RESEARCH CENTER

FIELD

Activity Report 2016

Section Software

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ABS Project-Team

5. New Software and Platforms

5.1. The Structural Bioinformatics Library

5.1.1. The SBL : overview

The `SBL` (http://sbl.inria.fr) is a generic C++/python library providing algorithms and applications to solve complex problems in computational structural biology (CSB). [20].

For Biologists, the key advantages are:

- comprehensive in silico environment providing software applications,
- answering complex bio-physical problems (modeling interfaces and contacts, modeling the flexibility of proteins, and modeling macro-molecular assemblies),
- 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.

5.1.2. 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.

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[0] The design has been guided by that used in the Computational Geometry Algorithm Library (CGAL), see http://www.cgal.org

5.1.3. 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.

5.1.4. 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.

5.1.5. The SBL for low-level developers and contributors: SBL-CORE, and SBL-MODELS

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 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.

5.1.6. 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 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/).

5.1.7. 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 Project-Team

6. New Software and Platforms

6.1. 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 visualisation 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 project-team 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 visualisation of building performances (heat, structural) in relation to the Building Information Modeling BIM framework.

AIRSEA Project-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 and Cyril Mazauric
- 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. DiceDesign

Designs of Computer Experiments
FUNCTIONAL DESCRIPTION

This package is useful for conducting design and analysis of computer experiments.

- Contact: Céline Hartweg
- URL: https://cran.r-project.org/web/packages/DiceDesign/index.html

6.4. DiceEval

Construction and Evaluation of Metamodels
FUNCTIONAL DESCRIPTION

This package is useful for conducting design and analysis of computer experiments. Estimation, validation and prediction of models of different types : linear models, additive models, MARS,PolyMARS and Kriging.

- Contact: Céline Hartweg
- URL: https://cran.r-project.org/web/packages/DiceEval/index.html

6.5. 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

6.6. 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

ALICE Project-Team

6. New Software and Platforms

6.1. GEOGRAM

GEOGRAM : A functions library for geometric programming
KEYWORD: 3D modeling
GEOGRAM is a programming library with a set of basic geometric algorithms, such as search data structures (AABB tree, Kd tree), geometric predicates, triangulations (Delaunay triangulation, Regular triangulation), intersection between a simplicial mesh and a Voronoi diagram (restricted Voronoi diagram). GEOGRAM also includes a code generator for predicates (PCK: Predicate Construction Kit) and an efficient implementation of expansion arithmetics in arbitrary precision. GEOGRAM is shipped with WARPDRIVE, the first program that computes semi-discrete optimal transport in 3D.

- Participant: Bruno Lévy
- Contact: Bruno Lévy
- URL: http://alice.loria.fr/software/geogram/doc/html/index.html

6.2. GLE

GraphiteLifeExplorer
KEYWORDS: 3D modeling - Biology
GLE is a 3D modeler, developed as a plugin of Graphite, dedicated to molecular biology. 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 for fine-tuning of atoms position and, most importantly, exports to PDB (the Protein Daba Bank file format).

- Participant: Samuel Hornus
- Partner: Fourmentin Guilbert foundation
- Contact: Samuel Hornus
- URL: https://members.loria.fr/samuel.hornus/FFG/gle.html

6.3. Graphite

Graphite: The Numerical Geometry Workbench
KEYWORDS: 3D modeling - Numerical Geometry - Texturing - Lighting - CAD - Visualization
Graphite is an experimental 3D modeler, built on 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 a dedicated software platform in numerical geometry that enables, among other things, 3D modelling and texture baking.

- Participants: Dobrina Boltcheva, Samuel Hornus, Bruno Lévy, David Lopez, Jeanne Pellerin and Nicolas Ray
- Contact: Bruno Lévy
- URL: http://alice.loria.fr/software/graphite

6.4. IceSL

The software allows us to modelize throught CSG's operations 3D's objects. These objects can be directly prepared to be send through a 3d printer without forming an intermediary mesh.

- Participants: Sylvain Lefebvre, Jérémie Dumas, Jean Hergel, Frederic Claux, Jonas Martinez Bayona and Samuel Hornus
- Contact: Sylvain Lefebvre
- URL: http://shapeforge.loria.fr/icesl

6.5. LibSL

LibSL: Simple Library For Graphics
LibSL is a toolbox for rapid prototyping of computer graphics algorithms, under both OpenGL, DirectX 9/10, Windows and Linux.

- Participant: Sylvain Lefebvre
- Contact: Sylvain Lefebvre
- URL: http://members.loria.fr/Sylvain.Lefebvre/libsl

6.6. OpenNL

OpenNL: Open Numerical Library
KEYWORDS: 3D modeling - Numerical algorithm
SCIENTIFIC DESCRIPTION

Open Numerical Library is a library for solving sparse linear systems, especially designed for the Computer Graphics community. The goal of OpenNL is to be as small as possible, while offering the subset of functionalities required by this application field. The Makefiles of OpenNL can generate a single .c + .h file, very easy to integrate in other projects. The distribution includes an implementation of the Least Squares Conformal Maps parameterization method.

- Participants: Bruno Lévy, Rhaleb Zayer and Nicolas Ray
- Contact: Bruno Lévy
- URL: http://alice.loria.fr/index.php/software/4-library/23-opennl.html

6.7. VORPALINE

VORPALINE mesh generator
KEYWORDS: 3D modeling - Unstructured heterogeneous meshes
VORPALINE is a surfacic and volumetric mesh generator, for simplicial meshes (triangles and tetrahedra), for quad-dominant and hex-dominant meshes.

- Participant: Bruno Lévy
- Contact: Bruno Lévy
- URL: http://alice.loria.fr/index.php/erc-vorpaline.html

ALPAGE Project-Team

5. New Software and Platforms

5.1. Alexina

Atelier pour les LEXiques INformatiques et leur Acquisition
FUNCTIONAL DESCRIPTION

Alexina is Alpage's 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/

5.2. 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 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, Djame Seddah and Benoît Crabbe
- Contact: Marie-Hélène Candito
- URL: http://alpage.inria.fr/statgram/frdep/fr_stat_dep_parsing.html

5.3. 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: Djame Seddah

5.4. 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: Eric Villemonte De La Clergerie
- Contact: Eric Villemonte De La Clergerie
- URL: http://dyalog.gforge.inria.fr/

5.5. FDTB1

- Contact: Laurence Danlos

5.6. 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: Djame Seddah

5.7. FRMG

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

5.8. Extreme UGC corpus

FUNCTIONAL DESCRIPTION

The Extreme UGC corpus is French three-domain data set focusing on user-generated content, made up of noisy question headlines from a cooking forum, live game chat logs and associated forums from two popular online games (MINECRAFT and LEAGUE OF LEGENDS). Building such an out of domain corpus, allowed us to consider the limits of our current normalization approaches. Currently annotated with part-of-speech, we plan to add other annotations layers.

- Contact: Djame Seddah

5.9. LexConn

- Contact: Laurence Danlos

5.10. LexViz

FUNCTIONAL DESCRIPTION

In the context of the industrial collaboration of ALPAGE with the company Lingua & 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: Eric Villemonte De La Clergerie and Mickaël Morardo
- Contact: Eric Villemonte De La Clergerie

5.11. 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

5.12. 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: Eric Villemonte De La Clergerie and Paul Bui-Quang
- Contact: Eric Villemonte De La Clergerie
- URL: http://alpage.inria.fr/frmgwiki/

5.13. 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 designed for the analysis and manipulation of attributed oriented and multi-relational graphs. Itis currently being used to convert existing universal dependencies for French to the upcoming 2.0 scheme to be used for the next "big" CoNLL parsing Shared Task of 2017.

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

5.14. 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/

5.15. 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: Djame Seddah

5.16. 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, Eric Villemonte De La Clergerie and Djame Seddah
- Contact: Benoît Sagot
- URL: http://lingwb.gforge.inria.fr/

5.17. Verb∋net

- Contact: Laurence Danlos

5.18. dyalog-sr

KEYWORD: Parsing
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

5.19. hyparse

Alpage Hybrid Parser
KEYWORDS: Parsing - NLP
FUNCTIONAL DESCRIPTION

Multilingual Phrase Structure Parser

- Contact: Benoît Crabbe
- URL: http://hyparse.gforge.inria.fr

5.20. vera

- Participants: Benoît Sagot and Dimitri Tcherniak
- Partner: Verbatim Analysis
- Contact: Benoît Sagot

ALPINES Project-Team

6. New Software and Platforms

6.1. BFD

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, Remi Lacroix and Frédéric Nataf
- Partners: CNRS - UPMC
- Contact: Laura Grigori
- URL: https://who.rocq.inria.fr/Laura.Grigori/

6.2. CALU : communication optimal algorithms for linear algebra

KEYWORDS: Communication avoiding - Linear algebra
FUNCTIONAL DESCRIPTION

CALU solves linear systems of equations Ax=b using Communication Avoiding LU.

- Contact: Laura Grigori
- URL: https://who.rocq.inria.fr/Laura.Grigori/

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/

6.4. 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 2^d-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: Frédéric Hecht
- URL: http://www.freefem.org/ff++/

6.5. 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
- URL: https://github.com/hpddm

6.6. LORASC

LORASC preconditioner

KEYWORD: Preconditioner

- Participants: Laura Grigori and Remi Lacroix
- Contact: Laura Grigori
- URL: not available

6.7. NFF

NFF Nested Filtering Factorization

KEYWORDS: Preconditioner - Interactive method - Linear system

- Participants: Laura Grigori, Frédéric Nataf and Long Qu
- Partners: Université Paris-Sud - UPMC
- Contact: Laura Grigori
- URL: not available

6.8. SparseToolbox

KEYWORDS: Preconditioner - Interactive method - Linear system

- Participants: Laura Grigori and Remi Lacroix
- Contact: Laura Grigori
- URL: not available

AMIB Project-Team

4. New Software and Platforms

4.1. GenRGenS

GENeration of Random GENomic Sequences
KEYWORDS: Bioinformatics - Genomic sequence
FUNCTIONAL DESCRIPTION

A software dedicated to the random generation of sequences. Supports different lasses of models, including weighted context-free grammars, Markov models, ProSITE patterns..

- Participants: Yann Ponty and Alain Denise
- Contact: Yann Ponty
- URL: https://www.lri.fr/~genrgens/

4.2. VARNA

Interactive drawing and editing of the RNA secondary structure
KEYWORDS: Bioinformatics - Structural Biology
SCIENTIFIC DESCRIPTION

VARNA is Java lightweight Applet dedicated to drawing the secondary structure of RNA. It is also a Swing component that can be very easily included in an existing Java code working with RNA secondary structure to provide a fast and interactive visualization.

Being free of fancy external library dependency and/or network access, the VARNA Applet can be used as a base for a standalone applet. It looks reasonably good and scales up or down nicely to adapt to the space available on a web page, thanks to the anti-aliasing drawing primitives of Swing.
FUNCTIONAL DESCRIPTION

Varna is a new tool for the automated drawing, visualization and annotation of the secondary structure of RNA, designed as a companion software for web servers and databases.

Varna implements four drawing algorithms, supports input/output using the classic formats dbn, ct, bpseq and RNAML and exports the drawing as five picture formats, either pixel-based (JPEG, PNG) or vector-based (SVG, EPS and XFIG).

It also allows manual modification and structural annotation of the resulting drawing using either an interactive point and click approach, within a web server or through command-line arguments.

- Participants: Alain Denise and Yann Ponty
- Partners: CNRS - Ecole Polytechnique - Université Paris-Sud
- Contact: Yann Ponty
- URL: http://varna.lri.fr/

ANGE Project-Team

6. New Software and Platforms

6.1. Freshkiss3D (FREe Surface Hydrodynamics using KInetic SchemeS)

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

- Participants: Nora Aïssiouene, Marie-Odile Bristeau, David Froger, Jacques Sainte-Marie, Fabien Souillé
- Formerly: Emmanuel Audusse, Anne-Céline Boulanger, Alain Dervieux, Raouf Hamouda, Bijan Mohammadi
- Partners: CEREMA – UPMC
- Contact: Jacques Sainte-Marie

A review of last developments is given in § 7.5.1 . See [20] for recent numerical results obtained thanks to the Freshkiss3D software.

6.2. TSUNAMATHS

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

ANJA Team

5. New Software and Platforms

5.1. New Software

5.1.1. Law

In order for our research to become used in a non-technological domain as is law, we make special efforts to develop user-friendly software tools. We have already made available an iOS application for computing the amount of child support. Another application is currently being developed for spousal support.

Future user-friendly software we intend to propose will be concerned with the areas of personal injury and intellectual property.

5.1.2. Economy and finance

The software toolbox FracLab (http://fraclab.saclay.inria.fr) contains a number of tools related to multistable processes, including their simulation and calibration. We intend to pursue these developments in particular by proposing methods dealing with self-stabilizing processes.

We also hope to be able to collaborate with financial institutions, in view of advancing the idea that current regulations, because they are model-based, perform the economy in a way that needs to be carefully scrutinized.

5.1.3. Archaeology

Our software ChronoModel provides a set of Bayesian statistical tools for constructing chronologies using measurement coming from different dating methods (e.g. 14C, TL/OSL, AM, typo-chronology). Chronomodel is a free and open-source cross-platform software that can be downloaded at http://www.chronomodel.fr

It offers a user-friendly interface for entering both data and archaeological facts : stratigraphy, temporal order constraints, contemporaneous events.

ChronoModel is currently used by researchers in laboratories of archaeology and earth science, and also by archaeologists working in the organizations of rescue archaeology.

ANTIQUE Project-Team

6. New Software and Platforms

6.1. 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/

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

6.3. 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/

6.4. 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

6.5. 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

6.6. 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

6.7. 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/

6.8. 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

6.9. 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

6.10. 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

6.11. 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/

6.12. DAFT

DAFT

FUNCTIONAL DESCRIPTION

DAFT is a distributed file management system in user-space, with a command-line interface. DAFT is intended at computational scientists, involved in data-intensive, distributed experiments and when no distributed filesystem is available on computing nodes. DAFT is secure; all messages are cryptographically signed and encrypted by default.

- Participants: Francois Berenger and Camille Coti.
- Contact: Francois Berenger and Camille Coti.
- URL: https://github.com/UnixJunkie/daft.

AOSTE Project-Team

5. New Software and Platforms

5.1. EVT Kopernic

Extreme Value Theory for Keeping Worst Reasoning Appropriate for Different Criticalities
FUNCTIONAL DESCRIPTION This software provides a probabilistic bound on the worst case execution time of a program. Its third version, released in March 2016, covers the case of statistically dependent execution times. Currently integrated in Rapitime (Rapita tool chain), a lighter version is under preparation for integration in FUI Waruna framework as well as in the preparation of hybrid versions to be released in 2017 as output of Capacites project.

- Participants: Liliana Cucu and Adriana Gogonel
- Contact: Liliana Cucu
- URL: https://who.rocq.inria.fr/Liliana.Cucu/Software.html

5.2. KPASSA

K-Periodic Asap Static Schedule Analyser
FUNCTIONAL DESCRIPTION This software is dedicated to the simulation, analysis, and static scheduling of Event/Marked Graphs, SDF and KRG extensions. A graphical interface allows to edit the Process Networks and their time annotations (latency, ...). Symbolic simulation and graph-theoretic analysis methods allow to compute and optimize static schedules, with best throughputs and minimal buffer sizes. In the case of KRG the (ultimately k-periodic) routing patterns can also be provided and transformed for optimal combination of switching and scheduling when channels are shared. KPASSA also allows for import/export of specific description formats such as UML-MARTE, to and from our other TimeSquare tool.

- Participants: Jean Vivien Millo and Robert De Simone
- Contact: Robert de Simone
- URL: http://www-sop.inria.fr/members/Jean-Vivien.Millo/kpassa/index.php

5.3. Lopht

Logical to Physical Time Compiler
SCIENTIFIC DESCRIPTION Lopht is a system-level compiler for embedded systems. Its input is formed of three objects:

- A functional specification in a high-level synchronous language.
- A description of the implementation platform, defining the topology of the parallel execution platform, and the capacity of its elements.
- A set of non-functional requirements, provided under the form of annotations on both functional specification and platform description.

The algorithmic core of Lopht is formed of allocation and scheduling heuristics which rely on two fundamental choices: the use of table-based static scheduling and the use of low-complexity heuristics based on list scheduling. The output of Lopht is formed of all the C code and configuration information needed to allow real deployment on the physical target platform.

FUNCTIONAL DESCRIPTION Accepted input languages for functional specifications include Heptagon and Scade v4. Lopht uses as f ront-end a modified version of the Heptagon compiler developed at Inria. The use of this front-end also allows the use of legacy/business C code satisfying the Heptagon calling convention.

Regarding scheduling, the originality of Lopht resides in a strong focus on classical compiler optimizations e.g. software pipelining), on novel architectural targets (many-core chips and time-triggered embedded systems), and the possibility to handle multiple, complex non-functional requirements covering real-time (release dates a nd deadlines possibly larger than the period, end-to-end flow constraints), ARINC 653 partitioning, the possibility to preempt or not each task, and allocation.
The output of Lopht is formed of all the C code and configuration information needed to allow compilation, linking/loading, and real-time execution on the target platform. Lopht fully automates the creation of tasks, partition, the full synthesis of C code compliant with the target API (e.g. C/APEX for ARINC 653 platforms), including communication code, and OS configuration for each computer), as well as the synthesis of communication schedules for the system

Two Lopht back-ends provide distinct input languages for platform description:

- One for distributed time-triggered architectures using ARINC 653-based processing nodes (SBCs) and Time-Triggered Ethernet networks
- One for many-core processors with support with timing predictability.

An ongoing research effort aims at providing a unified, formal platform description language allowing the unification of these back-ends.

- Participants: Dumitru Potop Butucaru, Raul Gorcitz, and Keryan Didier
- Contact: Dumitru Potop Butucaru

5.4. 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/

5.5. 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 and Meriem Zidouni
- URL: http://www.syndex.org

5.6. 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: Frederic Mallet, and Julien Deantoni
- Contact: Frederic Mallet
- URL: http://timesquare.inria.fr

5.7. Vercors

KEYWORD:

- Participants: Eric Madelaine, Oleksandra Kulankhina, Jimmy Awk, Xudong Qin
- Contact: Eric Madelaine
- URL: http://www-sop.inria.fr/oasis/Vercors

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.

We have achieved this year a major version of the platform frontend, named VCE-v4, that is now distributed on our website, and used by some of our partners. This version features a full chain of tools from the design of systems in the graphical component editors (VCE), the checking of static semantics correcteness, the generation of a semantic model suitable for model-checking, and finally the generation of executable code for the Proactive/GCM platform. These new features, and the tool architecture, have been described in [29] and [18].

APICS Project-Team (section vide)

ARAMIS Project-Team

6. New Software and Platforms

6.1. Clinica

KEYWORDS: Multimodal neuroimaging - anatomical MRI - diffusion MRI - functional MRI - PET - EEG/MEG

FUNCTIONAL DESCRIPTION

Clinica is a software platform for multimodal brain image analysis in clinical research studies. It aims at integrating a comprehensive set of processing tools for the main neuroimaging modalities: MRI (anatomical, functional, diffusion), PET and EEG/MEG. For each modality, it allows to easily extract various types of features (regional measures, parametric maps, surfaces, curves, networks) that can be subsequently used as input of machine learning, statistical modeling, morphometry or network analysis methods. Processing pipelines are based on combinations of freely available tools developed by the community and in-house developments. It provides an integrated data management system to store raw and processing data.

- Participants: Olivier Colliot, Stanley Durrleman, Fabrizio De Vico Fallani, Michael Bacci, Alexandre Routier, Jorge Samper-Gonzalez, Junhao Wen, Jérémy Guillon, Sabrina Fontanella, Thomas Jacquemont
- Contact: Olivier Colliot

6.2. 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

6.3. 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, Cedric Doucet, Michael Bacci and Barbara Gris
- Partners: Université de Montpellier 2 - Université Paris-Descartes - University of Utah
- Contact: Stanley Durrleman
- URL: http://www.deformetrica.org/

6.4. 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

6.5. 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

6.6. 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

ARIC Project-Team

5. New Software and Platforms

5.1. FPLLL

SCIENTIFIC DESCRIPTION

The fplll library is used or has been adapted to be integrated within several mathematical computation systems such as Magma, Sage, and PariGP. It is also used for cryptanalytic purposes, to test the resistance of cryptographic primitives.

FUNCTIONAL DESCRIPTION

fplll contains implementations of several lattice algorithms. The implementation relies on floating-point orthogonalization, and the LLL algorithm is central to the code, hence the name. It includes implementations of floating-point LLL reduction algorithms, offering different speed/guarantees ratios. It further includes an implementation of the BKZ reduction algorithm and variants thereof. It includes an implementation of the Kannan-Fincke-Pohst algorithm that finds a shortest non-zero lattice vector. For the same task, the GaussSieve algorithm is also available. Finally, it contains a variant of the enumeration algorithm that computes a lattice vector closest to a given vector belonging to the real span of the lattice.

- Participants: Martin Albrecht, Shi Bai, Guillaume Bonnoron, Léo Ducas, Damien Stehlé and Marc Stevens
- Contact: Damien Stehlé
- URL: https://github.com/fplll/fplll

5.2. HPLLL

hplll is an experimental C++ library companion to fplll.

FUNCTIONAL DESCRIPTION

hplll provides a specific LLL reduction algorithm using Householder orthogonalization, and HPC preliminary solutions especially for integer relation finding.

- Contact: Gilles Villard
- URL: http://perso.ens-lyon.fr/gilles.villard/hplll

5.3. 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.

There have been two new releases in 2016: 3.1.4 and 3.1.5. An MPFR-MPC developers meeting took place on 23 and 24 May 2016.

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

5.4. Gfun

A Maple package for solutions of linear differential or recurrence equations

FUNCTIONAL DESCRIPTION

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

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

5.5. Sipe

KEYWORDS: Floating-point - Correct Rounding

FUNCTIONAL DESCRIPTION

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. The currently supported operations are addition, subtraction, multiplication (possibly with the error term), fused multiply-add/subtract (FMA/FMS), and miscellaneous comparisons and conversions. Sipe provides two implementations of these operations, with the same API and the same behavior: one based on integer arithmetic, and a new one based on floating-point arithmetic.

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

5.6. 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.

- Participants: Clément Pernet, Gilles Villard
- Contact: Clément Pernet
- URL: http://www.linalg.org

AROMATH Project-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).

ASAP Project-Team

5. New Software and Platforms

5.1. Asapknn (MediEgo)

KEYWORDS: Widget web - Social network - Recommendation
FUNCTIONAL DESCRIPTION

Asapknn (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, Sebastien Campion, Rachid Guerraoui, Davide Frey and Arnaud Jegou
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Sebastien Campion

5.2. 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: Raziel Carvajal Gomez

5.3. 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 P2P-AllYours.

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

5.4. 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/

5.5. HEAP

Heterogeneity-aware gossip protocol

FUNCTIONAL DESCRIPTION

A video streaming platform based on HEAP. The platform is particularly suited for environment characterized by heterogeneous bandwidth capabilities such as those comprising ADSL edge nodes. HEAP is, in fact, able to dynamically leverage the most capable nodes and increase their contribution to the protocol, while decreasing by the same proportion that of less capable nodes. During the last few months, we have integrated HEAP with the ability to dynamically measure the available bandwidth of nodes, thereby making it independent of the input of the user.

- Participants: Davide Frey, Arnaud Jegou, Anne-Marie Kermarrec, Vivien Quema, Maxime Monod and Rachid Guerraoui
- Contact: Davide Frey

5.6. HyRec

Hybrid Recommender System

FUNCTIONAL DESCRIPTION

The motivation of this work is to explore solutions that could in some sense democratize personalization by making it accessible to any content provider company without generating huge investments. HyRec implements a user-based collaborative filtering scheme and offloads CPU-intensive recommendation tasks to front-end client browsers, while retaining storage and orchestration tasks within back-end servers. HyRec seeks to provide the scalability of p2p approaches without forcing content providers to give up the control of the system.

- Participants: Antoine Boutet, Davide Frey, Anne Marie Kermarrec, Arnaud Jegou and Rachid Guerraoui
- Contact: Davide Frey

5.7. WebGC

Web-based Gossip Communication

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

5.8. 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

5.9. 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, P2P-AllYours, and Behave.

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

5.10. 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 P2P-AllYours.
- 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. 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/

5.2. 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.

- Participants: Jaime Garcia Guevara, Theodore Papadopoulo, Olivier Commowick, Rene-Paul Debroize, Guillaume Pasquier, Laurence Catanese, Olivier Commowick, Alexandre Abadie, Benoit Bleuze, Clement Philipot, Fatih Arslan, Florian Vichot, John Stark, Julien Wintz, Loïc Cadour, Maxime Sermesant, Michael Knopke, Nicolas Toussaint, Olivier Clatz, Pierre Fillard, Sergio Medina, Stephan Schmitt and Hakim Fadil
- Partners: HARVARD Medical School - IHU LIRYC - King's College London - UPF Barcelona - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

5.3. MUSIC

Multi-modality Platform for Specific Imaging in Cardiology

KEYWORDS: Health - Cardiac - Computer-assisted interventions - Cardiac Electrophysiology - Medical imaging

FUNCTIONAL DESCRIPTION

MUSIC is a software 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.

- Participants: Loïc Cadour, Maxime Sermesant, Florian Vichot, Hakim Fadil, Florent Collot and Mathilde Merle
- Contact: Maxime Sermesant
- URL: https://team.inria.fr/asclepios/software/music/

5.4. 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.

A software consortium around SOFA is currently being set up to strengthen the perenial developement of the plateform https://www.sofa-framework.org/consortium/. The software is available under the LGPL licence.

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

5.5. VP2HF

Virtual Physiological Human for Heart Failure Platform

KEYWORDS: Health - Cardiac - Medical - Image - Processing - Medical imaging

FUNCTIONAL DESCRIPTION

The 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, KCL, and specific tools provided by Philips (algorithms of segmentation, scar segmentation, ...). 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 Loïc Cadour
- Contact: Maxime Sermesant
- URL: http://www.vp2hf.eu

ASCOLA Project-Team

6. New Software and Platforms

6.1. 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 Yousri Kouki
- Contact: Thomas Ledoux
- URL: http://www.emn.fr/z-info/csla/

6.2. CSQL

Cryptographic Composition for Query Language

SCIENTIFIC DESCRIPTION

C2QL is a compositional language of security techniques for information privacy in the cloud. A cloud service can use security techniques to ensure information privacy. These techniques protect privacy by converting the client's personal data into unintelligible text. But they also cause the loss of some functionalities of the service. As a solution, CSQL permits to compose security techniques to ensure information privacy without the loss of functionalities. But, the composition makes the writing of programs more intricate. To help the programmer, C2QL defines a query language for the definition of cloud services that enforces information privacy with the composition of security techniques. This language comes with a set of algebraic laws to, systematically, transform a local service without protection into its cloud equivalent that is protected by composition.

FUNCTIONAL DESCRIPTION

C2QL is implemented in Idris, a functional language of the Haskell family. The implementation harnesses the Idris dependant type system to ensure the correct composition of security mechanisms and provides a transformation of the implementation into a π-calculus. This transformation serves two purposes. First, it makes the distribution explicit, showing how a computation is distributed over SaaS, PaaS and client applications. Then, it helps defining an encoding into ProVerif to check that the service preserves the privacy of its clients.

- Participants: Ronan-Alexandre Cherrueau, Rémi Douence, Mario Südholt
- Contact: Ronan-Alexandre Cherrueau
- URL: https://github.com/rcherrueau/C2QL

6.3. EScala

SCIENTIFIC DESCRIPTION

EScala extends the idea of events as object members, as realized by C# events, with the possibility to define events declaratively by expressions over other events. The occurrences of an event can be defined by various set operations, such as union, intersection and difference, applied on the occurrences of other events. Events can be filtered by arbitrary conditions, the data attached to the events can be transformed by arbitrary functions. Event expressions make it possible to define events in terms of other events, at the lowest level relying on primitive events.

FUNCTIONAL DESCRIPTION

EScala is an extension of Scala programming language with support for events as attributes of objects. The support for events in EScala, combine the ideas of event-driven, aspect-oriented and functional-reactive programming.

- Participants: Jacques Noyé and Jurgen Van Ham
- Contact: Jurgen Van Ham
- URL: http://www.stg.tu-darmstadt.de/research/escala/index.en.jsp

6.4. JEScala

FUNCTIONAL DESCRIPTION

JEScala extends EScala with support for concurrent programming. Events can be declared as asynchronous so that their handling takes place concurrently. A new composition operator, the join operator, inspired by the join calculus, can also be used to synchronize the concurrent activities created by asynchronous events and communicate between them.

- Participants: Jurgen Van Ham and Jacques Noyé
- Contact: Jurgen Van Ham
- URL: http://www.stg.tu-darmstadt.de/research/jescala_menu/index.en.jsp

6.5. SimGrid

Scientific Instrument for the study of Large-Scale Distributed Systems

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

FUNCTIONAL DESCRIPTION

SimGrid is a toolkit that provides core functionalities 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.

- Participants: Frederic Suter, Martin Quinson, Arnaud Legrand, Takahiro Hirofuchi, Adrien Lebre, Jonathan Pastor, Mario Sudholt, Luka Stanisic, Augustin Degomme, Jean Marc Vincent, Florence Perronnin and Jonathan Rouzaud-Cornabas
- Partners: CNRS - ENS Rennes - Université de Nancy
- Contact: Martin Quinson
- URL: http://simgrid.gforge.inria.fr/

6.6. 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: Takahiro Hirofuchi, Adrien Lebre, Jonathan Pastor, Flavien Quesnel and Mario Sudholt
- Contact: Adrien Lebre
- URL: http://beyondtheclouds.github.io/VMPlaceS/

6.7. 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 Louet, Frederic Dumont and Jean-Marc Menaud
- Contact: Jean-Marc Menaud
- URL: http://www.btrcloud.org/btrCloud/index_EN.html

ASPI Project-Team (section vide)

ATHENA Project-Team

6. New Software and Platforms

6.1. 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. In 2016 a new generation of this software has been coded, which will be released publicly in 2017. It is being tested outside of Inria by a few beta-testers.

- Participants: Nathanaël Foy, Dieter Devlaminck, Loic Mahe, Maureen Clerc, Théodore Papadopoulo, Emmanuel Maby and Jérémie Mattout
- Partner: INSERM
- Contact: Maureen Clerc
- http://openvibe.inria.fr/coadapt-p300-stimulator-tutorial/

6.2. 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/

6.3. The White Matter Query Language

KEYWORDS: Neuroanatomy - Diffusion MRI - Automatic Segmentation - DSL
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.

