocessor systems of independent tasks, scheduled according to static priority scheduling. A public release is planned for 2016.

- Contact: Sophie Quinton.

SPECFUN Project-Team

5. New Software and Platforms

5.1. Coq

KEYWORDS: Proof - Certification - Formalisation

FUNCTIONAL DESCRIPTION

Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

- Participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Denes, Stéphane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pédrot, Loïc Pottier, Matthias Puech, Yann Régis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliâtre
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Hugo Herbelin
- URL: http://coq.inria.fr/

5.2. DynaMoW

Dynamic Mathematics on the Web

FUNCTIONAL DESCRIPTION

Programming tool for controlling the generation of mathematical websites that embed dynamical mathematical contents generated by computer-algebra calculations. Implemented in OCaml.

- Participants: Frédéric Chyzak, Alexis Darrasse and Maxence Guesdon
- Contact: Frédéric Chyzak
- URL: http://ddmf.msr-inria.inria.fr/DynaMoW/

5.3. ECS

Encyclopedia of Combinatorial Structures

FUNCTIONAL DESCRIPTION

On-line mathematical encyclopedia with an emphasis on sequences that arise in the context of decomposable combinatorial structures, with the possibility to search by the first terms in the sequence, keyword, generating function, or closed form.

- Participants: Stéphanie Petit, Alexis Darrasse, Frédéric Chyzak and Maxence Guesdon
- Contact: Frédéric Chyzak
- URL: http://algo.inria.fr/encyclopedia/

5.4. Math-Components

Mathematical Components library

FUNCTIONAL DESCRIPTION

The Mathematical Components library is a set of Coq libraries that cover the mechanization of the proof of the Odd Order Theorem.

- Participants: Andrea Asperti, Jeremy Avigad, Yves Bertot, Cyril Cohen, François Garillot, Georges Gonthier, Stéphane Le Roux, Assia Mahboubi, Sidi Ould Biha, Ioana Pasca, Laurence Rideau, Alexey Solovyev, Enrico Tassi and Russell O'connor
- Contact: Assia Mahboubi
- URL: http://www.msr-inria.fr/projects/mathematical-components-2/

5.5. Ring

FUNCTIONAL DESCRIPTION

Coq normalization tool and decision procedure for expressions in commutative ring theories. Implemented in Coq and OCaml. Integrated in the standard distribution of the Coq proof assistant since 2005.

- Contact: Assia Mahboubi

5.6. Ssreflect

FUNCTIONAL DESCRIPTION

Ssreflect is a tactic language extension to the Coq system, developed by the Mathematical Components team.

- Participants: Cyril Cohen, Yves Bertot, Laurence Rideau, Enrico Tassi, Laurent Théry, Assia Mahboubi and Georges Gonthier
- Contact: Yves Bertot
- URL: http://ssr.msr-inria.inria.fr/

SPHINX Team

6. New Software and Platforms

6.1. GPELab

Gross-Pitaevskii equations Matlab toolbox
KEYWORDS: 3D - Quantum chemistry - 2D
FUNCTIONAL DESCRIPTION

GPELab is a Matlab toolbox developed to help physicists for computing ground states or dynamics of quantum systems modeled by Gross-Pitaevskii equations. This toolbox allows the user to define a large range of physical problems (1d-2d-3d equations, general nonlinearities, rotation term, multi-components problems...) and proposes numerical methods that are robust and efficient.

- Contact: Xavier Antoine
- URL: http://gpelab.math.cnrs.fr/

6.2. GetDDM

KEYWORDS: Large scale - 3D - Domain decomposition - Numerical solver
FUNCTIONAL DESCRIPTION

GetDDM combines GetDP and Gmsh to solve large scale finite element problems using optimized Schwarz domain decomposition methods.

- Contact: Xavier Antoine
- URL: http://onelab.info/wiki/GetDDM

6.3. Platform: Vir'Volt

Vir'Volt is a prototype build in ESSTIN, an engineering school of Université de Lorraine, as part of a student project. The prototype enters low-consumption vehicle race, where the winner covers a given distance (depending upon the race, around 20 km) at a given average speed (around 25 km/h) with the lowest energy consumption. Thomas Chambrion has been in charge of the embedded automatic speed control of Vir'Volt for 6 years. In 2016, Vir'Volt will take part in the European Shell Eco Marathon organized in London. The sloping track (up to 5% uphill and 4% downhill) required a complete rebuild of the transmission parts. The proposed configuration has been obtained after intensive numerical simulations.

- Contact: Thomas Chambrion
- URL: http://www.ecomotionteam.org/blog/?page_id=3072

SPIRALS Project-Team

6. New Software and Platforms

6.1. APISENSE®

Participants: Clive Ferret-Canape, Julien Duribreux, Maria Gomez Lacruz, Christophe Ribeiro, Romain Rouvoy, Antoine Veuiller.

- Contact: Romain Rouvoy
- URL: https://bil.inria.fr/fr/software/view/614/tab

In 2015, APISENSE® has been extended to include the support for iOS smartphones and tablets. The infrastructure, hosted by the LHS (*Laboratoire Haute Sécurité*), is now fully secured to protect the privacy of contributors.

APISENSE® is a distributed platform dedicated to crowd-sensing activities. Crowd-sensing intends to leverage mobile devices to seamlessly collect valuable dataset for different categories of stakeholders. APISENSE® intends to be used in a wide variety of scientific and industrial domains, including network quality monitoring, social behavior analysis, epidemy predictions, emergency crisis support, open maps initiatives, debugging of applications in the wide. APISENSE® is composed of HIVE delivered as a *Platform-as-a-Service* (PaaS) to the stakeholders who can pilot and customize their own crowd-sensing environment [79], and *Bee* supporting participants with a mobile application to control the sensors to be shared with the rest of the world [68], [69]. The platform is used by the Metroscope consortium, an Internet scientific observatory initiative supported by Inria. APISENSE® originates as the output of Nicolas Haderer PhD thesis [67].

APISENSE® is at the core of the Inria ADT Focus CrowdLab project (see Section 9.2) and of an industrial transfer action that aims at creating the Crowdify spin-off company.

Registered with the APP (*Agence pour la Protection des Programmes*) under reference FR.001.080006.000.S.P.2013.000.10000. License: Proprietary.

6.2. PowerAPI

Participants: Maxime Colmant, Loïc Huertas, Romain Rouvoy.

- Contact: Romain Rouvoy
- URL: https://bil.inria.fr/fr/software/view/1642/tab

In 2015, POWERAPI has been further extended to support the monitoring of *Software-as-a-Service* (SaaS) [23] by including a support for hypervision technologies like KVM (*Kernel-based Virtual Machine*), and Docker.

POWERAPI is a Scala-based library for monitoring energy in software systems. It is based on a modular and asynchronous event-driven architecture using the Akka library. POWERAPI differs from existing energy process-level monitoring tool in its pure software, fully customizable and modular aspect which let users precisely define what they want to monitor, without plugging any external device. POWERAPI offers an API which can be used to express requests about energy spent by a process, following its hardware resource utilization (in terms of CPU, memory, disk, network, etc.). Its applications cover energy-driven benchmarking [75], [62], [60], [61], energy hotspots and bugs detection [76], [77], and real-time distributed system monitoring. POWERAPI originates as the output of Adel Noureddine PhD thesis [78].

POWERAPI is at the core of the Inria ADT eSurgeon project (see Section 9.2).

Web site: http://www.powerapi.org. Registered with the APP (Agence pour la Protection des Programmes) under reference IDDN.FR.001.400015.000.S.P.2012.000.10000. License: AGPL.

6.3. Saloon

Participants: Laurence Duchien, Daniel Romero Acero, Lionel Seinturier [correspondant].

- Contact: Lionel Seinturier
- URL: https://bil.inria.fr/fr/software/view/1492/tab

In 2015, SALOON was extended to fit with the requirements of the FP7 PaaSage project (see Section 9.3). New mechanisms were added to deal with ontologies for describing cloud computing commercial offers.

SALOON is a framework for the selection and configuration of Cloud providers according to application requirements. The framework enables the specification of such requirements by defining ontologies. Each ontology provides a unified vision of provider offers in terms of frameworks, databases, languages, application servers and computational resources (i.e., memory, storage and CPU frequency). Furthermore, each provider is related to a Feature Model (FM) with attributes and cardinalities, which captures its capabilities. By combining the ontology and FMs, the framework is able to match application requirements with provider capabilities and select a suitable one. Specific scripts to the selected provider are generated in order to enable its configuration. SALOON originates as the output of Clément Quinton PhD thesis [82].

Registered with the APP (Agence pour la Protection des Programmes) under reference IDDN.FR.001.300002.000.S.P.2014.000.10800.

6.4. Spoon

Participants: Thomas Durieux, Matias Martinez, Martin Monperrus, Gérard Paligot, Nicolas Petitprez.

- Contact: Martin Monperrus
- URL: https://bil.inria.fr/fr/software/view/251/tab

SPOON is a library for analyzing and transforming Java source code [18] [80]. In 2015, there was one engineer (Géradar Paligot) working full-time on Spoon. This has incredibly boosted the project. In particular, the new features of SPOON are: a) the complete support for Java 8 (incl. lambda expressions) b) the support for Maven and Gradle build systems. Also, a major testing effort has been done and consequently, the code quality now meets the highest standards, using a comprehensive test suite as well three continuous integration servers (incl. the Inria one). Spoon has an an international community of users and contributors, which is very active on the Github project.

SPOON is at the core of the Inria ADT Spoon3R project (see Section 9.1) SPOON is the foundation behind an industrial transfer action that aims at creating the Spoonware spin-off company on automatic hot patching.

Web site: http://spoon.gforge.inria.fr. Registered with the APP (Agence pour la Protection des Programmes) under reference IDDN.FR.001.070037.000.S.P.2007.000.10600. License: CeCILL-C.

STARS Project-Team

6. New Software and Platforms

6.1. CLEM

FUNCTIONAL DESCRIPTION

The Clem Toolkit is a set of tools devoted to design, simulate, verify and generate code for LE programs. LE is a synchronous language supporting a modular compilation. It also supports automata possibly designed with a dedicated graphical editor and implicit Mealy machine definition.

- Participants: Daniel Gaffé and Annie Ressouche
- Contact: Annie Ressouche
- URL: http://www-sop.inria.fr/teams/pulsar/projects/Clem/

6.2. EGMM-BGS

FUNCTIONAL DESCRIPTION

This software implements a generic background subtraction algorithm for video and RGB-D cameras, which can take feedback from people detection and tracking processes. Embedded in a people detection framework, it does not classify foreground / background at pixel level but provides useful information for the framework to remove noise. Noise is only removed when the framework has all the information from background subtraction, classification and object tracking. In our experiment, our background subtraction algorithm outperforms GMM, a popular background subtraction algorithm, in detecting people and removing noise.

- Participants: Anh Tuan Nghiem, François Brémond and Vasanth Bathrinarayanan
- Contact: François Brémond

6.3. MTS

FUNCTIONAL DESCRIPTION

This software consists of a retrieval tool for a human operator to select a person of interest in a network of cameras. The multi-camera system can re-identify the person of interest, wherever and whenever (s)he has been observed in the camera network. This task is particularly hard due to camera variations, different lighting conditions, different color responses and different camera viewpoints. Moreover, we focus on non-rigid objects (i.e. humans) that change their pose and orientation contributing to the complexity of the problem. In this work we design two methods for appearance matching across non-overlapping cameras. One particular aspect is the choice of the image descriptor. A good descriptor should capture the most distinguishing characteristics of an appearance, while being invariant to camera changes. We chose to describe the object appearance by using the covariance descriptor as its performance is found to be superior to other methods. By averaging descriptors on a Riemannian manifold, we incorporate information from multiple images. This produces mean Riemannian covariance that yields a compact and robust representation. This new software has made digital video surveillance systems a product highly asked by security operators, especially the ones monitoring large critical infrastructures, such as public transportation (subways, airports, and harbours), industrials (gas plants), and supermarkets.

- Participants: Slawomir Bak and François Brémond
- Contact: François Brémond

6.4. Person Manual Tracking in a Static Camera Network (PMT-SCN)

FUNCTIONAL DESCRIPTION

This software allows tracking a person in a heterogeneous camera network. The tracking is done manually. The advantage of this software is to give the opportunity to operators in video-surveillance to focus on tracking the activity of a person without knowing the positions of the cameras in a considered area. When the tracked person leaves the field-of–view (FOV) of a first camera, and enters the FOV of a second one, the second camera is automatically showed to the operator. This software was developed conjointly by Inria and Neosensys.

- Participants: Bernard Boulay, Anaïs Ducoffe, Sofia Zaidenberg, Anais Ducoffe, Annunziato Polimeni and Julien Gueytat
- Partner: Neosensys
- Contact: Anaïs Ducoffe

6.5. PrintFoot Tracker

FUNCTIONAL DESCRIPTION

This software implements a new algorithm for tracking multiple persons in a single camera. This algorithm computes many different appearance-based descriptors to characterize the visual appearance of an object and to track it over time. Object tracking quality usually depends on video scene conditions (e.g. illumination, density of objects, object occlusion level). In order to overcome this limitation, this algorithm presents a new control approach to adapt the object tracking process to the scene condition variations. More precisely, this approach learns how to tune the tracker parameters to cope with the tracking context variations. The tracking context, or video context, of a video sequence is defined as a set of six features: density of mobile objects, their occlusion level, their contrast with regard to the surrounding background, their contrast variance, their 2D area and their 2D area variance. The software has been experimented with three different tracking algorithms and on long, complex video datasets.

- Participants: Duc Phu Chau, François Brémond and Monique Thonnat
- Contact: François Brémond

6.6. Proof of Concept Néosensys (Poc-NS)

FUNCTIONAL DESCRIPTION

This is a demonstration software which gathers different technologies from Inria and Neosensys: PMT-SCN, re-identification and auto-side switch. This software is used to approach potential clients of Neosensys.

- Participants: Bernard Boulay, Sofia Zaidenberg, Julien Gueytat, Slawomir Bak, François Brémond, Annunziato Polimeni and Yves Pichon
- Partner: Neosensys
- Contact: François Brémond

6.7. SUP

Scene Understanding Platform
KEYWORDS: Activity recognition - 3D - Dynamic scene
FUNCTIONAL DESCRIPTION

SUP is a software platform for perceiving, analyzing and interpreting a 3D dynamic scene observed through a network of sensors. It encompasses algorithms allowing for the modeling of interesting activities for users to enable their recognition in real-world applications requiring high-throughput.

- Participants: François Brémond, Carlos Fernando Crispim Junior and Etienne Corvée
- Partners: CEA - CHU Nice - USC Californie - Université de Hamburg - I2R
- Contact: François Brémond
- URL: https://team.inria.fr/stars/software

6.8. VISEVAL

FUNCTIONAL DESCRIPTION

ViSEval is a software dedicated to the evaluation and visualization of video processing algorithm outputs. The evaluation of video processing algorithm results is an important step in video analysis research. In video processing, we identify 4 different tasks to evaluate: detection, classification and tracking of physical objects of interest and event recognition.

- Participants: Bernard Boulay and François Brémond
- Contact: François Brémond
- URL: http://www-sop.inria.fr/teams/pulsar/EvaluationTool/ViSEvAl_Description.html

6.9. py_ad

py action detection

FUNCTIONAL DESCRIPTION

Action Detection framework which allows user to detect action in video stream. It uses model trained in py_ar.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.10. py_ar

py action recognition

FUNCTIONAL DESCRIPTION

Action Recognition training/evaluation framework. It allows user do define action recognition experiment (on clipped videos). Train, test model, save the results and print the statistics.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.11. py_sup_reader

FUNCTIONAL DESCRIPTION

This is a library which allows to read video saved in SUP format in Python.

- Participant: Michal Koperski
- Contact: Michal Koperski

6.12. py_tra3d

py trajectories 3d

SCIENTIFIC DESCRIPTION

New video descriptor which fuse trajectory information with 3D information from depth sensor.

FUNCTIONAL DESCRIPTION

3D Trajectories descriptor Compute 3D trajectories descriptor proposed in (http://hal.inria.fr/docs/01/05/49/49/PDF/koperski-icip.pdf)

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.13. sup_ad

sup action detection

SCIENTIFIC DESCRIPTION

This software introduces the framework for online/real-time action recognition using state-of-the-art features and sliding window technique.

FUNCTIONAL DESCRIPTION

SUP Action Detection Plugin is a plugin for SUP platform which performs action detection using sliding window and Bag of Words. It uses an input data model trained in py_ar project.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

STEEP Project-Team

5. New Software and Platforms

5.1. QGISTranusReports

FUNCTIONAL DESCRIPTION

This software allows to graphically visualise data output by the TRANUS LUTI model (and possibly, of any other data of the same structure). In particular, this concerns any data items defined per zone of a modelled territory (productions, indicators, etc.). The software is designed as a plugin for the geographical information system platform QGIS and can be run interactively as well as by the command line or by a call from within another software. The interactive mode (within QGIS) allows the user to define graphical outputs to be generated from TRANUS output files (type of graphs to be generated â 2D or 3D â color coding to be used, choice of data to be displayed, etc.). Visualisation of data is done in the form of 2D graphs or 3D models defined using java-script.

- Contact: Peter Sturm

5.2. REDEM

REDuction Of EMission
FUNCTIONAL DESCRIPTION

REDEM soft is a tool designed for the benchmarking of national GHG emission reduction trajectories. The actual version of the software is implemented in Visual Basic under Microsoft Excel in order to facilitate handling and diffusion to climate/energy economists.

- Participants: Patrick Criqui, Constantin Ilasca, Olivier Boucher and Hélène Benveniste
- Partners: EDDEN - IPSL
- Contact: Emmanuel Prados
- URL: http://redem.gforge.inria.fr/

5.3. Wassily

SCIENTIFIC DESCRIPTION

The software is structured in three different modules:

the database module stores all the input-output data coming from Eurostat, OCDE, Insee or other sources.

the computation module performs the input-output calculations

the visualization module displays the results in a synthetic manner.

The database module is based on the SQlite format and makes use of SQL to manipulate the various tables involved in the process. The goal of this module is to provide a normalized data interface for the computation module, from various types of input-output data which are often stored as Excel sheet on web sites.
FUNCTIONAL DESCRIPTION

The purpose of this software is to automatize most of the work of standard input-output analysis and to visualize the results in a user-friendly way in order to efficiently address related environmental questions.

- Participants: Julien Alapetite and Jean-Yves Courtonne
- Contact: Julien Alapetite

5.4. Contribution to the R package “sensitivity"

FUNCTIONAL DESCRIPTION

The contribution to the R package “sensitivity” includes the development of the function “sobolroalhs” performing global sensitivity analysis of a numerical model. This function implements the estimation of the Sobol’ sensitivity indices introduced by [19] using two Orthogonal Array-based Latin Hypercubes. This function allows the estimation of all first-order indices or all closed second-order indices (containing the sum of the second-order effect between two inputs and the individual effects of each input) at a total cost of $2 \times N$. For closed second-order indices, $N = q^2$ where $q >= d - 1$ is a prime number denoting the number of levels of the orthogonal array, and where d is the number of factors of the model.

- Participants: Laurent Gilquin, Elise Arnaud, Clémentine Prieur
- Partners: AIRSEA (Inria / UJF)
- Contact: Laurent Gilquin
- URL: https://cran.r-project.org/web/packages/sensitivity/index.html

STORM Team

6. New Software and Platforms

6.1. Chameleon

KEYWORDS: HPC - Dense linear algebra - Task-based algorithm - Runtime system - Task scheduling

SCIENTIFIC DESCRIPTION

Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

We expect advances in three directions based first on strong and closed interactions between the runtime and numerical linear algebra communities. This initial activity will then naturally expand to more focused but still joint research in both fields.

1. Fine interaction between linear algebra and runtime systems. On parallel machines, HPC applications need to take care of data movement and consistency, which can be either explicitly managed at the level of the application itself or delegated to a runtime system. We adopt the latter approach in order to better keep up with hardware trends whose complexity is growing exponentially. One major task in this project is to define a proper interface between HPC applications and runtime systems in order to maximize productivity and expressivity. As mentioned in the next section, a widely used approach consists in abstracting the application as a DAG that the runtime system is in charge of scheduling. Scheduling such a DAG over a set of heterogeneous processing units introduces a lot of new challenges, such as predicting accurately the execution time of each type of task over each kind of unit, minimizing data transfers between memory banks, performing data prefetching, etc. Expected advances: In a nutshell, a new runtime system API will be designed to allow applications to provide scheduling hints to the runtime system and to get real-time feedback about the consequences of scheduling decisions.

2. Runtime systems. A runtime environment is an intermediate layer between the system and the application. It provides low-level functionality not provided by the system (such as scheduling or management of the heterogeneity) and high-level features (such as performance portability). In the framework of this proposal, we will work on the scalability of runtime environment. To achieve scalability it is required to avoid all centralization. Here, the main problem is the scheduling of the tasks. In many task-based runtime environments the scheduler is centralized and becomes a bottleneck as soon as too many cores are involved. It is therefore required to distribute the scheduling decision or to compute a data distribution that impose the mapping of task using, for instance the so-called “owner-compute” rule. Expected advances: We will design runtime systems that enable an efficient and scalable use of thousands of distributed multicore nodes enhanced with accelerators.