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

6.4. 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 electroencephalogrphy (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

6.5. 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 will be at the heart of the new dMRI module to be included in the *Olea Sphere* platform.

- Participants: Aurobrata Ghosh, Théodore Papadopoulo, Rachid Deriche and Demian Wassermann
- Contact: Rachid Deriche

6.6. 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, Rene-Paul Debroize, Guillaume Pasquier, Laurence Catanese, Olivier Commowick, Alexandre Abadie, Benoit Bleuze, Clement Philipot, Fatih Arslan, Florian Vichot, John Stark, Julien Wintz, Loïc Cadour, Maxime Sermesant, Michael Knopke, Nicolas Toussaint, Olivier Clatz, Pierre Fillard, Sergio Medina, Stephan Schmitt and Hakim Fadil
- Partners: HARVARD Medical School - IHU - LIRYC - IHU - Strasbourg - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

6.7. 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. OpenMEEG is being used for functional neuroimaging, through third-party software (Brainstorm and Fieldtrip), as can be noticed by the citations to our articles [9] and [89].

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

6.8. 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 Legeny, Jussi Tapio Lindgren, Alison Cellard, Loic Mahe, Guillaume Serriere, Marsel Mano, Maureen Clerc, Théodore Papadopoulo, Laurent Bougrain, Jeremy Frey and Nathanaël Foy
- Partners: CEA-List - GIPSA-Lab - INSERM
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

AVALON Project-Team

5. New Software and Platforms

5.1. Active Data

Participants: Gilles Fedak [correspondant], Valentin Lorentz, Laurent Lefevre.

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

5.2. DIET

Participants: Daniel Balouek-Thomert, Yves Caniou, Eddy Caron, Arnaud Lefray.

FUNCTIONAL DESCRIPTION

DIET (Distributed Interactive Engineering Toolbox) is a middleware designed for high-performance computing in a heterogeneous and distributed environment (workstations, clusters, grids, clouds). Three main developments are done in 2016:

Proxmox support: DIET has a new Cloud extension that can be used to interact with this PVE (Proxmox Virtual Environment) solution. Proxmox is a complete open source server virtualization management software, based on KVM virtualization and container-based virtualization. It manages KVM virtual machines, Linux containers (LXC), storage, virtualized networks, and HA clusters. This extension is a contribution provided by the NewGeneration-SR company.

DaaS support: The goal of this development was to add Data-as-a-Service (DaaS) functionality to the DIET middleware via an optional module. We have added the GDConnect plug-in to the DIET Data manager that provides the capability to deal with Google's Cloud Storage.

Energy Support: We designed, implementation and evaluation of an energy-efficient resource management system that builds upon DIET and NSDE-divisible tasks with precedence constraints.

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

5.3. Execo

Participant: Matthieu Imbert.

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. Execo is used directly by 15 to 30 users, in and out of the Avalon team, and is also used by a few Grid'5000 tools such as kwapi, funk, topo5k, g5k_bench_flops.

- Contact: Matthieu Imbert
- URL: http://execo.gforge.inria.fr

5.4. Kaapi

Participant: Thierry Gautier.

Kaapi is a library for high performance applications running on multi-cores/multi- processors with support for multi-GPUs. Kaapi provides ABI compliant implementations of libGOMP (GCC runtime for OpenMP) and libomp.so (CLANG and Intel compiler). It was one of the target runtime of the K'Star compiler (http://kstar.gforge.inria.fr).

Web site:

- Partners: EPI Corse (Philippe Virouleau, François Broquedis)
- Contact: Thierry Gautier
- URL: http://kaapi.gforge.inria.fr

5.5. Kwapi

Participants: Jean-Patrick Gelas, Laurent Lefevre.

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.

- Contact: Laurent Lefevre
- URL: https://launchpad.net/kwapi

5.6. L2C and DirectL2C

Participants: Hélène Coullon, Vincent Lanore, Christian Perez, Jérôme Richard.

FUNCTIONAL DESCRIPTION

L2C (http://hlcm.gforge.inria.fr) 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.

DirectL2C is an extension to L2C that enables efficient and consistent reconfiguration of large scale L2C based assemblies. It provides an assembly model enhanced with domains, tranformations, and transformation adapters.

- Partners: CEA/Maison de la Simulation (Julien Bigot)
- Contact: Christian Perez
- URL: http://hlcm.gforge.inria.fr/l2c:start

5.7. Sam4C

Participants: Eddy Caron, Arnaud Lefray, Marc Pinhede, Mathieu Veyrand.

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 (https://gforge.inria.fr/projects/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.

- Contact: Eddy Caron
- URL: https://gforge.inria.fr/projects/sam4c/

5.8. SimGrid

Participant: Frédéric Suter.

FUNCTIONAL DESCRIPTION

SimGrid is a toolkit that provides core functionalities 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.

- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson (EPC Myriads)
- URL: http://simgrid.gforge.inria.fr/

5.9. Grid'5000

Participants: Laurent Lefevre, Simon Delamare, David Loup, Christian Perez.

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. In 2016, a new cluster financially supported by Inria has been deployed on the Grid5000 Lyon site.

- Contact: Laurent Lefevre
- URL: https://www.grid5000.fr/

AVIZ Project-Team

6. New Software and Platforms

6.1. Zooids

Participants: Mathieu Le Goc [correspondant], Lawrence Kim, Ali Parsaei, Jean-Daniel Fekete, Pierre Dragicevic, Sean Follmer.

Zooids are autonomous robots that handle both display and interaction. We distribute them as an open-source open-hardware platform for developing tabletop swarm interfaces [24]. All information, related content and material can be found at http://www.aviz.fr/swarmui.

Figure 3. Zooids can be held as tokens, manipulated collectively or individually, behave as physical pixels, act as handles and controllers, and can move dynamically under machine control. They are building blocks for a new class of user interface we call swarm user interfaces.

6.2. Reorder.js

Participant: Jean-Daniel Fekete [correspondant].

Visualizing data tables and graph/network can be done using a matrix visualization. Jacques Bertin, the French cartographer and visualization pioneer explained in his book "Semiology of Graphics" that, to make sense of a matrix, it should first be correctly ordered. This is what the `Reorder.js` library is doing.

Ordering is also useful for other purposes. For example, if you want to visualize with Parallel Coordinates, you should provide an order for the dimension axes. Reorder.js can be used to find a suitable order. See also the poster paper [48].

The library also provide examples of visualizations using reordering; they are based on the d3.js library. For more information, see our survey of methods for matrix reordering [3].

6.3. NetworkCube

Participants: Jean-Daniel Fekete [correspondant], Nathalie Henry-Riche, Benjamin Bach.

Network visualizations support research in a range of scientific domains from biology to humanities. NetworkCube is a platform to bridge the gap between domain scientists and visualisation researchers; NetworkCube 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 [45].

NetworkCube is made of three parts: a core, the Vistorian which is specialized for visualizations for historians, and the Connectoscope which is specialized for Brain Researchers. NetworkCube provides multiple representations for dynamic networks, allowing complex explorations from Web clients.

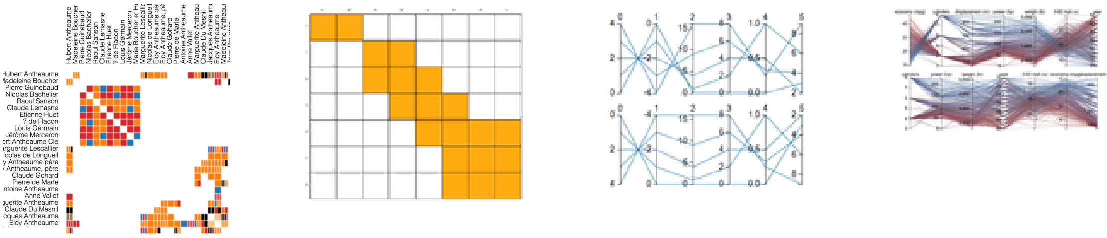


Figure 4. Correctly ordered matrices of a network (left), and parallel coordinate plots with dimensions ordered according to their correlation (right)

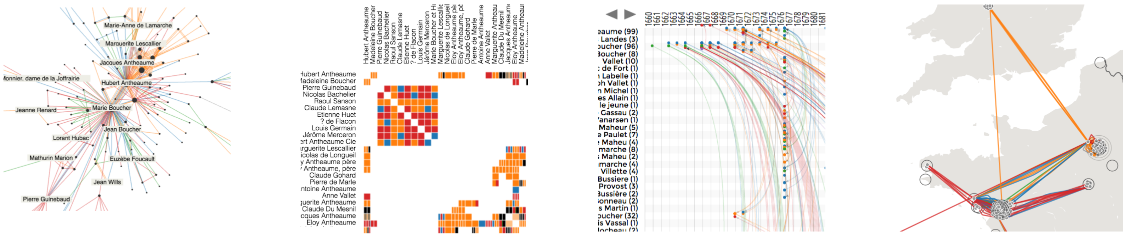


Figure 5. Four different visualization techniques to explore dynamic networks provided by NetworkCube

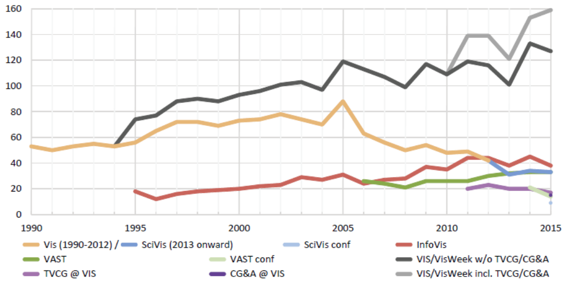


Figure 6. Overview of the files included in the dataset.

6.4. Vispubdata

Participants: Petra Isenberg [correspondant], Florian Heimerl, Steffen Koch, Tobias Isenberg, Panpan Xu, Charles Stolper, Michael Sedlmair, Torsten Möller, John Stasko.

We have created and made available to all a dataset with information about every paper that has appeared at the IEEE Visualization (VIS) set of conferences: InfoVis, SciVis, VAST, and Vis. The information about each paper includes its title, abstract, authors, and citations to other papers in the conference series, among many other attributes. This data is meant to be useful to the broad data visualization community to help understand the evolution of the field and as an example document collection for text data visualization research.

6.5. Time Curves

Participants: Benjamin Bach, Pierre Dragicevic [correspondant], Conglei Shi, Nicolas Heulot.

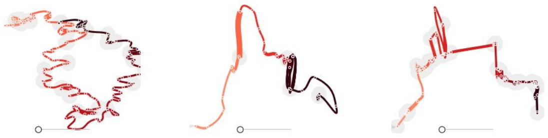


Figure 7. Wikipedia article on abortion illustrated with time curves.

We introduced *time curves* as a general approach for visualizing patterns of evolution in temporal data [2]. 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. In our paper and on the online Website, we illustrate how time curves can visually reveal informative patterns in a range of different datasets.

More on the project Web page: www.aviz.fr/ bbach/timecurves.

6.6. 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

Editors' Notes 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 and Jean-Daniel Fekete
- Contact: Jean-Daniel Fekete
- URL: https://github.com/CENDARI/editorsnotes

6.7. Hybrid Image Visualisation

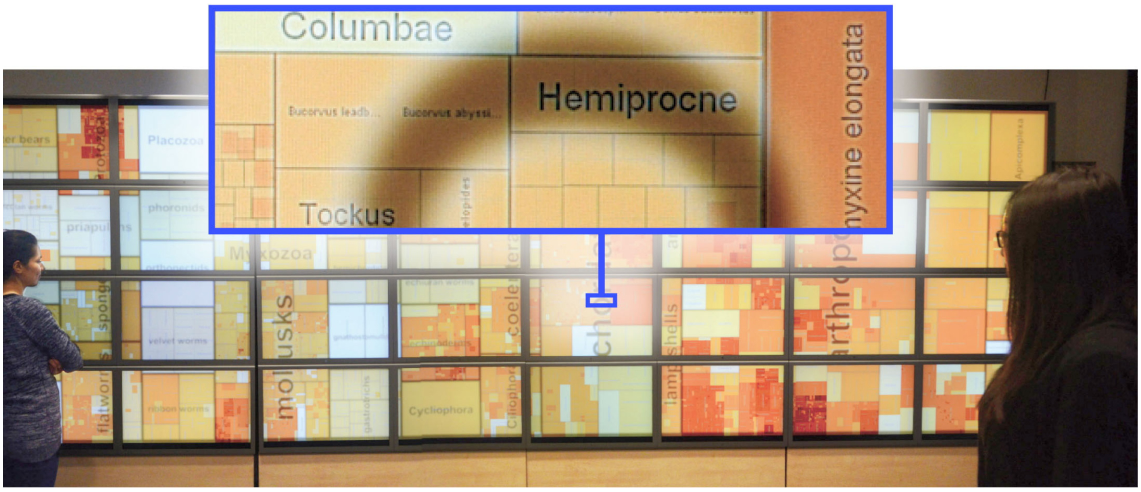


Figure 8. Hybrid image visualization software for the creation of visualizations for distant and close viewing on large displays.

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 8 .

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

6.8. Sparklificator

KEYWORDS: Information visualization - Data visualization - Visualization
SCIENTIFIC DESCRIPTION

Sparklificator is a general open-source jQuery library that eases the process of integrating word-scale visualizations into HTML documents.
FUNCTIONAL DESCRIPTION

Sparklificator's name comes from adding sparklines to a textual document. It is a general open-source jQuery library that eases the process of integrating wordscale visualizations into HTML documents. Sparklificator provides a range of options for adjusting the position (on top, to the right, as an overlay), size, and spacing of vizualisations within the text. The library includes default visualizations, including small line charts and bar charts, and can also be used to integrate custom word-scale visualizations created using webbased 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

5. New Software and Platforms

5.1. Consulting for Industry

Josiane Zerubia is a scientific consultant for the Galderma company (http://www.galderma.com/AboutGalderma/Worldwide-presence/R-D-Locations)

BEAGLE Project-Team

5. New Software and Platforms

5.1. DeCoSTAR

KEYWORDS: Bioinformatics - Evolution

FUNCTIONAL DESCRIPTION Given a set of gene trees, a species tree and adjacency relations between extant genes, DeCoSTAR reconstructs adjacencies between ancestral genes

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

5.2. EvoEvo

Evolution of 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/

5.3. 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 : 1) Select regions of interest in each image (detect the colony) 2) Denoise and renormalize the images 3) Identify each cells in each image (segmentation) 4) Follow cells through the whole movie (tracking) 5) Detect divisions and construct cell lineage in the population FluoBacTracker is an open-source software (under a tailored license agrement), downloadable free of charge for academics.

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

5.4. Tewep

Simulator of the dynamics of Transposable Elements Within Expanding Populations

KEYWORDS: Simulator - Transposable elements - Population genetics - Geographic expansion

FUNCTIONAL DESCRIPTION Transposable elements, found in the genomes of most living organisms (including humans), are pieces of DNA able to replicate themselves and to proliferate. Their presence is a source of mutations which are, most of the time, detrimental to their host. As a consequence, natural selection usually limits their spread. There are, however, some conditions where natural selection cannot be efficient enough to remove them, for example when the population size is small. It is also hypothesized that when a population geographically expands, the efficiency of natural selection could be reduced at the expansion front. TEWEP is an individual-based simulator designed to test whether transposable elements could proliferate in large expanding populations. It combines several population genetics models to simulate the evolution of the number of transposable elements in each individual of an expanding population.

- Partner: Laboratoire de Biométrie et Biologie Evolutive (LBBE) - UMR CNRS 5558
- Contact: Carole Knibbe
- URL: https://gforge.inria.fr/projects/tewep/

5.5. 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, Bérénice Batut, David Parsons, Vincent Liard, Dusan Misevic and Antoine Frénoy
- Partners: Insa de Lyon - INSERM - UCBL Lyon 1 - Université Paris-Descartes
- Contact: Carole Knibbe
- URL: http://www.aevol.fr/

5.6. evowave

KEYWORDS: Data stream - Clustering - Evolution - Wireless network

FUNCTIONAL DESCRIPTION This package is a toolbox to analyse signal strength in wifi activity logfiles. It includes three main modules. The first is a preprocessing module to agregate logfile contents. The second one is a subspace clustering module, based on an evolutionary algorithm, to identify similar wifi activity contexts. This similarity is defined on signal strength of wifi devices and the clusters can change over time. The third module is a visualisation tool to display the cluster modifications over time.

- Participants: Jonas Abernot, Guillaume Beslon, Leo Lefebvre, Sergio Peignier, Anthony Rossi and Christophe Rigotti
- Contact: Christophe Rigotti
- URL: http://evoevo.liris.cnrs.fr/download/4_-_deliverables/wp5/Deliverable_D5.1_software_archive.zip

BIGS Project-Team

6. New Software and Platforms

6.1. AGH

KEYWORDS: statistical analysis, ordered trees
SCIENTIFIC DESCRIPTION

The Matlab toolbox AGH provides methods for statistical analysis of ordered trees from their Harris paths in a user-friendly environment. More precisely it allows to easily compute estimators of the relative scale of trees which share the same shape. These estimators have been introduced for Galton-Watson trees conditioned on their number of nodes but may be computed for any ordered tree. The theoretical study of these estimators is presented in the associated paper [30] which should be consulted in parallel.

FUNCTIONAL DESCRIPTION

The Matlab toolbox AGH provides methods for statistical analysis of ordered trees from their Harris paths in a user-friendly environment.

- Participants: Romain Azaïs, Alexandre Genadot, Benoît Henry
- Contact: romain.azais@inria.fr
- URL: http://agh.gforge.inria.fr

BIOCORE Project-Team

6. New Software and Platforms

6.1. In@lgae

Numerical simulator of microalgae based processes
KEYWORDS: Simulation - Microalgae system - Productivity
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 nitrogen fluxes, lipid and sugar accumulation are predicted.

- Participants: Étienne Delclaux, Francis Mairet, Quentin Béchet and Olivier Bernard
- Contact: Olivier Bernard

6.2. Odin

Platform for advanced monitoring, control and optimisation of bioprocesses
KEYWORDS: Bioinformatics - Biotechnology
SCIENTIFIC DESCRIPTION

This C++ application enables researchers and industrials to easily develop and deploy advanced control algorithms through the use of a Scilab interpreter. It also contains a Scilab-based process simulator which can be harnessed for experimentation and training purposes. 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 is very modular in order to adapt to any plant and to run most of the algorithms, and it can handle the high level of uncertainties that characterises the biological processes through explicit management of confidence indexes.

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, Florian Guenn, Fabien Dilet, Olivier Calabro, Romain Primet, Serigne Sow, Olivier Bernard, Mathieu Lacage and Francesco Novellis
- Contact: Olivier Bernard
- URL: https://team.inria.fr/biocore/software/odin/

BIOVISION Team

5. New Software and Platforms

5.1. Virtual Retina: A biological retina model with contrast gain control for large scale simulations

KEYWORDS: Neurosciences - Simulation - Biology - Health
SCIENTIFIC DESCRIPTION

The Virtual Retina software 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 [65], [66], [67], [41], [17]. It has recently been shown to predict spikes in a mouse retina more accurately than linear-nonlinear (LN) models [79]. 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 RGCs. All parameters for the different stages of the model are customizable so that the visual field can be paved with different RGC types.

FUNCTIONAL DESCRIPTION.

Virtual Retina is a simulation software that allows large-scale simulations of biologically-plausible retinas.

- Participants: Bruno Cessac, Maria-Jose Escobar, Pierre Kornprobst, Selim Kraria, Daniela Pamplona, Selma Souihel, Thierry Vieville and Adrien Wohrer.
- Contact: Pierre Kornprobst
- URL: https://enas.inria.fr/virtual-retina.html

5.2. ENAS: Event Neural Assembly Simulation

KEYWORDS: Neurosciences - Health - Physiology
SCIENTIFIC DESCRIPTION

As one gains more intuitions and results on the importance of concerted activity in spike trains, models are developed to extract potential canonical principles underlying spike coding. These methods shed a new light on spike train dynamics. However, they require time and expertise to be implemented efficiently, making them hard to use in a daily basis by neuroscientists or modelers. To bridge this gap, we developed the license free multiplatform software ENAS (https://enas.inria.fr) integrating tools for individual and collective spike analysis and simulation, with some specificities devoted to the retina. The core of ENAS is the statistical analysis of population codes. One of its main strength is to provide statistical analysis of spike trains using Maximum Entropy-Gibbs distributions taking into account both spatial and temporal correlations as constraints, allowing to introduce causality and memory in statistics. It also generates simulated population raster from an user-specified Gibbs distribution.

We hope that ENAS will become a useful tool for neuroscientists to analyse spike trains and we hope to improve it thanks to user feedback. Our goal is to progressively enrich it with the latest research results, in order to facilitate transfer of new methods to the community.

FUNCTIONAL DESCRIPTION. ENAS is developed joinly by the Biovision, CORTEX/Mnemosyne, and DREAM Inria teams, under CeCILL-C licence, APP logiciel ENAS : IDDN.FR.OO1.190004.000.S.P.2014.000.31235. It can be freely loaded. ENAS has a friendly Graphical User Interface that avoids any scripting or writing code from user. Most methods have been implemented to run in parallel to reduce the time and memory consumption.

- Participants: Bruno Cessac, Pierre Kornprobst, Selim Kraria, Hassan Nasser, Thierry Vieville, Daniela Pamplona, Geoffrey Portelli, Selma Souihel.
- Contact: Bruno Cessac
- URL: https://enas.inria.fr

5.3. The Enas–Virtual Retina platform

In 2016 we merged Enas and Virtual Retina to produce the Enas platform https://enas.inria.fr. The initial version of Virtual retina has been extended to include lateral connections in the Inner Plexiform Layer. We can then simulate the response of the retina to visual stimuli (movies), including the effect of lateral connectivity, analyse the collective spike response to this stimulus using Gibbs distributions, and reproduce a similar raster using learning methods shaping the connectivity in the Inner Plexiform Layer.

This work has been presented in [27] and submitted to Frontiers in Neuroinformatics [3].

BIPOP Project-Team

5. New Software and Platforms

5.1. ACEF

- Participants: Vincent Acary and Olivier Bonnefon (previous Expert Engineer now at INRA).
- Contact: Vincent Acary.

5.2. Approche

KEYWORD: Geometric computing

- Participants: Alexandre Derouet-Jourdan, Florence Descoubes and Joelle Thollot
- Contact: Florence Descoubes
- URL: http://bipop.inrialpes.fr/~bertails/Papiers/floatingTangents3d.html

5.3. CloC

Super Space Clothoids in C
KEYWORD: Physical simulation
FUNCTIONAL DESCRIPTION

Reference software implementing the paper "Super Space Clothoids", R. Casati and F. Bertails-Descoubes, ACM Transactions on Graphics, 2013

- Participants: Florence Descoubes and Romain Casati
- Partner: UJF
- Contact: Florence Descoubes
- URL: http://bipop.inrialpes.fr/people/casati/publications/codes/ssc.html

5.4. MECHE-COSM

Modeling Entangled fiber with frictional Contact in Hair
KEYWORDS: Physical simulation - Frictional contact - Thin elastic rod
FUNCTIONAL DESCRIPTION

Implements super-helices [Bertails et al. 2006] coupled together by a hybrid algorithm for frictional contact [Daviet et al. 2011].

- Participants: Gilles Daviet, Florence Bertails Descoubes and Florent Cadoux
- Contact: Florence Descoubes

5.5. SALADYN MULTIBODY

- Participants: Vincent Acary and Olivier Bonnefon
- Contact: Vincent Acary

5.6. SICONOS

KEYWORDS: NSDS - MEMS - DCDC - SD - Collision - Friction - Mechanical multi-body systems
FUNCTIONAL DESCRIPTION

Siconos is an open-source scientific software primarily targeted at modeling and simulating nonsmooth dynamical systems in C++ and in Python: - Mechanical systems (rigid or solid) with unilateral contact and Coulomb friction and impact (nonsmooth mechanics, contact dynamics, multibody systems dynamics or granular materials). - Switched Electrical Circuit such as electrical circuits with ideal and piecewise linear components: power converter, rectifier, Phase-Locked Loop (PLL) or Analog-to-Digital converter. - Sliding mode control systems. - Biology (Gene regulatory network). Other applications are found in Systems and Control (hybrid systems, differential inclusions, optimal control with state constraints), Optimization (Complementarity systems and Variational inequalities), Fluid Mechanics, and Computer Graphics.

- Participants: Vincent Acary, Olivier Bonnefon, Maurice Bremond and Franck Perignon
- Contact: Bernard Brogliato
- URL: http://siconos.gforge.inria.fr

5.7. Platforms: SICONOS

5.7.1. 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. BCALM 2

KEYWORDS: Bioinformatics - NGS - Genomics - Metagenomics - De Bruijn graphs

SCIENTIFIC DESCRIPTION

BCALM 2 is a bioinformatics tool for constructing the compacted de Bruijn graph from sequencing data. It is a parallel algorithm that distributes the input based on a minimizer hashing technique, allowing for good balance of memory usage throughout its execution. It is able to compact very large datasets, such as spruce or pine genome raw reads in less than 2 days and 40 GB of memory on a single machine.

FUNCTIONAL DESCRIPTION

BCALM 2 is an open-source tool for dealing with DNA sequencing data. It constructs a compacted representation of the de Bruijn graph. Such a graph is useful for many types of analyses, i.e. de novo assembly, de novo variant detection, transcriptomics, etc. The software is written in C++ and makes extensive use of the GATB library.

- Participants: Rayan Chikhi, Antoine Limasset and Paul Medvedev
- Contact: Rayan Chikhi
- URL: https://github.com/GATB/bcalm

6.2. NORINE

Nonribosomal peptides resource

KEYWORDS: Bioinformatics - Biotechnology - Biology - Genomics - Graph algorithmics - Chemistry - Knowledge database - Drug development - Computational biology

SCIENTIFIC DESCRIPTION

Since its creation in 2006, Norine remains the unique knowledgebase dedicated to non-ribosomal peptides (NRPs). These secondary metabolites, produced by bacteria and fungi, harbor diverse interesting biological activities (such as antibiotic, antitumor, siderophore or surfactant) directly related to the diversity of their structures. The Norine team goal is to collect the NRPs and provide tools to analyze them efficiently. We have developed a user-friendly interface and dedicated tools to provide a complete bioinformatics platform. The knowledgebase gathers abundant and valuable annotations on more than 1100 NRPs. To increase the quantity of described NRPs and improve the quality of associated annotations, we are now opening Norine to crowdsourcing. We believe that contributors from the scientific community are the best experts to annotate the NRPs they work on. We have developed MyNorine to facilitate the submission of new NRPs or modifications of stored ones. Norine is freely accessible from the following URL: http://bioinfo.lifl.fr/NRP.

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 Leclere, Laurent Noe, Yoann Dufresne, Juraj Michalik and Stéphane Janot
- Partners: CNRS - Institut Charles Viollette - Université Lille 1 v
- Contact: Maude Pupin
- URL: http://bioinfo.lille.inria.fr/NRP

6.3. Olo

KEYWORDS: Bioinformatics - Indexation - Sequence alignment - Biological sequences - Approximate string matching

SCIENTIFIC DESCRIPTION

Approximate string matching of short sequences in a text often starts by a filtering step. That step relies on seed searching, which are shorter than the pattern. Usually in those seeds the number of errors is constrained, to allow more efficient computations. We designed the 01*0 seeds which offer a good trade-off between the number of false positives and filtering time.

FUNCTIONAL DESCRIPTION

We applied the 01*0 seeds to the similarity search of miRNA targets in a reference genome (Bwolo software) and to the similarity search between a pre-miRNA and mature miRNAs (Piccolo software).

- Participants: Sébastien Bini, Mikaël Salson, Hélène Touzet and Christophe Vroland
- Partners: CNRS - Université Lille 1
- Contact: Helene Touzet
- URL: http://bioinfo.lifl.fr/olo/

6.4. 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 against 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 an 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: CHRU Lille - CNRS - Inria - Université de Lille
- Contact: Mathieu Giraud
- URL: http://www.vidjil.org

CAGIRE Project-Team

6. New Software and Platforms

6.1. AeroSol

Participants: Simon Delmas [Université de Bordeaux], Sébastien de Brye [Université de Bordeaux], 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 Adaptive wall treatment for a second moment closure in the industrial context

- **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 [27].

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 2015, AeroSol had the following features:

- **Boundary conditions** Periodic boundary conditions, time-dependent inlet and outlet boundary conditions. Adiabatic wall and isothermal wall. Steger-Warming based boundary condition. Synthetic Eddy Method for generating turbulence.
- **C++/Fortran interface** Tests for binding fortran with C++.
- **Development environment** An upgraded use of CMake for compilation (gcc, icc and xlc), CTest for automatic tests and memory checking, lcov and gcov for code coverage reports. A CDash server for collecting the unitary tests and the memory checking. An under development interface for functional tests. Optional linking with HDF5, PAPI, with dense small matrices libraries (BLAS, Eigen). An updated shared project Plafrim and joint project Aerosol/Scotch/PaMPA project on the continuous integration platform. An on-going integration of SPack for handling dependencies. A fixed ESSL interface.
- **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.
- **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.
- **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).
- **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. Linearized Euler equations, and Sutherland model for non isothermal diffusive flows. Shallow-water model.
- **Multigrid** Development of p-multigrid methods. This includes also the possibility of beginning a computation with 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. In progress implementation of h-multigrid, with the development of tests of the aggregation methods of PaMPA, and the definition of finite element basis on arbitrary cells.
- **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.

- **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. In progress optimization by stocking the geometry for advection problems. SUPG and Residual distribution 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.
- **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 (BlueGene). Weighted load balancing for hybrid meshes.
- **Postprocessing** High order projections over line postprocessing, possibility of stocking averaged data, such as the average flow and the Reynolds stresses.
- **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.
- **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.
- **Validation** Poiseuille, Taylor-Green vortex. Laplace equation on a ring and Poiseuille flow on a ring. Volumic forcing based on wall dissipation.Turbulent channel flow.

In 2016, the following features have been added:

- Geometric multigrid methods: aggregation of the mesh based on PaMPA, definition of finite element basis on arbitrary shape cells. Definition of geometry, quadratures and numerical schemes on aggregated finite elements.
- Sutherland law in the Navier-Stokes equations.
- Mass matrix free implementation of discontinuous Galerkin methods.
- Improvement of installation documentation. Spack based installation.
- Implementation of Boussinesq type models and Shallow water discretizations with well balancing, positivity preserving, wet-dry handling, limiters based on entropy viscosity,
- Implementation of Barotropic Euler equations
- Implementation of Taylor-based basis on simplices.

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 designed an extensible source-to-source compiler infrastructure that takes advantage of leading edge model-driven object-oriented software engineering principles and technologies.