3. Linear algebra. Because of its central position in HPC and of the well understood structure of its algorithms, dense linear algebra has often pioneered new challenges that HPC had to face. Again, dense linear algebra has been in the vanguard of the new era of petascale computing with the design of new algorithms that can efficiently run on a multicore node with GPU accelerators. These algorithms are called “communication-avoiding” since they have been redesigned to limit the amount of communication between processing units (and between the different levels of memory hierarchy). They are expressed through Direct Acyclic Graphs (DAG) of fine-grained tasks that are dynamically scheduled. Expected advances: First, we plan to investigate the impact of these principles in the case of sparse applications (whose algorithms are slightly more complicated but often rely on dense kernels). Furthermore, both in the dense and sparse cases, the scalability on thousands of nodes is still limited, new numerical approaches need to be found. We will specifically design sparse hybrid direct/iterative methods that represent a promising approach.

Overall end point. The overall goal of the MORSE associate team is to enable advanced numerical algorithms to be executed on a scalable unified runtime system for exploiting the full potential of future exascale machines.
FUNCTIONAL DESCRIPTION

Chameleon is a dense linear algebra software relying on sequential task-based algorithms where sub-tasks of the overall algorithms are submitted to a Runtime system. A Runtime system such as StarPU is able to manage automatically data transfers between not shared memory area (CPUs-GPUs, distributed nodes). This kind of implementation paradigm allows to design high performing linear algebra algorithms on very different type of architecture: laptop, many-core nodes, CPUs-GPUs, multiple nodes. For example, Chameleon is able to perform a Cholesky factorization (double-precision) at 80 TFlop/s on a dense matrix of order 400 000 (e.i. 4 min).

- Participants: Marc Sergent, Suraj Kumar, Samuel Thibault, Andra Hugo, Terry Cojean, Nathalie Furmento
- Partners: Innovative Computing Laboratory (ICL) - King Abdullha University of Science and Technology - University of Colorado Denver
- Contact: Emmanuel Agullo
- URL: https://project.inria.fr/chameleon/

6.2. KLANG-OMP

The Klang-Omp OpenMP Compiler
KEYWORDS: Compilers - Task scheduling - OpenMP - Source-to-source compiler - Data parallelism
FUNCTIONAL DESCRIPTION

The Klang-Omp software is a source-to-source OpenMP compiler for languages C and C++. The Klang-Omp compiler translates OpenMP directives and constructs into API calls from the StarPU runtime system or the XKaapi runtime system. The Klang-Omp compiler is virtually fully compliant with OpenMP 3.0 constructs. The Klang-Omp compiler supports OpenMP 4.0 dependent tasks and accelerated targets.

- Participants: Olivier Aumage, Nathalie Furmento, Samuel Pitoiset and Samuel Thibault
- Contact: Olivier Aumage
- URL: http://kstar.gforge.inria.fr/#!index.md

6.3. KaStORS

The KaStORS OpenMP Benchmark Suite
KEYWORDS: Benchmarking - HPC - Task-based algorithm - Task scheduling - OpenMP - Data parallelism
FUNCTIONAL DESCRIPTION

The KaStORS benchmarks suite has been designed to evaluate implementations of the OpenMP dependent task paradigm, introduced as part of the OpenMP 4.0 specification.

- Participants: Olivier Aumage, François Broquedis, Pierrick Brunet, Nathalie Furmento, Thierry Gautier, Samuel Thibault and Philippe Virouleau
- Contact: Thierry Gautier
- URL: http://kastors.gforge.inria.fr/#!index.md

6.4. MAQAO

SCIENTIFIC DESCRIPTION

MAQAO relies on binary codes for Intel x86 and ARM architectures. For x86 architecture, it can insert probes for instrumentation directly inside the binary. There is no need to recompile. The static/dynamic approach of MAQAO analysis is the main originality of the tool, combining performance model with values collected through instrumentation.

MAQAO has a static performance model for x86 and ARM architectures. This model analyzes performance of the codes on the architectures and provides some feed-back hints on how to improve these codes, in particular for vector instructions.

The dynamic collection of data in MAQAO enables the analysis of thread interactions, such as false sharing, amount of data reuse, runtime scheduling policy, ...

FUNCTIONAL DESCRIPTION

MAQAO is a performance tuning tool for OpenMP parallel applications. It relies on the static analysis of binary codes and the collection of dynamic information (such as memory traces). It provides hints to the user about performance bottlenecks and possible workarounds.

- Participants: Denis Barthou, Olivier Aumage, Christopher Haine and James Tombi A Mba
- Contact: Denis Barthou
- URL: https://gforge.inria.fr/projects/maqao

6.5. P-EDGE

An Efficient and Portable Library for Error Correction Code Design and Optimization

KEYWORDS: Code generation - Error Correction Code

FUNCTIONAL DESCRIPTION

The P-Edge library joins genericity techniques together with code generation capabilities to enable implementing efficient and portable error correction codes. The genericity offered allows to easily experiment with a large panel of algorithmic variants.

- Authors: Adrien Cassagne, Olivier Aumage, Bertrand Le Gal, Camille Leroux and Denis Barthou
- Partner: IMS
- Contact: Adrien Cassagne

6.6. StarPU

The StarPU Runtime System

KEYWORDS: HPC - Scheduling - GPU - Multicore - Performance

SCIENTIFIC DESCRIPTION

Traditional processors have reached architectural limits which heterogeneous multicore designs and hardware specialization (e.g. coprocessors, accelerators, ...) intend to address. However, exploiting such machines introduces numerous challenging issues at all levels, ranging from programming models and compilers to the design of scalable hardware solutions. The design of efficient runtime systems for these architectures is a critical issue. StarPU typically makes it much easier for high performance libraries or compiler environments to exploit heterogeneous multicore machines possibly equipped with GPGPUs or Cell processors: rather than handling low-level issues, programmers may concentrate on algorithmic concerns.Portability is obtained by the means of a unified abstraction of the machine. StarPU offers a unified offloadable task abstraction named "codelet". Rather than rewriting the entire code, programmers can encapsulate existing functions within codelets. In case a codelet may run on heterogeneous architectures, it is possible to specify one function for each architectures (e.g. one function for CUDA and one function for CPUs). StarPU takes care to schedule and execute those codelets as efficiently as possible over the entire machine. In order to relieve programmers from the burden of explicit data transfers, a high-level data management library enforces memory coherency over the machine: before a codelet starts (e.g. on an accelerator), all its data are transparently made available on the compute resource.Given its expressive interface and portable scheduling policies, StarPU obtains portable performances by efficiently (and easily) using all computing resources at the same time. StarPU also takes advantage of the heterogeneous nature of a machine, for instance by using scheduling strategies based on auto-tuned performance models.

StarPU is a task programming library for hybrid architectures

The application provides algorithms and constraints: - CPU/GPU implementations of tasks - A graph of tasks, using either the StarPU's high level GCC plugin pragmas or StarPU's rich C API

StarPU handles run-time concerns - Task dependencies - Optimized heterogeneous scheduling - Optimized data transfers and replication between main memory and discrete memories - Optimized cluster communications

Rather than handling low-level scheduling and optimizing issues, programmers can concentrate on algorithmic concerns!

FUNCTIONAL DESCRIPTION

StarPU is a runtime system that offers support for heterogeneous multicore machines. While many efforts are devoted to design efficient computation kernels for those architectures (e.g. to implement BLAS kernels on GPUs), StarPU not only takes care of offloading such kernels (and implementing data coherency across the machine), but it also makes sure the kernels are executed as efficiently as possible.

- Participants: Samuel Thibault, Nathalie Furmento, Jérôme Clet-Ortega, Pierre-André Wacrenier, Terry Cojean, Andra Hugo, Raymond Namyst, Olivier Aumage, Marc Sergent and Samuel Pitoiset.
- Contact: Raymond Namyst
- URL: http://starpu.gforge.inria.fr/

6.7. hwloc

Hardware Locality

KEYWORDS: HPC - Topology - Open MPI - Affinities - GPU

FUNCTIONAL DESCRIPTION

Hardware Locality (hwloc) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices.

It builds a widely-portable abstraction of these resources and exposes it to the application so as to help them adapt their behavior to the hardware characteristics.

hwloc targets many types of high-performance computing applications, from thread scheduling to placement of MPI processes. Most existing MPI implementations, several resource managers and task schedulers, and multiple other parallel libraries already use hwloc .

- Participants: Brice Goglin and Samuel Thibault
- Contact: Brice Goglin
- URL: http://www.open-mpi.org/projects/hwloc/

SUMO Project-Team

6. New Software and Platforms

6.1. SIMSTORS

SIMSTORS is a simulator for regulated stochastic timed Petri nets. These Petri nets are a variant of stochastic and timed nets, which execution is controlled by a regulation policy an a predetermined theoretical schedule. The role of the regulation policy is to control the system to realize the schedule with the best possible precision. This software allows not only for step by step simulation, but also for performance analysis of systems such as production cells or train systems.

SIMSTORS was used successfully during a collaboration with Alstom transport to model existing urban railway systems and their regulation schemes. Alstom transport is willing to transfer this software and use it during early design phase of regulation algorithms in their metro lines.

Future extensions of the software will deal with verification of several new properties such as the robustness of proposed schedules.

- Participants: Loïc Hélouët and Abd El Karim Kecir
- Contact: Loïc Hélouët

6.2. Sigali

FUNCTIONAL DESCRIPTION

Sigali is a model-checker that operates on ILTS (Implicit Labeled Transition Systems, an equational representation of an automaton), an intermediate model for discrete event systems. It offers functionalities for verification of reactive systems and discrete controller synthesis. The techniques used consist in manipulating the system of equations instead of the set of solutions, which avoids the enumeration of the state space. Each set of states is uniquely characterized by a predicate and the operations on sets can be equivalently performed on the associated predicates. Therefore, a wide spectrum of properties, such as liveness, invariance, reachability and attractivity, can be checked. Algorithms for the computation of predicates on states are also available. Sigali is connected with the Polychrony environment (Tea project-team) as well as the Matou environment (VERIMAG), thus allowing the modeling of reactive systems by means of Signal Specification or Mode Automata and the visualization of the synthesized controller by an interactive simulation of the controlled system.

- Contact: Hervé Marchand

6.3. Tipex

TImed Properties Enforcement during eXecution
FUNCTIONAL DESCRIPTION

We are implementing a prototype tool named Tipex (TImed Properties Enforcement during eXecution) for the enforcement of timed properties. Tipex is based on the theory and algorithms that we develop for the synthesis of enforcement monitors for properties specified by timed automata (TA). The prototype is developped in python, and uses the PyUPPAAL and DBMpyuppaal libraries of the UPPAAL tool . It is currently restricted to safety and co-safety timed property. The property provided as input to the tool is a TA that can be specified using the UPPAAL tool, and is stored in XML format. The tool synthesizes an enforcement monitor from this TA, which can then be used to enforce a sequence of timed events to satisfy the property. Experiments have been conducted on a set of case studies. This allowed to validate the architecture and feasibility of enforcement monitoring in a timed setting and to have a first assessment of performance (and to what extent the overhead induced by monitoring is negligible).

- Contact: Thierry Jéron, Hervé Marchand
- URL: http://srinivaspinisetty.github.io/Timed-Enforcement-Tools/

6.4. ReaX

ReaX is a tool developed by Nicolas Berthier that investigates the control of safety properties for infnite reactive synchronous systems modeled by arithmetic symbolic transition systems. It provides effective algorithms allowing to solve the safety control problem (including the dead-lock free case), and report some experiments. Its aim is to replace Sigali, which is limited to finite state systems described by boolean variables.

- Contact : Nicolas Berthier, Hervé Marchand
- URL : http://reatk.gforge.inria.fr/

6.5. Open Agora Core

Christophe Morvan participates to the implementation of a sophisticated voting system: Open Agora Core. It currently implements several voting methods among which *Condorcet* (Schulze method) or *instant runoff*. It is integrated into a Slack [0] polling plugin. This development serves as a basic building block in the process of elaborating Open Agora, a startup that should be created during 2016.

- Contact : Christophe Morvan
- URL : http://www.open-agora.com

---

[0] Slack, `http://slack.com`, is an industrial team communication tool.

TACOMA Team

5. New Software and Platforms

5.1. THEGAME: data fusion for Smart Home and Smart Building

KEYWORDS: Smart home - Smart building

- Participants: Aurélien Richez
- Partner: Université de Rennes 1
- Contact: Frédéric Weis
- URL: https://github.com/bpietropaoli/THEGAME/

DESCRIPTION

Context-aware applications have to sense the environment in order to adapt themselves and provide with contextual services. This is the case of Smart Homes equipped with sensors and augmented appliances. However, sensors can be numerous, heterogeneous and unreliable. Thus the data fusion is complex and requires a solid theory to handle those problems. The aim of the data fusion, in our case, is to compute small pieces of context we call context attributes. Those context attributes are diverse and could be for example the presence in a room, the number of people in a room or even that someone may be sleeping in a room. For this purpose, we developed an implementation of the belief functions theory (BFT). THE GAME (THeory of Evidence in a lanGuage Adapted for Many Embedded systems) is made of a set of C-Libraries. It provides the basics of belief functions theory, computations are optimized for an embedded environment (binary representation of sets, conditional compilation and diverse algorithmic optimizations).

THE GAME is published under apache licence. It is maintained and experimented within a sensor network platform developed by TACOMA since June 2013.

5.2. Platforms

5.2.1. Platform Pervasive_RFID

KEYWORDS: Composite objects - RFID

- Participants: Paul Couderc and Nebil Ben Mabrouck
- Partner: Université de Rennes 1 (IETR)
- Contact: Paul Couderc

SCIENTIFIC DESCRIPTION

In 2015 we completed the RFID experiment testbed realized in 2014 in collaboration with IETR (see Figure 1).

This system allows both interactive testing as well as long running experiments of RFID reading protocols. It comprises a software platform (see Figure 2) allowing fine control over all dynamic aspects influencing RFID readings: movements for target and antenna, RFID reader configuration, and smart antenna configuration (diversity and power control). This testbed supports the reproduction of most situations found in real applications. We achieved the following improvements on the testbed in 2015:

- The implementation of a software controllable smart antenna, with dynamic radiating pattern, was completed along with its the hardware interface. This is an important feature when experimenting pervasive application, in particular to determine the radio performance improvements expectable from antenna diversity.

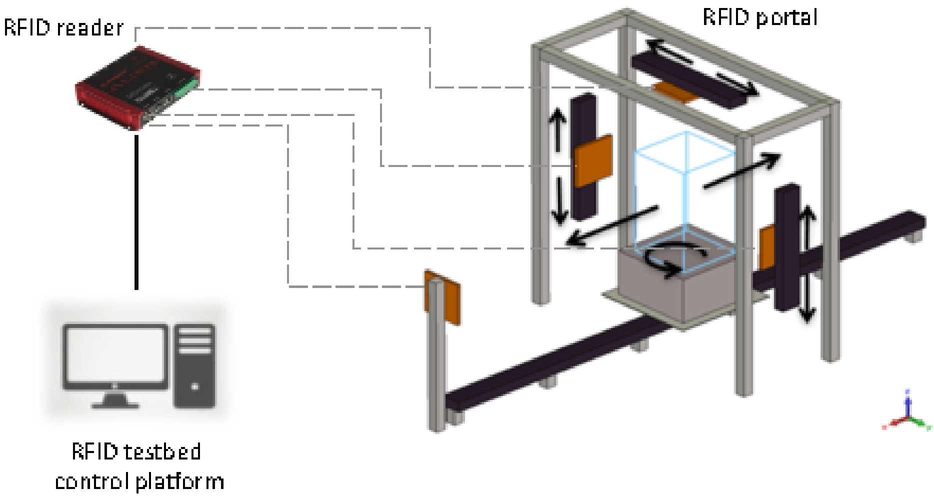


Figure 1. RFID testbed

- A particular effort was put on improving the operational performance and robustness of the system: the initial implementation was completed in 2014 in a context tightly coupled with our on-going RFID research, and with an important dependency on the technical expertise of short term positions staff-member. In order to widen the testbed?s perspectives as a research tool, two aspects were improved:
    1. a high-level scripting interface was added to offer easy automatized experimentation campaign. Iterative RFID experiments with fine-tuning parameters can be specified using a variety of script languages, and further executed in a remote fashion via the added interface.
    2. A virtualization of RFID readers and motion drives was also developed to simulate the behavior of critical experiments or new software updates before executing them on the real testbed.
    3. Functional tests were developed to ascertain that crucial functions of the testbed would work correctly after future software updates, thus ensuring the maintainability and sustainability of the system.

5.2.2. On-demand room

KEYWORDS: Smart Home - Metamorphic House

- Partner: Université de Rennes 1
- Partner: Université de Rennes 1 (Fondation Rennes 1)
- Contact: Michele Dominici and Frédéric Weis

DESCRIPTION

As part of the demonstration activities, we realized a prototype of the on-demand room as an immersive interactive virtual-reality application, leveraging the Immersia platform. Two iterations were achieved so far.

For the first iteration of the demonstrator, we realized a three-dimensional model of the on-demand room and two adjacent apartments, using the software SketchUp. This model was then imported in Unity3D and MiddleVR, which allow to display and navigate inside the model using the virtual reality platform Immersia [0].

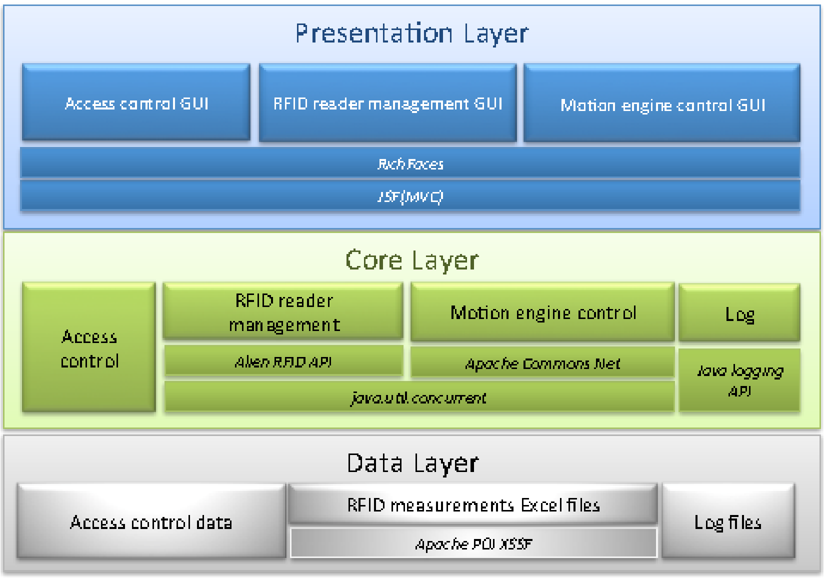


Figure 2. Software architecture of the RFID testbed

We then implemented the application logic of the on-demand room using Unity scripting facilities. By wearing 3D glasses and a marker on their hand, users can literally walk inside the apartments, open doors and observe how the configuration of the room changes to become a part of one dwelling or another, as shown in Figure 3 .

Figure 3. 3D model in the Immersia platform

---

[0] http://www.irisa.fr/immersia/

The second (and current) iteration of the demonstrator introduced a major feature: the real/virtual integration. Actual domestic appliances can now be connected to Immersia and participate to the on-demand room demonstration. In this phase we showed that a real light switch, located in the virtual on-demand room, can change its behavior and alternatively control one of the two real lamps, each located in one of the apartments, as shown in Figure 4 .

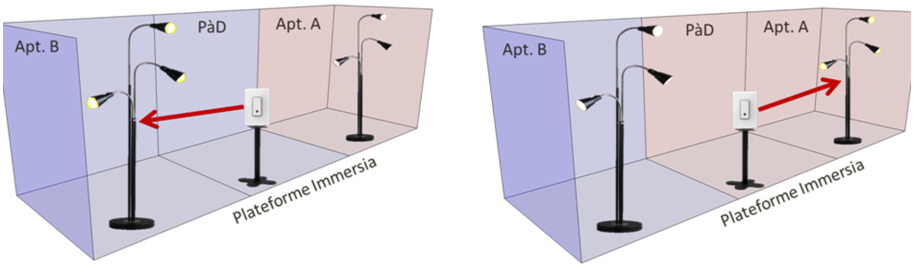


Figure 4. Integration of real devices

To develop the real/virtual integration feature, we used home automation controllers and devices implementing the KNX standard. After wiring and programming the domotic network, we developed an application that leverages the Falcon library, provided by the KNX association, to dynamically change the behavior of the real light switch.

TADAAM Team

5. New Software and Platforms

5.1. Hardware Locality

KEYWORDS: Topology - Locality

FUNCTIONAL DESCRIPTION

Hardware Locality (HWLOC) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices.

It builds a widely-portable abstraction of these resources and exposes it to the application so as to help them adapt their behavior to the hardware characteristics. HWLOC also offers monitoring abilities to identify application bottlenecks [12]. Moreover it focuses on modeling the network topology by embedding the NETLOC subproject in its future releases.

HWLOC targets many types of high-performance computing applications [1], [2], from thread scheduling to placement of MPI processes. Most existing MPI implementations, many resource managers, task schedulers and parallel libraries already use HWLOC.

HWLOC is developed in collaboration within the OPEN MPI consortium. The core development is carried out by Brice GOGLIN and other members of TADAAM team-project, with external contribution from many academic and industrial partners.