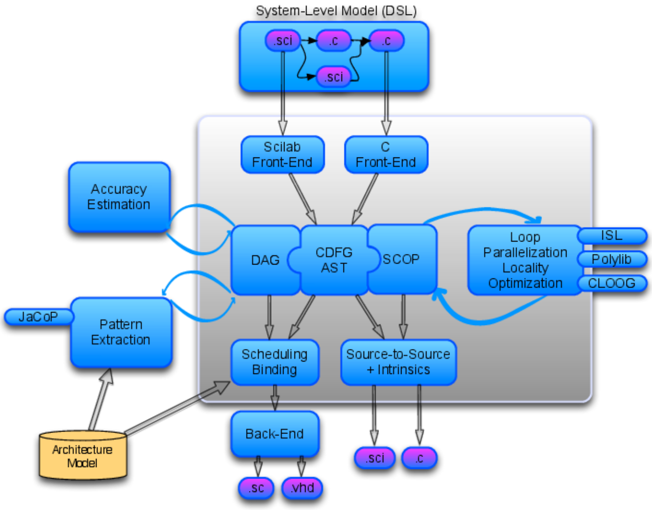


Figure 2. CAIRN*'s general software development framework.*

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 ASIC/FPGA 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.
- A polyhedral-based loop transformation and parallelization engine (mostly targeted at HLS).
- A custom instruction extraction flow (for ASIP and dynamically reconfigurable architectures). **Durase** is developed for the compilation and the synthesis targeting reconfigurable platforms and the automatic synthesis of application specific processor extensions. It uses advanced technologies, such as graph matching 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).

Gecos, ID.Fix or Durase have been demonstrated during "University Booths" in various conference such as IEEE/ACM DAC or DATE.

6.2. Gecos

KEYWORDS: Source-to-source compiler - Model-driven software engineering - Retargetable compilation

SCIENTIFIC DESCRIPTION

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 between 2012 and 2015 it was used in the context of the FP7 ALMA European project. The Gecos infrastructure will also be used by the EMMTRIX start-up, a spin-off from the ALMA project which aims at commercializing the results of the project and in the context of the H2020 ARGO European project.

FUNCTIONAL DESCRIPTION

Gecos provides a program transformation toolbox facilitating parallelisation of applications for heterogeneous multiprocessor embedded platforms. This includes a polyhedral loop transformation toolbox, efficient SIMD code generation for fixed point arithmetic data-types, coarse-grain parallelization engine targeting the data-flow actor model, and a Matlab/Scilab front-end. In addition to targeting programmable processors, Gecos can regenerate optimized code for High Level Synthesis tools.

- Participants: Steven Derrien, Nicolas Simon, Imen Fassi, and Ali Hassan El-Moussawi
- Partner: Université de Rennes 1
- Contact: Steven Derrien
- URL: http://gecos.gforge.inria.fr/doku/doku.php

6.3. ID-Fix

KEYWORDS: Energy efficiency - Embedded systems - Analytical accuracy evaluation - Fixed-point arithmetic - Accuracy optimization - Dynamic range evaluation - Code optimisation

SCIENTIFIC DESCRIPTION

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 different fixed-point data types. 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).

FUNCTIONAL DESCRIPTION

ID.Fix focuses on computational accuracy and can provide an optimised specification using fixed point arithmetic from a C source code with floating point data types. Fixed point arithmetic is very widely used in embedded systems as it provides better performance and is much more energy efficient. ID.Fix used an analytical model of the software code, which means it can explore more solutions and thereby produce much more efficient code than classical simulation-based tools.

- Participants: Olivier Sentieys, Benjamin Barrois and Nicolas Simon
- Partner: Université de Rennes 1
- Contact: Olivier Sentieys
- URL: http://idfix.gforge.inria.fr/doku.php

6.4. Zyggie

KEYWORDS: Health - Biomechanics - Wireless body sensor networks - Low power - Gesture recognition - Hardware platform - Software platform - Localization

SCIENTIFIC DESCRIPTION

Zyggie is a hardware and software wireless body sensor network platform. Each sensor node, attached to different parts of the human body, contains inertial sensors (IMU) (accelerometer, gyrometer, compass and barometer), an embedded processor and a low-power radio module to communicate data to a coordinator node connected to a computer, tablet or smartphone. One of the system's key innovations is that it collects data from sensors as well as on distances estimated from the power of the radio signal received to make the 3D location of the nodes more precise and thus prevent IMU sensor drift and power consumption overhead. Zyggie can be used to determine posture or gestures and mainly has applications in sport, healthcare and the multimedia industry.

FUNCTIONAL DESCRIPTION

The Zyggie sensor platform was developed 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 a processor, a radio transceiver and different sensors including an Inertial Measurement Unit (IMU) with 3-axis accelerometer, gyrometer, and magnetometer. Zyggie is used for evaluating data fusion algorithms, low power computing algorithms, wireless protocols, and body channel characterization in the BoWI project.

The Zyggie V2 prototype includes new features: a 32-bit microcontroller to manage a custom MAC layer and processe quaternions based on IMU measures, and an UWB radio from DecaWave to measure distances between nodes with Time of Flight (ToF).

- Participants: Arnaud Carer and Olivier Sentieys
- Partners: Lab-STICC - Université de Rennes 1
- Contact: Olivier Sentieys
- URL: http://www.bowi.cominlabs.ueb.eu/fr/zyggie-wbsn-platform

Figure 3. CAIRN*'s Ziggie platform for WBSN*

CAMIN Team

6. New Software and Platforms

6.1. Software and platforms

6.1.1. HILECOP

Participants: Baptiste Colombani, David Andreu, Thierry Gil [LIRMM], Robin Passama [LIRMM].

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.5), 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.

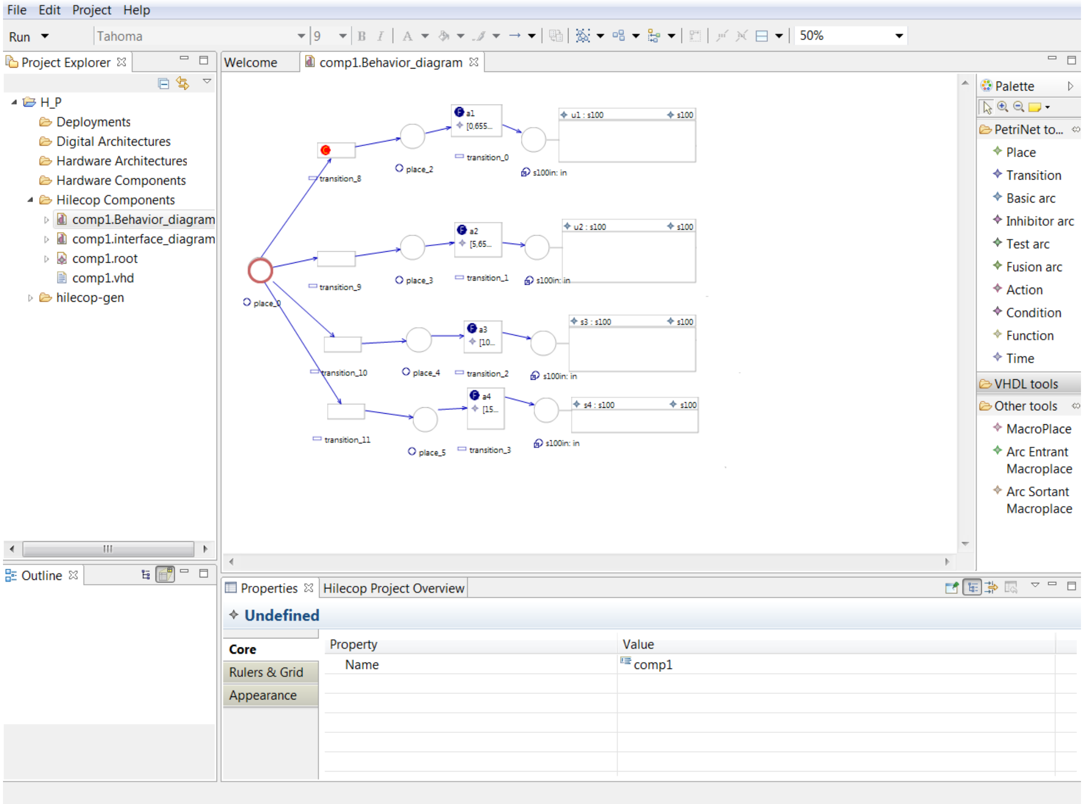
Undergoing work concerns the integration, in the HILECOP tool, of the formalism evolutions that allow behavior agregation as well as exception handling, both for analysis and implementation sides.

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).

6.1.2. PersoBalance: A Personalized Balance Assessment in Home Rehabilitation

Participants: Maxime Tournier, Alejandro Gonzalez, Philippe Fraisse, Mitsuhiro Hayashibe.

In 2014-2015, the team demonstrated the feasibility of a personalized balance assessment system using low-end sensors for home rehabilitation. The corresponding software (PersoBalance) performs an identification of inertial parameters for a subject using a depth camera and a connected balance board (in this case, a Nintendo Wii BalanceBoard) through a dedicated Kalman filter as the subject assumes various body postures. When the inertial parameters are estimated, the software is then able to compute a stability index for the subject based on criteria found in robotics and biomechanics literature. This year, in order to exploit the newer, more accurate and more robust sensors such as the Microsoft Kinect v2, a new version of the PersoBalance software was engineered. While the core method remainsthe same, several improvement have been made regarding efficiency, user interface and extensibility. The new system is faster, more accurate and robust. It automatically registers the balance board during identification, and features improved graphical feedback during both identification and stability estimation phases. New stability measures were added, and support for online inverse dynamics is on the way. Most of the new version uses a scripting language (Python) except for time-critical algorithm, making the software easily extensible without recompilation. It is supported by Inria ADT PersoBalance2. Currently the software is being adapted to embedded computers in order to provide monitoring data in the City4Age project.



Undefined

Property	Value
Name	comp1

Figure 5. HILECOP screenshot

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 6. PersoBalance: Online stability estimation, from left to right: as a subject undergoes an unexpected external push, the system automatically estimates the ground reaction forces (pink arrow) and computes a stability index from the position of the ZRAM point relative to the support polygon (white/orange). The skeleton colour changes from green to red as the stability index decreases.

6.1.3. Sensbiotk

Participants: Christine Azevedo Coste, Roger Pissard-Gibollet, Benoît Sijobert.

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.

http://sensbio.github.io/sensbiotk/

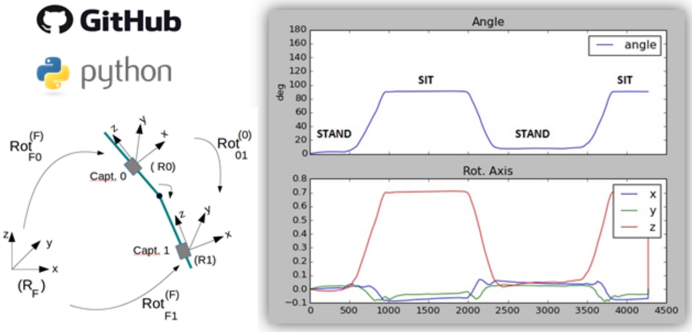


Figure 7. Sensbiotk toolbox for the calibration, the acquisition, the analysis and visualization of motion capture Inertial Measurement Units (IMU)

6.1.4. MOS2SENS

Participants: Mélissa Dali, Olivier Rossel, David Guiraud.

From Model Optimization and Simulation To Selective Electrical Neural Stimulation: it allows to manipulate 3D modeling of nerve and cuff electrodes taking into account anisotropy and the most advanced HH models of the myelinated axons. Based on optimized computing scheme, it allows to predict the acivation areas induced by a complex 3D spreading of the current over a multicontact electrodes. Moreover, the tool allows for performing optimization of the needed current to target a specific cross section of the nerve. Version 1.0 (IDDN.FR.001.490036.000.S.P.2014.000.31230) has been relaesed on december 2014 and v2.0 will be realeased January 2017. The last version includes full interface with OpenMEEG and COMSOL, and many other enhancements concerning both the model itself and the computation scheme.

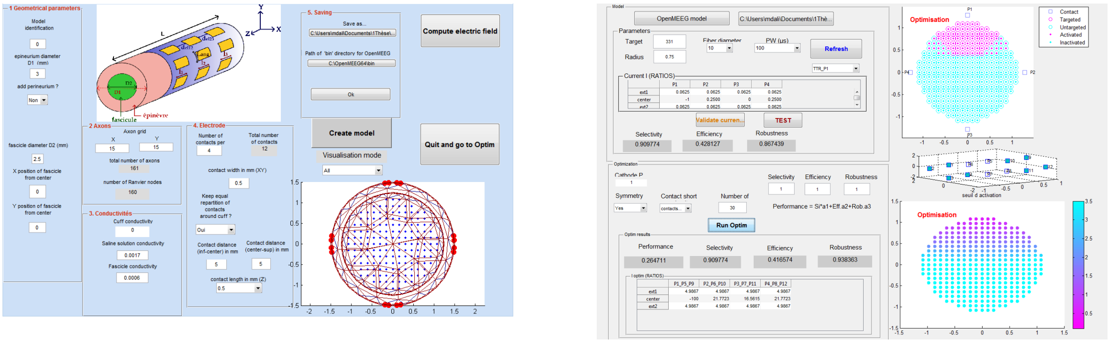


Figure 8. Graphical interface of software MOS2SENS, left: modeling multicontact CUFF electrode, right: optimization for spatial selectivity

6.1.5. STIMEP: An advanced real-time stimulation system based on a distributed architecture

Participants: Arthur Hiairrassary, David Andreu, David Guiraud, Olivier Rossel, Thomas Guiho.

The STIMEP has been developed within the EPIONE project (see section 9.3.1) which aims at assessing the use of invasive stimulation to relieve phantom pain. This innovative wearable stimulator allows to safely manipulate sensory afferent signals of an amputee through 4 TIME-4H intra fascicular electrodes, for a total of 56 channels.

The STIMEP is also designed to be controlled in real-time by a hand-prosthesis to generate feedback sensations; it permits as well a complex impedance follow-up.

The STIMEP is based on a distributed architecture and embeds:

- 1 x controller implemented on μC/OS-II RTOS exchanging data with a PC (USB) or an external device (SPI),
- 4 x neural stimulators with efficient modulation mechanisms to drive up to 4 multicontact electrodes simultaneously and independently,
- 6 x fully configurable procedures (formally modeled by Petri nets):
  - Contacts check, thresholds search, sensations characterization, therapy,
  - Real-time modulation of frequency, intensity and pulse-width,
  - Complex impedance measurement.
- 2 x smart and independent synchronization outputs,
- User and technical logs of relevant information.

The STIMEP is currently used in human trials and drives simultaneously 4 multicontact intrafascicular electrodes with real time control of the intensity, pulse-width and frequency of the stimulation to remove phantom pain and elicit very accurate sensation feedback.

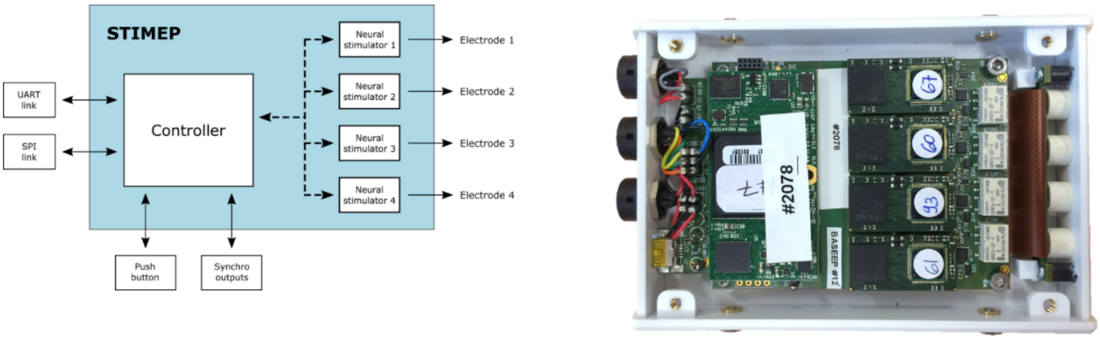


Figure 9. The STIMEP (STIMulator EPione)

CAMUS Team

6. New Software and Platforms

6.1. Apollo

Automatic speculative POLyhedral Loop Optimizer
KEYWORD: Automatic parallelization
FUNCTIONAL DESCRIPTION

Apollo is 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 can apply on-the-fly any kind of polyhedral transformations, including tiling, and can handle nonlinear loops, as while-loops referencing memory through pointers and indirections.

- Participants: Manuel Selva, Juan Manuel Martinez Caamaño, Artiom Baloian, and Philippe Clauss
- Contact: Philippe Clauss
- URL: http://apollo.gforge.inria.fr

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
- 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: Philippe Clauss and Cédric Bastoul
- Contact: Philippe Clauss
- URL: http://xfor.gforge.inria.fr

6.6. 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/

6.7. 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/

6.8. ORWL and P99

ORWL is a reference implementation of the Ordered Read-Write Lock tools as described in [1]. 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/.

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

6.9. Stdatomic and Musl

We implement the library side of the C11 atomic interface. It needs compiler support for the individual atomic operations and provides library support 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 [2]. A short version of it has been presented at 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/

CAPSID Project-Team

6. New Software and Platforms

6.1. Hex

KEYWORDS: 3D rendering - Bioinformatics - 3D interaction - Structural Biology

SCIENTIFIC DESCRIPTION The underlying algorithm uses a novel polar Fourier correlation technique to accelerate the search for close-fitting orientations of the two molecules.

FUNCTIONAL DESCRIPTION Hex is an interactive protein docking and molecular superposition program. Hex understands protein and DNA structures in PDB format, and it can also read small-molecule "SDF" files. Hex will run on most Windows-XP, Linux and Mac OS X PCs. The recent versions now 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. The calculations can be accelerated by using an optional disc cache (strongly recommended) of about 1 GB of disc space.

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

6.2. Kbdock

FUNCTIONAL DESCRIPTION Database 3D protein domain-domain interactions with a web interface

- Authors: Anisah Ghoorah, Anisah Ghoorah, David Ritchie and Marie Dominique Devignes
- Contact: David Ritchie
- URL: http://kbdock.loria.fr

6.3. Kpax

KEYWORDS: Bioinformatics - Structural Biology

SCIENTIFIC DESCRIPTION To align and superpose the 3D structures of protein molecules.

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

6.4. Sam

Symmetry Assembler

FUNCTIONAL DESCRIPTION To predict the three-dimentional structures of symmetrical protein complexes using spherical polar Fourier representations

- Authors: David Ritchie and Sergey Grudinin
- Partner: CNRS
- Contact: David Ritchie
- URL: http://sam.loria.fr

6.5. ECDomainMiner

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. Platforms

6.6.1. 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

CARAMBA Project-Team

6. New Software and Platforms

6.1. Belenios

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

Belenios is an online voting system that provides confidentiality and verifiability. End-to-end verifiability relies on the fact that the ballot box is public (voters can check that their ballots have been taken into account) and on the fact that the tally is publicly verifiable (anyone can recount the votes). Confidentiality relies on the encryption of the votes and the distribution of the decryption key.

Belenios builds upon Helios, a voting protocol used in several elections. The main design enhancement of Belenios vs Helios is that the ballot box can no longer add (fake) ballots, due to the use of credentials.

In 2016 our online platform has been used for several elections, for instance: representatives at the “comité de centre” in several Inria research centers, at the “conseil de laboratoire” at IRISA, and for the head of the “GT Calcul Formel” of the GDR-IM.

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

6.2. Kalray-ECM

KEYWORDS: Factorization - Kalray
FUNCTIONAL DESCRIPTION

Implementation of the factorization algorithm based on elliptic curves (ECM) for the MPPA-256 Kalray processor.

- Authors: Jérémie Detrey, Pierrick Gaudry and Masahiro Ishii
- Partner: Nara Institute of Science and Technology, Japan
- Contact: Jérémie Detrey
- URL: https://gforge.inria.fr/projects/kalray-ecm

6.3. TinyGB

- Author: Pierre-Jean Spaenlehauer
- Contact: Pierre-Jean Spaenlehauer
- URL: https://gforge.inria.fr/projects/tinygb/
- Licence: LGPL-3.0+

`TinyGB` is a software implementing tools for computing Gröbner bases of ideals in polynomial rings over finite fields. It has been released in April 2016.

It is not competitive with state-of-art software for computations over small prime fields. However, for polynomial systems over $\mathbb{Z}/p\mathbb{Z}$, with $p > 2^{31}$, its timings are competitive with the computer algebra system `Magma-2.22-2` (although the `Magma` is much better in terms of memory requirements). This is due to the fact that `TinyGB` relies on the library `MPFQ` (developed in the Caramba team) for the efficient arithmetic over large prime fields. For instance, computing the grevlex Gröbner basis of a system of 13 dense homogeneous quadratic equations in 13 variables over the field $\mathbb{Z}/(2^{31}+11)\mathbb{Z}$ can be achieved within 907 seconds with `TinyGB`, whereas `Magma-2.22-2` requires 4459 seconds (on an Intel Core i5-4590@3.30GHz).

The distribution of `TinyGB` contains the libraries `OpenBLAS`, `FFLAS-FFPACK` and `MPFQ`.

CARDAMOM Project-Team

5. New Software and Platforms

5.1. AeroSol

Participants: Simon Delmas [Universit de Bordeaux], Sbastien de Brye [Universit de Bordeaux], 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 Adaptive wall treatment for a second moment closure in the industrial context

- **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 [108].

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 2015, AeroSol had the following features:

- **Boundary conditions** Periodic boundary conditions, time-dependent inlet and outlet boundary conditions. Adiabatic wall and isothermal wall. Steger-Warming based boundary condition. Synthetic Eddy Method for generating turbulence.
- **C++/Fortran interface** Tests for binding fortran with C++.
- **Development environment** An upgraded use of CMake for compilation (gcc, icc and xlc), CTest for automatic tests and memory checking, lcov and gcov for code coverage reports. A CDash server for collecting the unitary tests and the memory checking. An under development interface for functional tests. Optional linking with HDF5, PAPI, with dense small matrices libraries (BLAS, Eigen). An updated shared project Plafrim and joint project Aerosol/Scotch/PaMPA project on the continuous integration platform. An on-going integration of SPack for handling dependencies. A fixed ESSL interface.
- **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.
- **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.
- **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).
- **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. Linearized Euler equations, and Sutherland model for non isothermal diffusive flows. Shallow-water model.
- **Multigrid** Development of p-multigrid methods. This includes also the possibility of beginning a computation with 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. In progress implementation of h-multigrid, with the development of tests of the aggregation methods of PaMPA, and the definition of finite element basis on arbitrary cells.
- **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.

- **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. In progress optimization by stocking the geometry for advection problems. SUPG and Residual distribution 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.
- **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). Weighted load balancing for hybrid meshes.
- **Postprocessing** High order projections over line postprocessing, possibility of stocking averaged data, such as the average flow and the Reynolds stresses.
- **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.
- **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.
- **Validation** Poiseuille, Taylor-Green vortex. Laplace equation on a ring and Poiseuille flow on a ring. Volumic forcing based on wall dissipation.Turbulent channel flow.

In 2016, the following features have been added:

- Geometric multigrid methods: aggregation of the mesh based on PaMPA, definition of finite element basis on arbitrary shape cells. Definition of geometry, quadratures and numerical schemes on aggregated finite elements.
- Sutherland law in the Navier-Stokes equations.
- Mass matrix free implementation of discontinuous Galerkin methods.
- Improvement of installation documentation. Spack based installation.
- Implementation of Boussinesq type models and Shallow water discretizations with well balancing, positivity preserving, wet-dry handling, limiters based on entropy viscosity,
- Implementation of Barotropic Euler equations
- Implementation of Taylor-based basis on simplices.

5.2. CAKE

KEYWORDS: Moving bodies, Rarefied flows

- Contact: Luc Mieussens
- URL: http://www.cake-solver.com/

FUNCTIONAL DESCRIPTION

Cake (Cut cell Algorithm for Kinetic Equations) can simulate 2D plane rarefied flows around moving obstacles, by using an immersed boundary technique with Cartesian grids. This code can simulate flows induced by temperature gradients, like the thermal creep flow. It has for instance been applied to the simulation of the Crookes radiometer.

5.3. Crysa

KEYWORDS: Image processing, structural analysis, 2D crystallography

- Participants: Jean Mercat and Cécile Dobrzynski
- Partners: ISM - LCPO - LCTS (UMR 5801)
- Contact: Cécile Dobrzynski

Crysa is a library allowing to study the organization of objects once placed in an hexagonal grid thus allowing to analyze the crystal structure/organization of an image. The library allows to detect regions of coherence in an image of crystals, and it allows to determine e.g. the good separation of objects in an experiment (new polymeric materials, plasma, ...).

5.4. Cut-ANOVA

KEYWORDS: Stochastic models - Uncertainty quantification

- Participants: Pietro-Marco Congedo
- Contact: Pietro-Marco Congedo

SCIENTIFIC DESCRIPTION

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.

FUNCTIONAL DESCRIPTION

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.

5.5. Fmg

KEYWORDS: Mesh adaptation, mesh deformation, elasticity, laplacian mesh equation

- Participants: Cécile Dobrzynski, Mario Ricchiuto, Leo Nouveau and Luca Arpaia
- Contact: Cécile Dobrzynski

FUNCTIONAL DESCRIPTION

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. This year a new semi-linear elasticity formulation has been implemented involving a constant coefficient PDE with a nonlinear *force* accounting for the smoothness of the target function. The advantage of this approach is that the non-linearity does not influence the elastic differential operator thus leading to a description of the deformation governed by a time-invariant matrix even in unsteady simulations. Other developments currently implemented in SLOWS are being imported in FMG.

5.6. MMG3D

KEYWORDS: Mesh - Anisotropic - Mesh adaptation

- Participants: Cécile Dobrzynski, Pascal Frey, Charles Dapogny and Algiane Froehly
- Partners: CNRS - IPB - Université de Bordeaux - UPMC
- Contact: Cécile Dobrzynski
- URL: http://www.mmgtools.org

SCIENTIFIC DESCRIPTION

Mmg3d is an open source software for tetrahedral remeshing. It performs local mesh modifications. The mesh is iteratively modified until the user prescriptions satisfaction.

Mmg3d can be used by command line or using the library version (C, C++ and Fortran API) : - It is a new version af the MMG3D4 software. It remesh both the volume and surface mesh of a tetrahedral mesh. It performs isotropic and anisotropic mesh adaptation and isovalue discretization of a level-set function.

Mmg3d allows to control the boundaries approximation: The "ideal" geometry is reconstruct from the piecewise linear mesh using cubic Bezier triangular partches. The surface mesh is modified to respect a maximal Hausdorff distance between the ideal geometry and the mesh.

Inside the volume, the software perform local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).

FUNCTIONAL DESCRIPTION

Mmg3d is one of the software of the Mmg platform. Is is dedicated to the modification of 3D volume meshes. It perform the adaptation and the optimization of a tetrahedral mesh and allow to discretize an isovalue.

Mmg3d perform local mesh modifications. The mesh is iteratively modified until the user prescription satisfaction.

5.7. Mmg platform

KEYWORDS: Mesh - Mesh generation - Anisotropic - Mesh adaptation - Isovalue discretization

- Participants: Cécile Dobrzynski, Charles Dapogny, Pascal Frey and Algiane Froehly
- Partners: CNRS - IPB - Université de Bordeaux - UPMC
- Contact: Cécile Dobrzynski
- URL: http://www.mmgtools.org

SCIENTIFIC DESCRIPTION

The Mmg platform gathers open source software for two-dimensional, surface and volume remeshing. The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescriptions satisfaction.

The 3 softwares can be used by command line or using the library version (C, C++ and Fortran API) : - Mmg2d performs mesh generation and isotropic and anisotropic mesh adaptation. - Mmgs allows isotropic and anisotropic mesh adaptation for 3D surface meshes. - Mmg3d is a new version af the MMG3D4 software. It remesh both the volume and surface mesh of a tetrahedral mesh. It performs isotropic and anisotropic mesh adaptation and isovalue discretization of a level-set function.

The platform software allow to control the boundaries approximation: The "ideal" geometry is reconstruct from the piecewise linear mesh using cubic Bezier triangular partches. The surface mesh is modified to respect a maximal Hausdorff distance between the ideal geometry and the mesh.

Inside the volume, the software perform local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).

FUNCTIONAL DESCRIPTION

The Mmg plateform gathers open source software for two-dimensional, 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 isovalue discretization

The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescription satisfaction.

5.8. NOMESH

- Participants: Cécile Dobrzynski and Algiane Froehly
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Cécile Dobrzynski

KEYWORDS: Mesh - Curved mesh - Tetrahedral mesh

FUNCTIONAL DESCRIPTION

NOMESH is a software allowing the generation of three 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.

5.9. SLOWS

KEYWORDS: Free surface flows, Unstructured meshes, shallow water equations, Boussinesq equations

- Participants: Luca Arpaia, Andrea Filippini, Maria Kazolea, Mario Ricchiuto and Nikolaos Pattakos
- Contact: Mario Ricchiuto

FUNCTIONAL DESCRIPTION

SLOWS (Shallow-water fLOWS) 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. The kernel of the CODE is a shallow water solver based on second order residual distribution or second and third order finite volume schemes. Three different approaches are available to march in time, 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. Linear algebraic sparse systems arising in the discretization are solved with This year several enhancements have been implemented

- a correction of both the residual distribution and finite volume methods to solve the shallow water equations in spherical (or Mercator) curvilinear coordinates;

- mass-conserving mesh movement to adapt an initial grid to wet-dry interfaces as well as to other physical features of the flow;
- a new library has been developed to enhance the shallow water equations. This library computes an algebraic source term by inverting an elliptic (grad-div type) PDE. The addition of this term to the shallow water version of SLOWS allows to recover the a fully nonlinear weakly dispersive Green-Naghdi solver. The solution of the elliptic PDE is performed with a classical Galerkin FEM approach, and MUMPS is the MUMPS library is used to invert the resulting matrix;
- Initial optimization and OpenMP parallelization of the shallow water kernel.

SLOWS is our main simulation tool in both the TANDEM and Tides projects.

5.10. Sparse-PDD

Adaptive sparse polynomial dimensional decomposition for global sensitivity analysis
KEYWORDS: Stochastic models - Uncertainty quantification

- Participants: Pietro-Marco Congedo
- Contact: Pietro-Marco Congedo

SCIENTIFIC DESCRIPTION

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.

FUNCTIONAL DESCRIPTION

This code allows an efficient meta-modeling for a complex numerical system featuring a moderate-to-large number of uncertain parameters. This innovative approach involves polynomial representations combined with the Analysis of Variance decomposition, with the objective to quantify the numerical output uncertainty and its sensitivity upon the variability of input parameters.

5.11. TUCWave

KEYWORDS: fre surface flows, Boussinesq equaions, weakly nonlinear models, unstructured grids

- Participants: Maria Kazolea, Argiris Delis and Ioannis Nikolos
- Contact: Maria Kazolea

FUNCTIONAL DESCRIPTION

Fortran Planform which accounts for the study of near shore processes. TUCWave uses a high-order well-balanced unstructured finite volume (FV) scheme on triangular meshes for modeling weakly nonlinear and weakly dispersive water waves over varying bathymetries, as described by the 2D depth-integrated extended Boussinesq equations of Nwogu (1993), rewritten in conservation law form. 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 developed follows an efficient edge based structured technique. For the advective fluxes, the scheme utilizes an approximate Riemann solver along with a well-balanced topography source term up-winding. Higher order accuracy in space and time is achieved through a MUSCL-type reconstruction technique and through a strong stability preserving explicit Runge-Kutta time stepping. Special attention is given to the accurate numerical treatment of moving wet/dry fronts and boundary conditions. Furthermore, the model is applied to several examples of wave propagation over variable topographies and the computed solutions are compared to experimental data. TUCWave is used in the TANDEM project to provide reference solutions with a weakly nonlinear and dispersive model.

CARMEN Project-Team

6. New Software and Platforms

6.1. CEPS: a Cardiac ElectroPhysiology Simulator

The Carmen team develops a software library to perform high-performance numerical simulations in cardiac electrophysiology using unstructured three-dimensional grids. The software, called CEPS (*Cardiac Electrophysiology Simulation*) is developed 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 facilitate the development of new numerical methods and new physical models.

Compared to other existing software, 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. The largest part of CEPS was developed by the Junior Engineer M. Juhoor, supervised by N. Zemzemi, during the CEPS ADT (*Action de Développement Technologique*).

To enforce a sound development process, some engineering and validation tools are used:

- Git hosted at the Inria GForge (ceps) to manage versions;
- Cmake for the building process
- Jenkins, hosted at the Inria continuous integration service, which runs a test suite of about 200 tests after every commit.

Main users and developers of CEPS are the PhD students of Carmen, i.e.

- A. Gérard, who uses CEPS for patient-specific modeling, has implemented a bilayer model using coupled nodes.
- Charlie Douanla-Lountsi currently works on high-order temporal integration methods, for later integration in CEPS.
- P. E. Bécue is developing a code to run microscopic-scale models (section 3.4) and wrote a coupled node assembler to support this work.

Since January 2015, M. Fuentes from the *Service d'Experimentation et de Développement* (SED), is responsible for developing new features in CEPS, improve robustness, efficiency, and documentation. M. Juhoor, who has previously worked on CEPS, and works on the IDAM project, brings us from time to time his expertise. Actions done in 2016 include:

- support for P2 Lagrange finite Elements
- node partitioning using the PTScotch partitioner
- input files and VtkReader (M. Juhoor)
- code refactoring
- documentation writing

6.2. IDAM

The goal of the IDAM project is to define a collection of plugins in the MUSIC software in order to create realistic meshes for the CEPS code. MUSIC is a multimodal platform for cardiac imaging developed by the imaging team at IHU LIRYC (https://bil.inria.fr/fr/software/view/1885/tab). Information comes from magnetic resonance imaging and cardiac tomography performed in the clinic and in the LIRYC laboratories. Building complete cardiac models directly from imaging data requires expert knowledge and is time-consuming and error-prone: specific expertise and multiple software tools are often needed to process data stemming from medical imaging into realistic meshes and parameter distributions.

IDAM aims to streamline the workflow of a complete cardiac simulation: anatomical mesh generation from patient-specific data, description of simulation parameters, and eventually analysis of simulation results obtained by simulation packages like CEPS (https://bil.inria.fr/fr/software/view/2630/tab). IDAM integrates tools from other Inria teams by using specialized libraries, for example MMG (https://bil.inria.fr/fr/software/view/2824/tab) for high-quality mesh generation.

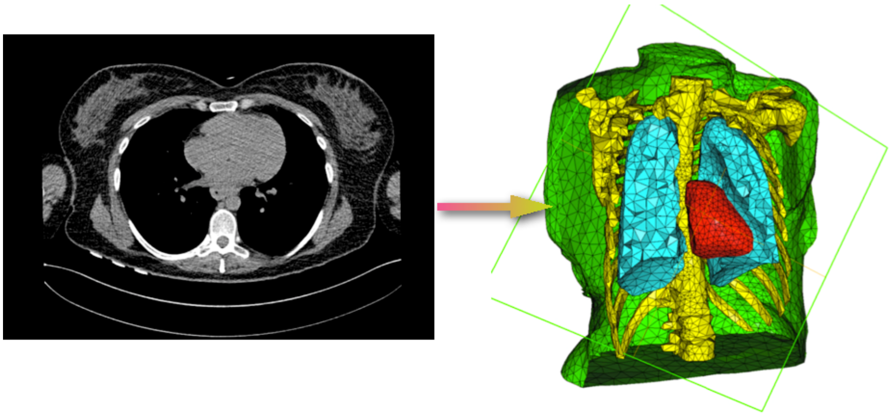


Figure 1. Mesh of a human torso and one of the X-ray computed-tomography slices on which it was based.

6.3. Platforms

6.3.1. Propag-5

Applied modeling studies performed by the Carmen team, especially M. Potse and M. Kania, in collaboration with IHU Liryc and foreign partners [39], [43], [18], [20], [14] [45], rely to a great extent on high-performance computations on the national supercomputers Curie, Occigen, and Turing. While the newly developed CEPS code is not ready to run efficiently on these systems we rely on an older code named Propag-5. This code is the result of a decades-long development first at the *Université de Montréal* in Canada, then at Maastricht University in the Netherlands, and finally at the Institute of Computational Science of the *Università della Svizzera italiana* in Lugano, Switzerland. Relatively small contributions to this code have been made by the Carmen team.

The predecessor of Propag-5, named Propag-4, was developed by M. Potse at the *Université de Montréal* [8]. It was based on earlier model code developed there by the team of Prof. R. Gulrajani [50], [53], and was parallellized with OpenMP to utilize the shared-memory SGI supercomputers available there at the time. Propag-4 was the first code ever able to run a bidomain reaction-diffusion model of the entire human ventricles; a problem 30 times larger than what had been reported before [8].

In order to utilize the more recent distributed-memory architectures Propag-4 was transformed into the hybrid MPI-OpenMP code Propag-5 at the Institute of Computational Science in Lugano by D. Krause and M. Potse [49]. The resulting code has been used for numerous applied studies. An important limitation of the Propag code is that it relies on a semi-structured mesh with a uniform resolution. On the other hand, the code scales excellently to large core counts and, as it is controlled completely with command-line flags and configuration files, it can be used by non-programmers. It also features

- a plugin system for membrane models,
- a completely parallel workflow, including the initial anatomy input and mesh partitioning, which allows it to work with meshes of more than 10^9 nodes,

- a flexible output scheme allowing hundreds of different state variables and transient variables to be output to file, when desired, using any spatial and temporal subsampling,
- a configurable, LUSTRE-aware parallel output system in which groups of processes write HDF5/netCDF files, and
- CWEB documentation of the entire code base.

The code has been stable and reliable for several years, and only minor changes are being made currently. It can be considered the workhorse for our HPC work until CEPS takes over.

6.3.2. Gepetto

Gepetto, named after a famous model maker, is a sofware suite that transforms a surface mesh of the heart into a set of (semi-)structured meshes for use by the Propag software or others. It creates the different fiber orientations in the model, including the transmurally rotating ventricular fibers and the various bundle structures in the atria (figure 2), and creates layers with possibly different electrophysiological properties across the wall. A practically important function is that it automatically builds the matching heart and torso meshes that Propag uses to simulate potentials in the torso (at a resolution of 1 mm) after projecting simulation results from the heart model (at 0.1 to 0.2 mm) on the coarser torso mesh [52]. Like Propag, the Gepetto software results from a long-term development that started in Montreal, Canada, around 2002. The code for atrial fiber structure was developed by our team.

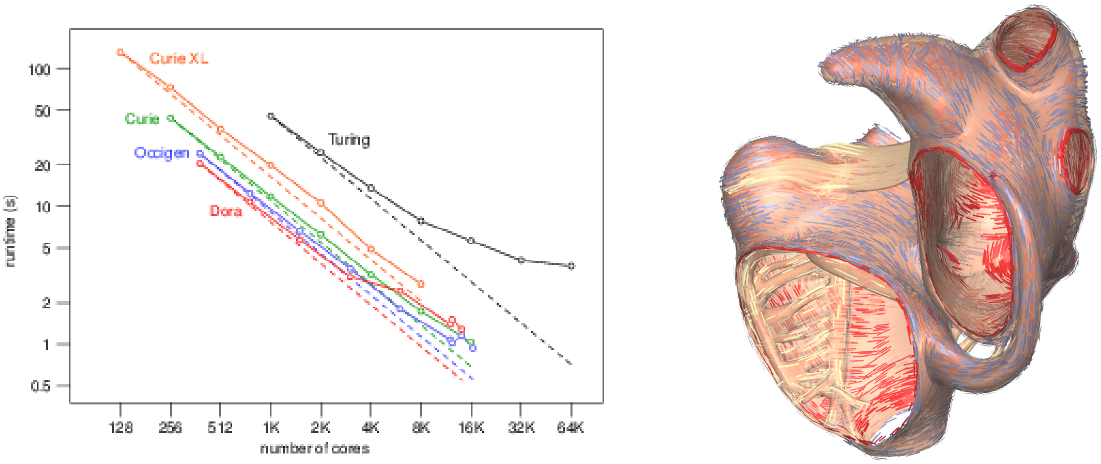


*Figure 2. **Left:** Strong scaling of the Propag-5 code on a monodomain reaction-diffusion equation for four systems: The Bull clusters Curie (small nodes and large nodes, XL) and Occigen, The Cray XC30 "Piz Dora" at the Swiss supercomputing center CSCS and the IBM BlueGene/Q "Turing". The graph shows the runtime needed for 10 ms of propagated activity using an explicit (forward) Euler integration. Dashed lines indicate the ideal scaling line with respect to the lowest number of cores measured. **Right:** Bundle structures and different layers of fiber orientation created by the Gepetto software.*

6.3.3. MUSIC

MUSIC is a multimodal platform for cardiac imaging developed by the imaging team at IHU LIRYC in collaboration with the Inria team Asclepios (https://bil.inria.fr/fr/software/view/1885/tab). It is based on the medInria software also developed by the Asclepios team. MUSIC is a cross-platform software for segmentation of medical imaging data, meshing, and ultimately also visualization of functional imaging data and model results.

Several members of the Carmen team use MUSIC for their work. The team also contributes a series of plugins for MUSIC through the IDAM project (section 6.2).

CARTE Team (section vide)

CASCADE Project-Team (section vide)

CASTOR Project-Team

4. New Software and Platforms

4.1. 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. A deposit with APP (Agence pour la protection des programmes) has been done in 2016.

- Participants: Jacques Blum, Cedric Boulbe and Blaise Faugeras
- Contact: Blaise Faugeras

4.2. 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. VacTH is foreseen to be used in the real-time plasma control loop on the WEST tokamak.

- Contact: Blaise Faugeras

4.3. CEDRES++

Functional Description

In Tokamaks, at the slow resistive diffusion time scale, the magnetic configuration in the plasma 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 P_1 finite element code CEDRES++ solves this free boundary equilibrium problem in direct and inverse mode and in static and evolutive formulations. 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) for the static case and the voltages applied to PF supplies in the evolutive one. The aim of the inverse problem is to find currents in the PF coils in order to best fit a given plasma shape. The code is one of the free boundary codes avalaible in the european Eurofusion - WPCD (WorkPackage Code Development for integrated modelling) platform.

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

4.4. FEEQS.M

Finite Element Equilibrium Solver in MATLAB
FUNCTIONAL DESCRIPTION

FEEQS.M (Finite Element Equilibrium Solver in Matlab) is a MATLAB implementation of the numerical methods in [Heumann2015] 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 (see [4]). The recent developments include:

- the comparison of FEM-BEM coupling (with B. Faugeras),
- overlapping mesh methods for free-boundary equilibrium,
- direct and inverse modes for simulations and optimal control approach to breakdown (with Eric Nardon, CEA Cadarache)
- 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: Remi Abgrall, Boniface Nkonga, Michael Papin and Mario Ricchiuto
- Contact: Boniface Nkonga

4.6. Jorek-Django

FUNCTIONAL DESCRIPTION

Jorek-Django is a new version of the JOREK software, for MHD modelling of plasma dynamic in tokamaks 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, Ayoub Iaagoubi, Ahmed Ratnani
- Contact: Hervé Guillard
- URL: https://gforge.inria.fr/projects/jorek/

4.7. 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 integration in time is based on a Strang splitting and Runge-Kutta schemes, with implicit treatment of the Lorentz terms (DIRK scheme). 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 the code is under development.

- Contact: Sebastian Minjeaud

4.8. 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

CEDAR Team

6. New Software and Platforms

6.1. New Software

6.1.1. CliqueSquare

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.

6.1.2. Compact

Compact reformulates conjunctive queries in the setting of ontology-based query anwering. It takes as input a conjunctive query and an ontology, and outputs a first-order rewriting of that query whenever it exists (without termination guarantee when it does not exists). To ease its use and dissemination, a novel version has been implemented by M. Thomazo based on the framework GRAAL, developed within the Inria Sophia-Antipolis team GraphIK by C. Sipieter, an engineer funded by an ADT. It will in particulary ease the integration with Semantic Web standards, as well as the use of query optimization techniques developed within Cedar for RDFS and DL-Lite$_\mathcal{R}$ to more general ontology languages.

6.1.3. RDF-Commons

RDF-Commons is a set of modules providing the abilities to *i)* load and store RDF data in a DBMS *ii)* parse RDF conjunctive queries *iii)* encode URIs and literals into integers *iv)* encode RDF conjunctive queries *v)* build statistics on RDF data *vi)* estimate the cost of the evaluation of a conjunctive query *vii)* saturate the RDF data, with respect to an RDF Schema *viii)*reformulate a conjunctive query with respect to an RDF Schema (ix) propose algebraic plans.

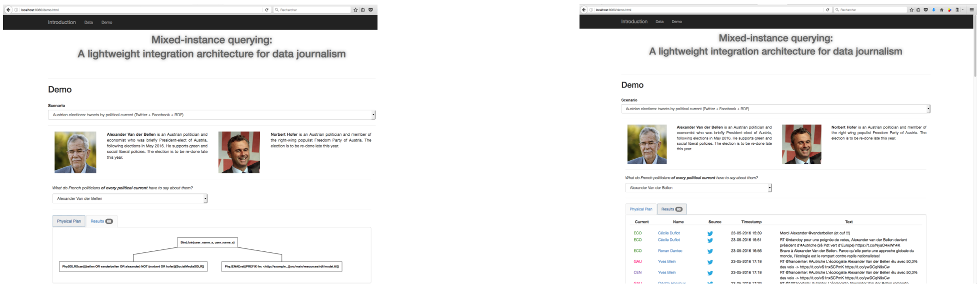
The algebraic plan part has been developed by A. Solimando and D. Bursztyn. An ADT funding for two years has been granted to consolidate and extend the development of RDF-Commons. The hiring process is ongoing.

6.1.4. RDFSummary

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.

6.1.5. Tatooine

We developed lightweight data integration system called Tatooine, based on our discussions with our journalist partners in the ANR ContentCheck project from the team “Les Décodeurs”. Tatooine allows to exploit heterogeneous data sources of different data models, which we view as a mixed data instance, by querying them together; Tatooine combines data from various sources within an integrated engine complemented by information extraction and data visualization modules. Figure 1 illustrates the functioning of Tatooine through screen captures: a set of tweets (JSON documents stored in SOLR) obtained through a full-text search are combined with information about their authors (RDF metadata stored in Jena TDB) and the results are presented to the users highlighting the political affiliation of the tweet authors.



Mixed-instance querying:
A lightweight integration architecture for data journalism

Demo

Scenario: Austrian elections: tweets by political current (Twitter + Facebook + RDF)

Alexander Van der Bellen is an Austrian politician and economist who was briefly President-elect of Austria, following elections in May 2016. He supports green and social liberal policies. The election is to be re-done late this year.

Norbert Hofer is an Austrian politician and member of the right-wing populist Freedom Party of Austria. The election is to be re-done late this year.

What do French politicians ***of every political current*** *have to say about them?*

Alexander Van der Bellen

Current	Name	Source	Timestamp	Text
ECO	Cécile Duflot	🐦	23-05-2016 15:39	Merci Alexander @vanderbellen (et ouf !!!)
ECO	Cécile Duflot	🐦	23-05-2016 15:51	RT @rdandoy pour une poignée de votes, Alexander van der Bellen devient président d'#Autriche (2è Pdt vert d'Europe) https://t.co/NyaO4wWh4K
ECO	Ronan Dantec	🐦	23-05-2016 16:56	Bravo à Alexander Van der Bellen. Parce qu'elle porte une approche globale du monde, l'écologie est le rempart contre replis nationalistes!
GAU	Yves Blein	🐦	23-05-2016 17:18	RT @franceinter: #Autriche L'écologiste Alexander Van der Bellen élu avec 50,3% des voix -> https://t.co/vS1nxSCPmK https://t.co/ywDCqN9xCw
CEN	Yves Blein	🐦	23-05-2016 17:18	RT @franceinter: #Autriche L'écologiste Alexander Van der Bellen élu avec 50,3% des voix -> https://t.co/vS1nxSCPmK https://t.co/ywDCqN9xCw

Figure 1. Tweet enrichment in Tatooine: evaluation plan (left) and results (right).

CELTIQUE Project-Team

3. New Software and Platforms

3.1. JSCert

Certified JavaScript
FUNCTIONAL DESCRIPTION

The JSCert project aims to develop a formal understanding of the JavaScript programming language. 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/

3.2. 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: Frederic Besson, David Pichardie, Pierre Vittet, Laurent Guillo, Laurent Hubert, Tiphaine Turpin and Nicolas Barre
- Contact: Frederic Besson
- URL: http://sawja.inria.fr/

3.3. SAWJA

Static Analysis Workshop for Java
KEYWORDS: Security - Software - Code review - Smart card
SCIENTIFIC 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.

See also the web page http://sawja.inria.fr/.

Version: 1.5

Programming language: Ocaml
FUNCTIONAL DESCRIPTION

Sawja is a toolbox for developing static analysis of Java code in bytecode format. Sawja provides advanced algorithms for reconstructing high-level programme representations. The SawjaCard tool dedicated to JavaCard is based on the Sawja infrastructure and automatically validates the security guidelines issued by AFSCM (http://www.afscm.org/). SawjaCard can automate the code audit process and automatic verification of functional properties.

- Participants: Frederic Besson, David Pichardie and Laurent Guillo
- Partners: CNRS - ENS Rennes
- Contact: Frederic Besson
- URL: http://sawja.inria.fr/

3.4. Timbuk

KEYWORDS: Proof - Ocaml - Program verification - 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/

3.5. 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).

Notably, the middle-end features:

- new important optimizations (Sparse Conditional Constant Propagation, and a coalescing phase on Conventional SSA)
- a generic dominance-based proof framework that rationalizes the proof process
- improved performance regarding compilation time

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

FUNCTIONAL DESCRIPTION

This software implements the HSBOF (Hybrid Sampling Bayesian Occupancy Filter) on GPU. It facilitates the integration of the model in an embedded chip.

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

6.2. DATMO (Detection and Tracking of Moving Objects)

FUNCTIONAL DESCRIPTION

This software is developped in the context of the autonomous driving assistance. It allows to detect, to track, and to classify mobile objects from LIDAR and mono-camera data. It can be linked or not with our previous implementation of the HSBOF software. The software is divided in 4 modules : Fusion, Detection, Tracking and Classification.

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

6.3. E.R.C.I.

Estimation of collision risks at road 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
FUNCTIONAL DESCRIPTION

This software is an implementation of the Occupancy Bayesian Filter (BOF) 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

Software in C++ for estimation based on the closed form solution

- Authors: Guillaume Fortier and Agostino Martinelli
- Contact: Agostino Martinelli

6.8. kinetics

FUNCTIONAL DESCRIPTION

Software computing decision support strategies and decision-making

- 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 for a single node (Android and Linux kernel, JVM) and a set of nodes (monitoring of flows between linux machines).
FUNCTIONAL DESCRIPTION

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

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

6.2. ELVIS

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

The studies that were performed since 2012 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 2013 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.
FUNCTIONAL DESCRIPTION

ELVIS is a visualisation tool geared to system security which enables analysts to visually explore log files using relevant representations. The tool accepts many different types of log file and can easily be extended to accept new ones opportunistically. Thanks to its data typing mechanisms, it can automatically choose relevant representations depending on the type of data that the analyst wants to observe.

- Participant: Nicolas Prigent
- Partner: SUPELEC
- Contact: Nicolas Prigent
- URL: https://hal.inria.fr/hal-00875668

6.3. GEPETO

GEoPrivacy-Enhancing TOolkit
KEYWORDS: Cyber attack - 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: CNRS - Université de Rennes 1
- 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: SUPELEC
- Contact: Eric Totel
- URL: http://www.rennes.supelec.fr/ren/perso/etotel/GNG/index.html

6.5. GroddDroid

KEYWORDS: Android - Detection - Malware
FUNCTIONAL DESCRIPTION

GroddDroid

1- locates suspicious code in Android application

2-computes execution paths towards suspicious code

3- forces executions of suspicious code

- Partners: CentraleSupélec - Insa Centre Val-de-Loire
- Contact: Valérie Viet Triem Tong
- URL: http://kharon.gforge.inria.fr/grodddroid.html

6.6. Kharon platform

KEYWORDS: Android - Malware - Dynamic Analysis
FUNCTIONAL DESCRIPTION

This platform executes Android applications and computes a graph representing all the information flows that occurred in the operating system due to a malicious execution. It can then classify observed behavior as benign or malicious. Access to this platform is currently in physically controlled at the high security laboratory (LHS) of Rennes.

- Partners: CentraleSupélec - Insa Centre Val-de-Loire
- Contact: Valérie Viet Triem Tong
- URL: http://kharon.gforge.inria.fr/

6.7. 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/

6.8. VEGAS

Visualizing, Exploring and Grouping AlertS
KEYWORDS: Security - Visualization - Cybersecurity - Intrusion Detection Systems (IDS) - SIEM
SCIENTIFIC DESCRIPTION

VEGAS explore the hypothesis that is is possible to offer to front-line security operators a visualization tool that allows the to perform a first informed triage of the alerts that were received from IDSes so as to group them and transmit them to security analysts in a relevant way.

FUNCTIONAL DESCRIPTION

VEGAS is a visualization tool that allows to easily identify, explore and group alerts generated by an IDS. This tool allows security operators to easily dispatch similar alerts to security analyst to help them study them more efficiently.

- Participants: Damien Cremilleux, Frédéric Majorczyk and Nicolas Prigent
- Partner: SUPELEC
- Contact: Damien Crémilleux

CLIME Project-Team

6. New Software and Platforms

6.1. Heimdali

- Participants: Isabelle Herlin, Dominique Bereziat and David Froger
- Contact: Isabelle Herlin

SCIENTIFIC DESCRIPTION

The main components of Heimdali concern:

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

FUNCTIONAL DESCRIPTION

The initial aim of the image processing library Heimdali was to replace an internal Inria library (named Inrimage) by 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 assimilation based on ITK (Insight Segmentation and Registration Toolkit http://www.itk.org). In reverse provide tools to ITK and contribute to the ITK community. Our software corresponds to issues related to satellite acquisitions but could be of interest for processing medical image sequences.

6.2. Image Forecast

- Authors: Isabelle Herlin and Yann Lepoittevin
- Contact: Isabelle Herlin

SCIENTIFIC DESCRIPTION

From a given number of images, Image Forecast synthetizes the future images at a given and short temporal horizon.

FUNCTIONAL DESCRIPTION

Image forecast includes two components:

- it estimates the dynamics from an image sequence. Various options are available in the software: stationarity, Lagrangian conservation, description of structures. The result is the motion field explaining the temporal evolution of image data.
- the estimated dynamics is applied for forecasting future images at short temporal horizon.

6.3. Polyphemus

- Participants: Sylvain Doré (CEREA, École des Pont ParisTech) and Vivien Mallet
- Contact: Vivien Mallet
- URL: http://cerea.enpc.fr/polyphemus/

FUNCTIONAL DESCRIPTION

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 forecast 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.

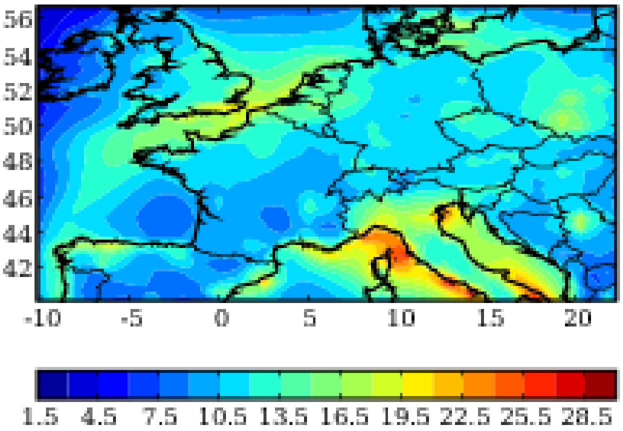


Figure 1. Map of the relative standard deviation (or spread, %) of an ensemble built with Polyphemus (ozone simulations, $\mu g\ m^{-3}$). The standard deviations are averaged over the summer of 2001. They provide an estimation of the simulation uncertainties.

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).

6.4. SoundCity - Ambiciti

- Authors: Pierre-Guillaume Raverdy (SED), Fadwa Rebhi (Mimove), Cong Kinh Nguyen (Mimove), Rajiv Bhatia (TheCivicEngine), Vivien Mallet and Valerie Issarny (Mimove)
- Contact: Valerie Issarny (Mimove)

FUNCTIONAL DESCRIPTION

Ambiciti measures the actual noise levels to which you are exposed. It can monitor noise levels throughout the day and inform you about your instantaneous, hourly and daily exposures.

Ambiciti also computes the air quality index in your region or at the exact location where you stand. You can also access to forecasts.

Ambiciti includes a lot of features:

- Measuring noise level, anytime on demand or automatically during the day,
- Air quality indexes, in the past, present and future hours or days,
- Pollution levels for nitrogen dioxide, fine particulate matter and ozone,
- Statistics on exposure to pollutions, hourly, daily, during daytime and nighttime,
- Maps with your noise measurements,
- Hourly air quality maps, at street resolution in Paris, San Francisco, Oakland, Richmond (California), at present time,
- The recommendation of pedestrian routes which minimize the exposure to noise pollution or to air pollution,
- The ability to take pictures with pollution levels on top.

6.5. Urban noise analysis

- Authors: Vivien Mallet, Raphael Ventura and Guillaume Cherel
- Contact: Vivien Mallet

FUNCTIONAL DESCRIPTION

This software merges noise simulations and mobile observations. It can extract a given region of a noise map and filter out the buildings. It extends a previous software for data assimilation of air pollution observations at city scale. This prior software computes the so-called best linear unbiased estimator (BLUE), with a special background error covariance model that depends on the city geometry. The extension for noise introduces special treatments for the errors in mobile observations, and includes more statistical verifications.

The software also comes with a Python module for the management of a large database of mobile noise measurements, especially with many filters relying the observations metadata.

The software finally includes the automatic generation of a report based on intensive measurements in a city district. This report targets participants of crowdsensing experiments.

6.6. Verdandi

- Participants: Vivien Mallet, Gautier Bureau (Medisim), Dominique Chapelle (Medisim), Sébastien Gilles (Medisim) and Philippe Moireau (Medisim)
- Contact: Vivien Mallet
- URL: http://verdandi.gforge.inria.fr/

FUNCTIONAL DESCRIPTION

Verdandi is a free and open-source (LGPL) library for data assimilation. It includes various 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.

COAST Project-Team

4. New Software and Platforms

4.1. MUTE

Multi-User Text Editor

FUNCTIONAL DESCRIPTION

MUTE (Multi-User Text Editor) is a web-based text editing tool that allows users to edit documents collaboratively in real-time. It implements our recent work on collaborative editing algorithms and more specifically the LogootSplit+ approach. 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.

- Participants: Gérald Oster, François Charoy, Claudia-Lavinia Ignat, Phillippe Kalitine, Matthieu Nicolas and Victorien Elvinger
- Contact: Gérald Oster
- URL: https://github.com/coast-team/mute/

4.2. NetFlux

Peer-to-Peer Network Library over WebRTC

FUNCTIONAL DESCRIPTION

NetFlux is a Nodejs library that allows users to deploy a peer-to-peer network between web browsers using the WebRTC technology.

- Participants: Gérald Oster, Phillippe Kalitine, Matthieu Nicolas.
- Contact: Gérald Oster
- URL: https://github.com/coast-team/netflux

4.3. MUTE-structs

Peer-to-Peer Network Library over WebRTC

FUNCTIONAL DESCRIPTION

MUTE-structs is a Nodejs module that provides an implementation of the LogootSplit CRDT algorithm. It is an optimistic replication algorithm that ensures eventual consistency on replicated text sequences. It is used in the MUTE real-time collaborative text editor.

- Participants: Gérald Oster, Claudia-Lavinia Ignat, Phillippe Kalitine, Matthieu Nicolas and Victorien Elvinger
- Contact: Gérald Oster
- URL: https://github.com/coast-team/mute-structs

4.4. Replication Benchmarker

FUNCTIONAL DESCRIPTION

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 event traces. These event traces can be produced randomly according to different parameters, can be extracted from actual 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 terms of execution time, memory footprint and quality of merge result (compared to manual merge history stored in git repositories).

- Participants: Pascal Urso and Gérald Oster
- Contact: Pascal Urso
- URL: https://github.com/score-team/replication-benchmarker/

4.5. Rivage

Real-tIme Vector grAphic Group Editor
FUNCTIONAL DESCRIPTION

Rivage is a real-time collaborative graphical editor. Several users can edit at the same time and in real-time a graphical document, user changes being immediately seen by the other users. The editor relies on a peer-to-peer architecture where users can join and leave the group at any time. Each user has a copy of the shared document and user changes on the document copies are merged in real-time by using a CRDT (Commutative Replicated Data Type) algorithm.

- Participant: Claudia-Lavinia Ignat
- Contact: Claudia-Lavinia Ignat
- URL: https://github.com/stephanemartin/rivage/

COATI Project-Team

6. New Software and Platforms

6.1. BigGraphs

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 : 240GB on disk, 398M vertices, 23G edges, average degree of 58 and max degree of 24635412.