HWLOC is composed of 100,000 lines of C.

- Participants: Brice Goglin, Nicolas Denoyelle, Cyril Bordage
- Contact: Brice Goglin
- URL: http://www.open-mpi.org/projects/hwloc/

5.2. NewMadeleine

KEYWORDS: High-performance computing - MPI communication

FUNCTIONAL DESCRIPTION

NewMadeleine is the fourth incarnation of the Madeleine communication library. The new architecture aims at enabling the use of a much wider range of communication flow optimization techniques. Its design is entirely modular: drivers and optimization strategies are dynamically loadable software components, allowing experimentations with multiple approaches or on multiple issues with regard to processing communication flows.

The optimizing scheduler SchedOpt targets applications with irregular, multi-flow communication schemes such as found in the increasingly common application conglomerates made of multiple programming environments and coupled pieces of code, for instance. SchedOpt itself is easily extensible through the concepts of optimization strategies (what to optimize for, what the optimization goal is) expressed in terms of tactics (how to optimize to reach the optimization goal). Tactics themselves are made of basic communication flows operations such as packet merging or reordering.

The communication library is fully multi-threaded through its close integration with PIOMan. It manages concurrent communication operations from multiple libraries and from multiple threads. Its MPI implementation Mad-MPI fully supports the MPI_THREAD_MULTIPLE multi-threading level.

- Participants: Alexandre Denis
- Contact: Alexandre Denis
- URL: http://pm2.gforge.inria.fr/newmadeleine/

5.3. PaMPA

KEYWORDS: parallel numerical solvers, unstructured heterogeneous meshes, dynamic load balancing, subdomain decomposition, parallel remeshing
FUNCTIONAL DESCRIPTIONPAMPA (“Parallel Mesh Partitioning and Adaptation”) is a library dedicated to the management of distributed meshes. Its purpose is to relieve solver writers from the tedious and error-prone task of writing again and again service routines for mesh handling, data communication and exchange, remeshing, and data redistribution. It is based on a distributed data structure that represents meshes as a set of entities (elements, faces, edges, nodes, etc.), linked by relations (that is, computation dependencies).

PAMPA interfaces with SCOTCH for mesh redistribution, and with MMG3D for parallel remeshing of tetrahedral elements. Other sequential remeshers can be plugged-in, in order to handle other types of elements.

Version 1.0 of PAMPA allows users to declare distributed meshes, to declare values attached to the entities of the meshes (e.g. temperature attached to elements, pressures to the faces, etc.), to exchange values between overlapping entities located at the boundaries of subdomains assigned to different processors, to iterate over the relations of entities (e.g. iterate over the faces of elements), to remesh in parallel the areas of a mesh that need to be remeshed, and to redistribute evenly the remeshed mesh across the processors of the parallel architecture. PAMPA is already used as the data structure manager for the AeroSol solver developed by teams CARDAMOM and CAGIRE.

Version 2.0 of PAMPA features parallel remeshing using any sequential remesher. At the time being, PAMPA is interfaced with the MMG3D tetrahedral remesher designed within team CARDAMOM. Its coupling with Tetgen is in progress. Meshes above one billion elements are generated with a quality similar to that offered by the sequential remesher alone. More than 1 billion of elements are obtained on a cluster with 600 processors in less than 20 minutes. Tests show a quite good weak scalability up to 600 processors, limited by cluster size. Extensive scalability testing will be performed during year 2016. An collaboration with Dassault Aviation demonstrated the use of PAMPA with their meshes during solver computations.

- Participants: Cédric Lachat, François Pellegrini, Cécile Dobrzynski.
- Contact: Cédric Lachat, François Pellegrini
- URL: project.inria.fr/pampa

5.4. Scotch

KEYWORDS: parallel graph partitioning, parallel static mapping, parallel sparse matrix block ordering, graph repartitioning, fixed vertices, mesh partitioning.
FUNCTIONAL DESCRIPTION

SCOTCH is a software package for parallel and sequential sparse matrix ordering, parallel and sequential graph partitioning, as well as sequential static mapping and remapping, without and with fixed vertices, and mesh and hypergraph partitioning.

The initial purpose of SCOTCH was to compute high-quality static mappings of valuated graphs representing parallel computations, onto target architectures of arbitrary topologies. Taking into account the topology and heterogeneity of the target architecture, in terms of processor speed and link bandwidth, allows SCOTCH to provide partitions that maximize communication locality.

This feature, which was meant for the NUMA machines of the 1980’s, has not been widely used in the past because high performance computers in the 1990’s were UMA architectures, thanks to hardware advances. As today’s high-end architectures are NUMA again, the mapping feature is regaining popularity.

The SCOTCH package consists of two libraries: the sequential SCOTCH library, and the parallel PT-SCOTCH library (for “Parallel Threaded SCOTCH”) that operates according to the distributed memory paradigm, using MPI. SCOTCH was the first full 64-bit implementation of a general purpose graph partitioner.

Version `6.0`, released on December 2012, corresponding to the 20th anniversary of SCOTCH, offers many new features: static mapping with fixed vertices, static remapping, and static remapping with fixed vertices. Several critical algorithms of the formerly strictly sequential SCOTCH library can now run in a multi-threaded way. All of these features, which exist only in the sequential version, will be ported to the parallel PT-SCOTCH library in the upcoming `6.1` major release.

A recent work on branch `6.0` enables SCOTCH to map onto (possibly disconnected) parts of a regular architecture, thanks to the new `sub` target architecture. This feature aims at allowing programs to distribute their data so as to maximize locality, according to the assignment of nodes performed by the batch scheduler, which do not always represent a regular, nor a connected, part of a parallel machine.

SCOTCH has been integrated into numerous third-party software, which indirectly contribute to its diffusion.

- Participants: François Pellegrini, Cédric Lachat, Astrid Casadei.
- Contact: François Pellegrini
- URL: https://gforge.inria.fr/projects/scotch/

5.5. TreeMatch

KEYWORDS: High-performance computing. Process Placement
FUNCTIONAL DESCRIPTION

TreeMatch is a library for performing process placement based on the topology of the machine and the communication pattern of the application. TreeMatch provides a permutation of the processes to the processors/cores in order to minimize the communication cost of the application. Important features are : the number of processors can be greater than the number of applications processes ; it assumes that the topology is a tree and does not require valuation of the topology (e.g. communication speeds) ; it implements different placement algorithms that are switched according to the input size. Some core algorithms are parallel to speed-up the execution. TreeMatch is integrated into various software such as the Charm++ programming environment as well as in both major open-source MPI implementations: Open MPI.

- Participants: Emmanuel Jeannot, Guillaume Mercier, François Tessier.
- Contact: Emmanuel Jeannot
- URL: http://treematch.gforge.inria.fr

5.6. Platforms

5.6.1. Platform: The Daltons

The Daltons are a set of machines available for the team members and the STORM team members enabling fast prototyping and benchmarking of our solutions, algorithms and software. It features up-to-date hardware (e.g. latest infiniband or GPU card) with the most recent processors.

TAO Project-Team

6. New Software and Platforms

6.1. CMA-ES

Covariance Matrix Adaptation Evolution Strategy
KEYWORDS: Numerical optimization - Black-box optimization - Stochastic optimization
SCIENTIFIC DESCRIPTION

The CMA-ES is considered as state-of-the-art in evolutionary computation and has been adopted as one of the standard tools for continuous optimisation in many (probably hundreds of) research labs and industrial environments around the world. The CMA-ES is typically applied to unconstrained or bounded constraint optimization problems, and search space dimensions between three and a hundred. The method should be applied, if derivative based methods, e.g. quasi-Newton BFGS or conjugate gradient, (supposedly) fail due to a rugged search landscape (e.g. discontinuities, sharp bends or ridges, noise, local optima, outliers). If second order derivative based methods are successful, they are usually faster than the CMA-ES: on purely convex-quadratic functions, f(x)=xTHx, BFGS (Matlabs function fminunc) is typically faster by a factor of about ten (in terms of number of objective function evaluations needed to reach a target function value, assuming that gradients are not available). On the most simple quadratic function f(x)=||x||2=xTx BFGS is faster by a factor of about 30.

FUNCTIONAL DESCRIPTION

The CMA-ES is an evolutionary algorithm for difficult non-linear non-convex black-box optimisation problems in continuous domain.

- Participants: Nikolaus Hansen and Emmanuel Benazera
- Contact: Nikolaus Hansen
- URL: https://www.lri.fr/~hansen/cmaesintro.html

6.2. COCO

COmparing Continuous Optimizers
KEYWORDS: Benchmarking - Numerical optimization - Black-box optimization - Stochastic optimization
SCIENTIFIC DESCRIPTION

COmparing Continuous Optimisers (COCO) is a tool for benchmarking algorithms for black-box optimisation. COCO facilitates systematic experimentation in the field of continuous optimization. COCO provides: (1) an experimental framework for testing the algorithms, (2) post-processing facilities for generating publication quality figures and tables, (3) LaTeX templates of articles which present the figures and tables in a single document.

The COCO software is composed of two parts: (i) an interface available in different programming languages (C/C++, Java, Matlab/Octave, R, Python) which allows to run and log experiments on multiple test functions testbeds of functions (noisy and noiseless) are provided (ii) a Python tool for generating figures and tables that can be used in the LaTeX templates.

FUNCTIONAL DESCRIPTION

The Coco Platform provides the functionality to automatically benchmark optimization algorithms for unbounded, unconstrained optimization problems in continuous domains. Benchmarking is a vital part of algorithm engineering and a necessary path to recommend algorithms for practical applications. The Coco platform releases algorithm developers and practitioners alike from (re-)writing test functions, logging, and plotting facilities by providing an easy-to-handle interface in several programming languages. The Coco platform has been developed since 2007 and has been used extensively within the "Blackbox Optimization Benchmarking (BBOB)" workshop series since 2009. Overall, 123 algorithms and algorithm variants by contributors from all over the world have been benchmarked with the platform so far and all data is publicly available for the research community for the submissions to BBOB-2013).

- Participants: Dimo Brockhoff, Tea Tulsar, Dejan Tulsar, Thanh-Do Tran, Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara and Asma Atamna
- Partners: Université technique de Dortmund - Université technique de Prague
- Contact: Dimo Brockhoff
- URL: http://coco.gforge.inria.fr/doku.php

6.3. PTraces

Personal digital Traces
KEYWORDS: Information retrieval - Taxonomy induction - Personal Big Data - Ontology
SCIENTIFIC DESCRIPTION Personal digital Traces (PTraces) is a platform for fetching and annotating personal data. Ptraces provides us a demonstration platform for personal semantics and ontology induction. Ptraces includes: (1) modules for securely fetching personal data from external applictions (2) an annotation component that annotates personal information with user-chosen taxonomies (facets). These facets arean experimental framework for testing the algorithms, (3) an information retrieval component

The PTraces software is composed of two parts: (i) A Java backbone, built on Elastic Search (ii) a web-browser user interface for configuring the system (choosing data sources, choosing ontologies to activate) and for query retrieved data.
FUNCTIONAL DESCRIPTION

The system accepts taxonomies in the SKOS format. These taxonomies are presented to the user, along with a number of connectors to otuside data sources (gmail, twitter, facebook, fitbit, ...). The user chooses which sources to index, and which taxonomies to apply. After this initialisation, the system accesses the sources using the indentification tokens that the user has supplied, fetches the user data, annotates the data using the activated taxonomies, and sets up a local server that that user can access to search in their own data, using a browser interface.

- Participants: Gregory Grefenstette, Lawrence Muchemi, Mohamed Bouatira
- Contact: Mohamed Bouatira
- URL: https://gforge.inria.fr/scm/browser.php?group_id=7217

6.4. Cartolabe

FUNCTIONAL DESCRIPTION

Scientific cartography from articles

- Contact: Philippe Caillou
- URL: (project starting in 2016 - no url yet)

6.5. GO

Grid Observatory
KEYWORDS: Green computing - Autonomic computing
FUNCTIONAL DESCRIPTION

The Grid Observatory (GO) software suite collects and publishes traces of the EGI (European Grid Initiative) grid usage. With the release and extensions of its portal, the Grid Observatory has made a database of grid usage traces available to the wider computer science community since 2008. These data are stored on the grid, and made accessible through a web portal without the need of grid credentials. The GO is fully integrated with the evolution of EGI monitoring.

- Participants: Cécile Germain-Renaud, Julien Nauroy and Martine Sebag
- Contact: Cécile Germain-Renaud
- URL: http://grid-observatory.org/

6.6. METIS

KEYWORDS: Optimization - Energy
FUNCTIONAL DESCRIPTION

Many works in Energy Optimization, in particular in the case of high-scale sequential decision making, are based on one software per application, because optimizing the software eventually implies losing generality. Our goal is to develop with Artelys a platform, METIS, which can be used for several applications. In 2012 we interfaced existing codes in Artelys and codes developed in the TAO team, experiments have been performed and test cases have been designed. Several codes have been developped, tested on real world problems, and are (depending on which code) under the process of (i) open source diffusion (ii) code protection.

A big work is the development of a new, independent, open source, simulator for the French power grid, currently under extension to other European countries.

- Participants: Olivier Teytaud, Jérémie Decock, Jean-Joseph Christophe, Vincent Berthier, Marie-Liesse Cauwet and Sandra Cecilia Astete Morales
- Partner: Artelys
- Contact: Olivier Teytaud
- URL: http://www.lri.fr/~teytaud

6.7. Game Test Bed

KEYWORDS: An open source game test bed.
FUNCTIONAL DESCRIPTION

GTB is an open source library of games, including solvers. It includes an interface to noisy continuous optimization of parametric policies, and noise-free continuous optimization, leading to a preliminary continuous optimization platform with real-world test cases.

- Participants: Olivier Teytaud is the only developer, some feedback from Sandra Astete-Morales, and an interfacing with works by Marcus Gallagher at Univ. Queensland in under discussion.
- URL: https://gforge.inria.fr/projects/gametestbed/

6.8. MOGO

KEYWORDS: Computer Go - Monte-Clarlo - UCT
FUNCTIONAL DESCRIPTION

MoGo and its Franco-Taiwanese counterpart MoGoTW is a Monte-Carlo Tree Search program for the game of Go, which made several milestones of computer-Go in the past (first wins against professional players in 19x19, first win with disadvantageous side in 9x9 Go). Recent results include 7 wins out of 12 against professional players (in Brisbane, 2012) in 7x7, and recently an optimization of the random seed which brings a significant improvement in Go and (unpublished) on the difficult case of phantom-Go. However, the work in the UCT-SIG has now shifted to energy management.

- Participants: Sylvain Gelly, Rémi Munos, Olivier Teytaud, Yizao Wang and Jean-Baptiste Hoock
- Contact: Olivier Teytaud
- URL: https://www.lri.fr/~teytaud/taiwanopen2009.html

6.9. MultiBoost

multi-purpose boosting package
KEYWORDS: Multi-class - Multi-label classification
FUNCTIONAL DESCRIPTION

The MultiBoost package provides a fast C++ implementation of multi-class/multi-label/multi-task boosting algorithms. It is based on AdaBoost.MH but it also implements popular cascade classifiers, Arc-GV , and FilterBoost . The package contains common multi-class base learners (stumps, trees, products, Haar filters). Further base learners and strong learners following the boosting paradigm can be easily implemented in a flexible framework.

- Participants: Balasz Kegl, Robert Busa-Fekete and Djalel Benbouzid
- Contact: Balasz Kegl
- URL: http://www.multiboost.org/

6.10. io.datascience

FUNCTIONAL DESCRIPTION

This Data as a Service (DaaS) platform [54] is developed in the context of the Center for Data Science and the TIMCO project. Its overall goals is to exploit the advances in semantic web techniques for efficient sharing and usage of scientific data. A related specific software is the Tester for Triplestore (TFT) software suite [49], which benchmarks the compliance of sparql databases wrt the RDF standard and publishes the results through the SparqlScore service.

- Contact: Cécile Germain
- URL: https://io.datascience-paris-saclay.fr/

TASC Project-Team

6. New Software and Platforms

6.1. AIUR

(Artificial Intelligence Using Randomness)
FUNCTIONAL DESCRIPTION

The main idea is to be unpredictable by making some stochastic choices. The AI starts a game with a "mood" randomly picked up among 5 moods, dictating some behaviours (aggressive, fast expand, macro-game, ...). In addition, some other choices (productions, timing attacks, early aggressions, ...) are also taken under random conditions.

Learning is an essential part of AIUR . For this, it uses persistent I/O files system to record which moods are efficient against a given opponent, in order to modify the probability distribution for the mood selection. The current system allows both on-line and off-line learning.

- Contact: Florian Richoux
- URL: https://github.com/AIUR-group/AIUR

6.2. CHOCO

SCIENTIFIC DESCRIPTION

For fourth consecutive year, CHOCO has participated at the MiniZinc Challenge , an annual competition of constraint programming solvers. Since then, in concurrency with 16 other solvers, CHOCO has won two silver medals and four bronze medals in three out of four categories (Free search, Parallel search and Open class). Five versions have been released all year long, the last one (v3.3.3, Dec. 22th) has the particularity to be promoted on Maven Central Repository. The major modifications were related to an improvement of the overall solver (efficiency, stability and robustness) but also a simplification of the API. As an example, more flexibility has been injected to the search loop, a central concept of the solver.
FUNCTIONAL DESCRIPTION

CHOCO is a Free and Open-Source Software dedicated to Constraint Programming. It is a Java library written under BSD 4-clause license (700 classes, 134K lines of code). It aims at describing hard combinatorial problems in the form of Constraint Satisfaction Problems and solving them with Constraint Programming techniques. The user models its problem in a declarative way by stating the set of constraints that need to be satisfied in every solution. Then, CHOCO solves the problem by alternating constraint filtering algorithms with a search mechanism. In addition to native explanations system, soft constraints and global constraints, the library is, in practice, open, easy to integrate and to tweak. A User Guide is now available: 164 pages describing how to use CHOCO, together with responsive online support (forums and mailing-lists).

- Participants: Charles Prud'homme, Nicolas Beldiceanu, Jean-Guillaume Fages, Xavier Lorca, Thierry Petit and Rémi Douence
- Partner: Ecole des Mines de Nantes
- Contact: Charles Prud'homme
- URL: http://www.choco-solver.org/

6.3. GCCat

Global Constraint Catalog
KEYWORDS: Constraint Programming - Global constraint - Catalogue - Graph - Automaton - Transducer - First order formula - meta-data - ontology - symmetry - counting -

FUNCTIONAL DESCRIPTION

This global constraint catalog presents a catalogue of global constraints where each constraint is explicitly described in terms of graph properties and/or automata and/or first order logical formulae with arithmetic. When available, it also presents some typical usage as well as some pointers to existing filtering algorithms. This year we were preparing a second volume of the catalog focused on time-series constraints. It presents a restricted set of finite transducers used to synthesise structural time-series constraints described by means of a multi-layered functions composition scheme. Second it provides the corresponding synthesised catalogue of structural time-series constraints where each constraint is explicitly described in terms of automata with accumulators.

- Participants: Nicolas Beldiceanu, Mats Carlsson, Sophie Demassey and Helmut Simonis
- Contact: Nicolas Beldiceanu
- URL: http://sofdem.github.io/gccat/gccat/index.html

6.4. GHOST

General meta-Heuristic Optimization Solving Tool
FUNCTIONAL DESCRIPTION

GHOST, i.e. General meta-Heuristic Optimization Solving Tool, is a template C++ library designed for StarCraft:BroodWartm. GHOST implements a meta-heuristic solver aiming to solve any kind of combinatorial and optimization RTS-related problems represented by a csp /cop. The solver handles dedicated geometric and assignment constraints in a way that is compatible with very strong real time requirements.

- Contact: Florian Richoux
- URL: http://github.com/richoux/GHOST

6.5. IBEX

pour le calcul ensembliste (calcul numérique garanti avec propagation rigoureuse d'incertitudes)
KEYWORD: Constraint Programming
SCIENTIFIC DESCRIPTION

In 2014 the development on IBEX has focused on the following points:

Rejection test based on first-order conditions (see First Order Rejection Tests For Multiple-Objective Optimization, A. Goldsztejn et al. [42]).

Q-intersection (see Q-intersection Algorithms for Constraint-Based Robust Parameter Estimation, C. Carbonnel et al., AAAI 2014)
FUNCTIONAL DESCRIPTION

IBEX is a C++ library for solving nonlinear constraints over real numbers. The main feature of Ibex is its ability to build solver/paver strategies declaratively through the contractor programming paradigm. It also comes with a black-box solver and a global optimizer.

- Participants: Ignacio Araya, Gilles Chabert, Bertrand Neveu, Ignacio Salas Donoso and Gilles Trombettoni
- Partners: ENSTA - Ecole des Ponts ParisTech
- Contact: Gilles Chabert
- URL: http://www.ibex-lib.org/

TEA Project-Team

6. New Software and Platforms

6.1. The Eclipse project POP

Participants: Loïc Besnard, Thierry Gautier, Paul Le Guernic, Jean-Pierre Talpin.