We started the project in 2014 with the evaluation of existing middlewares (GraphX / Spark and Giraph / Hadoop). After having tested some useful algorithms (written according to the BSP model) we decided to develop our own platform.

This platform is based on the existing BIGGRPH library and we are now in the phasis 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 also have solved problems of scalability, in particular concerning the communication layer with billions of messages exchanged between BSP steps. 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.

- Participants: Luc Hogie, Nicolas Chleq, David Coudert, Michel Syska.
- Partner: This project is a joint work of the three EPI COATI, DIANA and SCALE and is supported by an ADT grant.
- Contact: Luc Hogie
- URL : http://www.i3s.unice.fr/~hogie/biggrph/

ADDITIONAL SOFTWARES

The following software are useful tools that bring basic services to the platform (they are not dedicated to BIGGRPH). Participants : Luc Hogie, Nicolas Chleq

- JAC-A-BOO is a framework aiming at facilitating the deployment and the bootstrapping of distributed Java applications over Share-Nothing Clusters (SNCs). The primary motivation for developing JAC-A-BOO is to have an efficient and comprehensive deployment infrastructure for the BIGGRPH distributed graph library. http://www.i3s.unice.fr/~hogie/jacaboo
- LDJO (Live Distributed Java Objects) is a framework for the development and the deployment of Java distributed data structures. Alongside with data aspect of distributed data structures, LDJO comes with mechanisms for processing them in a distributed/parallel way. In particular it provides implementations of Map/Reduce and Bulk Synchronous Parallel (BSP). http://www.i3s.unice.fr/~hogie/ldjo
- OCTOJUS provides an object-oriented RPC (Remote Procedure Call) implementation in Java. At a higher abstraction level, OCTOJUS provides a framework for the development of systolic algorithms, a batch scheduler, as well as an implementation of Map/Reduce. The latter is used in the BIGGRPH graph computing platform. http://www.i3s.unice.fr/~hogie/octojus

6.2. GRPH

The high performance graph library for Java

FUNCTIONAL DESCRIPTION

GRPH is an open-source Java library for the manipulation of graphs. Its main design objectives are to make it simple to use and extend, efficient, and, according to its initial motivation: useful in the context of graph experimentation and network simulation. GRPH also has the particularity to come with tools like an evolutionary computation engine, a bridge to linear solvers, a framework for distributed computing, etc.

GRPH achieves great efficiency through the use of multiple code optimization techniques such as multi-core parallelism, caching, performant data structures and use of primitive objects, interface to CPLEX linear solver, exploitation of low-level processor caches, on-the-fly compilation of specific C/C++ code, etc.

Unlike other graph libraries which impose the user to first decide if he wants to deal with directed, undirected, hyper (or not) graph, the model offered by GRPH is unified in a very general class that supports mixed graphs made of undirected and directed simple or hyper edges.

We have identified more than 600 users of GRPH since 2013. Inside Inria we collaborate with the AOSTE EPI, for example we recently added a new algorithm (proposed by N. Cohen / LRI) for iterating over the cycles of a given graph in the TimeSquare tool. We also have integrated the discrete-events simulation engine of DRMSIM and some dynamic models (evolution of the connectivity with the mobility of nodes) to GRPH. GRPH includes bridges to other graph libraries such as JUNG, JGraphT, CORESE (a software developed by the WIMMICS team Inria-I3S), LAD (C. Solnon, LIRIS), Nauty (B. D. McKay) or Sagemath. L. Viennot has proposed an implementation of the 4-sweep diameter algorithm designed at LIAFA .

- Participants: Luc Hogie, Nathann Cohen, David Coudert and Michel Syska.
- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/grph/

6.3. Sagemath

SageMath
SageMath is a free open-source mathematics software system, initially created by William Stein (Professor of mathematics at Washington University), and now maintained by a large community of contributors. 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.
We contribute the addition of new graph algorithms along with their documentations and the improvement of underlying data structures.

- Contact: David Coudert
- URL: http://www.sagemath.org/

COFFEE Project-Team

5. New Software and Platforms

5.1. APPartFlow

FUNCTIONAL DESCRIPTION

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

5.2. Compass

FUNCTIONAL DESCRIPTION

Compass 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.

- Participants: Thierry Goudon, Roland Masson, Cindy Guichard, Chang Yang and Robert Eymard
- Contact: Roland Masson
- URL: http://math.unice.fr/~massonr/ComPASSHighEnergyGeothermy.html

5.3. NS2DDV

FUNCTIONAL DESCRIPTION

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.

- Contact: Creusé Emmanuel
- URL: math.univ-lille1.fr/~simpaf/SITE-NS2DDV/home.html

5.4. SimBiof

FUNCTIONAL DESCRIPTION

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: Thierry Goudon

COMETE Project-Team

6. New Software and Platforms

6.1. libqif - A Quantitative Information Flow C++ Toolkit Library

Participants: Konstantinos Chatzikokolakis [correspondant], Susheel Suresh, Tymofii Prokopenko.

https://github.com/chatziko/libqif

The goal of libqif is to provide an efficient C++ toolkit implementing a variety of techniques and algorithms from the area of quantitative information flow and differential privacy. We plan to implement all techniques produced by Comète in recent years, as well as several ones produced outside the group, giving the ability to privacy researchers to reproduce our results and compare different techniques in a uniform and efficient framework.

Some of these techniques were previously implemented in an ad-hoc fashion, in small, incompatible with each-other, non-maintained and usually inefficient tools, used only for the purposes of a single paper and then abandoned. We aim at reimplementing those – as well as adding several new ones not previously implemented – in a structured, efficient and maintainable manner, providing a tool of great value for future research. Of particular interest is the ability to easily re-run evaluations, experiments and case-studies from all our papers, which will be of great value for comparing new research results in the future.

The library was under constant development in 2016 with several new features added this year. The project's git repository shows for this year 77 commits by 2 contributors, containing 5697 line additions and 4067 line removals. Some of the techniques already implemented are:

- Standard leakage measures: Shannon, min-entropy, guessing entropy
- Measures from the g-leakage framework [26]
- Channel factorization
- Hyper distribution produced by a channel run under a prior
- Standard differential privacy mechanisms from the literature
- The planar Laplace mechanism of [27]
- The planar Geometric mechanism
- The tight-constraints mechanism of [29] (also with equality constraints)
- Optimal mechanism construction under DP
- The standard Kantorovich metric as well as the multiplicative variant from [28]
- Additive capacity for specific prior over all gain functions [2]
- All operations are supported for both doubles (for precision) and floats (for memory efficiency)
- All operations involving only rational quantities are supported using arbitrary precision rational arithmetic, allowing to obtain exact results
- Native linear programing for rationals
- Simple installation in OSX via Homebrew

Many more are scheduled to be added in the near future.

6.2. D-SPACES - constraint systems with space and extrusion operators

Participants: Frank Valencia, Yamil Salim Perchy.

http://www.lix.polytechnique.fr/~perchy/d-spaces/

D-SPACES is an implementation of constraint systems with space and extrusion operators. Constraint systems are algebraic models that allow for a semantic language-like representation of information in systems where the concept of space is a primary structural feature. We give this information mainly an epistemic interpretation and consider various agents as entities acting upon it. D-SPACES is coded as a c++11 library providing implementations for constraint systems, space functions and extrusion functions. The interfaces to access each implementation are minimal and thoroughly documented. D-SPACES also provides property-checking methods as well as an implementation of a specific type of constraint systems (a boolean algebra). This last implementation serves as an entry point for quick access and proof of concept when using these models. In [22] an illustrative example of using the library is given, in the form of a small social network where users post their beliefs and utter their opinions.

6.3. Trace Slicer for Timed Concurrent Constraint Programming

Participants: Catuscia Palamidessi, Carlos Olarte.

http://subsell.logic.at/slicer/

Concurrent Constraint Programming (CCP) is a declarative model for concurrency aimed at specifying reactive systems, i.e. systems that continuously interact with the environment. Some previous works have developed (approximated) declarative debuggers for CCP languages. However, the task of debugging concurrent programs remains difficult. This tool is a companion for the existing debugging techniques. Slicing in our proposal consists of considering partial computations, which show the presence of bugs. Often, the quantity of information in a trace is overwhelming, and the user gets easily lost, since she cannot focus on the sources of the bugs. Our slicer allows for marking part of the state of the computation and assists the user to eliminate most of the redundant information in order to highlight the errors. See [19] for further details.

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, Benjamin Heymann and Jinyan Liu
- 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
- URL: http://www.safety-line.fr

6.3. Bocop HJB

- Participants: Joseph Frédéric Bonnans, Pierre Martinon, Benjamin Heymann and Jinyan Liu
- Contact: Joseph Frédéric Bonnans
- URL: http://bocop.org

COMPSYS Team

6. New Software and Platforms

6.1. 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. Status: proof of concept, see related paper [2].

- Partner: ENS Lyon
- Contact: Alexandre Isoard

6.2. PolyOrdo

Polynomial Scheduler
FUNCTIONAL DESCRIPTION

Computes a polynomial schedule for a sequential polyhedral program having no affine schedule, in lieu of multidimensional schedules. Uses algorithms for finding positive polynomials in semi-algebraic sets. Status: proof of concept software, see related paper [14].

- Contact: Paul Feautrier

6.3. OpenOrdo

OpenStream scheduler
FUNCTIONAL DESCRIPTION

Finds polynomial schedules for the streaming language OpenStream. Main use: detecting deadlocks. The scheduler has been extended to bound the size of stream buffers, either directly or as a side-effect of constructing bounded delay schedules. An effort for bounding the number of in-flight tasks is under way.

Status: proof of concept, see related paper [1].

- Contact: Paul Feautrier

6.4. 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.

Status: proof of concept, unfinished, see Alexandre Isoard's thesis [17].

- Partner: ENS Lyon
- Contact: Alexandre Isoard

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 [34] 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 [40], [39] 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 [35] 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,

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[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 [42], CTL [30], ACTL [32], etc.) to be defined in XTL.
- PBG (*Partitioned BCG Graph*) is a file format implementing the theoretical concept of *Partitioned LTS* [38] 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 [50] 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 [36] 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 TRAIAN Compiler

Participants: Hubert Garavel [correspondent], Frédéric Lang, Wendelin Serwe.

We develop a compiler named TRAIAN, see § 5.2), for translating LOTOS NT descriptions into C programs, which will be used for simulation, rapid prototyping, verification, and testing.

The current version of TRAIAN, which handles LOTOS NT types and functions only, has useful applications in compiler construction [37], being used in all recent compilers developed by CONVECS.

The TRAIAN compiler can be freely downloaded from the CONVECS Web site [0].

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[0] http://convecs.inria.fr/software/traian

CORSE Project-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 creation of a machine description library for all parts of the TIREX project, secondly, the development of tools for parsing assembly code.

We developed `archinfo`, a LLVM based library that allows programatic access to descriptors for a target CPUs instructions and registers. The focus was to expose information that was not already available from LLVM, such as machine operand types (float or integer, bitwidth, ...) and flags describing the high level behaviour of the instructions.

The, also LLVM based, assembly parser is intended to be used for translating assembly files generated by common compilers to TIREX, but it can also handle a number of idioms usually found in hand written assembly code. It reconstructs some high level information required for the TIREX format, such as the control flow and call graph, from the assembly code. We also started investigating how our existing tools can be extended to directly parse binary code and reconstruct information from them.

5.2. QEMU plugins

We have collaborated with STMicroelectronics on extending the QEMU CPU emulator with a plugin system. These plugins allow users to observe and modify the machine code emitted by QEMUs binary translator.

We have leveraged this to start development on a number of tools for profiling and performance debugging.

- cachesim: A QEMU plugin that feeds memory accesses observed during program execution into the DineroIV cache simulator. This allows estimating the number of a cache misses caused by each instruction of a program. Using this information we can also estimate the amount of memory bandwidth required by a program. This in turn can be used to diagnose if the applications performance is constrained by memory or CPU resources.
- dep-rate: A QEMU plugin that uses a shadow memory to detects data dependencies between instructions and correlates them with cache misses reported by DineroIV to estimate the performance impact of these dependencies.
- cpath: A QEMU plugin that estimates the optimal execution time of a program on an infinitely parallel CPU and compares it to that for a more realistic model of a CPU. This comparison is used to judge the amount of instruction level parallelism existing in a program.

5.3. Givy

Givy is a runtime developed as part of the PhD thesis of François Gindraud. It is designed for architectures with distributed memories, with the Kalray MPPA as the main target. It executes dynamic data-flow task graphs, annotated with memory dependencies. It automatically handles scheduling and placement of tasks (using the memory dependency hints), and generate memory transfers between distributed memory nodes when needed by using a software cache coherence protocol. An important part of the work corresponds on implementing and testing a memory allocator with specific properties that is a building block of the whole run time. This memory allocator is also tuned to work on the MPPA and its constraints, turning with very little memory and being efficient in the context of multith readed calls.

5.4. Dynamic Dependence Graph (DDG)

By instrumenting the memory accesses, at the LLVM IR level, of a hand selected region of a program, the DDG tool builds a graph with all dynamic instructions. Each instruction, i.e. a node in the graph, is identified by a statement identifier, mapping the dynamic instruction to a static statement, and an induction vector, containing the trip counters of loops surrounding the related statement. Edges connecting these nodes represent either data dependence, reuse or anti-dependence among the instructions, obtained by using the shadow memory technique, that labels ownership to a given written memory position to a dynamic instruction, and creating relationship to it to instructions that read the exact same memory position. Instructions that have a statically known formula (SCEVs) are not tracked, allowing our technique to remove, for example, obvious dependencies from a loop iteration to the next, and still track integer instructions. As the number of dynamic instructions, even in very simple applications, grows extremely fast, the generated graph does not to fit in main memory just after a few hundred loop iterations, our tool allows limiting the number of loop iterations that are tracked. Dependencies between iterations outside the observed iteration space can either be ignored or clamped as being generated by a single instruction. The generated graph can be used to guide loop optimizers, that could not extract precise dependencies. It can also be used by performance debugging tools, in order to determine if it is possible to obtain a new instruction schedule that would improve locality.

5.5. Integer polynomial Fourier-Motzkin elimination

Quantifier elimination is the process of removing existential variables of a given formula, obtaining one that is simpler in the number of variables, and that is implied by the original formula. A very well known algorithm is the Fourier-Motzkin elimination process, that given a system (or formula) of inequalities removes variables by combining all upper and lower bounds of such variables. At each step a variable is selected and eliminated. The very first limitation of this algorithm is the fact that it is designed for linear systems, where all coefficients of the variable being eliminated are numeric values, and the inequality can be classified as either a upper or lower bound. When dealing with polynomials, all possible values, positive, negative, or zero, for an coefficient, that is, a symbolic expression, must be explored. To avoid this requirement we use the positiveness algorithm, proposed by Mark Schweighofer, to retrieve symbolic coefficient signs. In fact, this algorithm is of major importance when resolving system over integer variables, instead of reals, as it is used in many other techniques required to preserve the precision of the simplified formula, such as symbolic normalization, convex hull detection, redundancy removing. Our C++ implementation uses GiNaC for symbolic expressions manipulation.

5.6. 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 can be dowloaded at this address https://forge.imag.fr/projects/boast/.

BOAST was already used to generate and optimize the computing kernels of three scientific applications:

- BigDFT: A massively parallel electronic structure code using wavelet basis set.
- SPECFEM: Computational Infrastructure for Geodynamics.
- Gysela: Fusion plasma simulations.

BOAST is currently used in the context of the European H2020/HPC4E project. The computing kernels of two scientific applications are currently studied with BOAST:

- Alya: Large Scale Computational Mechanics.
- Hou10ni: Solutions to accoustics wave propagation problems. This code is developed by the Magique3D Inria team (Pau, Julien Diaz).

Frédéric Desprez presented BOAST at the CSCD workshop http://www.netlib.org/utk/people/JackDongarra/CCDSC-2016/ in October 2016. After this workshop, a paper was submited at the Internationaj Journal on High Performance Computing Applications (IJHPCA).

BOAST was also used in the Bulldog project during the last CERMACS summer school http://smai.emath.fr/cemracs/cemracs16/ in July 2016. A joint paper with CEA researchers from Cadarache and Maison de la Simulation was also submitted to present the results of the Bulldog project.

5.7. mcGDB: Interactive debugging of OpenMP programs

MCGDB introduced the concept of *programming-model centric* source-level interactive debugging as an extension of the traditional language-level interactive debugging. The idea was to integrate into debuggers the notion of *programming models*, as abstract machines running over the physical ones. These abstract machines, implemented by runtime libraries and programming frameworks, provide the high-level primitives required for the implementation of today's parallel applications.

We developed a proof-of-concept, mcGDB, as a Python extension of GDB, the debugger of the GNU project. mcGDB was initially developed by Kevin Pouget during his thesis with STMicroelectronics. mcGDB is currently extended with the Nano2017/DEMA project.

We proposed the new support of mcGDB for OpenMP task-based programming. This support consists of task-based execution representation and control improvements, in cooperation with Temanejo graphical debugger. We also studied import implementation details of mcGDB, related to the support of multiple OpenMP environments and CPU architectures; the separation of cross-cutting concerns (user interaction and execution representing) through aspect-oriented programming, and the first steps of mcGDB micro-benchmarking.

mcGDB [30] was presented at the second OpenMPCon developpers conference in Nara.

CQFD Project-Team

6. New Software and Platforms

6.1. 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

6.2. 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

6.3. 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

6.4. QuantifQuantile

FUNCTIONAL DESCRIPTION

QuantifQuantile is an R package that allows to perform quantization-based quantile regression. The different functions of the package allow the user to construct an optimal grid of N quantizers and to estimate conditional quantiles. This estimation requires a data driven selection of the size N of the grid that is implemented in the functions. Illustration of the selection of N is available, and graphical output of the resulting estimated curves or surfaces (depending on the dimension of the covariate) is directly provided via the plot function.

- Isabelle Charlier, Jérôme Saracco
- Contact: Isabelle Charlier
- URL: https://cran.r-project.org/web/packages/QuantifQuantile/index.html

6.5. biips

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: Francois Caron and Adrien Todeschini
- 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

CTRL-A Team

6. New Software and Platforms

6.1. Heptagon BZR

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.

Heptagon BZR is an extension of Heptagon, equipped with a behavioral contract mechanisms, where assumptions can be described, as well as an "enforce" property part. Its main feature is to include discrete controller synthesis within its compilation. The semantics of contracts is that the property should be enforced by controlling the behaviour of the node equipped with the contract. This property will be enforced by an automatically built controller, which will act on free controllable variables given by the programmer.

- Participants: Adrien Guatto, Marc Pouzet, Cédric Pasteur, Léonard Gerard, Brice Gelineau, Gwenael Delaval and Eric Rutten
- Contact: Gwenaël Delaval
- http://bzr.inria.fr

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: https://gforge.inria.fr/projects/grasp/

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: Eric 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: Eric 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. Queueing Systems

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/

6.6. Data analysis tools

6.6.1. Twitter link predictions

FUNCTIONAL DESCRIPTION

Inference, study and prediction of the dynamics of the Twitter mention network

- Participants: Hadrien Hours, Eric Fleury and Márton Karsai
- Contact: Márton Karsai
- URL: https://github.com/HadrienHours/TwitterMentionNetworkLinkPrediction

6.7. Platforms

6.7.1. 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 Researchâs âÃquipements dâExcellenceâ (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/

DATAMOVE Team

5. New Software and Platforms

5.1. 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).
The OAR ecosystem also include several associated software tools that proved to be useful independently from OAR. Among theses, two softwares play a major role in the support our research studies. The first one is Kameleon (http://kameleon.imag.fr), a tool to help enhancing reproducibility of experiments by guarantee the ability to reproduce the complete used software stacks. The second one is Batsim (https://gforge.inria.fr/projects/batsim) a RJMS simulator based on SimGrid. Batsim simulates job execution taking into account the target platform hardware capabilities through SimGrid, while scheduling is performed by an actual job management system. A comprehensive API enables to easily plug into BatSim various job management systems like OAR.

- Participants: Olivier Richard, Pierre Neyron, Salem Harrache and Bruno Bzeznik
- Partners: CIMENT - CNRS - Grid'5000 - LIG
- Contact: Olivier Richard
- URL: http://oar.imag.fr

5.2. FlowVR

KEYWORDS: HPC - In Situ Processing - Computational Steering
SCIENTIFIC DESCRIPTION FlowVR is an open source middelware to augment parallel simulations running on thousands of cores with in situ processing capabilities and live steering. FlowVR offers a very flexible environment while enabling high performance asynchronous in situ and in transit processing.
FUNCTIONAL DESCRIPTION FlowVR adopts the "data-flow" paradigm, where your application is divided as a set of components exchanging messages (think of it as a directed graph). FlowVR enables to encapsulate existing codes in components, interconnect them through data channels, and deploy them on distributed computing resources. FlowVR takes care of all the heavy lifting such as application deployment and message exchange.

- Participants: Bruno Raffin, Matthieu Dreher, Jérémy Jaussaud
- Contact: Bruno Raffin
- URL: http://flowvr.sf.net

5.3. Platforms

5.3.1. Grid’5000 (https://www.grid5000.fr/) and meso center Ciment (https://ciment.ujf-grenoble.fr)

We have been very active in promoting the factorization of compute resources at a regional and national level. We have a three level implication, locally to maintain a pool of very flexible experimental machines (hundreds of cores), regionally through the CIMENT meso center (Equipex Grant), and nationally by contributing to the Grid’5000 platform, our local resources being included in this platform. Olivier Richard is member of Grid’5000 scientific committee and Pierre Neyron is member of the technical committee. The OAR scheduler in particular is deployed on both infrastructures. We are currently preparing proposals for the next generation machines within the context of the new university association (Univ. Grenoble-Alpes).

DATASHAPE Team

6. New Software and Platforms

6.1. GUDHI

Geometric Understanding in Higher Dimensions
SCIENTIFIC DESCRIPTION

The current release of the GUDHI library includes:

- Data structures to represent, construct and manipulate simplicial and cubical complexes.
- Algorithms to compute simplicial complexes from point cloud data.
- Algorithms to compute persistent homology and multi-field persistent homology.
- Simplification methods via implicit representations.

FUNCTIONAL DESCRIPTION

The GUDHI open source library will provide the central data structures and algorithms that underlie 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.

- Participants: Jean-Daniel Boissonnat, Marc Glisse, Mariette Yvinec, Clément Maria, David Salinas, Paweł Dłotko, Siargey Kachanovich and Vincent Rouvreau
- Contact: Jean-Daniel Boissonnat
- URL: http://gudhi.gforge.inria.fr/

DEDUCTEAM Team

5. New Software and Platforms

5.1. Software of the team

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
  - Archsat: theorem prover using tableaux-like rules with a SAT core
- 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

5.2. Novelties of the year

The main novelties this year are:

- CoLoR has been ported to Coq 8.5.
- F. Blanqui started to develop a prototype for developing Dedukti proofs interactively.

DEFI Project-Team

6. New Software and Platforms

6.1. 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/

6.2. 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/

6.3. 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/

6.4. 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/

6.5. 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/

6.6. SAXS-EM

This software solves the inverse problem of determining nono-paticles size distrubutions from SAXS measurements.

FUNCTIONAL DESCRIPTION

This software is written in matlab and determine size distributions is isotropic samples from measurements of X-ray diffraction at small angles. It treats the case of diluted and dense particle distributions.

- Contact: Houssem Haddar, Zixian Jiang
- URL: http://www.cmap.polytechnique.fr/~haddar/

DEFROST Team

6. New Software and Platforms

6.1. SOFA

Simulation Open Framework Architecture

KEYWORDS: Real time - Multi-physics simulation - Medical applications

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.

Since 2016, SOFA development and maintenance is now coordinated by the SOFA Consortium.

DEFROST is an active member of the consortium steering committee; beside his mission of Inria continuous integration support team coordinator, Bruno Carrez is in charge of the continuous integration setup of the SOFA consortium.

- Participants: Christian Duriez, Jeremie Dequidt, Bruno Carrez, Damien Marchal, Eulalie Coevoet, Frederick Largilliere
- Partner: Sofa consortium, projet-team Mimesis, projet-team Imagine, projet-team Asclepios, In-Simo, Anatoscope
- Contact: Hugo Talbot
- URL: http://www.sofa-framework.org

6.2. Soft-robot plugin for Sofa

Soft-robot plugin for Sofa

KEYWORDS: Simulation - Soft-Robot - Inverse models - Finite Element Method - Quadratic Programmings

FUNCTIONAL DESCRIPTION The soft-robot plugin consists in a new framework to simulate and control soft robots. This framework is based on a mechanical modeling of the robot elements in Sofa combined with fast real-time direct/inverse FEM solvers.

The keypoint of the approach implemented is that the same modeling is used for interactive simulation of its behavior and interactive control of the fabricated robots. This plugin was developped during the ADT project SORBET that ended in 09/2016.

- Participants: Eulalie Coevoet, Olivier Goury, Frederick Largilliere, Bruno Carrez, Damien Marchal, Jérémie Dequidt and Christian Duriez
- Contact: Eulalie Coevoet and Christian Duriez
- URL: https://project.inria.fr/softrobot/

DIANA Project-Team

5. New Software and Platforms

5.1. ACQUA

Participants: Chadi Barakat [contact], Thierry Spetebroot, 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. 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], Mondi Ravi.

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 is supported by the UCN@Sophia Labex in 2016/2017 (funding the engineer Mondi Ravi) In August 2016, we released the first stable public release of ElectroSmart. On the 20th December 2016 we had 1502 downloads in Google Play, an average score of 4,66/5, 800 active users, 22 millions measured signals and 500k measured geographic zones.

- URL: http://es.inria.fr
- Version: 1.1
- 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-ng

Participants: Thierry Parmentelat [correspondant], Thierry Turletti, Mario Antonio Zancanaro.

During the past couple of years, we had developped NEPI, the Network Experimentation Programming Interface, as a wide spectrum tool for orchestrating network experiments on network experimentation platforms.

In the more specific context of R2lab, we have been facing more stringent requirements in terms of response time, especially when synchonizing the parallel parts of a wireless experiment. For that reason, and also because the NEPI codebase was starting to feel much too large for its actual usage, and consequently very brittle, we have decided to start and put together a new set of components, named **nepi-ng** for nepi new generation.

At this point, nepi-ng has a much smaller scope than NEPI used to have, in that it only supports remote control of network experiments over ssh. As a matter of fact, in practice, this is the only access mechanism that we need to have for running experiments on both R2lab, and PlanetLab Europe.

For that reason, the actual size of the nepi-ng codebase is about 12 times smaller than the one of NEPI. However, running the same experiment on R2lab turns out to be about 10 times faster using nepi-ng rather than NEPI, that in this context is impeded by its generic model for resources, that prevents NEPI from being as reactive as what can be achieved with nepi-ng.

The design of nepi-ng of course is modular, so that it will be perfectly possible to add other control mechanisms to this core if and when this becomes necessary.

- URL: http://nepi-ng.inria.fr
- Version: 0.5
- Keywords: networking experimentation, orchestration
- License: CC BY-SA 4.0
- Type of human computer interaction: python library
- OS/Middleware: Linux
- Required library or software: python-3.5 / asyncio
- Programming language: python3

5.4. 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 2016, OpenLISP is used to provide connectivity between satellite sites of the LISP-Lab project.

- 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: http://ddt-root.org

5.5. Platforms

5.5.1. Reproducible research laboratory ($\mathrm{R}^2\mathrm{lab}$*)*

Scientific evaluation of network protocols requires for experiment results to 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 the last couple of years, an anechoic chamber, with RF absorbers preventing radio waves reflections and with a 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 operated for 2 years now, 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.

During 2016, our focus regarding $\mathrm{R}^2\mathrm{lab}$ has been set on the following aspects. First, we have deployed USRPs (Universal Software Radio Peripherals) together with hardware devices for controlling these USRP extensions. This is extremely interesting, as it considerably widens the fields of application for the tesbed. In particular, and that was our second angle for improvements this year, we have taken advantage of the USRP hardware to provide support for OpenAirInterface-based deployments in the chamber. That feature was demonstrated for example during the formal opening that took place on November 9 this year, where it was demonstrated how to set up a private LTE network in 3 minutes.

For more details see http://r2lab.inria.fr.

DICE Team

5. New Software and Platforms

5.1. BitBallot

FUNCTIONAL DESCRIPTION

The BitBallot voting protocol is designed to target large scale communities. The protocol allows users to share only restricted amounts of their data and computation with central platforms as well as other peers. Convinced by the need of new election mechanisms, to support emerging forms of more continuous democracy, we are developing BitBallot, to allow elections to be organized independently of any central authority. The protocol guarantees the following properties, anonymity of the data sources, non interruptible run-time, global access to results, and non predictability of results through partial communication spying.

- Contact: Stéphane Grumbach, Ste´phane Frénot, Damien Reimert, Robert Riemann

5.2. C3PO

FUNCTIONAL DESCRIPTION

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 those networks. They rely 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 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.

- Contact: Ste´phane Frénot, Damien Reimert

5.3. 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.

FUNCTIONAL DESCRIPTION

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: Ste´phane Frénot, Ste´phane Grumbach
- URL: http://www.jumplyn.com

DIONYSOS Project-Team

6. New Software and Platforms

6.1. The Passive Test Tool (ttproto) and CoAP Testing Tool

`ttproto` is an experimental tool for implementing testing tools, for conformance and interoperability testing. It was first implemented to explore interesting features and concepts for the TTCN-3 standard. It was also used to implement a passive interoperability test suite we provided for the CoAP (Constrained Application Protocol) interoperability event held in Paris in March 2012. It is currently used for the purpose of developing testing tools (for interoperability and conformance testing) for the F-interop european project (see http://www.f-interop.eu/). This tool is implemented in `python3` and its design was influenced mainly by TTCN-3 (abstract model, templates, snapshots, behavior trees, communication ports, logging) and by Scapy (syntax, flexibility, customizability) Its purpose is to facilitate rapid prototyping and experimentation (rather than production use). We chose to maximize its modularity and readability rather than performances and real-time considerations.

- Participants: César Viho, Federico Sismondi
- Contact: César Viho, Federico Sismondi
- http://www.irisa.fr/tipi

6.2. T3DevKit and IPv6 testing tools

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).

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) provides an object oriented framework to manipulate TTCN-3 entities (values, ports, timers, external functions). T3DevKit offers an implementation of the TRI and TCI standard interfaces a default implementations for the system adapter (SA), platform adapter (PA), test management (TM), test logging (TL) and component handling (CH) modules and a default codec. Built-in scripts for the generation of executable test suite, which are tool-independent facilitate the distribution of test suite sources.

IPv6 test suites have been developed using the TTCN-3 environment. The full Abstract Test Suites are written in TTCN-3 and the source files for building the codecs and adapters with the help of T3DevKit.