The distribution of project POP [0] is a major achievement of the ESPRESSO (and now TEA) project-team. The Eclipse project POP is a model-driven engineering front-end to our open-source toolset Polychrony. It was finalised in the frame of project OPEES, as a case study: by passing the POLARSYS qualification kit as a computer aided simulation and verification tool. This qualification was implemented by CS Toulouse in conformance with relevant generic (platform independent) qualification documents. Polychrony is now distributed by the Eclipse project POP on the platform of the POLARSYS industrial working group. Project-team TEA aims at continuing its dissemination to academic partners, as to its principles and features, and industrial partners, as to the services it can offer.

Technically, project POP is composed of the Polychrony toolset, under GPL license, and its Eclipse framework, under EPL license. SSME (Syntactic Signal-Meta under Eclipse), is the metamodel of the Signal language implemented with Eclipse/Ecore. It describes all syntactic elements specified in Signal Reference Manual [0]: all Signal operators (e.g. arithmetic, clock synchronization), model (e.g. process frame, module), and construction (e.g. iteration, type declaration).

The metamodel primarily aims at making the language and services of the Polychrony environment available to inter-operation and composition with other components (e.g. AADL, Simulink, GeneAuto, P) within an Eclipse-based development toolchain. Polychrony now comprises the capability to directly import and export Ecore models instead of textual Signal programs, in order to facilitate interaction between components within such a toolchain.

The download site for project POP has opened in 2015 at: https://www.polarsys.org/projects/polarsys.pop. It should be noted that the Eclipse Foundation does not host code under GPL license. So, the Signal toolbox useful to compile Signal code from Eclipse is hosted on our web server.

6.2. The Polychrony toolset

Participants: Loïc Besnard, Thierry Gautier, Paul Le Guernic, Jean-Pierre Talpin.

The Polychrony toolset is an Open Source development environment for critical/embedded systems. It is based on Signal, a real-time polychronous dataflow language. It provides a unified model-driven environment to perform design exploration by using top-down and bottom-up design methodologies formally supported by design model transformations from specification to implementation and from synchrony to asynchrony. It can be included in heterogeneous design systems with various input formalisms and output languages.

The Polychrony toolset provides a formal framework to:

- validate a design at different levels, by the way of formal verification and/or simulation,
- refine descriptions in a top-down approach,
- abstract properties needed for black-box composition,
- assemble heterogeneous predefined components (bottom-up with COTS),
- generate executable code for various architectures.

---

[0] *Polychrony on POLARSYS (POP)*, an Eclipse project in the POLARSYS Industry Working Group, 2013. https://www.POLARSYS.org/projects/POLARSYS.pop

[0] *SIGNAL V4-Inria version: Reference Manual*. Besnard, L., Gautier, T. and Le Guernic, P. http://www.irisa.fr/espresso/Polychrony, 2010

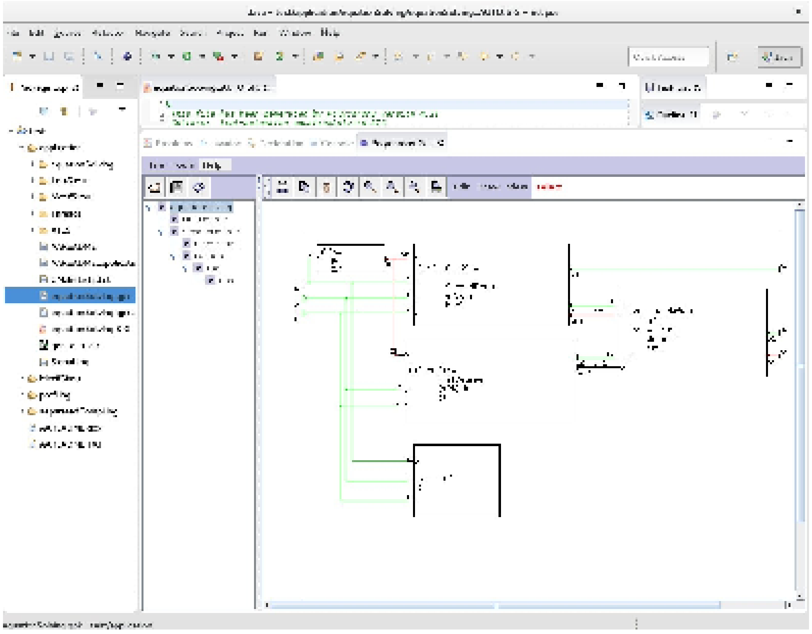


Figure 1. The Eclipse POP Environment

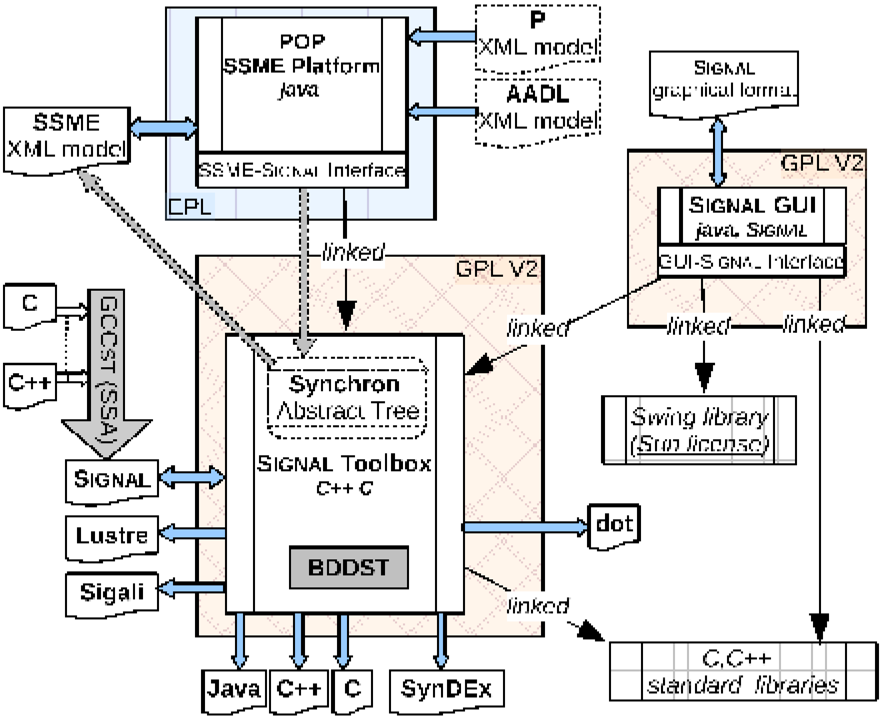


Figure 2. The Polychrony toolset high-level architecture

The Polychrony toolset contains three main components and an experimental interface to GNU Compiler Collection (GCC):

- The Signal toolbox, a batch compiler for the Signal language, and a structured API that provides a set of program transformations. Itcan be installed without other components and is distributed under GPL V2 license.
- The Signal GUI, a Graphical User Interface to the Signal toolbox (editor + interactive access to compiling functionalities). It can be used either as a specific tool or as a graphical view under Eclipse. In 2015, it has been transformed and restructured, in order to get a more up-to-date interface allowing multi-window manipulation of programs. It is distributed under GPL V2 license.
- The SSME platform, a front-end to the Signal toolbox in the Eclipse environment. It is distributed under EPL license.
- GCCst, a back-end to GCC that generates Signal programs (not yet available for download).

The Polychrony toolset also provides a large library of Signal programs and examples, user documentations and developer-oriented implementation documents, and facilities to generate new versions.

The Polychrony toolset can be freely downloaded on the following web sites:

- The Polychrony toolset public web site: http://polychrony.inria.fr/. This site, intended for users and for developers, contains downloadable executable and source versions of the software for differents platforms, user documentation, examples, libraries, scientific publications and implementation documentation. In particular, this is the site for the open-source distribution of Polychrony.
- The Inria GForge: https://gforge.inria.fr. This site, intended for internal developers, contains the whole sources of the environment and their documentation.

As part of its open-source release, the Polychrony toolset not only comprises source code libraries but also an important corpus of structured documentation, whose aim is not only to document each functionality and service, but also to help a potential developer to package a subset of these functionalities and services, and adapt them to developing a new application-specific tool: a new language front-end, a new back-end compiler. This multi-scale, multi-purpose documentation aims to provide different views of the software, from a high-level structural view to low-level descriptions of basic modules. It supports a distribution of the software "by apartment" (a functionality or a set of functionalities) intended for developers who would only be interested by part of the services of the toolset.

6.3. SigCert: translation validation from Signal to C

Participants: Van-Chan Ngo, Jean-Pierre Talpin, Thierry Gautier, Paul Le Guernic, Loïc Besnard.

Translation validation [00] is a technique that attempts to verify that program transformations preserve the program semantics. It is obvious to prove globally that the source program and its final compiled program have the same semantics. However, we believe that a better approach is to separate concerns and prove each analysis and transformation stage separately with respect to ad-hoc data-structures to carry the semantic information relevant to that phase.

In the case of the Signal compiler [1], [7], the preservation of the semantics can be decomposed into the preservation of clock semantics at the *clock calculation* phase [15] and that of data dependencies at the *static scheduling* phase[16], and, finally, value-equivalence of variables at the *code generation* phase[14].

Translation Validation for Clock Transformations in a Synchronous Compiler. The clock semantics of the source and transformed programs are formally represented as *clock models*. A clock model is a first-order logic formula that characterizes the presence/absence status of all signals in a Signal program at a given instant. Given two clock models, a *clock refinement* between them is defined which expresses the semantic preservation of clock semantics[15]. A method to check the existence of clock refinement is defined as a satisfiability problem which can be automatically and efficiently proved by a SMT solver [0].

---

[0] *Translation validation.* Pnueli A., Siegel M., and Singerman E. In Proceedings of TACAS'98, 1998.

[0] *Translation validation: From signal to c.* M. Siegel A. Pnueli and E. Singeman. In Correct Sytem Design Recent Insights and Advances, 2000.

[0] *Satisfiability modulo theories: An appetizer.* L. de Moura and N. Bjorner. In Brazilian Symposium on Formal Methods, 2009.

Precise Deadlock Detection for Polychronous Data-flow Specifications. Dependency graphs are a commonly used data structure to encode the streams of values in data-flow programs and play a central role in scheduling instructions during automated code generation from such specifications. We propose a precise and effective method that combines a structure of dependency graph and first order logic formulas to check whether multi-clocked data-flow specifications are deadlock-free before generating code from them. We represent the flow of values in the source programs by means of a dependency graph and attach first-order logic formulas to condition these dependencies. We use an SMT solver to effectively reason about the implied formulas and check deadlock freedom [16].

Implementation and Experiments. At a high level, our prototype tool *SigCert* ([14]) developed in OCaml could check the correctness of the compilation of Signal compiler w.r.t clock semantics, data dependence, and value-equivalence as given in Figure 3 . The individual modules designed in the context of this work are now being implemented and integrated in the open-source Polychrony toolset.

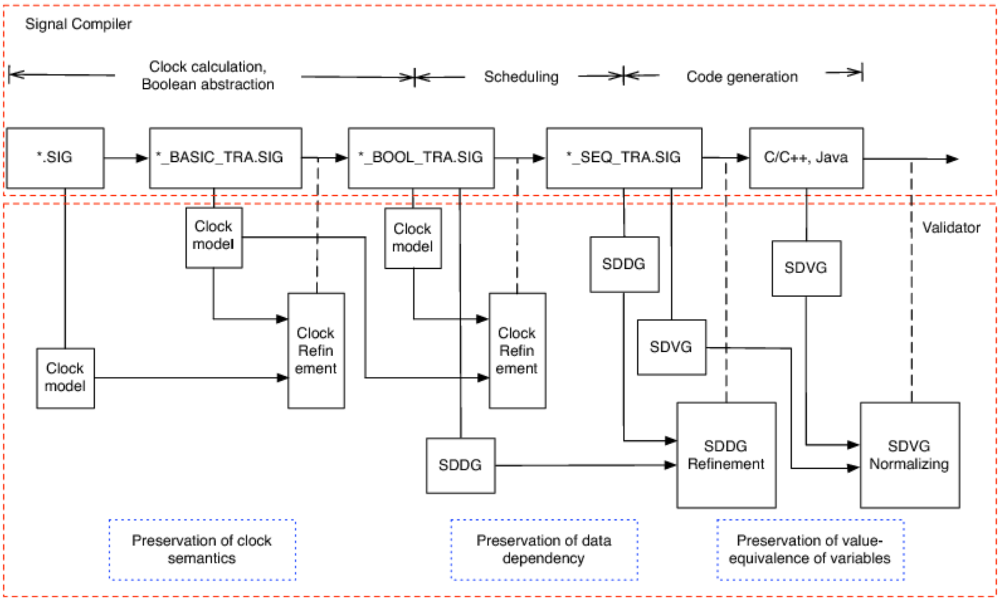


Figure 3. Our Integration within Polychrony Toolset

6.4. ADFG: Affine data-flow graphs scheduler synthesis under Eclipse

Participants: Alexandre Honorat, Jean-Pierre Talpin, Thierry Gautier, Loïc Besnard.

We have proposed a dataflow design model [2] of SCJ/L1 applications [0] in which handlers (periodic and aperiodic actors) communicate only through lock-free channels. Hence, each mission is modeled as a dataflow graph. The presented dataflow design model comes with a development tool integrated in the Eclipse IDE for easing the development of SCJ/L1 applications and enforcing the restrictions imposed by the design model. It consists of a GMF editor where applications are designed graphically and timing and buffering parameters can be synthesized. Indeed, abstract affine scheduling is first applied on the dataflow subgraph, that consists only of periodic actors, to compute timeless scheduling constraints (e.g. relation between the speeds of two actors) and buffering parameters. Then, symbolic fixed-priority schedulability analysis (i.e., synthesis of timing and scheduling parameters of actors) considers both periodic and aperiodic actors.

---

[0] *Safety critical Java technology specification*. JSR-302, Year = 2010

Through a model-to-text transformation, using Acceleo, the SCJ code for missions, interfaces of handlers, and the mission sequencer is automatically generated in addition to the annotations needed by the memory checker. Channels are implemented as cyclic arrays or cyclical asynchronous buffers; and a fixed amount of memory is hence reused to store the infinite streams of tokens. The user must provide the SCJ code of all the `handleAsyncEvent()` methods. We have integrated the SCJ memory checker [0] in our tool so that potential dangling pointers can be highlighted at compile-time. To enhance functional determinism, we would like to develop an ownership type system to ensure that actors are strongly isolated and communicate only through buffers.

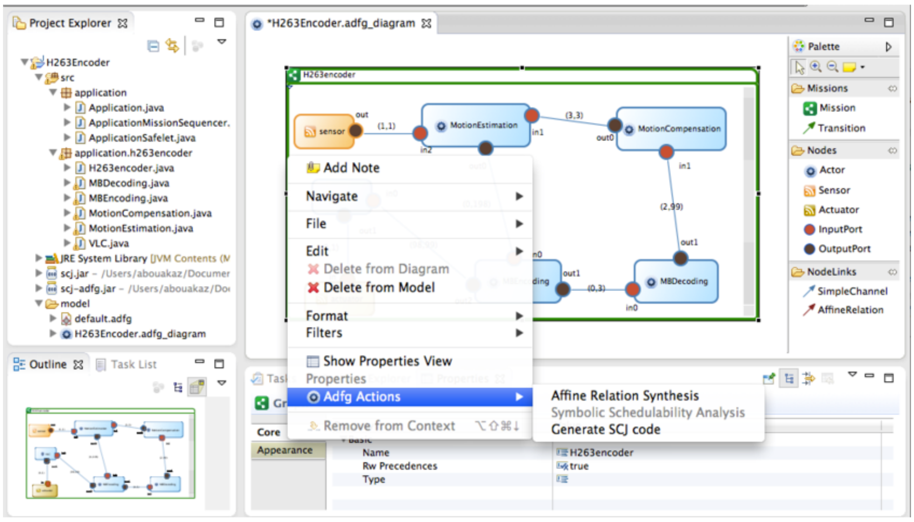


Figure 4. The ADFG Tool

The ADFG tool is being further developed in the context of the ADT "La vie d'AADL" in order to serve both as scheduler synthesis tool from AADL specifications and SCJ tasksets. We plan to further the front end analysis tools from Java task sets in order to build the input CSDF graphs from program analysis, in the context of a future PhD.

---

[0] *Static checking of safety critical Java annotations*. Tang, D. Plsek, A. and Vitek, J. International Workshop on Java Technologies for Real-Time and Embedded Systems, 2010

TITANE Project-Team

6. New Software and Platforms

6.1. CGAL Barycentric coordinates 2D

SCIENTIFIC DESCRIPTION

The package 2D Generalized Barycentric Coordinates offers an efficient and robust implementation of two-dimensional closed-form generalized barycentric coordinates defined for simple two-dimensional polygons. If coordinates with respect to multivariate scattered points instead of a polygon are required, please refer to natural neighbour coordinates from the package 2D and Surface Function Interpolation. The package includes an implementation of Wachspress, mean value, and discrete harmonic coordinates and provides some extra functions to compute barycentric coordinates with respect to segments (segment coordinates) and triangles (triangle coordinates).

- Participants: Pierre Alliez and Dmitry Anisimov
- Contact: Pierre Alliez

6.2. Module CGAL: Point Set Processing

SCIENTIFIC DESCRIPTION

This component implements methods to analyze and process unorganized point sets. The input is an unorganized point set, possibly with normal attributes (unoriented or oriented). The point set can be analyzed to measure its average spacing, and processed through functions devoted to the simplification, outlier removal, smoothing, normal estimation, normal orientation and feature edges estimation.

- Participants: Pierre Alliez, Laurent Saboret and Clément Jamin
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Point_set_processing_3/index.html

6.3. Module CGAL: Scale-space surface reconstruction

KEYWORD: Geometric algorithms
SCIENTIFIC DESCRIPTION

This package implements a surface reconstruction method which takes as input an unordered point set and computes a triangulated surface mesh interpolating the point set. We assume that the input points were sampled from the surface of an object. The method can also process point sets sampled from the interior of the object, although we cannot provide guarantees on the output. This method can handle a decent amount of noise and outliers. The point set may greatly undersample the object in occluded regions, although no surface will be reconstructed to fill these regions.

See http://doc.cgal.org/latest/Scale_space_reconstruction_3/index.html
FUNCTIONAL DESCRIPTION

This method reconstructs a surface that interpolates a set of 3D points. This method provides an efficient alternative to the Poisson surface reconstruction method. The main difference in output is that this method reconstructs a surface that interpolates the point set, as opposed to approximating the point set. How the surface connects the points depends on a scale variable, which can be estimated semi-automatically.

- Participants: Pierre Alliez and Thijs Van Lankveld
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Scale_space_reconstruction_3/index.html

6.4. Skeleton-Blockers

Skeleton-Blockers data-structure
KEYWORDS: C++ - Mesh - Triangulation - Topology - 3D
FUNCTIONAL DESCRIPTION

Skeleton-Blockers is a compact, efficient and generic data-structure that can represent any simplicial complex. The implementation is in C++11.

- Participant: David Salinas
- Contact: David Salinas
- URL: https://project.inria.fr/gudhi/software/

6.5. Structure-preserving Decimation

KEYWORDS: Mesh - 3D - Multi-View reconstruction
FUNCTIONAL DESCRIPTION

Structure-preserving decimation is a software that can simplify 3D meshes while preserving some of their structure. Simplification is performed through either a command line or a graphical user interface that can combine several operations including several simplification methods.

- Participants: David Salinas, Pierre Alliez and Florent Lafarge
- Contact: David Salinas

TOCCATA Project-Team

6. New Software and Platforms

6.1. Alt-Ergo

Automated theorem prover for software verification
KEYWORDS: Software Verification - Automated theorem proving
FUNCTIONAL DESCRIPTION

Alt-Ergo is an automatic solver of formulas based on SMT technology. It is especially designed to prove mathematical formulas generated by program verification tools, such as Frama-C for C programs, or SPARK for Ada code. Initially developed in Toccata research team, Alt-Ergo's distribution and support are provided by OCamlPro since September 2013.

- Participants: Sylvain Conchon, Évelyne Contejean, Mohamed Iguernelala, Stéphane Lescuyer and Alain Mebsout
- Partner: OCamlPro
- Contact: Sylvain Conchon
- URL: http://alt-ergo.lri.fr

6.2. CFML

Interactive program verification using characteristic formulae
KEYWORDS: Coq - Software Verification - Deductive program verification - Separation Logic
FUNCTIONAL DESCRIPTION

The CFML tool supports the verification of OCaml programs through interactive Coq proofs. CFML proofs establish the full functional correctness of the code with respect to a specification. They may also be used to formally establish bounds on the asymptotic complexity of the code. The tool is made of two parts: on the one hand, a characteristic formula generator implemented as an OCaml program that parses OCaml code and produces Coq formulae, and, on the other hand, a Coq library that provides notation and tactics for manipulating characteristic formulae interactively in Coq.

- Contact: Arthur Charguéraud
- URL: http://www.chargueraud.org/softs/cfml/

6.3. Coq

KEYWORDS: Proof - Certification - Formalisation
FUNCTIONAL DESCRIPTION

Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

- Participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Denes, Stéphane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pédrot, Loïc Pottier, Matthias Puech, Yann Régis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliâtre
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Hugo Herbelin
- URL: http://coq.inria.fr/

6.4. CoqInterval

Interval package for Coq
KEYWORDS: Interval arithmetic - Coq
FUNCTIONAL DESCRIPTION

CoqInterval is a library for the proof assistant Coq. CoqInterval provides a method for proving automatically the inequality of two expression of real values.

The Interval package provides several tactics for helping a Coq user to prove theorems on enclosures of real-valued expressions. The proofs are performed by an interval kernel which relies on a computable formalization of floating-point arithmetic in Coq.

The Marelle team developed a formalization of rigorous polynomial approximation using Taylor models inside the Coq proof assistant, with a special focus on genericity and efficiency for the computations. In 2014, this library has been included in CoqInterval.

- Participants: Guillaume Melquiond, Érik Martin-Dorel, Nicolas Brisebarre, Miora Maria Joldes, Micaela Mayero, Jean-Michel Muller, Laurence Rideau and Laurent Théry
- Contact: Guillaume Melquiond
- URL: http://coq-interval.gforge.inria.fr/

6.5. Coquelicot

The Coquelicot library for real analysis in Coq
KEYWORDS: Coq - Real analysis
FUNCTIONAL DESCRIPTION

Coquelicot is library aimed for supporting real analysis in the Coq proof assistant. It is designed with three principles in mind. The first is the user-friendliness, achieved by implementing methods of automation, but also by avoiding dependent types in order to ease the stating and readability of theorems. This latter part was achieved by defining total function for basic operators, such as limits or integrals. The second principle is the comprehensiveness of the library. By experimenting on several applications, we ensured that the available theorems are enough to cover most cases. We also wanted to be able to extend our library towards more generic settings, such as complex analysis or Euclidean spaces. The third principle is for the Coquelicot library to be a conservative extension of the Coq standard library, so that it can be easily combined with existing developments based on the standard library.

- Participants: Sylvie Boldo, Catherine Lelay and Guillaume Melquiond
- Contact: Sylvie Boldo
- URL: http://coquelicot.saclay.inria.fr/

6.6. Cubicle

The Cubicle model checker modulo theories
KEYWORDS: Model Checking - Software Verification
FUNCTIONAL DESCRIPTION

Cubicle is an open source model checker for verifying safety properties of array-based systems, which corresponds to a syntactically restricted class of parametrized transition systems with states represented as arrays indexed by an arbitrary number of processes. Cache coherence protocols and mutual exclusion algorithms are typical examples of such systems.

- Participants: Sylvain Conchon and Alain Mebsout
- Contact: Sylvain Conchon
- URL: http://cubicle.lri.fr/

6.7. Flocq

The Flocq library for formalizing floating-point arithmetic in Coq
KEYWORDS: Floating-point - Arithmetic code - Coq
FUNCTIONAL DESCRIPTION

The Flocq library for the Coq proof assistant is a comprehensive formalization of floating-point arithmetic: core definitions, axiomatic and computational rounding operations, high-level properties. It provides a framework for developers to formally certify numerical applications.

Flocq is currently used by the CompCert certified compiler for its support of floating-point computations.

- Participants: Guillaume Melquiond and Sylvie Boldo
- Contact: Sylvie Boldo
- URL: http://flocq.gforge.inria.fr/

6.8. Gappa

The Gappa tool for automated proofs of arithmetic properties
KEYWORDS: Floating-point - Arithmetic code - Software Verification - Constraint solving
FUNCTIONAL DESCRIPTION

Gappa is a tool intended to help verifying and formally proving properties on numerical programs dealing with floating-point or fixed-point arithmetic. It has been used to write robust floating-point filters for CGAL and it is used to certify elementary functions in CRlibm. While Gappa is intended to be used directly, it can also act as a backend prover for the Why3 software verification plateform or as an automatic tactic for the Coq proof assistant.

- Contact: Guillaume Melquiond
- URL: http://gappa.gforge.inria.fr/

6.9. Why3

The Why3 environment for deductive verification
KEYWORDS: Formal methods - Trusted software - Software Verification - Deductive program verification
FUNCTIONAL DESCRIPTION

Why3 is an environment for deductive program verification. It provides a rich language for specification and programming, called WhyML, and relies on external theorem provers, both automated and interactive, to discharge verification conditions. Why3 comes with a standard library of logical theories (integer and real arithmetic, Boolean operations, sets and maps, etc.) and basic programming data structures (arrays, queues, hash tables, etc.). A user can write WhyML programs directly and get correct-by-construction OCaml programs through an automated extraction mechanism. WhyML is also used as an intermediate language for the verification of C, Java, or Ada programs.

- Participants: Jean-Christophe Filliâtre, Claude Marché, Guillaume Melquiond, Andriy Paskevych, François Bobot, Martin Clochard and Levs Gondelmans
- Partners: CNRS - Université Paris-Sud
- Contact: Claude Marché
- URL: http://why3.lri.fr/

TONUS Team

6. New Software and Platforms

6.1. SCHNAPS

Participants: Emmanuel Franck, Pierre Gerhard, Philippe Helluy [correspondent], Michel Massaro, Malcolm Roberts, Bruno Weber.

Solveur pour les lois de Conservation Hyperboliques Non-linéaires Appliqué aux PlasmaS
SCIENTIFIC DESCRIPTION

It is clear now that future computers will be made of a collection of thousands of interconnected multicore processors. Globally, it appears as a classical distributed memory MIMD machine. But at a lower level, each of the multicore processors is itself made of a shared memory MIMD unit (a few classical CPU cores) and a SIMD unit (a GPU). When designing new algorithms, it is important to adapt them to this kind of architecture. Our philosophy will be to program our algorithms in such a way that they can be run efficiently on this kind of computers. Practically, we will use the MPI library for managing the coarse grain parallelism, while the OpenCL library will efficiently operate the fine grain parallelism.

We have invested for several years until now into scientific computing on GPUs, using the open standard OpenCL (Open Computing Language). We were recently awarded a prize in the international AMD OpenCL innovation challenge thanks to an OpenCL two-dimensional Vlasov-Maxwell solver that fully runs on a GPU. OpenCL is a very interesting tool because it is an open standard now available on almost all brands of multicore processors and GPUs. The same parallel program can run on a GPU or a multicore processor without modification. OpenCL programs are quite complicated to construct. For instance it is difficult to distribute efficiently the computation or memory operations on the different available accelerators. StarPU http://starpu.gforge.inria.fr/ is a runtime system developed at Inria Bordeaux that simplifies the distribution of tasks on heterogeneous compute units. We have started to use this software tool in SCHNAPS.

Because of the envisaged applications, which may be either academic or commercial, it is necessary to conceive a modular framework. The heart of the library is made of generic parallel algorithms for solving conservation laws. The parallelism can be both fine-grained (oriented towards GPUs and multicore processors) and coarse-grained (oriented towards GPU clusters). The separate modules allow managing the meshes and some specific applications. With our partner AxesSim, we also develop a C++ specific version of SCHNAPS for electromagnetic applications.
FUNCTIONAL DESCRIPTION

SCHNAPS is a generic Discontinuous Galerkin solver, written in C, based on the OpenCL, MPI and StarPU frameworks.

- Partner: AxesSim
- Contact: Philippe Helluy
- URL: http://schnaps.gforge.inria.fr/

6.2. Selalib

Participants: Sever Adrian Hirstoaga, Michel Mehrenberger [correspondent], Pierre Navaro, Laurent Navoret, Thi Trang Nhung Pham, Christophe Steiner.

SEmi-LAgrangian LIBrary
KEYWORDS: Plasma physics - Semi-Lagrangian method - PIC - Parallel computing - Plasma turbulence
SCIENTIFIC DESCRIPTION

The objective of the Selalib project (SEmi-LAgrangian LIBrary) is to develop a well-designed, organized and documented library implementing several numerical methods for kinetic models of plasma physics. Its ultimate goal is to produce gyrokinetic simulations.

Another objective of the library is to provide to physicists easy-to-use gyrokinetic solvers, based on the semi-Lagrangian techniques developed by Eric Sonnendrücker and his collaborators in the past CALVI project. The new models and schemes from TONUS are also intended to be incorporated into Selalib.

FUNCTIONAL DESCRIPTION

Selalib is a collection of modules conceived to aid in the development of plasma physics simulations, particularly in the study of turbulence in fusion plasmas. Selalib offers basic capabilities from general and mathematical utilities and modules to aid in parallelization, up to pre-packaged simulations.

- Partners: Max Planck Institute - Garching - IRMA, Université de Strasbourg - IRMAR, Université Rennes 1 - LJLL, Université Paris 6
- Contact: Michel Mehrenberger
- URL: http://selalib.gforge.inria.fr/

6.3. Django

Participants: Emmanuel Franck [correspondent], Boniface Nkonga, Ahmed Ratnani.

- Scientific description:
  The JOREK code is one of the most important MHD codes in Europe. This code written 15 years ago allows to simulate the MHD instabilities which appear in the TOKAMAK. Using this code the physicist has obtained some important results. However to run larger and more complex test cases it is necessary to evolve the numerical methods used.
  In 2014, the DJANGO code has been created, the aim of this code is double: have a numerical library to implement, test and validate new numerical methods for MHD, fluid mechanics and Electromagnetic equations in the finite element context and prepare the future new JOREK code. This code is a 2D-3D code based on implicit time schemes and IsoGeometric (B-Splines, Bezier curves) for the spatial discretization.
- Functional description:
  DJANGO is a finite element implicit solver written in Fortran 2003 with a Basic MPI framework. The code is coupled with the PETSC library for the linear solvers and the code CAID (A. Ratnani) for the mesh.
- Authors:
  Ahmed Ratnani (Max Planck Institut of Plasma Physic, Garching, Germany), Boniface NKonga (University of Nice and Inria Sophia-Antipolis, France), Emmanuel Franck (Inria Nancy Grand Est, TONUS Team)
- Contributors:
  Laura Mendoza, Mustafa Gaja (PhD), Jalal Lakhlili, Celine Caldini-Queiros, Matthias, Hoelzl, Eric Sonnendrücker (Max Planck Institut of Plasma Physic, Garching, Germany), Ayoub Iaagoubi (ADT), Hervé Guillard (University of Nice and Inria Sophia-Antipolis, France), Virginie Grandgirard, Guillaume Latu (CEA Cadarache, France)
- Year 2015:
  The year 2015 is an important year for the JOREK code. Indeed, after the year 2014 where the IsoParametric (Bezier curves) finite element approach in 2D have been implemented for basic elliptic equations, in 2015 we have extended the code for more complex problems. Now the code can treat some hyperbolic, parabolic and elliptic models with different approaches (IsoParametric/IsoGeometric approach, Splines for triangle) in 2D and 3D by tensor product. The compilation of the code is more stable and some regression test cases have been added. To finish, two realistic MHD models (which come from to the JOREK code) have been implemented and must be validated. The Year 2016 will be the year of the first physical and realistic results.

TOSCA Project-Team

6. New Software and Platforms

6.1. ExitBM

FUNCTIONAL DESCRIPTION

The ExitBM library provides methods to simulate random variables related to the first exit time and position of the Brownian motion from simple domains, namely intervals, squares and rectangles. This is a new software of 2015.

- Participants: Madalina Deaconu and Antoine Lejay
- Contact: Antoine Lejay
- URL: http://exitbm.gforge.inria.fr/

6.2. SDM

Stochastic Downscaling Method
FUNCTIONAL DESCRIPTION

The computation of the wind at small scale and the estimation of its uncertainties is of particular importance for applications such as wind energy resource estimation. To this aim, we have developed a computer code belonging to the family of codes of atmospheric flow calculation, in the atmospheric boundary layer. SDM especially concerns the simulation of wind at small space scales (meaning that the horizontal resolution is one kilometer or less), based on the combination of an existing Numerical Weather Prediction model providing a coarse prediction, and a Lagrangian Stochastic Model for turbulent flows.

This year we added to SDM a software tool for Configuration Interface and Visualization (CIV) of the SDM simulations. This dedicated GUI restitutes the 3D simulation view of all SDM outputs (including the rendering of interactions with mills). It is also a key environment tool to visualize a coarse resolution input, to extract time boundary condition of any chosen subdomain simulation for a NetCDF (Network Common DataForm) input file, to prepare the compilation procedure of any simulation case of SDM, to execute codes.

- Participants: Mireille Bossy, Sélim Kraria
- Contact: Mireille Bossy
- URL: http://windpos.inria.fr

6.3. Triton

KEYWORDS: Image analysis - Oceanography
FUNCTIONAL DESCRIPTION

The Triton software aims at providing a toolbox to analyze nearshore waves images recorded by a camera on the beach. More precisely, it aims at estimating the height, length and speed of waves, to find speed and direction of currents, and to reconstruct the bathymetry from these images. This is a new software of 2015.

- Participants: Stanislas Larnier, Rafael Almar and Antoine Lejay
- Contact: Antoine Lejay

TYREX Project-Team

5. New Software and Platforms

5.1. CSS Analyzer

CSS Analyzer
FUNCTIONAL DESCRIPTION

This software now consists in two distinct prototypes: two static analyzers (with a different purpose) that share a common compiler for CSS. The first prototype is used for bug detection and verification of a cascading style sheet (CSS) file. It involves a compiler for CSS rules (and in particular selectors) into logical formulas, adapted for the semantics of CSS (see the initial WWW'12 paper). The second prototype performs automated refactoring for size reduction of CSS style sheets. It reuses the first compiler and the logical solver for detecting which rules can be refactored and how. It implements various optimisation techniques (like early pruning), for the purpose of dealing with large-size real CSS files. This prototype reduces the size of CSS files found in the most popular websites (such as CNN, facebook, Google Sites, Apple, etc.) by up to 30% while preserving their semantics [18].

- Participants: Pierre Genevès, Nabil Layaïda and Marti Bosch Padros
- Contact: Pierre Genevès
- URL: http://tyrex.inria.fr/websolver/

5.2. Interactive eXtensible Engine (IXE)

Interactive eXtensible Engine
FUNCTIONAL DESCRIPTION

PDRTrack is a localization utility running on iOS or Android smartphones used for recording and playing data sets (accelerometer, gyroscope, barometer and magnetometer values) to study the effect of different pedometer and map matching parameters on indoor and outdoor localization accuracy. This application uses the PDR library, written in C++, which provides the user's location in real time based on the interpretation of mobile phone sensors. Three main modules have been designed to build this localization system:

- a pedometer that estimates the distance the user has walked and his speed
- a motion manager that enables data set recording and simulation but also the creation of virtual sensors or filters (e.g gyroscope drift compensation, linear acceleration, altimeter)
- a map-matching algorithm that provides location estimates on a given OpenStreetMap description and the current user's trajectory

The PDR library is a central component of the VENTURI project. It has been used for applications such guiding a visually impaired people. Others partners have used this localisation system for retrieving a scale factor needed for the computer vision part (i.e SLAM).

GPS navigation systems, when used in an urban environment, are limited in precision and can only give instructions at the level of the street and not of the pavement or corridor. GPS is also limited to outdoor navigation and requires some transitioning system when switching to indoor navigation.

PDRTrack is embedded in IXE. IXE is an urban pedestrian navigation system based on Inertial Measurement Units (IMU) and running on mobile phones with onboard geographic data and a routing engine. IXE allows augmented reality queries on customised embedded geographical data. Queries on route nodes or POIs, on ways and relations are predefined for efficiency and quality of information. Following a web paradigm, IXE can be seen as web browser for XML documents describing navigation networks. by using the micro-format concept, one can define inside OpenStreetMap a complex format for pedestrian navigation networks allowing navigation at the level of pavements or corridors.

The big advantage of IXE is that it relies on a standard OpenStreetMap editor called JOSM to create navigation networks and augmented reality content. IXE browser reads OSM documents and produces from them visible or audible navigation information. IXE is composed of three engines, one for dead-reckoning navigation, one for interactive audio and the last one for Augmented Reality visual information.

- Participants: Nabil Layaïda, Pierre Genevès, Thibaud Michel and Mathieu Razafimahazo
- Contact: Nabil Layaïda
- URL: http://tyrex.inria.fr/mobile/

5.3. XML Reasoning Solver

XML Reasoning Solver
FUNCTIONAL DESCRIPTION

The XML Reasoning Solver is a tool for the static analysis of queries and schemas based on our theoretical advances [12]. It allows automated verification of properties that are expressed as logical formulas over trees. A logical formula may for instance express structural constraints or navigation properties (like e.g. path existence and node selection) in finite trees.

The reasoner is built on top of a finite tree logic solver for a new modal logic equipped with recursion and backward axes. The solver is very fast in practice and uses symbolic techniques (Binary Decision Diagrams). The solver has been recently extended to support functions, parametric functions and polymorphic subtyping. One notable difficulty was to elaborate many advanced optimizations with symbolic implementation techniques. The logical solver significantly advances the state of the art. In particular, it is the first implementation that effectively solves the query containment problem for a large fragment of the XPath query language. It supports all navigation axes and regular tree constraints. Although researchers had studied XPath satisfiability before, such prior works were either unimplementable or deemed to explode even for tiny examples. As of 2014, it is still the only implementation actually capable of solving this problem in practice for real world instances.

The reasoner includes compilers and various static analyzers for web query and schema languages. This includes compilers for XPath, for XML schemas (DTDs, XML Schemas, Relax NGs) into logical formulas, parsers, benchmarks, and libraries for automated testing. Various difficulties reside in the compilation of real-world queries, including compiling XPath queries into fixed-point logics, developing specific implementation techniques in order to avoid worst case blow-ups as much as possible when e.g. supporting unordered XML attributes among (ordered) XML elements, etc. The reasoner also generates counter-examples that allow program defects to be reproduced independently from the analyzer.

The off-line version of the solver (with a native library) is fast and up-to-date with the latest advances. We developed and deployed an interactive web interface to make the solver available to the international scientific community. For this purpose, we redesigned the libraries used for the manipulation of binary decision diagrams (BDDs) so that they could used in a fully concurrent and multithreaded manner. This is in order to allow several instances of the logical solver to run concurrently for several users on a web server (GWT-based), while decreasing performance as less as possible.
The reasoner helps us to guide and validate our approach. We continue to develop, maintain and use it on an almost-daily basis.

- Participants: Pierre Genevès, Nabil Layaïda, Louis Jachiet and Nils Gesbert
- Contact: Pierre Genevès
- URL: http://tyrex.inria.fr/websolver/

5.4. XQuery type-checker

XQuery type-checker
FUNCTIONAL DESCRIPTION

This prototype implements a sound static type-system for XQuery, which, as of december 2014, is the most precise type system known for XQuery. It supports the static typing of backward axes that no other does nor is supported in the XQuery recommendation. It also includes precise typing for conditional statements which is challenging as such statement are usually sensitive to the program context. Our type checker successfully verifies complex programs for which existing type-checkers (either known from the literature or those developed in commercial software) fail by reporting false alarms. One major benefit is to allow the cost of validation to be deferred from runtime to compile-time (once only). This prototype is implemented in Scala and interacts with the solver by issuing externals calls for deciding complex subtyping relations. This prototype is described in preprint [20].

- Participants: Pierre Genevès, Nabil Layaïda and Nils Gesbert
- Contact: Pierre Genevès
- URL: http://tyrex.inria.fr/websolver/

5.5. claireCourseMaker

Claire CourseMaker Library
FUNCTIONAL DESCRIPTION

The goal of the ClaireCourseMaker is to provide direct and visual editing tools for structuring, annotating and timeline-based authoring of continuous content such as audio or video. I it is mainly devoted to the synchronisation and layout of pedagogical material (video, slides, chaptering, etc.) and enables the incorporation of rich media content in MOOCs. The underlying technology is based on Web standards and relies on the open source JavaScript Popcorn library and Popcorn Maker web application developed by the Mozilla Foundation. The tool is a wysiwyg web-based authoring tool which benefits from the generic features of Popcorn and offers structuring methods such chaptering and container-based synchronisation.

ClaireCourseMaker is the direct follow-up tool of the Timesheet library developed in the project. Timesheet library is a cross-browser JavaScript implementation for scheduling the dynamic behaviour of HTML5 content. It uses and provides a reference implementation for declarative synchronisation markup such as SMIL Timing and Synchronization and SMIL Timesheets.

ClaireCourseMaker has been developed in collaboration with the OpenClassrooms company in the context of the Claire project.

- Participants: Cécile Roisin, Nabil Layaïda and Nicolas Hairon
- Contact: Cécile Roisin
- URL: https://github.com/NicolasHairon/popcorn.webmaker.org

URBANET Team

6. New Software and Platforms

6.1. PrivaMovApp

FUNCTIONAL DESCRIPTION

UrbaNet is leading the development of an Android application for user data collection purposes. The application is based on the Funf framework, and is currently available on Google Play.

- Participants: Patrice Raveneau, Hervé Rivano, Razvan Stanica.
- Contact: Razvan Stanica
- URL: http://liris.cnrs.fr/privamov/project/

6.2. TAPASCologne

Travel and Activity PAtterns Simulation Cologne

FUNCTIONAL DESCRIPTION

TAPASCologne is an initiative by the Institute of Transportation Systems at the German Aerospace Center (ITS-DLR), aimed at reproducing, with the highest level of realism possible, car traffic in the greater urban area of the city of Cologne, in Germany.

To that end, different state-of-art data sources and simulation tools are brought together, so to cover all of the specific aspects required for a proper characterization of vehicular traffic:

The street layout of the Cologne urban area is obtained from the OpenStreetMap (OSM) database, The microscopic mobility of vehicles is simulated with the Simulation of Urban Mobility (SUMO) software, The traffic demand information on the macroscopic traffic flows across the Cologne urban area (i.e., the O/D matrix) is derived through the Travel and Activity PAtterns Simulation (TAPAS) methodology, The traffic assignment of the vehicular flows described by the TAPASCologne O/D matrix over the road topology is performed by means of Gawron’s dynamic user assignment algorithm.