- Participants: César Viho, Federico Sismondi
- Contact: Federico Sismondi

6.3. 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 internal 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 (section vide)

DIVERSE Project-Team

6. New Software and Platforms

6.1. FAMILIAR

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.

FUNCTIONAL DESCRIPTION

Familiar is an environment for large-scale product customisation. From a model of product features (options, parameters, etc.), Familiar can automatically generate several million variants. These variants can take many forms: software, a graphical interface, a video sequence or even a manufactured product (3D printing). Familiar is particularly well suited for developing web configurators (for ordering customised products online), for providing online comparison tools and also for engineering any family of embedded or software-based products.

- Participants: Mathieu Acher, Guillaume Becan, Olivier Barais
- Contact: Mathieu Acher
- URL: http://familiar-project.github.com

6.2. GEMOC Studio

KEYWORDS: Model-driven engineering - Meta model - MDE - DSL - Model-driven software engineering - Dedicated langage - Language workbench - Meta-modelisation - Modeling language - Meta-modeling

SCIENTIFIC DESCRIPTION

The language workbench put together the following tools seamlessly integrated to the Eclipse Modeling Framework (EMF):

- Melange, a tool-supported meta-language to modularly define executable modeling languages with execution functions and data, and to extend (EMF-based) existing modeling languages.
- MoCCML, a tool-supported meta-language dedicated to the specification of a Model of Concurrency and Communication (MoCC) and its mapping to a specific abstract syntax and associated execution functions of a modeling language.
- GEL, a tool-supported meta-language dedicated to the specification of the protocol between the execution functions and the MoCC to support the feedback of the data as well as the callback of other expected execution functions.
- BCOoL, a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models.
- Sirius Animator, an extension to the model editor designer Sirius to create graphical animators for executable modeling languages.

FUNCTIONAL DESCRIPTION

The GEMOC Studio is an eclipse package that contains components supporting the GEMOC methodology for building and composing executable Domain-Specific Modeling Languages (DSMLs). It includes the two workbenches: The GEMOC Language Workbench: intended to be used by language designers (aka domain experts), it allows to build and compose new executable DSMLs. The GEMOC Modeling Workbench: intended to be used by domain designersto create, execute and coordinate models conforming to executable DSMLs. The different concerns of a DSML, as defined with the tools of the language workbench, are automatically deployed into the modeling workbench. They parametrize a generic execution framework that provide various generic services such as graphical animation, debugging tools, trace and event managers, timeline, etc.

- Participants: Benoit Combemale, Dorian Leroy, Thomas Degueule, Erwan Bousse, Fabien Coulon and Didier Vojtisek
- Contact: Benoit Combemale
- URL: http://gemoc.org

6.3. Kevoree

Kevoree Core

KEYWORDS: Cloud - Deployment - Embedded - Domotique - Heterogeneity - Software Components - Architecture - Software component - Dynamic adaptation - M2M - Dynamic deployment

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.

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: Jean Emile Dartois, Olivier Barais, Aymeric Hervieu, Johann Bourcier, Noel Plouzeau, Benoit Baudry, Maxime Tricoire, Jacky Bourgeois, Inti Gonzalez Herrera, Ivan Paez Anaya, Francisco Javier Acosta Padilla, Mohamed Boussaa and Manuel Leduc
- Partner: Université de Rennes 1
- Contact: Olivier Barais
- URL: http://kevoree.org/

6.4. Melange

KEYWORDS: Model-driven engineering - Meta model - MDE - DSL - Model-driven software engineering - Dedicated langage - Language workbench - Meta-modelisation - Modeling language - Meta-modeling

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-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 DSLs. 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 tightly integrated with the Eclipse Modeling Framework ecosystem and relies on the meta-language Ecore for the definition of the abstract syntax of DSLs. Executable meta-modeling is supported by weaving operational semantics defined with Xtend. Designers can thus easily design an interpreter for their DSL in a non-intrusive way. Melange is bundled as a set of Eclipse plug-ins.

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.

- Participants: Thomas Degueule, Benoit Combemale, Dorian Leroy, Erwan Bousse, Didier Vojtisek, Fabien Coulon, Jean-Marc Jezequel, Arnaud Blouin, Olivier Barais and David Mendez Acuna
- Contact: Benoit Combemale
- URL: http://melange-lang.org

6.5. Opencompare

KEYWORD: Software Product Line, Variability, MDE, Meta model, Configuration

FUNCTIONAL 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 – we are all using PCMs – 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 an ambitious 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.

- Participants: Mathieu Acher, Guillaume Becan and Sana Ben Nasr
- Contact: Mathieu Acher
- URL: http://opencompare.org

6.6. amiunique

KEYWORDS: Privacy - Browser fingerprinting

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 2014, FOSSA'14, FIC'15, ICT'15) and it has been visited by more than 100000 unique visitors in one year.

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).

- Participants: Benoit Baudry and Pierre Laperdrix
- Partner: INSA Rennes
- Contact: Benoit Baudry
- URL: https://amiunique.org/

DOLPHIN Project-Team

6. New Software and Platforms

6.1. 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, 140+ 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). A new extension towards bi-objective problems will be used for the BBOB-2016 workshop at GECCO.

- Participants: Dimo Brockhoff, Arnaud Liefooghe, Thanh-Do Tran, Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara, Asma Atamna, Tea Tusar and Dejan Tusar
- Partners: Université technique de Dortmund - Université technique de Prague
- Contact: Dimo Brockhoff
- URL: https://github.com/numbbo/coco

6.2. ParadisEO

KEYWORD: Metaheuristics, multi-objective optimization, Parallel metaheuristics

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: Université Lille 1
- Contact: El-Ghazali Talbi
- URL: http://paradiseo.gforge.inria.fr/

6.3. VRPsolve

KEYWORDS: C++ - Mobile Computing, Transportation - Optimization

- Participants: Clive Ferret-Canape, Arnaud Liefooghe and Sebastien Verel
- URL: http://gforge.inria.fr/projects/vrpsolve

6.4. Platform 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

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 binary decoder and a code-generator for VHDL simulation. New features of the HiHope language are described in more detail in Section.

- Contact: Vlad Rusu
- URL: https://gforge.inria.fr/frs/?group_id=3646

DYLISS Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: RDF - SPARQL - Querying - Graph
FUNCTIONAL DESCRIPTION

AskOmics allows to load heterogeneous bioinformatics data (formatted as tabular files or directly in RDF) into a Triple Store system using a user-friendly web interface. AskOmics also provides an intuitive graph-based user interface supporting the creation of complex queries that currently require hours of manual searches across tens of spreadsheet files. The elements of interest selected in the graph are then automatically converted into a SPARQL query that is executed on the users' data.

- Authors: Charles Bettembourg, Yvanne Chaussin, Anthony Bretaudeau, Olivier Filangi, Fabrice Legeai and Olivier Dameron
- Partners: CNRS - INRA - Université de Rennes 1
- Contact: Fabrice Legeai
- https://github.com/askomics/askomics

6.2. PADMet

PortAble Database for Metabolism
KEYWORDS: Bioinformatics - Toolbox - Metabolic networks - Standardization
FUNCTIONAL DESCRIPTION

The PADMet package allows conciliating genomics and metabolic network information used to produce a genome-scale constraint-based metabolic model within a database that traces all the reconstruction process steps. It allows representing the metabolic model in the form of a Wiki containing all the used/traced information. Other standard outputs are made available with the package. The main concept underlying PADMet-Package is to provide solutions that ensure the consistency, the internal standardization and the reconciliation of the information used within any workflow that combines several tools involving metabolic networks reconstruction or analysis. The PADMet package is at the core of the AuReMe workflow, dedicated to the primary reconstruction of genome-scale metabolic networks from raw data. It allows the study of organisms for which few experimental data are available. Its main feature is to undergo the reconstruction of the metabolic network by combining several heterogeneous knowledge and data sources, including the information reported by several scaffold metabolic networks for cousin species.

- Partners: CNRS - Inria - Université de Rennes 1 - University of Chile.
- Contact: Meziane Aite
- https://gitlab.inria.fr/DYLISS/padmet-toolbox

6.3. PowerGrASP

Power Graph compression in ASP
KEYWORDS: Bioinformatics - Constraint-based Programming - Data visualization - Optimization - Decomposition - Graph - Graph visualization - Pattern extraction - Answer Set Programming - Formal concept analysis
FUNCTIONAL DESCRIPTION

Implementation of graph compression methods oriented toward visualization, and based on power graph analysis. The method relies of formal concept analysis and is implemented in the declarative langage Answer Set Programming. It is applied to regulatory networks currently produced in the domain of bioinformatics.

- Participants: Lucas Bourneuf, Jacques Nicolas
- Partners: Inria - Université de Rennes 1 - INRA.
- Contact: Lucas Bourneuf
- URL: http://github.com/aluriak/powergrasp

6.4. Platforms and toolboxes

A goal of the team is to facilitate interplays between tools for biological data analysis and integration. Our tools 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 developed in collaboration with the GenOuest resource and data center hosted in the IRISA laboratory, including their computer facilities [more info]. It worths considering them into larger dedicated environments to benefit from the expertise of other research groups.

- The **BioShadock** repository allows one to share the different docker containers that we are developing [website].
- The **Inria chile Mobyle portal** gathers some of the tools that were developed in collaboration with Dyliss, such as meneco, shogen and lombarde [website].
- The **bioASP portal** gather most of ASP-based python packages that we are developping in collaboration with Potsdam university [website]
- The **GenOuest galaxy portal** now provides access to most tools for integrative biology and sequence annotation (access on demand).

6.4.1. AuReMe - Tracable reconstruction of metabolic networks

The toolbox **AuReMe** allows for the **Au**tomatic **Re**construction of **Me**tabolic networks based on the combination of multiple heteregeneous data and knowledge sources. Since 2016, the workflow has been made available as a Docker image to facilitate its distribution among the scientific community [web page].

- The **Model-management PADmet module** allows conciliating genomics and metabolic network information used to produce the metabolic model within a local database that traces all the reconstruction process steps and to connect software in the pipeline. This toolbox was completly redesigned in 2016. [package]
- The **meneco python package** allows filling the gaps of a metabolic network by using a qualitative approach to elaborate the biosynthetic capacities; the problem is viewed as a combinatorial optimization problem encoded in a Answer Set Programming Problem [87] [64]. [python package].
- The **shogen python package** allows aligning genome and metabolic network to identify genome units which contain a large density of genes coding for enzymes that regulate successive reactions of metabolic pathways; the problem is also encoded with an ASP program. [62]. [python package].
- The **Manual curation assistance PADmet module** allows for curating the reported metabolic networks and modify metadata [package].
- The **Wiki-export PADmet module** enables the export of the metabolic network and its functional genomic unit as a local wiki platform allowing the user-friendly investigation of the network together with the main steps used to reconstruct it. It was developed in 2016. [package].

6.4.2. Filtering interaction networks with graph-based optimization criteria

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.

- The **lombarde package** enables the filtering of transcription-factor/binding-site regulatory networks with mutual information reported by the response to environmental perturbations. The high level of false-positive interactions is filters according to graph-based criteria. Knowledge about regulatory modules such as operons or the output of the shogen package can be taken into account [48][13] [web server].
- The **KeyRegulatorFinder package** allows searching key regulators of lists of molecules (like metabolites, enzymes or genes) by taking advantage of knowledge databases in cell metabolism and signaling. The complete information is transcribed into a large-scale interaction graph which is filtered to report the most significant upstream regulators of the considered list of molecules [61] [package].
- The **powerGrasp python package** provides an implementation of graph compression methods oriented toward visualization, and based on power graph analysis. [package].
- The **iggy package** enables the repairing of an interaction graph with respect to expression data. 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. [5] [93] [Python package][web server].

6.4.3. Caspo - Studying synchronous boolean networks

The **caspo** pipeline is dedicated to 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.

Software provides an easy to use software for the study of synchronous logical (boolean) networks. In 2016, the tool was redesigned to enhance its functionalities and integrated in a docker container to facilitate its use on any platform [86] [28] [python package and docker container].

- The **caspo-learn module** performs an automated inference of logical networks from the observed response to different perturbations (phosphoproteomics datasets). It allows for identifying admissible large-scale logic models saving a lot of efforts and without any a priori bias. It is also included in the cellNopt package [0] [7] [94].
- The **caspo-classify, predict and visualize modules** allows for classifying a family of boolean networks with respect to their input–out- put predictions [7].
- The **caspo-design module** designs experimental perturbations which would allow for an optimal discrimination of rival models in a family of boolean networks [95].
- The **caspo-control module** identifies key-players of a family of networks: it computes robust 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 [73].
- **caspo-timeseries module** have been designed by our colleagues from LRI as an extension of the caspo pipeline to take into account time-series observation datasets in the learning procedure [23] [python package and docker container].

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[0] http://www.cellnopt.org/

6.4.4. cadbiom - Building and analyzing the asynchronous dynamics of enriched logical networks

Based on Guarded transition semantic, the **cadbiom** 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. In 2016, the tool was integrated in a docker container in order to facilitate its use on any platform [49] [docker container][web server].

- **The cadbiom graphical interface** is useful to build and study moderate size models. It provides means for model exploration, simulation and checking. For large-scale models, the graphical interface allows to focus on specific nodes of interest.
- **The cadbiom API** allows to load a model (including large-scale ones), perform static analysis (exploration, frontier computation, statistics, and dependence graph computation) and check temporal properties on a finite horizon in the future or in the past.
- **Exploring large-scale knowledge repositories** A main feature of cadbiom is that automatic translation of the large-scale PID repository (about 10,000 curated interactions) have been automatically translated into the cadbiom formalism. Therefore, the API allows for computing the upstream regulators of any set of genes based on this large-scale repository.

6.4.5. Protomata - Expressive pattern discovery on protein sequences

Protomata is a machine learning suite for the inference of *automata* characterizing (functional) families of proteins from available sequences. Based on a new kind of alignment said partial and local, it learns precise characterizations of the families – beyond the scope of classical sequence patterns such as PSSM, Profile HMM, or Prosite Patterns – allowing to predict new family members with a high specificity.

Protomata gives access to the three main modules as stand-alone programs, which are also integrated in a single workflow *protomata-learner*:

- **Paloma** builds partial local multiple alignments;
- **Protobuild** infers automata from these alignements;
- **Protomatch and Protoalign** scan, parse and align new sequences based on the automata infered previously. This module was improved in 2016 by embedding new options to score the sequences with respect to all accepting paths (Forward score) in addition to the scoring module based on the best path (Viterbi score). More generally, we have worked on the efficiency of the automata's weighting scheme based on the state-of-the-art schemes used for profile HMMs.

The suite is completed by many tools to handle or visualize data and can be used online via a [web interface].

6.4.6. Logol - Complex pattern modelling and matching

The **Logol** toolbox is a swiss-army-knife for pattern matching on DNA/RNA/Protein sequences, using a high-level grammatical formalism to permit a large expressivity for patterns [54]. A Logol pattern consists in a complex combination of motifs (such as degenerated strings) and structures (such as imperfect stem-loop ou repeats). Compared to other specialized pattern matching tools, some of the Logol key features are the possibilities to divide a pattern description into several sub-patterns, to enable the use of ambiguous models or to permit the inclusion of negative conditions in a pattern definition. Possible fields of application are the detection of mutated binding sites [32] or stem-loop identification (e.g. in CRISPR [0] [10]) [web page].

- The **Graphical designer** allows a user to iteratively build a complex pattern based on basic graphical patterns. The associated grammar file is an export of the graphical designer. In 2015, the efficiency of the tool was improved by slight evolutions of the underlying grammar.
- The **LogolMatch** parser takes as input a biological (nucleic or amino acid) sequence and a grammar file (i.e. a pattern). It combines a grammar analyzer, a sequence analyzer and a prolog Library. It returns a file containing all the occurrences of the pattern in the sequence with their parsing details.
- Full genome analysis, and connection to biological databases have been made available recently.

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[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

Aironum is an experimental software that solves the unsteady compressible Navier-Stokes equations with k-, LES-VMS (Large Eddy Simulation - Variational Multi-Scale) and hybrid turbulence modelling on parallel platforms, using MPI. The mesh model is unstructured tetrahedrization, with possible mesh motion.

Aironum was developed by Inria and University of Montpellier. It is used by Inria, University of Montpellier and University of Pisa. 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 (Reynolds Averaged Navier-Stokes) 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

Tapenade [10] is an Algorithmic Differentiation tool that transforms an original program into a new program that computes derivatives of the original program. Being an AD tool, Tapenade produces analytical derivatives exact up to machine precision, and in adjoint mode computes gradients at a cost independent of the number of input variables.

Tapenade implements the results of our research about models and static analyses for AD. 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. Tapenade accepts source programs written in Fortran77, Fortran90, or C. It provides differentiation in the following modes: tangent, vector tangent, adjoint, and vector adjoint.

Tapenade performs sophisticated data-flow analysis, flow-sensitive and context-sensitive, on the complete source program to produce an efficient differentiated code. Analyses performed are Type-Checking, Read-Write analysis, Pointer analysis, and AD-specific analyses including Activity analysis, Adjoint Liveness analysis, and TBR analysis.

- Participants: Laurent Hascoët, Valérie Pascual
- 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 DESCRIPTION

CIDANE 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 visualiser for host-parasite and gene-species trees evolution.

- Participants: Laurent Bulteau
- Contact: Laurent Bulteau (not Inria), Blerina Sinaimeri (for Inria ERABLE)
- 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 (not Inria), Marie-France Sagot (for Inria ERABLE)
- 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, Marie-France Sagot, Blerina Sinaimeri
- Contact: Christian Baudet (not Inria), Beatrice Donati (not Inria), and Marie-France Sagot (Inria ERABLE)
- 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 (Inria ERABLE)
- 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: http://hapcol.algolab.eu/

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 (contact: pierre.peterlongo@inria.fr).

- Participants: Vincent Lacroix, Pierre Peterlongo
- Contact: Pierre Peterlongo (EPI GenScale)
- URL: http://colibread.inria.fr/software/discosnp/

5.14. KisSplice

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.

- 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: Clara Benoit-Pilven, 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. MultiPus

FUNCTIONAL DESCRIPTION

MULTIPUS (for MULTIple species for the synthetic Production of Useful biochemical Substances) is an algorithm that, given a microbial consortium given as input, identifies all optimal sub-consortia to synthetically produce compounds that are either exogenous to it, or are endogenous but where interaction among the species in the sub-consortia could improve the production line.

- Participants: Laurent Bulteau, Alice Julien-Laferrière, Arnaud Mary, Alberto Marchetti-Spaccamela, Delphine Parrot, Marie-France Sagot, Leen Stougie and Susana Vinga
- Contact: Alice Julien-Laferrière, Arnaud Mary, Marie-France Sagot
- URL: http://multipus.gforge.inria.fr/

5.25. PepLine

FUNCTIONAL DESCRIPTION

Pipeline for the high-throughput analysis of proteomic data.

- Participants: Jérôme Garin, Alain Viari
- Contact: Alain Viari
- URL: Available upon request to the contact person

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. Sasita

FUNCTIONAL DESCRIPTION

SASITA is a software for the exhaustive enumeration of minimal stoichiometrically valid precursor sets in metabolic networks.

- Participants: Vicente Acuña, Ricardo Andrade, Alberto Marchetti-Spaccamela, Marie-France Sagot, Leen Stougie, Martin Wannagat
- Contact: Marie-France Sagot, Ricardo Andrade, Martin Wannagat
- URL: http://sasita.gforge.inria.fr/

5.30. Smile

FUNCTIONAL DESCRIPTION

Motif inference algorithm taking as input a set of biological sequences. A visualiser is currently being developed.

- Participants: Ricardo Andrade (visualiser), Mariana Ferrarini (visualiser), Laurent Marsan, Marie-France Sagot
- Contact: Ricardo Andrade, Marie-France Sagot
- URL: Soon available

5.31. Totoro & Kotoura

FUNCTIONAL DESCRIPTION

We proposed two methods to decipher the reaction changes during a metabolic transient state using measurements of metabolic concentrations. We called these *metabolic hyperstories*.

TOTORO (for TOpological analysis of Transient metabOlic RespOnse) is based on a qualitative measurement of the concentrations in two steady-states to infer the reaction changes that lead to the observed differences in metabolite pools in both conditions. In the currently available release, a pre-processing and a post-processing steps are included. After the post-processing step, the solutions can be visualised using DINGHY.

KOTOURA (for Kantitative analysis Of Transient metabOlic and regUlatory Response And control) infers quantitative changes of the reactions using information on measurement of the metabolite concentrations in two steady-states.

- Participants: Ricardo Andrade, Laurent Bulteau, Louis Duchemin, Alice Julien-Laferrière, Alberto Marchetti-Spaccamela, Arnaud Mary, Vincent Lacroix, Marie-France Sagot, Leen Stougie, Philippe Veber, Susana Vinga
- Contact: Alice Julien-Laferrière, Arnaud Mary, Ricardo Andrade, Marie-France Sagot
- URL: http://hyperstories.gforge.inria.fr/

5.32. WhatsHap and pWhatsHap

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. PWHATSHAP 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 and https://bitbucket.org/whatshap/whatshap/branch/parallel

EVA Project-Team

6. New Software and Platforms

6.1. OpenWSN (Software)

Participants: Tengfei Chang, Jonathan Muñoz, Malisa Vucinic, Thomas Watteyne.

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 2016:

- Development:
  - better (continuous) testing of the existing OpenWSN code.
  - Build a image for a RaspberryPi which contains the OpenVisualizer preinstalled.
  - Port OpenWSN to the First prototype of the "Single-Chip uMote" (SCuM), developed in Prof. Pister's lab at UC Berkeley.
  - Create a Virtual Machine image with all OpenWSN development tools preinstalled.
  - Implementation of 6TiSCH standards as they appear, including revisions.
  - Maintenance of the "Golden Image" used as a reference during interoperability testing
- Recognition:
  - OpenWSN remains ETSI's 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**
    Standards for the Industrial IoT: a Hands-on Tutorial with OpenWSN and OpenMote. Xavier Vilajosana, Pere Tuset-Peiro, Tengfei Chang, **Thomas Watteyne**. IEEE International Symposium on Personal, Indoor and Mobile Radio Communications (PIMRC), Valencia, Spain, 4-8 September 2016.
  - **Tutorial**
    Introduction to the IETF 6TiSCH stack with OpenWSN & OpenMote. **Thomas Watteyne**, Xavier Vilajosana, Pere Tuset-Peiro, Tengfei Chang. International Conference on Telecommunications (ICT), Thessaloniki, Greece, 16-18 May 2016.
  - **Interop Event**
    ETSI 6TiSCH 3 plugtests, 15-16 Juny 2016, Berlin, Germany
  - **Interop Event**
    ETSI 6TiSCH 2 plugtests, 2-4 Februay 2016, Paris, France

This software appears in https://bil.inria.fr/.

6.2. OPERA and OCARI (Software)

Participants: Erwan Livolant, Pascale Minet.

The OPERA software was developed by the Hipercom2 team in the OCARI project 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 2016, Erwan Livolant developed extensions to allow the remote management of the OCARI network and the transmission of commands to sensors and actuators.

6.3. F-Interop (Software)

Participants: Remy Leone, Thomas Watteyne.

F-Interop is revolutionizing the way interoperability events are conducted. We are building a cloud-based system which allows implementors to meet online to test their implementations against one another, verify compliance in a automated way, and verify the performance of their implementations on large scale testbeds. This significantly cuts down time-to-market for standards-based solutions, and eventually leads to more standards-based products on the market. The F-Interop platform starts by targeting 6TiSCH, 6LoWPAN and CoAP standards, but our ambition is for F-Interop to become the standard way of doing interoperability, at least at the IETF IoT level.

This implementation is done as part of the H2020 F-Interop project. More information at http://www.f-interop.eu/.

This software appears in https://bil.inria.fr/.

6.4. 6TiSCH Simulator (Software)

Participants: Malisa Vucinic, Thomas Watteyne.

The 6TiSCH simulator allows one to conduct high-level simulator of an IETF 6TiSCH network and answer questions such as How long does it take the nodes to join the network? What is the average power consumption? What does the latency distribution look like?

The simulator is written in Python. While it doesn't provide a cycle-accurate emulation, it does implement the functional behavior of a node running the full 6TiSCH protocol stack. This includes RPL, 6LoWPAN, CoAP and 6P. The implementation work tracks the progress of the standardization process at the IETF.

This implementation is done as part of the H2020 ARMOUR project and the standardization activities of the Inria-EVA team at the IETF. It is published under an open-source BSD license and maintained at https://bitbucket.org/6tisch/simulator/.

This software appears in https://bil.inria.fr/.

6.5. 6TiSCH Wireshark Dissector (Software)

Participants: Jonathan Muñoz, Thomas Watteyne.

The goal of this project is to maintain Wireshark dissectors for 6TiSCH (and 6TiSCH-related) standards up-to-date.

Implementation on the dissectors is done through an open-source repository, stable code is regularly contributed back to the main Wireshark code base.

This implementation is done as part of the collaboration with Gridbee and the standardization activities of the Inria-EVA team at the IETF. It is published under an open-source BSD license and maintained at https://github.com/openwsn-berkeley/dissectors.

This software appears in https://bil.inria.fr/.

6.6. Mercator (Software)

Participants: Keoma Brun-Laguna, Thomas Watteyne.

Mercator allows one to evaluate the connectivity in a low-power wireless network. It is a collection of tools, including the firmware to load on the devices, the scripts that automate the measurements of the connectivity and the tools to structure and display results.

The firmware is written as part of the OpenWSN project. Scripts and analysis tools are written in Python.

It is published under an open-source BSD license and maintained at https://github.com/openwsn-berkeley/mercator.

This software appears in https://bil.inria.fr/.

6.7. CONNEXION (Software)

Participants: Pascale Minet, Erwan Livolant.

In the CONNEXION project, the integration of the OCARI wireless sensor network in a Service-Oriented Architecture using the OPC-UA/ROSA middleware went on with Telecom ParisTech. More precisely, we developed the remote managment of the OCARI network as well as the possibility to generate commands to the sensors and actuators.

Erwan Livolant developed an OCARI frame dissector plugin for Wireshark (https://www.wireshark.org) available from the Git repository at OCARI website. 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.

6.8. SolSystem (Software)

Participants: Keoma Brun-Laguna, Thomas Watteyne.

SolSystem is a back-end solution for a low-power wireless mesh network based on SmartMesh IP. It defines how low-power wireless devices must format and transfer sensor data, and the tools to gather, store and display sensor data.

This system is used in several deployments, including http://savethepeaches.com/ and http://snowhow.io/.

The source code is composed of the definition of the SOL structure (https://github.com/realms-team/sol), the code that runs on the manager (https://github.com/realms-team/solmanager, written in Python) and the code that runs on the server receiving the data (https://github.com/realms-team/solserver, written in Python).

It is published under an open-source BSD license. Information and overview at http://www.solsystem.io/.

This software appears in https://bil.inria.fr/.

6.9. Argus (Software)

Participants: Remy Leone, Thomas Watteyne.

Share your low-power wireless sniffer through the cloud!

Imagine you are a team of low-power wireless enthusiasts developing the next generation of products in standards. One essential tool in your toolkit is a low-power wireless sniffer, which shows you the frames which fly through the air.

Rather than requiring each person in your team to have a sniffer, Argus allows you to put in a share a sniffer through the cloud.

There are three piece to Argus:

- The Argus Probe is the program which attaches to your low-power wireless sniffer and forwards its traffic to the Argus Broker.
- The Argus Broker sits somewhere in the cloud. Based on MQTT, it connect Argus Probes with Argus Clients based on a pub-sub architecture.
- Several Argus Clients can the started at the same time. It is a program which subscribes to the Argus Broker and displays the frames in Wireshark.

It is published under an open-source BSD license, maintained at https://github.com/openwsn-berkeley/argus.

This software appears in https://bil.inria.fr/.

6.10. SAHARA (Software)

Participants: Ines Khoufi, Erwan Livolant, Pascale Minet.

Ines Khoufi developed modules for the simulation of the Time Slotted Channel Hopping (TSCH) on the ns3 simulation tool. These modules include multi-interface management and transmission management according to a given schedule.

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.

6.11. FIT IoT-LAB (Platform)

Participants: Thomas Watteyne, Tengfei Chang.

Note well: IoT-lab is *not* 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 highlights Inria-EVA activity and contribution to the IoT-lab testbed in 2016.

The Inria-EVA team has been using the platform extensively throughout 2016. During the process, we have been interacting closely with the IoT-lab team of engineers.

IoT-lab-related activities include:

- **Running OpenWSN networks at scale**. The IoT-lab has been an incredibly powerful tool to verify the scalability of the protocols and implementations in OpenWSN (Section 6.1). *Lead: Tengfei Chang*.
- **Assessing connectivity with Mercator**. The Mercator project (Section 6.6) is targetted at measuring the connectivity of the IoT-lab platform in time, space and frequency. *Lead: Keoma Brun-Laguna*.
- **16-channel Sniffer with Argus**. We are currently working extending the Argus project (Section 6.9) with support for IoT-lab motes. That is, rather than using a 16-channel sniffer, turn 16 IoT-lab nodes into a distributed multi-frequency sniffer. *Lead: Remy Leone*.
- **IoT-lab for Interop Testing with F-Interop**. Through the H2020 F-Interop project, we are developing the tools (see Section 6.3) to run an F-Interop user's code on the IoT-lab to verify conformance and interoperability. *Lead: Remy Leone*.
- **Scalable Security Solution with H2020 ARMOUR**. Through the H2020 ARMOUR project, Inria-EVA is testing whether security solutions standardized at the IETF are scalable. *Lead: Malisa Vucinic*.

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], Olivier Gladin, 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.

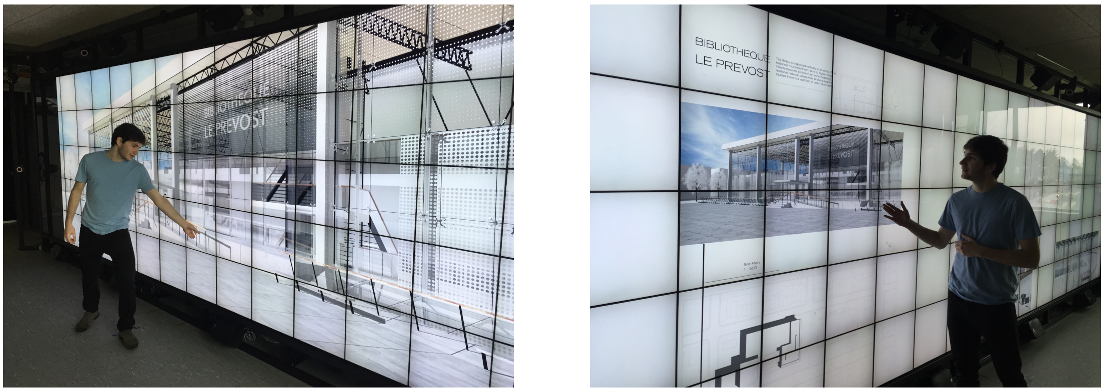


Figure 1. The WILDER platform.