- Participants: Marco Fiore, Diala Naboulsi and Razvan Stanica.
- Contact: Marco Fiore
- URL: http://kolntrace.project.citi-lab.fr/#download

6.3. Platforms

6.3.1. Sense in the City

Sense in the city is a lightweight experimentation platform for wireless sensor networks in development. The main objective of this platform is to be easily transferable and deployable on the field. It allows a simplified deployment of the code running on the sensors and the collection of logs generated by the instrumentation of the code on a centralized database. In the early stage of the platform, the sensors are powered by small PCs, e.g. Raspberry Pis, but we are investigating the integration of energy harvesting capabilities such as solar panels.

- Participants: Khaled Boussetta, Hervé Rivano.
- Contact: Khaled Boussetta

VEGAS Project-Team

5. New Software and Platforms

5.1. ISOTOP

Topology and geometry of planar algebraic curves
KEYWORDS: Topology - Curve plotting - Geometric computing

Isotop is a Maple software for computing the topology of an algebraic plane curve, that is, for computing an arrangement of polylines isotopic to the input curve. This problem is a necessary key step for computing arrangements of algebraic curves and has also applications for curve plotting.

This software, registered at the APP in June 2011, has been developed since 2007 in collaboration with F. Rouillier from Inria Paris - Rocquencourt. The distributed version is based on the method described in [3], which presents several improvements over previous methods. In particular, our approach does not require generic position. This version is competitive with other implementations (such as ALCIX and INSULATE developed at MPII Saarbrücken, Germany and TOP developed at Santander Univ., Spain). It performs similarly for small-degree curves and performs significantly better for higher degrees, in particular when the curves are not in generic position.

We are currently working on an improved version integrating a new bivariate polynomial solver based on several of our recent results published in [11], [22], [27]. This version is not yet distributed.

- Contact: Sylvain Lazard & Marc Pouget
- URL: http://vegas.loria.fr/isotop/

5.2. SubdivisionSolver

KEYWORDS: Numerical solver - Polynomial or analytical systems

The software SubdivisionSolver solves square systems of analytic equations on a compact subset of a real space of any finite dimension. SubdivisionSolver is a numerical solver and as such it requires that the solutions in the subset are isolated and regular for the input system (i.e. the Jacobian must not vanish). SubdivisionSolver is a subdivision solver using interval arithmetic and multiprecision arithmetic to achieve certified results. If the arithmetic precision required to isolate solutions is known, it can be given as an input parameter of the process, otherwise the precision is increased on-the-fly. In particular, SubdivisionSolver can be interfaced with the Fast_Polynomial library (https://bil.inria.fr/en/software/view/2423/tab) to solve polynomial systems that are large in terms of degree, number of monomials and bit-size of coefficients.

The software is based on a classic branch and bound algorithm using interval arithmetic: an initial box is subdivided until its sub-boxes are certified to contain either no solution or a unique solution of the input system. Evaluation is performed with a centered evaluation at order two, and existence and uniqueness of solutions is verified thanks to the Krawczyk operator.

SubdivisionSolver uses two implementations of interval arithmetic: the C++ boost library that provides a fast arithmetic when double precision is enough, and otherwise the C mpfi library that allows to work in arbitrary precision. Considering the subdivision process as a breadth first search in a tree, the boost interval arithmetic is used as deeply as possible before a new subdivision process using higher precision arithmetic is performed on the remaining forest.

We used SubdivisionSolver for the experiments in [26], [14], see Section 6.3.2 .

- Contact: Rémi Imbach
- URL: https://bil.inria.fr/fr/software/view/2605/tab

5.3. CGAL Periodic Triangulations and Meshes

The CGAL library offers a package to compute the 3D periodic Delaunay triangulation of a point set in $\mathbb{R}^3$, more precisely the Delaunay triangulation of a point set in the 3-dimensional flat torus with cubic domain [30]. The package has been used in various fields. [0]

We have been extending this package in three directions:

First, a few new small functions have been added to the Delaunay triangulation class and integrated in CGAL 4.7.

We have developed and documented some new classes allowing to compute *weighted* periodic Delaunay triangulations. They have been submitted to the CGAL editorial board and accepted for inclusion in CGAL. The code still needs some polishing, and the testsuite must be completed, before a public distribution in CGAL.

We have continued our work to use this package together with the 3D mesh generation package of CGAL [29], in order to propose a construction of meshes of periodic volumes. Although last year's preliminary results were already convincing [32], [33], the work is not ready yet for being submitted to CGAL: the code requires to be completed, documented, and extensively tested.

- Contact: Monique Teillaud
- In collaboration with Aymeric Pellé (Geometrica project-team)
- This work was done in the framework of the Inria ADT *(Action de Développement Technologique)* OrbiCGAL http://www.loria.fr/~teillaud/ADT-OrbiCGAL/

---

[0] see http://www.cgal.org/projects.html

VERIDIS Project-Team

6. New Software and Platforms

6.1. The Redlog Computer Logic System

FUNCTIONAL DESCRIPTION

Redlog is an integral part of the interactive computer algebra system Reduce. It supplements Reduce's comprehensive collection of powerful methods from symbolic computation by supplying more than 100 functions on first-order formulas. Redlog has been publicly available since 1995 and is constantly being improved. The name Redlog stands for Reduce Logic System. Andreas Dolzmann from Schloss Dagstuhl Leibniz-Zentrum für Informatik is a co-developer of Redlog.

Reduce and Redlog are open-source and freely available under a modified BSD license at http://reduce-algebra.sourceforge.net/. The Redlog homepage is located at http://www.redlog.eu/. Redlog generally works with interpreted first-order logic in contrast to free first-order logic. Each first-order formula in Redlog must exclusively contain atoms from one particular Redlog-supported theory, which corresponds to a choice of admissible functions and relations with fixed semantics. Redlog-supported theories include Nonlinear Real Arithmetic (Real Closed Fields), Presburger Arithmetic, Parametric QSAT, and many more.

Effective quantifier elimination procedures for the various supported theories establish an important class of methods available in Redlog. For the theories supported by Redlog, quantifier elimination procedures immediately yield decision procedures. Besides these quantifier elimination-based decision methods there are specialized, and partly incomplete, decision methods, which are tailored to input from particular fields of application.

In 2015 there was further significant progress with the identification of bifurcations in biochemical models based on real reasoning [17], [33]. With existential real quantifier elimination Redlog can now produce unsatisfiable cores in the infeasible case [27]. This is of considerable relevance in the course of using Redlog as a theory solver in SMT contexts, e.g., within the SMArT project (section 9.2).

Redlog is a widely accepted tool and highly visible in mathematics, informatics, engineering and the sciences. The seminal article on Redlog [4] has received more than 300 citations in the scientific literature so far.

- Participants: Thomas Sturm, Marek Kosta, and Maximilian Jaroschek
- Contact: Thomas Sturm
- URL: http://www.redlog.eu/

6.2. SPASS

FUNCTIONAL DESCRIPTION

SPASS is an automated theorem prover based on superposition that handles first-order logic with equality and several extensions for particular classes of theories. It has been developed since the mid-1990s at the Max-Planck Institut für Informatik in Saarbrücken. Version 3.8 is the final release of the SPASS first-order prover built on a traditional "select given loop" design; it is distributed under the FreeBSD license at http://www.spass-prover.org.

SPASS will be released in the future in the form of various reasoners for different logics, including combinations of first-order logic with background theories, in particular some forms of arithmetic. In 2015, we have continued our efforts to improve the superposition calculus as well as to develop dedicated arithmetic decision procedures for various arithmetic theories, in particular linear integer arithmetic. Our results are:

- new calculi and decidability results for finite domain fragments,
- specialized reasoning support for finite subsets,
- specialized decision procedures for linear real arithmetic with one quantifier alternation,
- new efficient and complete procedures for (mixed) linear integer arithmetic,
- decidability results and respective procedures for various combinations of linear arithmetic with first-order logic.
- Participants: Martin Bromberger, Thomas Sturm, Marco Voigt, Uwe Waldmann, Christoph Weidenbach
- Contact: Christoph Weidenbach
- URL: http://www.spass-prover.org/

6.3. The TLA+ Proof System

FUNCTIONAL DESCRIPTION

TLAPS, the TLA$^+$ proof system developed at the Joint MSR-Inria Centre, is a platform for developing and mechanically verifying proofs about TLA$^+$ specifications. The TLA$^+$ proof language is hierarchical and explicit, allowing a user to decompose the overall proof into independent proof steps. TLAPS consists of a *proof manager* that interprets the proof language and generates a collection of proof obligations that are sent to *backend verifiers*. The current backends include the tableau-based prover Zenon for first-order logic, Isabelle/TLA$^+$, an encoding of TLA$^+$ as an object logic in the logical framework Isabelle, an SMT backend designed for use with any SMT-lib compatible solver, and an interface to a decision procedure for propositional temporal logic.

The current version 1.4.3 of TLAPS was released in June 2015, it is distributed under a BSD-like license. The prover fully handles the non-temporal part of TLA$^+$. Basic temporal logic reasoning is supported through an interface with a decision procedure for propositional temporal logic that performs on-the-fly abstraction of first-order subformulas. Symmetrically, subformulas whose main operator is a connective of temporal logic are abstracted before being sent to backends for first-order logic.

A complete rewrite of the proof manager has started in 2015. Its objectives are to replace the ad-hoc parser used so far with an interface to SANY, the standard parser and semantic analyzer for TLA$^+$, to extend the scope of the fragment of TLA$^+$ that is handled by TLAPS, and general code refactoring and performance improvements.

TLAPS has been used in several case studies in 2015, including the proof of determinacy of PharOS (section 8.1) and the verification of the Pastry routing protocol (section 7.2). These case studies feed back into the standard library of the distribution.

- Participants: Stephan Merz, Martin Riener, Hernán Vanzetto
- Contact: Stephan Merz
- URL: http://tla.msr-inria.inria.fr/tlaps/content/Home.html

6.4. The veriT Solver

FUNCTIONAL DESCRIPTION

VeriT is an open, trustable and efficient SMT (Satisfiability Modulo Theories) solver developed in cooperation with David Déharbe from the Federal University of Rio Grande do Norte in Natal, Brazil, on leave for Clearsy. The solver can handle large quantifier-free formulas containing uninterpreted predicates and functions, and arithmetic over integers and reals. It features efficient decision procedures for uninterpreted symbols and linear arithmetic. It also has some support for user-defined theories, quantifiers, and lambda-expressions. This allows users to easily express properties about concepts involving sets, relations, etc. The prover can produce explicit proof traces when it is used as a decision procedure for quantifier-free formulas with uninterpreted symbols and arithmetic. To support the development of the tool, non-regression tests use Inria's grid infrastructure; it allows us to extensively test the solver on thousands of benchmarks in a few minutes. The veriT solver is available as open source under the BSD license at the veriT Web site.

Efforts in 2015 have been focused on efficiency, stability, and expressiveness, with a new ability for handling non-linear arithmetic. The decision procedures for uninterpreted symbols and linear arithmetic have been further improved. The integration of the solver Redlog (section 6.1) for non-linear arithmetic in the context of the SMArT project (section 9.2) now works for quantifier-free formulas with non-linear real arithmetic, but is not yet complete for combinations.

The veriT solver participated in the SMT competition SMT-COMP 2015 with decent results.

We target applications where validation of formulas is crucial, such as the validation of TLA^+ and B specifications, and work together with the developers of the respective verification platforms to make veriT even more useful in practice. The solver is available as a plugin for the Rodin platform for discharging proof obligations generated in Event-B [53]; on a large repository of industrial and academic cases, this SMT-based plugin decreased by 75% the number of proof obligations requiring human interactions, compared to the original B prover.

- Participants: Pascal Fontaine, Pablo Dobal, David Déharbe, and Haniel Barbosa
- Partners: Université de Lorraine - Federal University of Rio Grande do Norte
- Contact: Pascal Fontaine
- URL: http://www.veriT-solver.org

VIRTUAL PLANTS Project-Team

5. New Software and Platforms

5.1. OpenAleaLab

KEYWORDS: Bioinformatics - Biology - Workflow - Modelling Environment
FUNCTIONAL DESCRIPTION

OpenAleaLab is an integrated modelling environment (IME) designed for scientists based on IPython and on OpenAlea components. This open source environment is extensible via plug-ins and allows user to work with a set of diverse modelling paradigms like imperative languages (Python, R), scientific workflows (visual programming) or rule-based language (L-System). This IME, built using PyQt, provides an IPython shell, a text editor, a project manager, a graphical package installer and a world, containing the objects and state variables shared by the different paradigms. The world can be graphically interpreted in 3D or 2D. Different paradigms and tools for plant modelling are available as plug-ins, such as a visual programming environment, a L-system language, a 3D viewer, and an R editor and interpreter. The plug-in system is based on setuptools entry-points and provide both functional and GUI components. This environment is designed to be easily extensible in order to include new plant modelling paradigms in the future or to be customized for other scientific domains. Several dedicated extensions (TissueLab, PlantLab) have been developed or are in development.

- Participants: Christophe Pradal, Guillaume Baty, Julien Coste, Christophe Godin.
- Contact: Christophe Pradal, Christophe Godin
- URL: http://virtualplants.github.io/

5.2. TissueLab

KEYWORDS: Bioinformatics - Biology - Modelling Environment
FUNCTIONAL DESCRIPTION

TissueLab is an OpenAleaLab extension dedicated to studies plant morphogenesis at the scale of tissues. This extension was built on the basis of several key concepts of OpenAleaLab (project, world, interactive panels, etc.) and using its plugin mechanism (dynamically discovered, modular, extensible, etc.). TissueLab enables the visualization, interaction, reconstruction, analysis and simulation of tissue development based on image sequences. It contains for instance the PyThor module, dedicated to 3D real-time interaction and modification of segmented images for the creation of ground truth segmentations.

- Participants: Sophie Ribes, Guillaume Baty, Guillaume Cerutti, Alizon Konig, Gregoire Malandain, Christophe Pradal, Christophe Godin.
- Contact: Christophe Godin
- URL: https://gforge.inria.fr/projects/oalab

5.3. TissueMeca

KEYWORDS: Bioinformatics - Biology - Mechanics - Morphogenesis
FUNCTIONAL DESCRIPTION

A mechanical model of growing tissue has been implemented using the open source software SOFA and OpenAlea. Using OpenAlea, a generic tissue representation can be defined with attributes giving structural, geometrical and physical parameters of the simulation. Then, based on SOFA and its modular approach, it is possible to combine different element types (triangle and edge elements), forces (elastic forces and turgor) and positional constraints within the same model to find the static elastic equilibrium, given a current configuration. The use of an implicit integration scheme makes it possible to achieve close-to interactive simulation of growth. The module implements also growth equations for the different cell walls after each elastic equilibrium step. Algorithms to simulate division and refinement of each element of the modelled tissue are also available.

- Participants: Frédéric Boudon, Olivier Ali, Jean-Philippe Bernard, Benjamin Gilles, Christophe Godin.
- Contact: Frédéric Boudon
- https://gforge.inria.fr/projects/tissuemeca/

5.4. PlantScan3D

KEYWORDS: Bioinformatics - Biology - Laser scanners - 3D Reconstruction
FUNCTIONAL DESCRIPTION

This software aims at semi-automatically reconstructing the 3D structures of plants from laser scans. For this, it encapsulates automatic reconstruction method developed by the Virtual Plants team (Preuksakarn et al., 2010) or by the literature (Vernoust and Lazarus, 2000). Once reconstructed the structure can be graphically edited by adding, deleting, repositioning or reorganizing segments in the structure. The original pointset can be processed with contraction operators to shift the points toward the center of the shape. Some post processing procedures are available to retrieve automatically botanical features such as divergence angle sequences.

- Participants: Frédéric Boudon, Chakkrit Preuksakarn, Christophe Godin
- Contact: Frédéric Boudon
- URL: http://plantscan3d.gforge.inria.fr/

5.5. ASTEC

KEYWORDS: Segmentation - Tracking - High resolution
FUNCTIONAL DESCRIPTION A new algorithmic pipeline, ASTEC (Adaptative Segmentation and Tracking of Embryonic Cells), has been developed to segment and track cell shapes in 3D from movies with high spatio-temporal resolution of embryos where the membranes have been labeled (using dye or genetic markers for example). To segment the 3D embryo image at a given time-point, ASTEC takes advantage of the high spatial resolution of the movie in order to propagate the segmentation of the previous time points. This, coupled to biological knwoledge on the studied system, allows to constrain the segmentation and to track cells throughout time simulataneously. Moreover, the propagation allows to bound the potential mistakes of segmentation (e.g. a cells cannot disapear) which enables powerfull post-correction based on the study of the resulting tracking.

- Participants: Léo Guignard, Grégoire Malandain, Patrick Lemaire, Christophe Godin
- Contact: Christophe Godin
- URL: https://gforge.inria.fr/projects/marsalt/

5.6. Alep

KEYWORDS: Foliar Fungus, Pathogen, FSPM, Epidemics, Infectious Cycle, Modelling framework
LONG: Architecture & Leaf Pathogens
FUNCTIONAL DESCRIPTION

Alep is a FSPM library implemented in Python that adapts the concepts and tools of OpenAlea to pathosystem modelling. The key components of Alep are two abstract classes that represent Dispersal Units and Lesions of foliar fungi in a generic form. The equations in these classes are specified to model a given species of fungus. Alep also contains several generic functions to manipulate these objects and define their contract: functions of dispersal by rain and by wind, functions managing the growth and competition of several lesions on the same leaf. A particular pathosystem is modeled by assembling a coherent set of components via a plugin system. This strategy allows the composition of existing algorithms as well as the extension or the inclusion of new algorithms. Their assembly and scheduling of execution uses scientific workflows defined in OpenAlea. This way, models can run at different time and spatial scales.

- Participants: Guillaume Garin, Christophe Pradal, Christian Fournier, Vianey Houles, Corinne Robert, Bruno Andrieu
- Contact: Christophe Pradal
- URL: https://gforge.inria.fr/projects/openaleapkg

5.7. AutoWIG

KEYWORDS: Syntaxic Analysis
FUNCTIONAL DESCRIPTION

The goal of AutoWIG (Automatic Wrapper and Interface Generator) is to provide an automatic approach for the process of Python interfacing of C++ libraries. This Python library relies on two main principles: i) automatic C++ code parsing using LLVM/clang, and ii) Python wrapper generation with C++ code introspection.

- Participants: Pierre Fernique, Christophe Pradal
- Contact: Pierre Fernique
- URL: https://github.com/VirtualPlants/AutoWIG

5.8. Phenomenal

KEYWORDS: Image Analysis
FUNCTIONAL DESCRIPTION

Phenomenal is a Python library that provides a set of algorithms to process images produce by Image-based phenotyping platforms. The library contains algorithms for i) plant image segmentation, ii) 3D reconstruction of plant organs and plant canopies, iii) calculation of intercepted light and radiation use efficiency. All these algorithms are integrated in the OpenAlea platform.

- Participants: Simon Artzet, Jérôme Chopard, Michael Mielewczik, Nicolas Brichet, Christian Fournier, Christophe Pradal
- Contact: Christophe Pradal
- URL: https://gforge.inria.fr/projects/phenomenal/

5.9. Platforms

5.9.1. Platform OpenAlea

OpenAlea is an open-software platform for interdisciplinary research in plant modeling and simulation. This scientific workflow platform is used for the integration and comparison of different models and tools provided by the research community. It is based on the Python (http://www.python.org) language that aims at being both a *glue* language for the different modules and an efficient modeling language for developing new models and tools. *OpenAlea* currently includes modules for plant simulation, analysis and modeling at different scales (*V-Plants* modules), for modeling ecophysiological processes (*Alinea* modules) such as radiative transfer, transpiration and photosynthesis (*RATP*, *Caribu*, *Adel*, *TopVine*, *Ecomeristem*) and for 3D visualization of plant architecture at different scales (*PlantGL*).

OpenAlea is the result of a collaborative effort associating 20 french research teams in plant modeling from Inria, CIRAD, INRA and ENS Lyon. The Virtual Plants team coordinates both development and modeling consortia, and is more particularly in charge of the development of the kernel and of some of the main data structures such as multi-scale tree graphs and statistical sequences.

OpenAlea is a fundamental tool to share models and methods in interdisciplinary research (comprising botany, ecophysiology, forestry, agronomy, applied mathematics and computer science approaches). Embedded in Python and its scientific libraries, the platform may be used as a flexible and useful toolbox by biologists and modelers for various purposes (research, teaching, rapid model prototyping, communication, etc.).

5.9.2. Platform Sofa

Our team is increasingly using the platform SOFA developed at Inria by other teams, in conjunction with OpenAlea, to model biomechanics of plant tissues. SOFA (https://www.sofa-framework.org) is an Open Source framework primarily targeted at real-time simulation, with an emphasis on biological simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods. It has been extensively used by our team in the recent years to conduct virtual mechanical experiments on plant tissues (see section 6.2.3).

VISAGES Project-Team

6. New Software and Platforms

6.1. Anima

KEYWORDS: Filtering - Medical imaging - Diffusion imaging - Registration - Relaxometry
SCIENTIFIC DESCRIPTION Anima is a set of libraries and tools developed by the team as a common repository of research algorithms. As of now, it contains tools for image registration, statistical analysis (group comparison, patient to group comparison), diffusion imaging (model estimation, tractography, etc.), quantitative MRI processing (quantitative relaxation times estimation, MR simulation), image denoising and filtering, and segmentation tools. All of these tools are based on stable libraries (ITK, VTK), making it simple to maintain.

- Participants: Laurence Catanese, Olivier Commowick, René-Paul Debroize, Florent Leray, Renaud Hédouin and Guillaume Pasquier
- Contact: Olivier Commowick
- URL: https://github.com/Inria-Visages/Anima-Public/wiki
- APP number: IDDN.FR.001.460020.000.S.P.2015.000.31230

6.2. MedInria

KEYWORDS: Segmentation - Health - DWI - Visualization - Medical imaging
SCIENTIFIC DESCRIPTION It aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010 and renewed in 2012. The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.
FUNCTIONAL DESCRIPTION MedInria is a free software platform dedicated to medical data visualization and processing as illustrated in figure 2 .

- Participants: Olivier Commowick, René-Paul Debroize, Guillaume Pasquier, Laurence Catanese
- Partners: HARVARD Medical School - IHU - LIRYC - IHU - Strasbourg - NIH
- Inria structures involved : ASCLEPIOS, ATHENA, PARIETAL, VISAGES
- Contact: Olivier Commowick
- URL: http://med.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230

6.3. autoMRI

KEYWORDS: Magnetic Resonance Imaging (MRI) - functional MRI (fMRI) - Arterial Spin Labeling (ASL) - functional ASL (fASL) - Statistical Parametric Mapping (SPM) - Automation
SCIENTIFIC DESCRIPTION This software is highly configurable in order to fit to a wide range of needs. Pre-processing includes segmentation of anatomical data, as well as co-registration, spatial normalization and atlas building of all data types. The analysis pipelines perform either within-group analysis or between-group or one subject-versus-group comparison and produce statistical maps of regions with significant differences. These pipelines can be applied to structural data to exhibit patterns of atrophy or lesions, to ASL (both pulsed or pseudo-continuous sequences) or PET data to detect perfusion or metabolic abnormalities (see figure 3 , left), to relaxometry data to detect deviations from a template (see figure 3 , right), to functional data - either BOLD or ASL - to outline brain activations related to block or event-related paradigms. In addition to the standard General Linear Model approach, the ASL pipelines implement an a contrario approach and, for patient-specific perfusion study, an heteroscedastic variance model. Besides, the vascular pipeline processes 4D MRA data and enables accurate assessment of hemodynamic patterns.

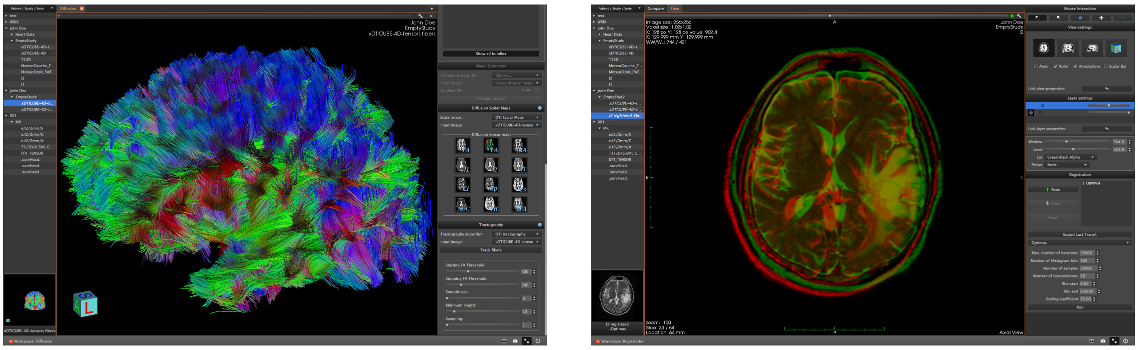


Figure 2. The medInria software platform: Tractography overlapped with 3D image (left), and Fused view of registered images (right)

FUNCTIONAL DESCRIPTION Based on MATLAB and the SPM8 toolbox, autoMRI provides complete pipelines to pre-process and analyze various types of images (anatomical, functional, perfusion, metabolic, relaxometry, vascular). A new version of the ASL post-processing part was developed in Python and Nipype, therefore not requiring the disponibility of Matlab licences.

- Participants: Isabelle Corouge, Cédric Meurée, Pierre Maurel and Elise Bannier
- Contact: Isabelle Corouge
- URL: http://www.irisa.fr/visages/

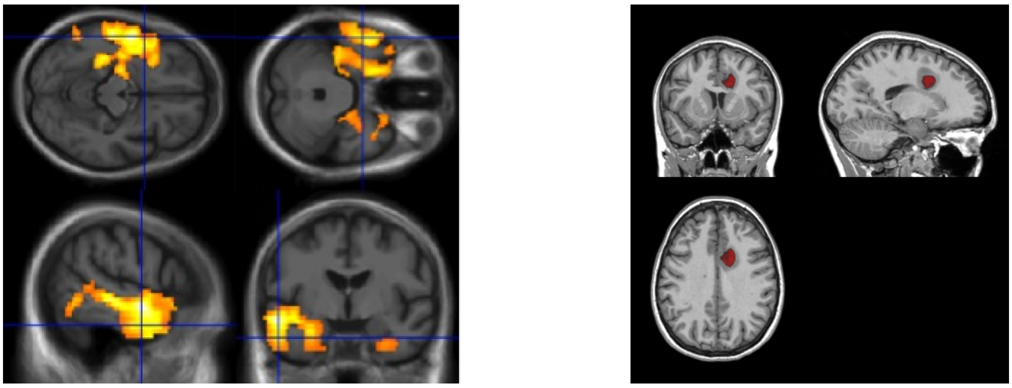


Figure 3. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (left) and detection of relaxometry defect in an MS patient (right).

6.4. Shanoir

KEYWORDS: Shanoir - Webservices - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS - Nifti

FUNCTIONAL DESCRIPTION SHAring NeurOImaging Resources (Shanoir, Previously InriaNeuroTk) is an open source software platform designed to structure, manage, archive, visualize and share neuroimaging data with an emphasis on multi-centric collaborative research projects. It provides common features of neuroimaging data management systems along with research-oriented data organization and enhanced accessibility (see figure 4).

Shanoir is a secured J2EE application running on a JBoss server, reachable via graphical interfaces in a browser or by third party programs via web services. It behaves as a repository of neuroimaging files coupled with a relational database hoding meta-data. The data model, based on OntoNeurolog, an ontology devoted to the neuroimaging field, is structured around the concept of "research study". A research study includes patients who themselves have examinations that either produce image acquisitions or clinical scores. Each image acquisition is composed of datasets represented by their acquisition parameters and image files. The system only keeps anonymous data.

Image file imports are possible from various sources (DICOM CDs, PACs, image files in NIfTI / Analyze format) using either online wizards, with completions of related meta-data, or commande line tools. Once de-identified during the import phase, DICOM header's customizable feature. Shanoir can also record any executed processing allowing to retrieve workflows applied to a particular dataset along with the intermediate data.

The clinical scores resulting from instrument based assessments (e.g. neuropsychological tests) can also be entered and easily retrieved and exported in different formats (Excel, CSV, Xml). Scores and image acquisitions are bound together which makes relationship analysis possible. The instrument database is scalable and new measures can be added in order to meet specific project needs, by use of intuitive graphical interfaces.

Using cross-data navigation and advanced search criteria, the users can quickly point to a subset of data to be downloaded. Client side applications have as well been developed to illustrate how to locally access and exploit data through the available web services. With regards to security, the system requires authentication and user rights are tunable for each hosted studies. A study responsible can thereby define the users allowed to see, download or import data into his study or simply make it public.

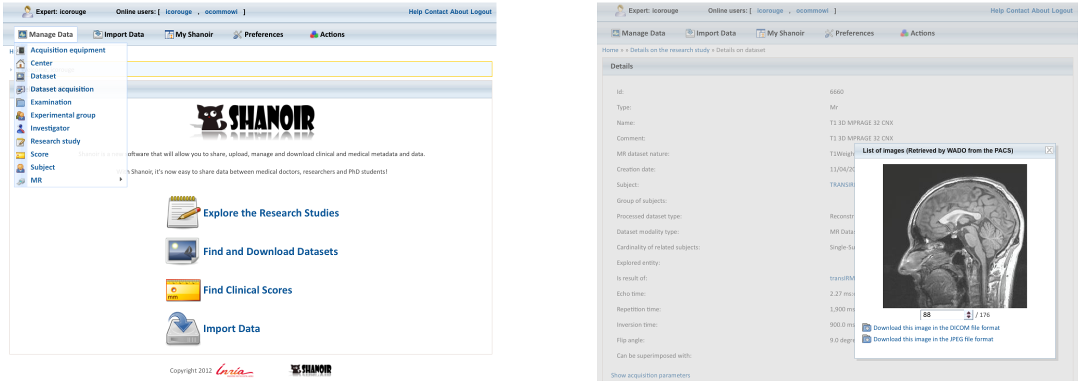
Shanoir serves neuroimaging researchers in organizing efficiently their studies while cooperating with other laboratories. By managing patient privacy, Shanoir allows the exploitation of clinical data in a research context. It is finally a handy solution to publish and share data with a broader community.

Shanoir integrates the enterprise search platform, Apache Solr, to provide the users a vast array of advanced features such as near real-time indexing and queries, full-text search, faceted navigation, autosuggestion and autocomplete.

- Participants: Michael Kain, Justine Guillaumont, Christian Barillot, Anthony Baire and Yao Yao
- Partners: Université de Rennes 1 - CNRS - INSERM
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.520021.003.S.A.2008.000.31230 (2014/08/20)

6.5. QtShanoir

KEYWORDS: Shanoir - Qt - Webservices - Soap - C++ - Health - DICOM - Plug-in - Medical imaging - Nifti
SCIENTIFIC DESCRIPTION QtShanoir is based on Qt/C++ librairie. It interacts with the Shanoir server using SOAP web services provided. This application queries the server and displays hierarchical data extracted in tree view. Data could also be easily downloaded or uploaded on the server. In order to extend the Shanoir environment, QtShanoir is developed to contain two shared libraries: - « GUI » that represents all user interfaces. - « DAO » that takes in charge the data model. This library assures the connection to the server and provides all QtShanoir services : research, download and upload of Processed Dataset (NIfTI). QtShanoir dynamic libraries are already reused and integrated in other projects: in the software medInria and in an under development command line program.



oftware that will allow you to share, upload, manage and download clinical and medical metadata and data.

h Shanoir, it's now easy to share data between medical doctors, researchers and PhD students!

Id: 6660
Type: Mr
Name: T1 3D MPRAGE 32 CNX
Comment: T1 3D MPRAGE 32 CNX
MR dataset nature: T1Weigh
Creation date: 11/04/20
Subject: TRANSIRI
Group of subjects:
Processed dataset type: Reconstr
Dataset modality type: MR Data
Cardinality of related subjects: Single-Su
Explored entity:
Is result of: transIRM
Echo time: 2.27 ms
Repetition time: 1,900 ms
Inversion time: 900.0 ms
Flip angle: 9.0 degre
Can be superimposed with:

Figure 4. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

FUNCTIONAL DESCRIPTION QtShanoir is a graphical client application of the medical imaging database Shanoir. This application provides various functionalities to satisfy researchers' needs. It allows users to: - explore neuroimaging data derived from multicenter research trials. Through an intuitive user interface, users could easily visualize voluminous amount of structured data: studies, patients and datasets extracted from Shanoir - download and to upload data from the server. This application is available on Windows, UNIX, MacOs X. It is integrated as a plugin in medInria, a multi-plateform for medical image processing and visualization.

- Participants: Olivier Commowick, Justine Guillaumont, Florent Leray, and Wefa Hakem
- Contact: Olivier Commowick
- URL: http://qtshanoir.gforge.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230 (2012/02/08)

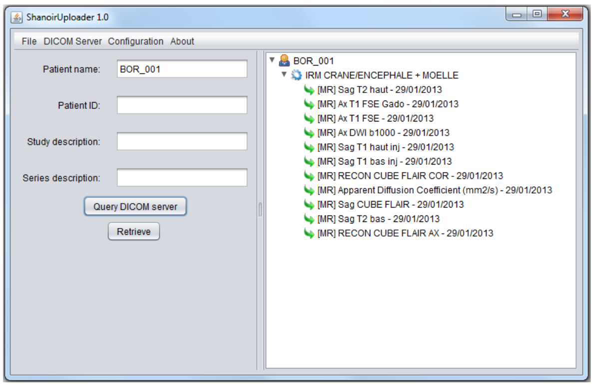
6.6. ShanoirUploader

KEYWORDS: Shanoir - Webservices - Java - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS

SCIENTIFIC DESCRIPTION ShanoirUploader is a desktop application on base of JavaWebStart (JWS). The application can be downloaded and installed using an internet browser. It interacts with a PACS to query and retrieve the data stored on it as illustrated in figure 5 . After this ShanoirUploader sends the data to a Shanoir server instance in order to import these data. This application bypasses the situation, that in most of the clinical network infrastructures a server to server connection is complicated to set up between the PACS and a Shanoir server instance.

FUNCTIONAL DESCRIPTION ShanoirUploader is a Java desktop application that transfers data securely between a PACS and a Shanoir server instance (e.g., within a hospital). It uses either a DICOM query/retrieve connection or a local CD/DVD access to search and access images from a local PACS or the local CD/DVD. After having retrieved the data, the DICOM files are locally anonymized and then uploaded to the Shanoir server. A possible integration of a hash creation application for patient identifiers is provided as well. The primary goals of that application are to enable mass data transfers between different remote server instances and therefore reduce the waiting time of the users, when importing data into Shanoir. Most of the time during import is spent with data transfers.

- Participants: Justine Guillaumont, Michael Kain, Christian Barillot, Yao Yao, Inès Fakhfakh
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.380026.000.S.P.2015.000.31230 (2015/09/11)



Patient name: BOR_001

Patient ID:

Study description:

Series description:

- BOR_001
  - IRM CRANE/ENCEPHALE + MOELLE
    - [MR] Sag T2 haut - 29/01/2013
    - [MR] Ax T1 FSE Gado - 29/01/2013
    - [MR] Ax T1 FSE - 29/01/2013
    - [MR] Ax DWI b1000 - 29/01/2013
    - [MR] Sag T1 haut inj - 29/01/2013
    - [MR] Sag T1 bas inj - 29/01/2013
    - [MR] RECON CUBE FLAIR COR - 29/01/2013
    - [MR] Apparent Diffusion Coefficient (mm2/s) - 29/01/2013
    - [MR] Sag CUBE FLAIR - 29/01/2013
    - [MR] Sag T2 bas - 29/01/2013
    - [MR] RECON CUBE FLAIR AX - 29/01/2013

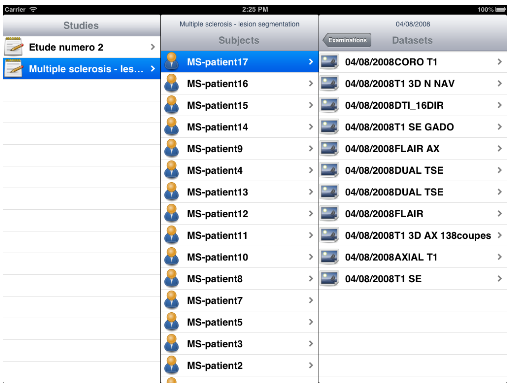
Figure 5. The ShanoirUploader software is a desktop application designed to interact with a PACS to query and retrieve the data stored on any PACS.

6.7. iShanoir

KEYWORDS: Shanoir - Biology - Health - Neuroimaging - Mobile application - Medical imaging - Biomedical imaging

FUNCTIONAL DESCRIPTION iShanoir is an iOS application, designed for iPhone and iPad. On base of this application a Shanoir server can be accessed. For this the Shanoir SOAP web-services are called. As shown in figure 6 , iShanoir can be used to access and navigate in the data tree structure, stored on a Shanoir server. iShanoir displays as well additional meta data corresponding to the data entities in the tree structure. On base of these informations image files (NIfTI and DICOM) can be selected and downloaded on a local iPhone/iPad in a temporary cache. From this cache the files can be opened and displayed with a viewer that the user has already installed on his device.

- Participants: Michael Kain, Christian Barillot
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr



Etude numero 2
Multiple sclerosis - les...

MS-patient17
MS-patient16
MS-patient15
MS-patient14
MS-patient9
MS-patient4
MS-patient13
MS-patient12
MS-patient11
MS-patient10
MS-patient8
MS-patient7
MS-patient5
MS-patient3
MS-patient2

04/08/2008CORO T1
04/08/2008T1 3D N NAV
04/08/2008DTI_16DIR
04/08/2008T1 SE GADO
04/08/2008FLAIR AX
04/08/2008DUAL TSE
04/08/2008DUAL TSE
04/08/2008FLAIR
04/08/2008T1 3D AX 138coupes
04/08/2008AXIAL T1
04/08/2008T1 SE

Figure 6. The iShanoir software is a desktop application designed to...

6.8. Integration of EEG and fMRI

Participants: Marsel Mano, Lorraine Perronnet.

Related to the project Hemisfer there have been development of new functions, scripts and demos for the acquisition and processing of the EEG and fMRI data in Real-time. These include:

- Functions for fMRI header info reader, volume reader, motion correction, slice time correction nifty output conversion, real time fMRI initialization, real time fMRI processing, z-score calculation, volume smoother, alignment, etc., functions for real time EEG data acquisition, filtering, power calculation and display.
- Scripts for various protocols used in offline fMRI experiments, real time processing loop for EEG and fMRI.
- Demo for real time acquisition of the EEG and fMRI data, demo for real time processing efficiency of the fMRI data, demo for the real time processing of EEG data, real time z-Score for fMRI data.
- Several small aux functions for I/O interfaces (e.g. com, serial)

In the current stage the prototype also relies on various other free toolboxes (e.g. SPM, pnet)

- Keywords: medical imaging, EEG, fMRI
- Software benefit: integration of EEG and fMRI processing
- Type of human computer interaction: C++ API, shell scripts
- OS/Middleware: Windows, Mac and Linux.
- Required library or software : SPM, pnet.
- Programming language: C++, shell scripts

6.9. Platforms

6.9.1. The Neurinfo Platform

VISAGES is the founding actor of an experimental research platform which was installed in August 2009 at the University Hospital of Rennes. The University of Rennes 1, Inria, Inserm for the academic side, and the University Hospital of Rennes and the Cancer Institute “Eugene Marquis“ for the clinical side, are partners of this neuroinformatics platform called Neurinfo (http://www.neurinfo.org). This platform has been supported under the “Contrat de Projets Etat-Région” (C. Barillot is the PI) and has received a total amount of 4.01 M€ for the period 2007–2014. European (FEDER), National (through Ministry of research, Inria, Inserm and ANR) and local councils (Brittany Region, Ille et Vilaine, and Rennes Metropole) have joined their effort to support this operation for a total amount of 4010 k€ (600 k€ for the infrastructures, 2850 k€ for the equipments and 560 k€ for the functioning). This application was set up through the Regional PIMATGI initiative coordinated by INSERM in Brittany (C. Roux). The overall PIMATGI initiative served for the financing of three distinct, but complementary, platforms: Neurinfo, TheraFONC as a technical platform dedicated to therapy guided by functional imaging especially in the oncology domain (Inserm U 650 - LaTIM, Dir. Ch. Roux, Brest), and TherA-Image as a platform dedicated to image guided mini-invasive surgery and therapy especially in the domain of cardio-vascular diseases (U642 -LTSI, Dir. L. Senhadji, Rennes).

Concerning the Neurinfo Platform, the activity domain is a continuum between methodological and technological research built around specific clinical research projects. The ambition is to do innovation in science, technology and medical technology transfer for the implementation on the clinical field. On the medical field, the translational research domain mainly concerns medical imaging and more specifically the clinical neurosciences. Among them are multiple sclerosis, epilepsy, neurodegenerative, neurodevelopmental and psychiatric diseases, surgical procedures of brain lesions, neuro-oncology and radiotherapy planning. Beyond these CNS applications, the platform is also open to alternative applications. Neurinfo ambitions to support the emergence of research projects based on their level of innovation, their pluri-disciplinarity and their ability to foster collaborations between different actors (public and private research entities, different medical specialties, different scientific profiles).

In this context, a new research 3T MRI system (Siemens Verio system) was acquired in summer 2009 in order to develop the clinical research in the domain of morphological, functional, structural and cellular in-vivo imaging. In 2014 a new equipment for simultaneous recording of EEG and MRI images has been acquired from Brain Product. In 2015, a mock scanner for experimental set-up has been acquired as well as a new High Performance Computing environment made of one large computing cluster and a data center that is shared and operated by the Inria center at IRISA (UMR CNRS 6074). The computation cluster (240 cores) and the data center (up to 50 TB) are dedicated to host and process imaging data produced by the Neurinfo platform, but also by other research partners that share their protocols on the Neurinfo neuroinformatics system (currently more than 30 sites).

Visages and its partners in the Neurinfo project are committed to use this new research platform for developing new regional, national and international collaborations around fundamental and applied clinical research projects dealing with in-vivo medical imaging.

WHISPER Project-Team

6. New Software and Platforms

6.1. Platforms

6.1.1. Coccinelle

Our recent research is in the area of code manipulation tools for C code, particularly targeting Linux kernel code. This work has led to the Coccinelle tool that we are continuing to develop. Coccinelle serves both as a basis for our future research and the foundation of our interaction with the Linux developer community.

The need to find patterns of code, and potentially to transform them, is pervasive in software development. Examples abound. When a bug is found, it is often fruitful to see whether the same pattern occurs elsewhere in the code. For example, the recent Heartbleed bug in OpenSSL partly involves the same fragment of code in two separate files. [0] Likewise, when the interface of an API function changes, all of the users of that function have to be updated to reflect the new usage requirements. This generalizes to the case of code modernization, in which a code base needs to be adapted to a new compiler, new libraries, or a new coding standards. Finding patterns of code is also useful in code understanding, *e.g.*, to find out whether a particular function is ever called with a particular lock held, and in software engineering research, *e.g.*, to understand the prevalence of various kinds of code structures, which may then be correlated with other properties of the software. For all of these tasks, there is a need for an easy to use tool that will allow developers to express patterns and transformations that are relevant to their source code, and to apply these patterns and transformations to the code efficiently and without disrupting the overall structure of the code base.

The Coccinelle program matching and transformation tool for C code addresses these needs. Coccinelle has been under development for over 10 years, and is mature software, available in a number of Linux distributions (Ubuntu, Debian, Fedora, etc.). It allows matching and transformation rules to be expressed in terms of fragments of C code, more precisely in the form of a *patch*, in which code to add and remove is highlighted by using + and −, respectively, in the leftmost column, and other, unannotated, code fragments may be provided to describe properties of the context. The C language is extended with a few operators, such as metavariables, for abstracting over subterms, and a notion of positions, which are useful for reporting bugs. The pattern matching rules can interspersed with rules written in Python or OCaml, for further expressiveness. The process of matching patterns against the source code furthermore takes into account some semantic information, such as the types of expressions and reachability in terms of a function's (intraprocedural) control-flow graph, and thus we refer to Coccinelle matching and transformation specifications as *semantic patches*.

Coccinelle was originally motivated by the goal of modernizing Linux 2.4 drivers for use with Linux 2.6, and was originally validated on a collection of 60 transformations that had been used in modernizing Linux 2.4 drivers [8]. Subsequent research involving Coccinelle included a formalization of the logic underlying its implementation [1] and a novel mechanism for identifying API usage protocols [45]. More recently, Coccinelle has served as a practical and flexible tool in a number of research projects that somehow involve code understanding or transformation. These include identifying misuses of named constants in Linux code [47], extracting critical sections into procedures to allow the implementation of a centralized locking service [53], generating a debugging interface for Linux driver developers [23], detecting resource release omission faults in Linux and other infrastructure software [64], and understanding the structure of device driver code in our current DrGene project [66].

---

[0] http://git.openssl.org/gitweb/?p=openssl.git;a=commitdiff;h=96db902

Throughout the development of Coccinelle, we have also emphasized contact with the developer community, particularly the developers of the Linux kernel. We submitted the first patches to the Linux kernel based on Coccinelle in 2007. Since then, over 4500 patches have been accepted into the Linux kernel based on the use of Coccinelle, including around 3000 by over 500 developers from outside our research group. Over 50 semantic patches are available in the Linux kernel source code itself, with appropriate infrastructure for developers to apply these semantic patches to their code within the normal `make` process. Many of these semantic are also included in a 0-day build-testing system for Linux patches maintained by Intel. [0] Julia Lawall was invited to the Linux Kernel Summit as a core attendee (invitation only) in 2010 and 2014, and has been invited to the internal 2014 SUSE Labs Conference. She has also presented Coccinelle at developer events such as LinuxCon Europe, Kernel Recipes (Paris), FOSDEM (Brussels), and RTWLS, and has supervised three interns using Coccinelle financed by the Linux Foundation, as part of the Outreachy internship program.

Finally, we are aware of several companies that use Coccinelle for modernizing code bases. These include Metaware in Paris, with whom we had a 5-month contract in 2013-2014 for the customization and maintenance of Coccinelle. We hope to be able to organize other such contracts in the future.

6.1.2. Better Linux

Over the past few years, Julia Lawall and Gilles Muller have designed and developed of a number of tools such as Coccinelle, Diagnosys [23] [22] and Hector [64], to improve the process of developing and maintaining systems code. The BtrLinux action aims to increase the visibility of these tools, and to highlight Inria's potential contributions to the open source community. We are developing a web site https://btrlinux.inria.fr/, to centralize the dissemination of the tools, collect documentation, and collect results. This action is supported by Inria by the means of a young engineer (ADT), Quentin Lambert. In the case of Coccinelle, we will focus on enhancing its visibility and its dissemination, by using it to find and fix faults in Linux kernel code, and by submitting the resulting patches to the Linux maintainers. Our work on Diagnosys and Hector is described below.

Diagnosys is a hybrid static and dynamic analysis tool that first collects information about Linux kernel APIs that may be misused, and then uses this information to generate wrapper functions that systematically log at runtime any API invocations or return values that may reflect such misuse. A developer can then use a specific make-like command to build an executable driver that transparently uses these wrapper functions. At runtime, the wrappers write log messages into a crash resilient region of memory that the developer can inspect after any crash. Diagnosys is complementary to Coccinelle in the kind of information that it provides to developers. While Coccinelle directly returns a report for every rule match across the code base, often including false positives that have to be manually isolated by the developer, Diagnosys only reports on conditions that occur in the actual execution of the code. Diagnosys thus produces less information, but the information produced is more relevant to the particular problem currently confronting the developer. As such, it is well suited to the case of initial code development, where the code is changing frequently, and the developer wants to debug a specific problem, rather than ensuring that the complete code base is fault free. Diagnosys is a complete functioning system, but it needs to be kept up to date with changes in the kernel API functions. As part of the BtrLinux action, we will regularly run the scripts that collect information about how to create the wrappers, and then validate and make public the results.

Hector addresses the problem of leaking resources in error-handling code. Releasing resources when they are no longer needed is critical, so that adequate resources remain available over the long execution periods characteristic of systems software. Indeed, when resource leaks accumulate, they can cause unexpected resource unavailability, and even single leaks can put the system into an inconsistent state that can cause crashes and open the door to possible attacks. Nevertheless, developers often forget to release resources, because doing so often does not make any direct contribution to a program's functionality. A major challenge in detecting resource-release omission faults is to know when resource release is required. Indeed, the C language does not provide any built-in support for resource management, and thus resource acquisition and release are typically implemented using ad hoc operations that are, at best, only known to core developers.

---

[0] E.g., http://comments.gmane.org/gmane.linux.kernel.kbuild/269

Previous work has focused on mining sequences of such functions that are used frequently across a code base, [35], [51] but these approaches have very high rates of false negatives and false positives [48]. We have proposed Hector, a static analysis tool that finds resource-release omission faults based on inconsistencies in the operations performed within a single function, rather than on usage frequency. This strategy allows Hector to have a low false positive rate, of 23% in our experiments, while still being able to find hundreds of faults in Linux and other systems.

Hector was developed as part of the PhD thesis of Suman Saha and was presented at DSN 2013, where it received the William C. Carter award for the best student paper. Hector is complementary to Coccinelle, in that it has a more restricted scope, focusing on only one type of fault, but it uses a more precise static analysis, tailored for this type of fault, to ensure a low false positive rate. Hector, like Coccinelle, is also complementary to Diagnosys, in that it exhaustively reports on faults in a code base, rather than only those relevant to a particular execution, and is thus better suited for use by experienced developers of relatively stable software. Over 70 patches have been accepted into Linux based on the results of Hector. The current implementation, however, is somewhat in a state of disarray. As part of the BtrLinux action, we are currently working on returning the code to working condition and then will actively use it to find faults in Linux. Based on these results, we will either submit appropriate patches to the Linux developers or notify the relevant developer when the corresponding fix is not clear.

6.2. New Software

6.2.1. coq-bitset library

As part of Arthur Blot's internship, we have developed the `coq-bitset` library, a certified library implementing bitsets in the Coq proof assistant [17]. It enables abstract and formal reasoning about efficient low-level code within a proof assistant, thus paving the way for further certified results in the field of low-level system code (such as device drivers).

As part of this effort, we have also extended a pre-existing formalization of bit vectors in Coq [41] with a trustworthy extraction mechanism. This enables manipulating and reasoning about native integers in the Coq proof assistant, while supporting an efficient execution in OCaml.

Both libraries have been made available on Github as well as on the `Coq-opam` repository.

WILLOW Project-Team

6. New Software and Platforms

6.1. Visual Place Recognition with Repetitive Structures

A new version of the open-source release of the software package for visual localization in urban environments has been made publicly available in July 2015. The software package implements the method [A. Torii et al., CVPR 2013] (journal version published this year in [5]) for representing visual data containing repetitive structures (such as building facades or fences), which often occur in urban environments and present significant challenge for current image matching methods. This is an extended version that includes geometric verification. The first version was made available in 2013 and has been updated in May 2014. The current version of the software is available at http://www.di.ens.fr/willow/research/repttile/download/repttile_demo_ver04.zip.

6.2. NetVLAD: CNN architecture for weakly supervised place recognition

Open source release of the software package for our paper "NetVLAD: CNN architecture for weakly supervised place recognition" [21]. It provides a full implementation of the method, including code for weakly supervised training of the CNN representation, testing on standard datasets, as well as trained models. Links to all of these are available at our project page http://www.di.ens.fr/willow/research/netvlad/.

6.3. 24/7 place recognition by view synthesis

Open source release of the software package for our paper "24/7 place recognition by view synthesis" [16]. It provides code for computing VLAD descriptors, performing feature matching and view synthesis. Link to the code is available at our project page http://www.ok.ctrl.titech.ac.jp/~torii/project/247/.

6.4. Weakly Supervised Object Recognition with Convolutional Neural Networks

Open-source release of the software package for weakly supervised object recognition with convolutional neural networks has been made publicly available in May 2015. The software package implements the method [M. Oquab et al., CVPR 2015] [14] for object category recognition and localization using convolutional neural networks with weak supervision (without bounding box annotations). The method (i) outputs accurate image-level labels, (ii) predicts approximate locations (but not extents) of objects, and (iii) performs comparably to its fully-supervised counterparts using object bounding box annotation for training. The current version of the software is available at http://www.di.ens.fr/willow/research/weakcnn/.

6.5. Unsupervised Object Discovery and Localization in the Wild

This package contains source code for unsupervised object discovery and localizatoin from image collections. From an arbitrary collection of images in the wild, the method effectively discover dominant object instances and localize them by bounding boxes. The localization accuracy of discovered objects measured at standard benchmarks for object localization is significantly better than the state-of-the-art methods in co-localization, while using no supervision on image collections. The package is available from http://www.di.ens.fr/willow/research/objectdiscovery/.

6.6. Joint Static and Dynamic Guidance Filter

Open-source release of the software package for depth upsampling, texture removal, and scale-space filtering has been made publicly available. The software package implements the newly developed method [10] for robust filtering with joint static and dynamic guidance. The software is available at http://www.di.ens.fr/willow/research/sdfilter/.

WIMMICS Project-Team

6. New Software and Platforms

6.1. CORESE

KEYWORDS: Semantic Web - Web of Data - RDF - SPARQL
FUNCTIONAL DESCRIPTION

Corese is a Semantic Web Factory, it implements W3C recommandations such as RDF, RDFS, SPARQL 1.1 Query and Update. It provides an Inference Rule language, a Transformation Language for RDF graphs and a function language on top of SPARQL. Furthermore, Corese integrates original features such as approximate search and extended Property Path. It also provides distributed federated query processing (cooperation with Johan Montagnat, I3S).

- Participants: Olivier Corby, Erwan Demairy, Fuqi Song.
- Partners: I3S, Mnemotix
- Contact: Olivier Corby
- URL: http://wimmics.inria.fr/corese

6.2. DBpedia

KEYWORDS: French chapter of DBpedia
FUNCTIONAL DESCRIPTION

DBpedia is an international crowd-sourced community effort to extract structured information from Wikipedia and make this information available on the semantic Web as linked open data. The DBpedia triple stores then allow anyone to solve sophisticated queries against Wikipedia extracted data, and to link the different data sets on these data. The French chapter of DBpedia was created and deployed by Wimmics and is now an online running platform providing data to several projects such as: QAKIS, Izipedia, zone47, Sépage, HdA Lab., JocondeLab, etc.

- Participants: Raphaël Boyer and Fabien Gandon
- Contact: Fabien Gandon
- URL: http://fr.dbpedia.org

6.3. Discovery Hub

KEYWORD: Search Engine
FUNCTIONAL DESCRIPTION

Discovery Hub is an Exploratory Search Engine on top of DBpedia.

- Participants: Nicolas Marie, Fabien Gandon, Emilie Palagi and Alain Giboin
- Partner: Alcatel-Lucent
- Contact: Fabien Gandon
- URL: http://discoveryhub.co

6.4. QAKiS

KEYWORD: Natural Language Question Answering
FUNCTIONAL DESCRIPTION Question-Answening wiki framework based system

The QAKiS system implements question answering over DBpedia. QAKiS allows end users to submit a query to an RDF triple store in English and obtain the answer in the same language, hiding the complexity of the non-intuitive formal query languages involved in the resolution process. At the same time, the expressiveness of these standards is exploited to scale to the huge amounts of available semantic data. Its major novelty is to implement a relation-based match for question interpretation, to convert the user question into a query language (e.g. SPARQL). English, French and German DBpedia chapters are the RDF data sets to be queried using a natural language interface.

- Participants: Elena Cabrio, Amine Hallili (SynchroNext), Alessio Palmero Aprosio (FBK Italy), Fabien Gandon and Serena Villata
- Contact: Elena Cabrio
- URL: http://www.qakis.org/

ZENITH Project-Team

6. New Software and Platforms

6.1. Hadoop_g5k

Participants: Reza Akbarinia, Miguel Liroz-Gistau, Patrick Valduriez.

URL: https://www.grid5000.fr/mediawiki/index.php/Hadoop_On_Execo

Apache Hadoop provides an open-source framework for reliable, scalable, parallel computing. It can be deployed and used in large-scale platforms such as Grid 5000. However, its configuration and management is very difficult, specially under the dynamic nature of clusters. Therefore, we built Hadoop_g5k (Hadoop easy deployment in clusters), a tool that makes it easier to manage Hadoop clusters and prepare reproducible experiments. Hadoop_g5k offers a set of scripts to be used in command-line interfaces and a Python interface. It is actually used by Grid5000 users, and helps them saving much time when doing their experiments with MapReduce.

6.2. LogMagnet

Participants: Julien Diener, Florent Masseglia.

URL: https://team.inria.fr/zenith/software/LogMagnet

LogMagnet is a software for analyzing streaming data, and in particular log data. Log data usually arrive in the form of lines containing activities of human or machines. In the case of human activities, it may be the behavior on a Web site or the usage of an application. In the case of machines, such log may contain the activities of software and hardware components (say, for each node of a computing cluster, the calls to system functions or some hardware alerts). Analyzing such data is often difficult and crucial in the meanwhile. LogMagnet allows to summarize this data, and to provide a first analysis as a clustering. This summary may also be exploited as easily as the original data.

6.3. MultiSite-Rec

Participants: Mohamed Reda Bouadjenek, Florent Masseglia, Esther Pacitti.

Recommender systems are used as a mean to supply users with content that may be of interest to them. They have become a popular research topic, where many aspects and dimensions have been studied to make them more accurate and effective. In practice, recommender systems suffer from cold-start problems. However, users use many online services, which can provide information about their interest and the content of items (e.g. Google search engine, Facebook, Twitter, etc). These services may be valuable data sources, which supply information to help a recommender system in modeling users and items' preferences, and thus, make the recommender system more precise. Moreover, these data sources are distributed, and geographically distant from each other, which raise many research problems and challenges to design a distributed recommendation algorithm. MultiSite-Rec is a distributed collaborative filtering algorithm, which exploits and combine these multiple and heterogeneous data sources to improve the recommendation quality.

6.4. ThePlantGame: crowdsourced plants identification

Participants: Maximilien Servajean [contact], Alexis Joly, Julien Champ.

URL: http://theplantgame.com/

The Plant Game is a participatory game whose purpose is the production of large masses of taxonomic data to improve our knowledge of biodiversity. The interest of the game is twofold: (i) train and progress in botany while having fun, and (ii) participate to a large citizen sciences project in biodiversity. The game relies on consistent scientific contributions compared to classical crowdsourcing models and algorithms that are not scalable to classification problems with thousands of complex classes such as plant species. The most remarkable one is the active training of the users based on innovative sub-task creation and assignment processes that are adaptive to the increasing skills of the user. The first public version of the game was released in July 2015. Nowadays, about 1000 players are registered and produce on average about 35 new validated plant observations per day. The accuracy of the produced taxonnomic tags is about 94%, which is quite impressive considering the fact that a majority of users are beginners when they start playing.

6.5. Pl@ntNet

Participants: Julien Champ, Hervé Goëau, Alexis Joly.

URL: http://goo.gl/CpSrr3

Pl@ntNet is an image sharing and retrieval application for the identification of plants. It is developed in the context of the Floris'tic project that involves four French research organisations (Inria, Cirad, INRA, IRD) and Tela Botanica social network. The key feature of the iOS and Android front ends is to help identifying plant species from photographs, through a server-side visual search engine based on several results of ZENITH team on content-based information retrieval. Since its first release in March 2013 on the apple store, the application was downloaded by around 1M users in more than 170 countries (between 2,500 and 10,000 active users daily with peaks occurring during the week-ends). The collaborative training set that allows the content-based identification is continuously enriched by the users of the application and the members of Tela Botanica social network. At the time of writing, it includes about 200K images covering more than 5000 French plant species about 4/5 of the whole French flora (this is actually the widest identification tool built anytime).

6.6. Snoop & SnoopIm

Participants: Alexis Joly, Julien Champ, Jean-Christophe Lombardo.

URL: http://otmedia.lirmm.fr/

Snoop is a generalist C++ library dedicated to high-dimensional data management and efficient similarity search. Its main features are dimension reduction, high-dimensional feature vectors hashing, approximate k-nearest neighbors search and Hamming embedding. Snoop is a refactoring of a previous library called PMH developed jointly with the French National Institute of Audiovisual. It is based on the joined research work of Alexis Joly and Olivier Buisson. SnoopIm is a content-based image search engine built on top of Snoop and allowing to retrieve small visual patterns or objects in large collections of pictures. The software is being experimented/used in several contexts including a logo retrieval application set up in collaboration with INA (DigInPix: http://diginpix.ina.fr), a whale's individuals matching application set up in collaboration with CetaMada NGO (IdentyWhale, to be publicly released soon), a hieroglyphs recognition application currently under development in collaboration with the Egyptology department of Montpellier University Paul-Valéry.

6.7. SciFloware

Participants: Dimitri Dupuis, Didier Parigot.

URL: http://www-sop.inria.fr/members/Didier.Parigot/pmwiki/Scifloware

SciFloware is an action of technology development (ADT Inria) with the goal of developing a middleware for the execution of scientific workflows in a distributed and parallel way. It capitalizes on our experience with SON and an innovative algebraic approach to the management of scientific workflows. SciFloware provides a development environment and a runtime environment for scientific workflows, interoperable with existing systems. We validate SciFloware with workflows for analyzing biological data provided by our partners CIRAD, INRA and IRD.

6.8. CloudMdsQL Compiler

Participants: Carlyna Bondiombouy, Boyan Kolev, Oleksandra Levchenko, Patrick Valduriez.

URL: http://cloudmdsql.gforge.inria.fr

The CloudMdsQL (Cloud Multi-datastore Query Language) compiler transforms queries expressed in a common SQL-like query language into an optimized query execution plan to be executed over multiple cloud data stores (SQL, NoSQL, HDFS, etc.) through a query engine. The compiler/optimizer is implemented in C++ and uses the Boost.Spirit framework for parsing context-free grammars. CloudMdsQL is being validated on relational, document and graph data stores in the context of the CoherentPaaS European project.

6.9. Chiaroscuro

Participants: Tristan Allard, Florent Masseglia, Esther Pacitti.

URL: http://people.irisa.fr/Tristan.Allard/chiaroscuro/

Chiaroscuro is a software developped in the context of a research contract with EDF. It aims at clustering time series with privacy preserving guarantees. It is a distributed system, working in a P2P environment. It is used by the team for experiments and by EDF as a proof-of-concept. Chiaroscuro is the first software for that purpose. It is written in Java. The distributed algorithm implemented in Chiaroscuro has been filed by EDF in a patent (with Inria and University of Montpellier)

6.10. FP-Hadoop

Participants: Reza Akbarinia, Miguel Liroz, Patrick Valduriez.

https://gforge.inria.fr/plugins/mediawiki/wiki/fp-hadoop

FP-Hadoop is an extension of Hadoop that efficiently deals with the problem of data skew in MapReduce jobs. In FP-Hadoop, there is a new phase, called intermediate reduce (IR), in which blocks of intermediate values, constructed dynamically, are processed by intermediate reduce workers in parallel, by using a scheduling strategy.