EXMO Project-Team

5. New Software and Platforms

5.1. Alignment API

SCIENTIFIC DESCRIPTION

Using ontologies is the priviledged way to achieve interoperability among heterogeneous systems within the semantic web. However, as the ontologies underlying two systems are not necessarily compatible, they may in turn need to be reconciled. Ontology reconciliation requires most of the time to find the correspondences between entities (e.g., classes, objects, properties) occuring in ontologies. We call a set of such correspondences an alignment.

We have designed a format for expressing alignments in a uniform way. 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. We have proposed and implemented an expressive extension called EDOAL [13].

The Alignment API [2] is an API and implementation for expressing and sharing ontology alignments.

FUNCTIONAL DESCRIPTION

The API itself 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 sample matchers,
- a library of renderers (XSLT, RDF, SKOS, SWRL, OWL, C-OWL, SPARQL, etc.),
- 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 APIs,
- parsers for different formats.

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.

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.

The Alignment API is used in the Ontology Alignment Evaluation Initiative data and result processing (§6.1.1). 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.

- Participants: Jérôme Euzenat, Jérôme David, Armen Inants
- Contact: Jérôme Euzenat
- URL: http://alignapi.gforge.inria.fr/

5.2. OntoSim

SCIENTIFIC DESCRIPTION

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 is a library offering similarity and distance measures between ontology entities as well as between ontologies themselves. It materialises our work towards better ontology proximity measures.

FUNCTIONAL DESCRIPTION

OntoSim is a Java API allowing to compute similarities between ontologies. It relies on the Alignment API for ontology loading so it is quite independent of the ontology API used (JENA or OWL API).

OntoSim provides a framework for designing various kinds of similarities. In particular, we differentiated similarities in the ontology space from those in the alignment space. The latter ones make use of available alignments in a network of ontologies 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.

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.

- Participants: Jérôme David, Jérôme Euzenat
- Contact: Jérôme David
- URL: http://ontosim.gforge.inria.fr/

FLOWERS Project-Team

6. New Software and Platforms

6.1. Poppy project

6.1.1. HiPi Board

FUNCTIONAL DESCRIPTION

Hipi is a board to control robots on Raspberry Pi. It is an extension of the Pixl board with the following features:

- A DC/DC power converter from 12V (motor) to 5V (Raspberry Pi) at 3A.
- A stereo audio amplifier 3W.
- A MPU9250 central motion unit .
- A RS232 and a RS485 bus connected to the Raspberry Pi by SPI for driving MX and RX Dynamixel motor series.

This board will be integrated soon in the new head of the Poppy Humanoid and Poppy Torso.

Using the Raspberry Pi for every Poppy robots will simplify the hardware complexity (we maintain 4 types of embedded boards, with different Linux kernel and configurations) and improve the usage and installation of new robots.

- Contact: Theo Segonds
- URL: https://forum.poppy-project.org/t/poppy-1-1-hipi/2137

6.1.2. IKPy

Inverse Kinematics Python Library
FUNCTIONAL DESCRIPTION

IKPy is a Python Inverse Kinematics library, designed to be simple to use and extend. It provides Forward and Inverse kinematics functionality, 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.

- Contact: Pierre Manceron
- URL: https://github.com/Phylliade/ikpy

6.1.3. Pixl Board

FUNCTIONAL DESCRIPTION

Pixl is a tiny board used to create low cost robots based on Raspberry Pi board and Dynamixel XL-320 motors. This board has 2 main features:

- The power part, allowing the user to plug a 7.5V AC/DC converter or a battery directly into the Pixl. This power is distributed to all XL320 motors and is converted to 5V for the Raspberry Pi board.
- The communication part, which converts full duplex to half duplex and vice-versa. The half duplex part switch between RX and TX automatically. Another connector allows the user to connect his XL320 network.

The board is used in the Poppy Ergo Jr robot.

- Contact: Theo Segonds
- URL: https://github.com/poppy-project/pixl

6.1.4. Poppy

FUNCTIONAL DESCRIPTION

The Poppy Project team develops open-source 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.

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 a unified system in which essential robotic components (actuators, sensors...) are independent modules connected with other modules through standardized interfaces:

- Unified mechanical interfaces, simplifying 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, making it easy to program each module independently.

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.

- Participants: Pierre Rouanet, Matthieu Lapeyre, Jonathan Grizou and Pierre-Yves Oudeyer
- Contact: Pierre-Yves Oudeyer
- URL: https://www.poppy-project.org/

6.1.5. Poppy Ergo Jr

FUNCTIONAL DESCRIPTION

Poppy Ergo Jr is an open hardware robot developed by the Poppy Project to explore the use of robots in classrooms for learning robotic and computer science.

It is available as a 6 or 4 degrees of freedom arm designed to be both expressive and low-cost. This is achieved by the use of FDM 3D printing and low cost Robotis XL-320 actuators. A Raspberry Pi camera is attached to the robot so it can detect object, faces or QR codes.

The Ergo Jr is controlled by the Pypot library and runs on a Raspberry pi 2 or 3 board. Communication between the Raspberry Pi and the actuators is made possible by the Pixl board we have designed.

The Poppy Ergo Jr robot has several 3D printed tools extending its capabilities. There are currently the lampshade, the gripper and a pen holder.

With the release of a new Raspberry Pi board early 2016, the Poppy Ergo Jr disk image was updated to support Raspberry Pi 2 and 3 boards. The disk image can be used seamlessly with a board or the other.

- Contact: Theo Segonds
- URL: https://github.com/poppy-project/poppy-ergo-jr

6.1.6. Poppy Ergo Jr Installer

FUNCTIONAL DESCRIPTION

An alternative way to install the Ergo Jr robot software is made available using containers.

Users can own their own operating system installation, then add the Ergo Jr required software in a sandboxed environment. This results in a non-intrusive installation on the host system.

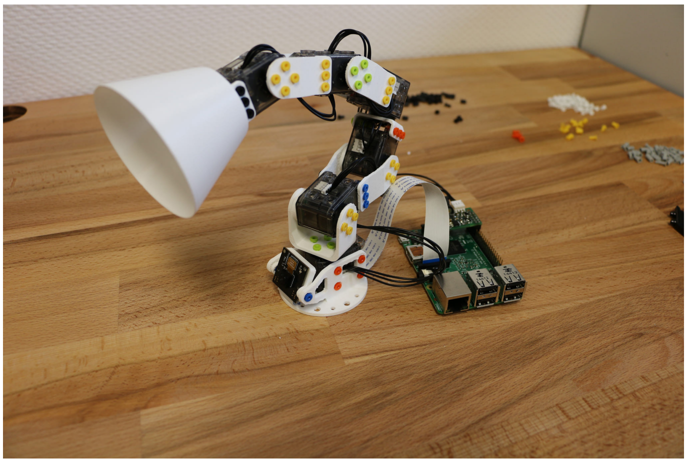


Figure 1. Poppy Ergo Jr, 6-DoFs arm robot for education

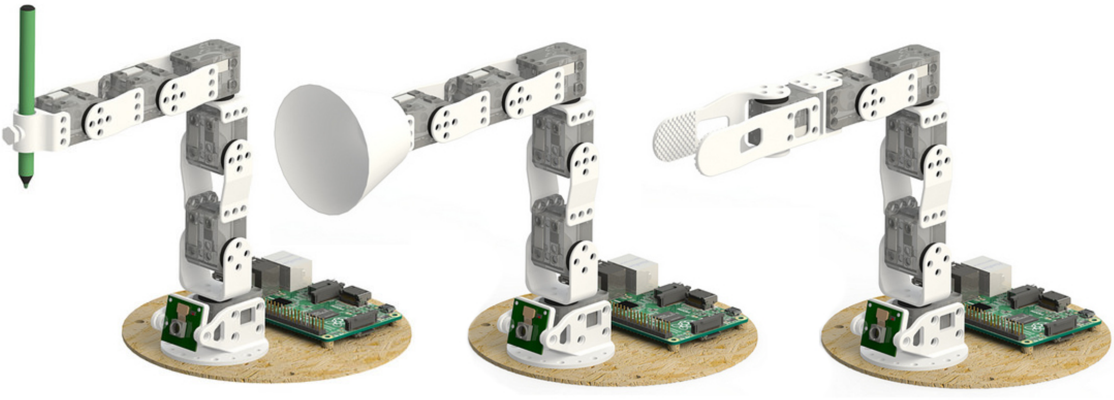


Figure 2. The available Ergo Jr tools: a pen holder, a lampshade and a gripper

Docker containers implementation were used, and image is hosted at Docker Hub.

- Contact: Damien Caselli
- URL: https://hub.docker.com/r/poppycommunity/ergo-jr/

6.1.7. Poppy Ergo Jr Simulator

FUNCTIONAL DESCRIPTION

Poppy Project, through Poppy Education, wants users to get used to robotics, even without owning a physical robot.

For that purpose, Poppy Project team created a dummy robot in Pypot that is meant to be used in conjunction with a consumer application. We choose to develop a web hosted application using a 3D engine (Threejs) to render the robot.

Our ambition is to have a completely standalone simulated robot with physics. Some prototypes were created to benchmark possible solutions.

- Contact: Damien Caselli
- URL: https://github.com/poppy-project/poppy-simu

6.1.8. PyPot

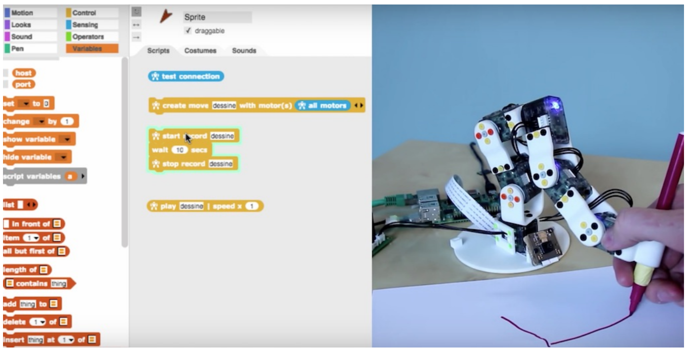
SCIENTIFIC DESCRIPTION

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. Pypot can be used to:

- control Robotis motors through a USB2serial device,
- define the structure of a custom 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 Poppy robots. This abstraction layer allows to seamlessly switch from a given 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 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.



```
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

FUNCTIONAL DESCRIPTION

Pypot is entirely written in Python to allow for fast development, easy deployment and quick scripting by non-expert developers. It can also benefit from the scientific and machine learning libraries existing in Python. The serial communication is handled through the standard library and offers high performance (10ms sensorimotor loop) for common Poppy uses. It is cross-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 with a single code base.

Finally, it has been developed to be easily and quickly extended for other types of motors and sensors.

It works with Python 2.7 or Python 3.3 or later, and has also been adapted to the Raspberry Pi board.

Pypot has been connected to Snap!, a variant of the famous Scratch visual language, developed to teach computer science to children. It is based on a drag-and-drop blocks interface to write scripts by assembling those blocks.

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*. Thanks to the Snap! HTTP block, users can control robots through this visual interfaces connecting to Pypot. A set of dedicated Snap! blocks has 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 to program the robot by demonstration. Using the *record* and *play* blocks, users can easily trigger kinesthetic recording of the whole robot or only a specific subpart, such as an arm. These records can then be played or "mixed" - either played in sequence or simultaneously - 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 recording tool has been developed and used in collaboration with artists who show interest in the concept of robotic moves.

- Participants: Pierre Rouanet, Matthieu Lapeyre, Steve Nguyen, Damien Caselli and Theo Segonds
- Contact: Theo Segonds
- URL: https://github.com/poppy-project/pypot

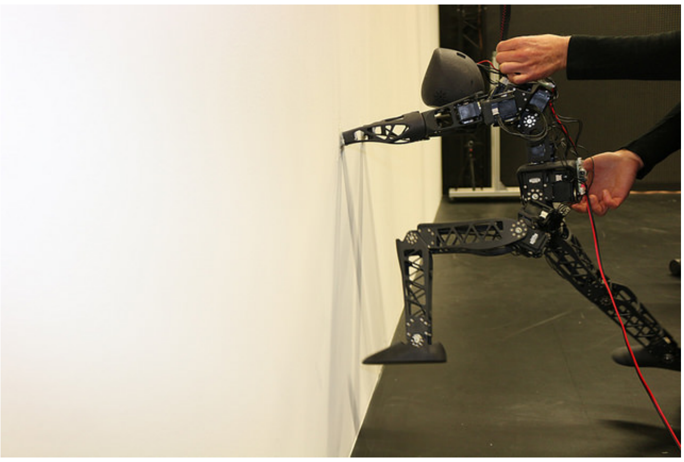


Figure 5. Artistic project exploring the concept of robotic move.

6.1.9. PyQMC

Python library for Quasi-Metric Control

FUNCTIONAL DESCRIPTION

PyQMC is a python library implementing the control method described in http://dx.doi.org/10.1371/journal.pone.0083411 It allows to solve discrete markovian decision processes by computing a Quasi-Metric on the state space. This model based method has the advantage to be goal independant and thus can produce a policy for any goal with relatively few recomputation. New addition to this method is the possibility of online learning of the transition model and the Quasi-Metric.

- Participant: Steve Nguyen
- Contact: Steve Nguyen
- URL: https://github.com/SteveNguyen/pyqmc

6.2. Explauto

an autonomous exploration library

SCIENTIFIC DESCRIPTION

An important challenge in developmental robotics is how robots can be intrinsically motivated to learn efficiently parametrized policies to solve parametrized multi-task reinforcement learning problems, i.e. learn the mappings between the actions and the problem they solve, or 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 optimize the parametrized policies. 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 real and simulated robotic agents. Explauto's scientific roots trace back from Intelligent Adaptive Curiosity algorithmic architecture [152], which has been extended to a more general family of autonomous exploration architectures by [3] and recently expressed as a compact and unified formalism [38]. The library is detailed in [39]. In Explauto, interest models are implementing the strategies of active selection of particular problems / goals in a parametrized multi-task reinforcement learning setup to efficiently learn parametrized policies. The agent can have different available strategies, parametrized problems, models, sources of information, or learning mechanisms (for instance imitate by mimicking vs by emulation, or asking help to one teacher or to another), and chooses between them in order to optimize learning (a processus called strategic learning [45]). Given a set of parametrized problems, a particular exploration strategy is to randomly draw goals/ RL problems to solve in the motor or problem space. More efficient strategies are based on the active choice of learning experiments that maximize learning progress using bandit algorithms, e.g. maximizing improvement of predictions or of competences to solve RL problems [152]. 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 strategies can act either on the motor or on the problem 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 effect, executing the command through the environment and observing the actual effect. Both the parametrized policies and interest models are finally updated according to this experience.
- Goal babbling consists in sampling goals in the problem space and to use the current policies to infer a motor action supposed to solve the problem (inverse prediction). The robot/agent then executes the command through the environment and observes the actual effect. Both the parametrized policies and interest models are finally updated according to this experience.It has been shown that this second strategy allows a progressive solving of problems much more uniformly in the problem space than with a motor babbling strategy, where the agent samples directly in the motor space [3].

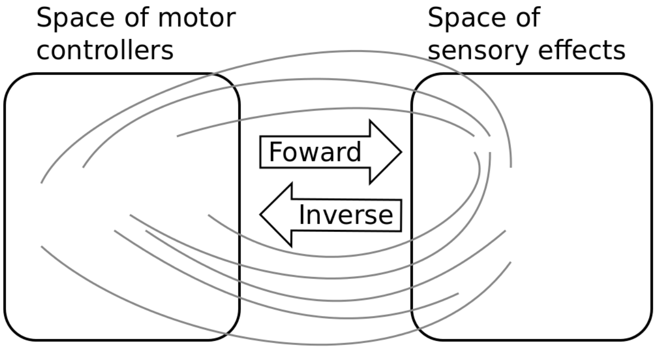


Figure 6. Complex parametrized policies involve high dimensional action and effect spaces. For the sake of visualization, the motor M and sensory S spaces are only 2D each in this example. The relationship between M and S is non-linear, dividing the sensorimotor space into regions of unequal stability: 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:

- Real and simulated robotic setups (Environment level),
- Incremental learning of parametrized policies (Sensorimotor level),
- Active selection of parametrized RL problems (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 parametrized policies 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 problems, 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 theenvironment 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.

Explauto environments now handle actions depending on a current context, as for instance in an environment where a robotic arm is trying to catch a ball: the arm trajectories will depend on the current position of the ball (context). Also, if the dynamic of the environment is changing over time, a new sensorimotor model (Non-Stationary Nearest Neighbor) is able to cope with those changes by taking more into account recent experiences. Those new features are explained in Jupyter notebooks.

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),
- acoustic 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.

- Contact: Sébastien Forestier
- URL: https://github.com/flowersteam/explauto

6.3. Tools for robot learning, control and perception

6.3.1. 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

6.3.2. Aversive++

FUNCTIONAL DESCRIPTION

Aversive++ is a C++ library that eases micro-controller programming. Its aim is to provide an interface simple enough to be able to create complex applications, and optimized enough to enable small micro-controllers 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 micro-controllers.

- Contact: Loïc Dauphin
- URL: http://aversiveplusplus.com/

6.3.3. DMP-BBO

Black-Box Optimization for Dynamic Movement Primitives
KEYWORD: -
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 has been extended to include the “unified model for regression”. The implementation of several of the function approximators have been made real-time compatible.

- Participant: Freek Stulp
- Partner: ENSTA
- Contact: Freek Stulp
- URL: https://github.com/stulp/dmpbbo

6.3.4. KERAS-QR

KERAS with Quick Reset
KEYWORDS: Library - Deep learning

- Participant: Florian Golemo
- Contact: Florian Golemo
- URL: https://github.com/fgolemo/keras

6.3.5. Multimodal

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

6.3.6. 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

6.3.7. 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

6.3.8. ThifloNet

KEYWORDS: Deep learning - Policy Learning
SCIENTIFIC DESCRIPTION

We created a software architecture that combines a state-of-the-art computer vision system with a policy learning framework. This system is able to perceive a visual scene, given by a still image, extract facts (“predicates”), and propose an optimal action to achieve a given goal. Both systems are chained into a pipeline that is trained by presenting images and demonstrating an optimal action. By providing this information, both the predicate recognition model and the policy learning model are updated.

Our architecture is based on the recent works of Lerer, A., Gross, S., & Fergus, R., 2016 ("Learning Physical Intuition of Block Towers by Example"). They created a large network able to identify physical properties of stacked blocks. Analogously our vision system utilizes the same network layout (without the image prediction auxiliary output), with an added output layer for predicates, based on the expected number and arity of predicates. The vision subsystem is not trained with a common cross-entropy or MSE loss function, but instead receives its loss form the policy learning subsystem. The policy learning module calculates the loss as optimal combination of predicates for the given expert action.

By using this combination of systems, the architecture as a whole requires significantly fewer data samples than other systems (which exclusively utilize neural networks). This makes the approach more feasible to real-life applciation with actual live demonstration.
FUNCTIONAL DESCRIPTION

The neural network consists of ResNet-50 (the currently best-performing computer vision system), with 50 layers, 2 layers for converting the output of ResNet to predicates and a varying amount of output neurons, corresponding to the estimated number of n-arity predicates. The network was pretrained on the ImageNet dataset. The policy learning module incorporates the ACE tree learning tool and a wrapper in Prolog.

Our example domain consists of 2-4 cubes colored in red, blue, green, and yellow and randomly stacked on top of each other in a virtual 3D environment. The dataset used for training and testing contains a total of 30000 elements, each with an image of the scene, the correct predicates, a list of blocks that are present and the corresponding expert action, that would lead to stacking the blocks to a tower.

- Participants: Florian Golemo, Thibaut Munzer and Manuel Lopes
- Contact: Florian Golemo

6.4. Tools for education

6.4.1. KidLearn

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. The library regrouping the different developed technologies is available on github.

- Participants: Benjamin Clement, Pierre Yves Oudeyer, Didier Roy and Manuel Lopes
- Contact: Manuel Lopes
- URL: https://flowers.inria.fr/research/kidlearn/, https://github.com/flowersteam/kidlearn

6.4.2. KidBreath

FUNCTIONAL DESCRIPTION

KidBreath is a web responsive application composed by several interactive contents linked to asthma and displayed to different forms: learning activities with quiz, short games and videos. There are profil creation and personalization, and a part which describes historic and scoring of learning activities, to see evolution of Kidreath use. To test Kidlearn algorithm, it is iadapted and integrated on this platform. Development in PHP, HTML-5, CSS, MySQL, JQuery, Javascript. Hosting in APACHE, LINUX, PHP 5.5, MySQL, OVH.

- Partner: ItWell SAS
- Contact: Alexandra Delmas
- URL: http://www.kidbreath.fr

6.4.3. Kidlearn: money game application

FUNCTIONAL DESCRIPTION

The games is instantiated in a browser environment where students are proposed exercises in the form of money/token games (see Figure 7). For an exercise type, one object is presented with a given tagged price and the learner has to choose which combination of bank notes, coins or abstract tokens need to be taken from the wallet to buy the object, with various constraints depending on exercises parameters. The games have been developed using web technologies, HTML5, javascript and Django.

- Contact: Benjamin Clement
- URL: https://flowers.inria.fr/research/kidlearn/

6.4.4. Kidlearn: script for Kidbreath use

FUNCTIONAL DESCRIPTION

A new way to test Kidlearn algorithms is to use them on Kidbreath Plateform. The Kidbreath Plateform use apache/PHP server, so to facilitate the integration of our algorithm, a python script have been made to allow PHP code to use easily the python library already made which include our algorithms.

Github link to explanation about it : https://github.com/flowersteam/kidlearn/tree/feature/kidbreath/module_php.

- Contact: Benjamin Clement
- URL: https://github.com/flowersteam/kidlearn/tree/feature/kidbreath/module_php

6.5. 3rdHand Project

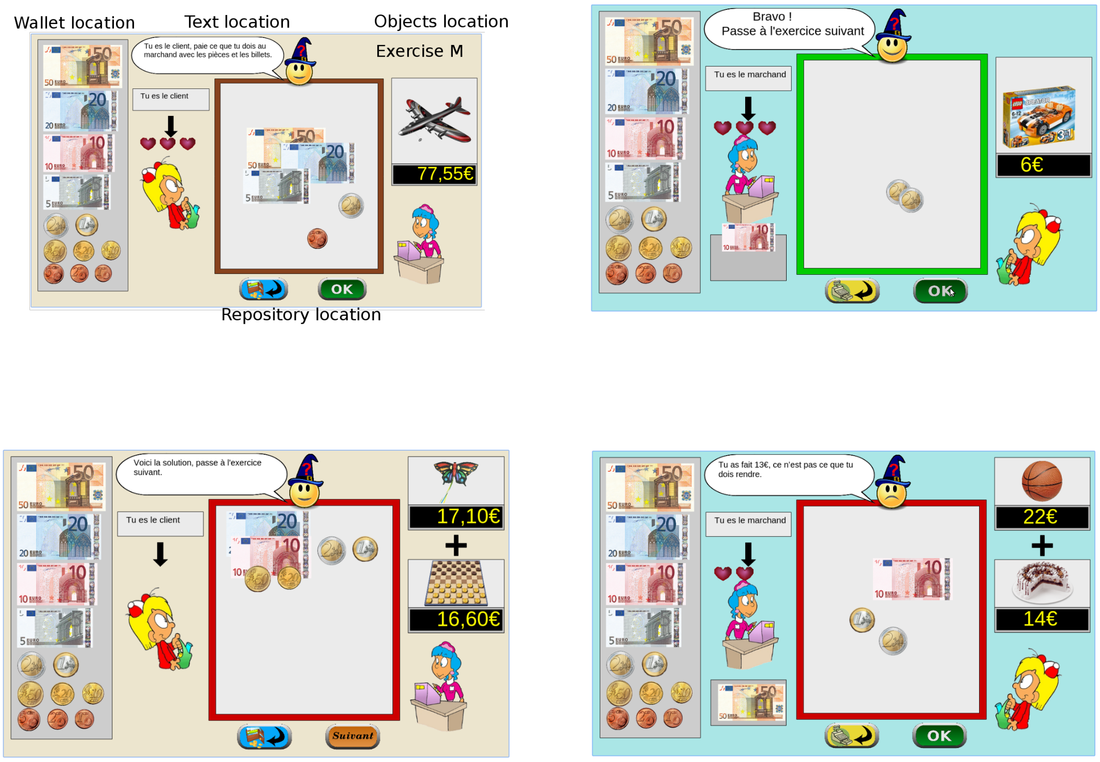
6.5.1. 3rdHand Infrastructure

KEYWORDS: Interaction - Robotics - Infrastructure software - Framework - Robot Operating System (ROS)

FUNCTIONAL DESCRIPTION

The infrastructure is predicate-based to handle relational actions and covers perception (scene description generation, human actions recognition), decision making (teleoperated, scripted or learning from demonstrations), interaction with end users (GUI, voice, gestures) and parallel executions of robotic actions (hold, pick, grasp, bring, ...).

- Contact: Yoan Mollard
- https://github.com/3rdHand-project/thr_infrastructure



Tu es le client, paie ce que tu dois au marchand avec les pièces et les billets.

Bravo !
Passe à l'exercice suivant

Voici la solution, passe à l'exercice suivant.

Tu as fait 13€, ce n'est pas ce que tu dois rendre.

Figure 7. Four principal regions are defined in the graphical interface. The first is the wallet location where users can pick and drag the money items and drop them on the repository location to compose the correct price. The object and the price are present in the object location. Four different types of exercises exist: M : customer/one object, R : merchant/one object, MM : customer/two objects, RM : merchant/two objects.

6.5.2. Kinect 2 Server

Kinect 2 server
KEYWORDS: Depth Perception - Speech recognition - Gesture recognition - Kinect
FUNCTIONAL DESCRIPTION

The server written in C# uses the Kinect SDK v2 to get the RGBD raw image, skeleton tracking information, recognized speech. It also uses the text-to-speech from Microsoft. Then it streams JSON data over the network using the Publisher/Subscriber pattern from the ZeroMQ network library. A Linux client has been written in Python but it can be written in any other language that is compatible with ZeroMQ. Features are controllable through a Graphical User Interface on Windows, or through the code from any Linux/Windows client. The clients can for instance enable features (speech recognition on, skeleton tracking off, . . .) and parameters (set new speech to recognize, change language, . . .) from remote.

- Contact: Yoan Mollard
- URL: https://github.com/baxter-flowers/kinect_2_server/

6.5.3. ProMP

Probabilistic Movement Primitives
KEYWORDS: Interaction - Robotics - Probability - Motion model - Robot Operating System (ROS)
FUNCTIONAL DESCRIPTION

Joint-space primitives with a task-space constraint: The primitives are stored in joint-space but demonstrations are provided both in joint space and task space, context. Thanks to this context, task-space goals can be requested to these joint-space primitives. The benefit is that requesting a new task-space goal does not require to call an IK method which would return demonstrations-agnostic joint configurations.

Vocal interactive learning and clustering: This work includes an interactive learning aspect which allows to automatically cluster motor primitives based on the standard deviation of their demonstrations. A new primitive is created automatically if the provided demonstration is out of 2 standard deviation of the existing primitives, otherwise the demonstration is distributed to an existing one.

- Contact: Yoan Mollard
- URL: https://github.com/baxter-flowers/promplib

6.5.4. ROS Optitrack Publisher

KEYWORDS: Target tracking - Robot Operating System (ROS)
FUNCTIONAL DESCRIPTION

This package allows to publish optitrack markers declared as rigid bodies as TF transforms. Data is gathered through the embedded VRPN server of Motive/Arena. Only rigid bodies are requested to the server, thus single points in 2D/3D are ignored. VRPN server can be enable in View > Data streaming in Motive.

- Contact: Yoan Mollard
- URL: https://github.com/baxter-flowers/optitrack_publisher

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 Memin
- Contact: Etienne Memin
- 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 (for the first time to our knowledge) 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 Memin
- 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.

- Participant: Etienne Memin
- Contact: Etienne Memin
- URL: http://fluid.irisa.fr/index.html

5.4. Low-Order-Motion

Estimation of low order representation of fluid motion

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: Etienne Memin and Anne Cuzol
- Contact: Etienne Memin
- 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 Derian, Christopher Mauzey and Etienne Memin
- Partner: CSU Chico
- Contact: Etienne Memin
- URL: http://phys.csuchico.edu/lidar/typhoon/

5.6. GRT3D

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.

- Participants: Yvan Crenner, Jocelyne Erhel
- Partner: ANDRA
- Contact: Jocelyne Erhel
- URL: http://www.irisa.fr/sage/recherche/chemistry.html

5.7. H2OLab

KEYWORDS: Simulation - Multiscale - Uncertainly - Heterogeneity - Hydrogeology - Groundwater - Contamination - Energy

SCIENTIFIC DESCRIPTION

The software platform contains a database which is interfaced through the web portal H2OWeb. It contains also software modules which can be used through the interface H2OGuilde. The platform H2OLab is an essential tool for the dissemination of scientific results. Currently, software and database are shared by the partners of the h2mno4 project.

FUNCTIONAL DESCRIPTION

The software platform H2OLab is devoted to stochastic simulations of groundwater flow and contaminant transport in highly heterogeneous porous and fractured geological media.

-Modeling and numerical simulation of aquifers -Porous and fractured heterogeneous media -Flow with mixed finite elements -Solute transport with a Lagrangian method -Stochastic modeling for data uncertainty.

- Participants: Jean-Raynald De Dreuzy, Jocelyne Erhel
- Partners: Université de Rennes 1 - CNRS - Université de Lyon - Université de Poitiers
- Contact: Jocelyne Erhel
- URL: http://h2olab.inria.fr/

5.8. PALMTREE

FUNCTIONAL DESCRIPTION

We present an easy-to-use package for the parallelization of Lagrangian methods for partial differential equations. In addition to the reduction of computation time, the code aims at satisfying three properties:

simplicity: the user just has to add the algorithm governing the behaviour of the particles. portability: the possibility to use the package with any compiler and OS. action-replay: the ability of the package to replay a selected batch of particles.

The last property allows the user to replay and capture the whole sample path for selected particles of a batch. This feature is very useful for debugging and catching some relevant information.

- Participants: Lionel Lenotre
- Contact: Jocelyne Erhel

FOCUS Project-Team

6. New Software and Platforms

6.1. AIOCJ

Adaptive Interaction-Oriented Choreographies in Jolie

SCIENTIFIC DESCRIPTION

AIOCJ is a framework for programming adaptive distributed systems based on message passing. AIOCJ comes as a plugin for Eclipse, AIOCJ-ecl, allowing one 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.

FUNCTIONAL DESCRIPTION

AIOCJ is an open-source choreography programming language for developing adaptive systems.

- Participants: Saverio Giallorenzo, Mila Dalla Preda, Maurizio Gabbrielli, Ivan Lanese and Jacopo Mauro
- 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 is currently extended with primitives for cloud-computing in the EU project ENVISAGE. ABS is very similar to ASP, developed by the former 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 analyzed by a back-end that uses a fix-point technique to derive in a deterministic way the deadlock information.

- Contact: Cosimo Laneve
- 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. 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 analyzed 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 analyzers. 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

FUNCTIONAL DESCRIPTION

HOCA is an abbreviation for Higher-Order Complexity Analysis, and is meant as a laboratory for the automated complexity analysis of higher-order functional programs. Currently, HOCA consists of one executable pcf2trs which translates a pure subset of OCaml to term rewrite systems, in a complexity-reflecting manner. As a first step, HOCA desugars the given program to a variation of Plotkin's PCF with data-constructors. Via Reynold's defunctionalization, the PCF program is turned into an applicative term rewrite system (ATRS for short), and call-by-value reductions of the PCF program are simulated by the ATRS step-by-step. On the ATRS, various complexity reflecting transformations are performed: inlining, dead-code-elimination, instantiation of higher-order variables through a call-flow-analysis and finally uncurrying. This results in a first-order rewrite system, whose runtime-complexity asymptotically reflects the complexity of the initial program.

- Participants: Ugo Dal Lago and Martin Avanzini
- Contact: Ugo Dal Lago
- URL: http://cbr.uibk.ac.at/tools/hoca/

6.4. JOLIE

Java Orchestration Language Interpreter Engine

KEYWORD: Microservices

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 2016

Jolie has transitioned from version 1.4.1 to version 1.6. The last version of Jolie that supports Java 1.6 is Jolie 1.5. Jolie 1.6 transitions from Java 1.6 to Java 1.8 and makes use of the new features and libraries found in the new version of Java. Version 1.6 of Jolie features:

- general performance improvements and bug fixes, in particular regarding concurrent data structures using Java lambdas,
- improvements of the standard library of the language,
- better error messages and improved compatibility with the main operating systems,
- support for type choices (AKA type sums),
- support of for-loop construct to iterate over arrays without explicit indexes,
- improved support for the HTTP protocol (and, by extension, web applications).
- Participants: Claudio Guidi, Fabrizio Montesi, Saverio Giallorenzo and Maurizio Gabbrielli
- Contact: Fabrizio Montesi
- 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: Cosimo Laneve
- 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 portfolio solver that allows one to solve a Constraint (Satisfaction/Optimization) Problem 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.

FUNCTIONAL DESCRIPTION

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: Maurizio Gabbrielli
- URL: https://github.com/CP-Unibo/sunny-cp

6.7. Blender

Aeolus Blender

KEYWORDS: Automatic deployment - Cloud applications management
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. FIT IoT-Lab

Participants: 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.

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. ECP

Part-Based Object Detection
FUNCTIONAL DESCRIPTION A DPM model gives rise to the energy function being optimized during inference and has to be learned offline beforehand. All functionality is accessible via a ROS interface. The work follows closely Felzenszwalb's "Object Detection with Discriminatively Trained Part Based Models", using the FFLD-library in the implementation and facilitating communication in a setup with NAO robots.

- Participants: Haithem Boussaid, Stefan Kinauer, Iasonas Kokkinos
- Contact: Stefan Kinauer
- URL: https://bitbucket.org/eu-reconfig/ecp

6.4. 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: Nikos Paragios
- URL: http://campar.in.tum.de/Main/Drop

6.5. 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/

6.6. 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

6.7. 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

6.8. 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

6.9. 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/

6.10. 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: Nikos Paragios
- Contact: Nikos Paragios
- URL: http://www.mrf-registration.net/

6.11. Newton-MRF

FUNCTIONAL DESCRIPTION MAP inference in MRFs can be performed through the LP relaxation approach. This project was a study of the feasibility and benefit of Newton-type methods for solving the optimization problem that is obtained by smoothing the dual of the LP relaxation. The project TRN-MRF is a trust-region Newton method that can address inference in higher order MRFs, for cases in which decomposition according to individual cliques leads to practical convergence. The project QN-MRF works for problems that need decomposition according to larger sub-problems (like chains of higher order cliques) and it works as long as a node is shared by exactly two sub-problems.

- Participants: Hariprasad Kannan, Nikos Paragios, Nikos Komodakis
- Contact: Hariprasad Kannan
- URL: https://github.com/neostrider/TRN-MRF, https://github.com/neostrider/QN-MRF

6.12. Relative MMD

FUNCTIONAL DESCRIPTION This software can be used to compare two distributions to a reference distribution. Applications include model selection and exploratory data analysis.

- Participants: Eugene Belilovsky, Wacha Bounliphone, Matthew Blaschko (in collaboration with researchers at UCL and Deepmind)
- Contact: Eugene Belilovsky
- URL: https://github.com/eugenium/MMD

6.13. Deep Graph Structure Discovery

FUNCTIONAL DESCRIPTION Novel approach to graph structure discovery using neural network. This software provides a much faster approach to discover underlying conditional independence structure in small sample data.

- Participants: Eugene Belilovsky
- Contact: Eugene Belilovsky
- URL: https://github.com/eugenium/LearnGraphDiscovery

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].

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 specifications, 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. Recent releases (“Seven”) provide a new license (Cecill-B), a simplified build process and numerous features, including a simple macro system that connects the C input language and LISA annotations.

- 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. OPAM Builder

Participant: Fabrice Le Fessant.

OPAM Builder checks in real time the installability on a computer of all packages after any modification of the OPAM repository. To achieve this result, it uses smart mechanisms to compute incremental differences between package updates, to be able to reuse cached compilations, and go down from quadratic complexity to linear complexity.

- URL: http://github.com/OCamlPro/opam-builder

6.6. PASL

Participants: Michael 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/

6.7. TLAPS

Participants: Damien Doligez [**contact**], Stefan Merz [team Veridis], Martin Riener [team Veridis].

TLAPS 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.

- URL: https://tla.msr-inria.inria.fr/tlaps/content/Home.html

6.8. 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://zenon-prover.org/

GAMMA3 Project-Team

3. New Software and Platforms

3.1. 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

3.2. 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

3.3. BL2D

KEYWORDS: Automatic mesher - Delaunay - Anisotropic - Planar domain

SCIENTIFIC DESCRIPTION

The meshing method is of controlled Delaunay type, isotropic or anisotropic. The internal point generation follows an advancing-front logic, and their connection is realized 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

3.4. 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 *a posteriori* error estimation 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

3.5. 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

3.6. 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 parametrization 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

3.7. 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 should have unit length edges with respect to the related Riemannian space (the so-called “unit mesh”). 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

3.8. 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

3.9. 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, Eric Saltel, Frédéric Alauzet and Adrien Loseille
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

3.10. 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, Eric Saltel, Frédéric Alauzet and Adrien Loseille
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

3.11. 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, Eric Saltel, Frédéric Alauzet, Adrien Loseille and Frederic Hecht
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

3.12. 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

3.13. 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

3.14. 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

3.15. 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/

3.16. 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, for details see thereafter.

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

3.17. 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

3.18. 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 a 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

3.19. 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 a 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

3.20. 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 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

3.21. 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

3.22. 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

3.23. 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

3.24. Wolf-Xfem

KEYWORD: Scientific calculation

SCIENTIFIC DESCRIPTION

Tool providing the mesh of the intersection between a surface mesh and a volume mesh in the goal of simulating mechanical fractures.

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

5. New Software and Platforms

5.1. big-graph-tools

FUNCTIONAL DESCRIPTION

Gang is developing software for big graph manipulation. A preliminary library offering diameter and skeleton computation is available online [0]. This library was used to compute the diameters of the worldwide road network (200M edges), skeleton subtrees of the shortest-path trees of continental-sized road networks, as well as the largest strongly connected component of the Twitter follower-followee graph (23G edges).

- Contact: Laurent Viennot
- URL: https://who.rocq.inria.fr/Laurent.Viennot/dev/big-graph-tools/

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[0] https://who.rocq.inria.fr/Laurent.Viennot/dev/big-graph-tools/

GECO Project-Team

6. New Software and Platforms

6.1. ARTIV1 INPAINTING

ARTIV1 INPAINTING
FUNCTIONAL DESCRIPTION

ARTIV1 INPAINTING is a software for reconstruction of corrupted and damaged images. One of the main features of the algorithm on which the software is based is that it does not require any information about the location and character of the corrupted places. Another important advantage is that this method is massively parallelizable, this allows to work with sufficiently large images. Theoretical background of the presented method is based on the model of geometry of vision due to Petitot, Citti and Sarti. The main step is numerical solution of the equation of 3D hypoelliptic diffusion. A new version of the software has just be submitted for protection at APP (Agence pour la protection des programmes).

- Contact: Ugo Boscain

GENSCALE Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: RDF - SPARQL - Querying - Graph
FUNCTIONAL DESCRIPTION

AskOmics allows to load heterogeneous bioinformatics data (formatted as tabular files) into a Triple Store system using a user-friendly web interface. AskOmics also provides an intuitive graph-based user interface supporting the creation of complex queries that currently require hours of manual searches across tens of spreadsheet files. The elements of interest selected in the graph are then automatically converted into a SPARQL query that is executed on the users' data.

- Authors: Charles Bettembourg, Yvanne Chaussin, Anthony Bretaudeau, Olivier Filangi, Fabrice Legeai and Olivier Dameron
- Partners: CNRS - INRA - Université de Rennes 1
- Contact: Fabrice Legeai
- URL: https://github.com/askomics/askomics

6.2. BBhash

Basic binary representation of successive hash
KEYWORDS: C++ - Indexation - Data structures
FUNCTIONAL DESCRIPTION

BBHash is a simple library for building minimal perfect hash function. Given a set of N input keys, it will compute a bijective function that will associate to each key an integer between 1 and N. This then allows to create an indexed array that will hold some data for each key. It is designed to handle large scale datasets (hundred billion and more elements). The function itself is just a little bit larger than other state-of-the-art libraries, it takes approximately 3 bits / elements (compared to 2.62 bits/elem for the emphf lib), but construction is faster and does not require additional memory.

- Participants: Guillaume Rizk, Pierre Peterlongo, Rayan Chikhi and Antoine Limasset
- Contact: Guillaume Rizk
- URL: https://github.com/rizkg/BBHash

6.3. BCALM 2

KEYWORDS: Bioinformatics - NGS - Genomics - Metagenomics - De Bruijn graphs
SCIENTIFIC DESCRIPTION

BCALM 2 is a bioinformatics tool for constructing the compacted de Bruijn graph from sequencing data. It is a parallel algorithm that distributes the input based on a minimizer hashing technique, allowing for good balance of memory usage throughout its execution. It is able to compact very large datasets, such as spruce or pine genome raw reads in less than 2 days and 40 GB of memory on a single machine.
FUNCTIONAL DESCRIPTION

BCALM 2 is an open-source tool for dealing with DNA sequencing data. It constructs a compacted representation of the de Bruijn graph. Such a graph is useful for many types of analyses, i.e. de novo assembly, de novo variant detection, transcriptomics, etc. The software is written in C++ and makes extensive use of the GATB library.

- Participants: Rayan Chikhi, Antoine Limasset and Paul Medvedev
- Contact: Rayan Chikhi
- URL: https://github.com/GATB/bcalm

6.4. BGREAT

De bruijn graph read alignment tool
KEYWORDS: Short reads - Genome assembling
FUNCTIONAL DESCRIPTION

Mapping genomic extracts (reads) on genomic references is a central and necessary task in most genomic studies. But reference sequences are mainly extracted from assembly graphs through an inexact process that both creates chimeras and losses biological pieces of information. This motivates the need of mapping sequences on references represented by graphs. BGREAT is conceived to map reads on de Bruijn graph, a widely used graph in genome assembly.

- Participants: Pierre Peterlongo and Antoine Limasset
- Contact: Pierre Peterlongo
- URL: https://github.com/Malfoy/BGREAT

6.5. GATB-Core

Genome Assembly and Analysis Tool Box
KEYWORDS: Bioinformatics - NGS - Genomics - Genome assembling
FUNCTIONAL DESCRIPTION

The GATB-Core library 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 processor (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-Core library is written in C++.

- Participants: Dominique Lavenier, Guillaume Rizk, Pierre Peterlongo, Charles Deltel, Patrick Durand and Claire Lemaitre
- Contact: Dominique Lavenier
- URL: http://gatb.inria.fr/

6.6. GATB-Core Tutorial

Online GATB-Core tutorial
KEYWORD: Bioinformatics
FUNCTIONAL DESCRIPTION

"GATB-Core tutorial" is an interactive learning tool that aims at learning software development relying on the bioinformatics toolkit GATB-Core without the need of installing it, its dependencies and a C++ compiler. The tutorial relies on a client-server system. The client is simply a web browser running a full-featured C++ code editor. In turns, it is embedded in templates for the purpose of displaying various lessons. The server side is a Linux-based VM capable of compiling and running "online" any C++ code snippets using GATB-Core. That VM is deployed on Inria's A||Go SaaS platform.

- Participant: Patrick Durand
- Contact: Patrick Durand
- URL: http://gatb-core.gforge.inria.fr/training/

6.7. MindTheGap

KEYWORDS: Bioinformatics - NGS - Genome assembling
FUNCTIONAL DESCRIPTION

MindTheGap performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It is designed to call insertions of any size, whether they are novel or duplicated, homozygous or heterozygous in the donor genome. The main algorithmic improvement of version 2.0.0 is to detect additionnal variants, such as SNPs and deletions. This feature improves the sensitivity of the insertion detection algorithm for insertions that are located near these other variants. Additionnally, 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.

- Participants: Claire Lemaitre and Guillaume Rizk
- Contact: Claire Lemaitre
- URL: https://gatb.inria.fr/software/mind-the-gap/

6.8. PLAST

Local alignment tool
KEYWORDS: Bioinformatics - Genomic sequence - Genomics
FUNCTIONAL DESCRIPTION

PLAST is a parallel alignment search tool for comparing large protein banks.

Sequence similarity searching is an important and challenging task in molecular biology and next-generation sequencing should further strengthen the need for faster algorithms to process such huge amount of data. At the same time, the internal architecture of current microprocessors is tending towards more parallelism, leading to the use of chips with two, four and more cores integrated on the same die. The main purpose of this work was to design an effective algorithm to fit with the parallel capabilities of modern microprocessors. A parallel algorithm for comparing large genomic banks and targeting middle-range computers has been developed and implemented in PLAST software. The algorithm exploits two key parallel features of existing and future microprocessors: the SIMD programming model (SSE instruction set) and the multithreading concept (multicore). Compared to multithreaded BLAST software, tests performed on an 8-processor server have shown speedup ranging from 3 to 6 with a similar level of accuracy.

- Participants: Dominique Lavenier, Erwan Drezen and Van Hoa Nguyen
- Contact: Dominique Lavenier
- URL: https://team.inria.fr/genscale/high-throughput-sequence-analysis/plast-intensive-sequence-comparison/

6.9. Simka

KEYWORDS: Comparative metagenomics - K-mer - Distance - Ecology
FUNCTIONAL DESCRIPTION

Simka is a comparative metagenomics method dedicated to NGS datasets. It computes a large collection of distances classically used in ecology to compare communities by approximating species counts by k-mer counts. The method scales to a large number of datasets thanks to an efficient and parallel kmer-counting strategy that processes all datasets simultaneoulsy.

- Participants: Gaetan Benoit, Claire Lemaitre, Pierre Peterlongo and Dominique Lavenier
- Contact: Gaetan Benoit
- URL: https://gatb.inria.fr/software/simka/

6.10. short read connector

KEYWORDS: Bioinformatics - Genomics - Metagenomics

SCIENTIFIC DESCRIPTION

Short read connector enables the comparisons of two read sets B and Q. For each read from Q it provides either:

The number of occurrences of each k-mers of the read in the set B (SRC_counter) or A list of reads from B that share enough k-mers with the tested read from B (SRC_linker)

FUNCTIONAL DESCRIPTION

This tool uses a data structure (BBHASH) adapted to the indexing of big data. Short Read Connector works on reads, which are sequencing data from high-throughput sequencers. Once the data is indexed, short read connector makes it possible either to find the similar reads in a dataset or to simply retrieve the approximate number of these similar reads.

- Participants: Pierre Peterlongo, Camille Marchet and Antoine Limasset
- Partner: UPMC
- Contact: Pierre Peterlongo
- URL: https://github.com/pierrepeterlongo/short_read_connector

GEOSTAT Project-Team

5. New Software and Platforms

5.1. Fluex

KEYWORDS: Signal - Signal processing

SCIENTIFIC DESCRIPTION

Fluex is a package consisting of the Microcanonical Multiscale Formalism for 1D, 2D 3D and 3D+t general signals.

FUNCTIONAL DESCRIPTION Fluex is a C++ library developed under Gforge. Fluex is a library in nonlinear signal processing. Fluex is able to analyze turbulent and natural complex signals, Fluex is able to determine low level features in these signals that cannot be determined using standard linear techniques.

- Participants: Rémi Paties and Hussein Yahia
- Contact: Hussein Yahia
- URL: https://geostat.bordeaux.inria.fr/index.php/downloads.html
- URL: https://bil.inria.fr/fr/software/view/2113/tab

5.2. FluidExponents

- Participants: Hussein Yahia and Antonio Turiel
- Contact: Hussein Yahia
- URL: https://bil.inria.fr/fr/software/view/336/tab

GRACE Project-Team

6. New Software and Platforms

6.1. ACTIS

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 have two directions for improvement: renewing the APIs to make them actually usable by researchers, and incorporating efficient programs for decoding, like J. Nielsen's CodingLib, which contains many new algorithms.

- Contact: David Lucas
- https://bil.inria.fr/fr/software/view/2114/tab

During the project, D. Lucas and J. Nielsen proposed a google summer of code project on rank-metric codes under our ACTIS framework. The intern was Arpit Merchant, who visited us for SageDays75.

6.2. muKummer

KEYWORD: Cryptography
FUNCTIONAL DESCRIPTION

A competitive, high-speed, open implementation of the Diffie–Hellman key exchange protocol and a Schnorr-type digital signature scheme, targeting the 128-bit security level on two microcontroller platforms: the classic AVR ATMega 8-bit platform and the more modern ARM Cortex M0 32-bit platform. These downloads contain mixed C and assembly sources for the implementations described in [16].

- Participant: Benjamin Smith
- Contact: Benjamin Smith
- ATMega implementation URL: http://www.cs.ru.nl/~jrenes/software/mukummer-avr.tar.gz
- Cortex M0 implementation URL: http://www.cs.ru.nl/~jrenes/software/mukummer-arm.tar.gz

GRAPHDECO Project-Team

5. New Software and Platforms

5.1. SWARPI-Unity

SWARPI-Unity (for Superpixel Warp for Image-based rendering for Unity)
This is a software module developed in collaboration with Testaluna in the context of the CR-PLAY EU project. It involves an implementation of the Image-Based rendering algorithms of the group in the Unity3D framework. The software was improved this year to support mobile Android devices and was used in the evaluation step of the CR-PLAY project and for multiple demos.

- Participants: Sebastien Bonopera, Jerome Esnault, George Drettakis and Gaurav Chaurasia
- Contact: George Drettakis

5.2. SIBR

SIBR (for Simple Image-Based Rendering)
This is a framework containing libraries and tools used internally for research projects based on Image-Base Rendering. It includes both preprocessing tools (computing data used for rendering) and rendering utilities. This new framework replaces the previously used IBR-COMMON tools.

- Participants: George Drettakis, Abdelaziz Djelouah, Rodrigo Ortiz Canyon, Theo Thonat, Sebastien Bonopera
- Contact: George Drettakis

5.3. MVIIR

MVIIR (for Multi-View Image Intrinsic Images and Relighting)
This package is the software implementation of the intrinsic image algorithm of Duchêne et al. It includes two libraries; one general-purpose that can be used to augment the functionalities of the previously mentioned SIBR framework, and another for specific logic concerning the relighting task. This package includes also programs to compute preprocess data required for the relighting of a dataset.

- Participants: George Drettakis, Sebastien Bonopera, Adrien Bousseau
- Contact: George Drettakis

5.4. SGTDGP

SGTDGP (for Synthetic Ground Truth Data Generation Platform)
We have started the development of a ground truth data generation platform based on complex and realistically rendered scenes built in 3D modelling packages such as 3DS Max. The platform includes an export module from 3DSMax with support for complex materials and shade trees such as those developed for the physically based rendering VRay platform. This module exports to the Mitsuba opensource renderer, and includes support for various operations using Mitsuba, as well as rendering on the Inria cluster. The platform is designed to generate ground truth data for learning as well as data for ground truth comparisons for image-based rendering projects in the group.

- Participants: George Drettakis, George Kopanas, Sai Bangaru
- Contact: George Drettakis

GRAPHIK Project-Team

5. New Software and Platforms

5.1. SudoQual

Participants: Michel Leclère, Michel Chein, Alain Gutierrez, Clément Sipieter, Brett Choquet.

Contact: Michel Leclère

SudoQual is a software suite that allows discovering and evaluating coreference links between individual entities references. It has been developed during the ANR project Qualinca. This software suite comprises:

- a generic API allowing to implement (thanks to a graphical interface) applications computing "same-as" and "different-from" links in knowledge bases;
- a generic application (whose specific parameters are defined in a configuration file) evaluating the quality of a knowledge base; it is available either as a standalone client or as a web service;
- a library dedicated to the comparison of individual entities' attributes;
- the specific configuration file dedicated to evaluating the quality of links in ABES' Sudoc catalogue.

Main developments this year are:

- adapting the API's architecture to the NetBeans IDE in order to benefit from its better edition functionalities;
- finalizing, testing and optimizing the linkage application;
- specifying and implementing the quality evaluation application;
- implementing this latter application as a web service.

5.2. GRAAL

Participants: Clément Sipieter, Jean-François Baget, Michel Leclère, Marie-Laure Mugnier, Swan Rocher.

Contact: Marie-Laure Mugnier (scientific contact), Clément Sipieter (technical contact)

Keywords: Data management - Ontologies - Query Answering

Web site: https://graphik-team.github.io/graal/

Scientific Description Graal is a generic platform for ontological query answering with existential rules. It implements various paradigms that fall into that framework. It is an open source software written in Java.

Functional Description See last year's report for a description of GRAAL's features http://raweb.inria.fr/rapportsactivite/RA2015/graphik/uid49.html.

New Features The main features developed in 2016 are:

- improvement of the semi-saturation algorithm with compilable rules;
- implementation of mappings allowing to query an existing database as it is, without prior loading it in GRAAL;
- design and implementation of classes that manage a knowledge base (i.e., the rules and the data). In particular, the results of the rule analyser Kiabora (that has been integrated within GRAAL) are used to automatically select the most appropriate algorithms for querying the knowledge base.

5.3. Cogui

Participants: Alain Gutierrez, Marie-Laure Mugnier, Michel Leclère, Michel Chein.

Contact: Marie-Laure Mugnier (scientific contact), Alain Gutierrez (technical contact)

Keywords: Graphical knowledge bases - Ontology Editor - Conceptual Graphs

Web site: http://www.lirmm.fr/cogui/

Scientific Description Cogui is a tool for building and verifying graphical knowledge bases. It is a freeware written in Java.

Functional Description See last year's report for a description of CoGui's features http://raweb.inria.fr/rapportsactivite/RA2015/graphik/uid41.html.

New features Cogui is currently under heavy refactoring to benefit from NetBeans graphical libraries.

5.4. CoGui-Capex

CoGui-Capex is a decision support tool dedicated to food industry. Its knowledge base represents the causal links between food descriptors and actions which can be undertaken by operators to control food quality on the line. The new version of CoGui-Capex developed in 2016 in a Neatbeans environnement is coupled with the so-called "Knowledge book" developed by INRA I2M team in Bordeaux [49]. This collaboration will be extended in the CASDAR Docamex national project (funded by the French Ministry of Agriculture), which will begin in January 2017 for 4 years with several cheese makers.

5.5. @Web

An extension of the 5 stars/FAIRS scientific data annotation platform called @Web (http://www6.inra.fr/cati-icat-atweb), managed by INRA, has been developped by Leandro Lovisolo (UBA master student) co-supervised by Federico Ulliana and Patrice Buche using semantic web languages (OWL, SPARQL, RDF). This extension permits to represent negative constraints expressed on annotated data and will be used in data curation phase.

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

6.2. Platforms

We describe here only the new platforms that have been developed in 2016 while we maintain a very large number of platforms (e.g. the cable-driven parallel robots of the MARIONET family, the ANG family of walking aids or our experimental flat).

6.2.1. GMSIVE ADT: virtual reality and rehabilitation

Inria has agreed to fund us for developing the platform GMSIVE whose purpose is to introduce end-user motion and their analysis in a virtual reality environment in order to make rehabilitation exercises more attractive and more appropriate for the rehabilitation process. For example we have developed an active treadmill whose slope will change according to the user place in the virtual world while the lateral inclination may be changed in order to regulate the load between the left and right leg. Such a system may be used in rehabilitation to simulate a walk in the mountain while increasing on-demand the load on an injured leg (that is usually avoided by the user) for a shorter rehabilitation time. At the same time the walking pattern is analyzed in order to assess the efficiency of the rehabilitation exercise.

The motion system is composed of two vertical columns whose height may be adjusted (they are used for actuating the treadmill), a 6 d.o.f motion base and a cable-driven parallel robot which may lift the user (in the walking experiment this robot may be used to support partly the user while he is walking allowing frail people to start the rehabilitation earlier). We intend to develop sailing and ski simulators as additional rehabilitation environment. Currently the columns and motion base are effective while the robot has been installed but not tested yet and we have started to study the coupling between the motion generators and the 3D visualization.

6.2.2. Activities detection platform

For non intrusive activities detection we use low cost distance and motion sensors that are incorporated in a 3D printed box (figure 1) and constitute a detection station. Several such station are implemented at appropriate place in the location that has to be monitored (e.g. the Valrose EHPAD where 15 such stations has been deployed at the end of 2016 while 17 stations will be deployed at Institut Claude Pompidou at the very beginning of 2017). Although the information provided by each station is relatively poor an appropriate network of such station allow us to provide the information requested by the medical community.

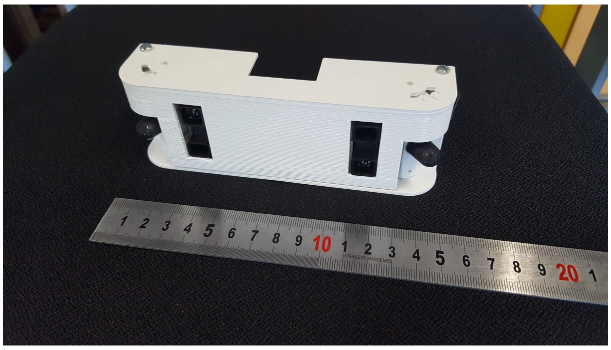


Figure 1. A station for activities detection. The 4 sensors allow to determine the presence of the subject in a given zone, his/her direction of motion and speed even at night

HIEPACS Project-Team

6. New Software and Platforms

6.1. Spack-morse

The radical change we have adopted in terms of methodology (task-based programming strongly) changes the software design. In particular, our codes become more and more modular and the complexity of their inter-dependencies is subsequently very high.

In order to address this complexity we have chosen to rely on the `Spack` flexible package manager designed to support multiple versions, configurations, platforms, and compilers (http://software.llnl.gov/spack developed and maintained at LLNL. We have integrated all our libraries above this package manager in the `Spack-Morse` extension that we maintain in HIEPACS.

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-3 (original software reusing known ideas and introducing new ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-3 (good quality middle-term maintenance).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web). source distribution or a commercially-distributed product).
- Contact: Florent Pruvost
- URL: http://morse.gforge.inria.fr/spack/spack.html

6.2. Chameleon

`Chameleon` is a dense linear algebra software relying on the STF sequential task-based programming paradigm. It implements the tile algorithms originally designed for multicore architectures in the `PLASMA` package and extends them so that they can be processed on by a runtime system to exploit any type of hardware architecture (multicore, GPU, heterogeneous, supercomputer). This software is central for the team as it allows to investigate in a relatively simple context (regular dense linear algebra algorithms) new types of designs before implementing them for the more irregular algorithms implemented in the software packages described below.

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-3 (good quality middle-term maintenance).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web). source distribution or a commercially-distributed product).
- Contact: Emmanuel Agullo
- URL: https://project.inria.fr/chameleon

6.3. HIPS

`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).

Thus, `HIPS` is a software library that provides several methods to build an efficient preconditioner in almost all situations.

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-2 (basic maintenance to keep the software alive).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Pierre Ramet
- URL: http://hips.gforge.inria.fr

6.4. MaPHYS

`MaPHyS` (Massively Parallel Hybrid Solver) is an hybrid iterative/direct parallel (MPI-threads) sparse linear solver based on algebraic domain decomposition technique for real/complex symmetric positive definite/unsym/-metric matrices. For a given number of MPI processes/domains, `MaPHyS` solves the Schur complement computed from the adjacency graph of the sparse matrix using a preconditioned Krylov subspace method (CG or GMRES). The provided preconditioners are variants of an algebraic Additive Schwarz methods. A prototype version of a two level precondionner using an algebraic coarse space is available but not yet publicly distributed (provided upon request for beta testers).

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-4 (well-defined and implemented plans for future maintenance and evolution).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Emmanuel Agullo
- URL: https://project.inria.fr/maphys/fr

6.5. MetaPart

`MetaPart` is a library that addresses 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 & ordering software packages such as `Scotch`, `PaToH`, `METIS`, `Zoltan`, `Mondriaan`, 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).

- Audience: A-1 (internal prototype).
- Software originality: SO-3 (original software reusing known ideas and introducing new ideas).
- Software maturity: SM-2 (basic usage works, terse documentation).
- Evolution and maintenance: EM-3 (good quality middle-term maintenance).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Aurélien Esnard
- URL: http://metapart.gforge.inria.fr

6.6. PaStiX

`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` solver 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.

- Audience: A-5 (wide audience, large user's community).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-4 (major software project, strong software engineering).
- Evolution and maintenance: EM-4 (well-defined and implemented plans for future maintenance and evolution).
- Software distribution and licensing: SDL-5 (external packaging and distribution, as part of a popular open source distribution or a commercially-distributed product).
- Contact: Pierre Ramet
- URL: http://pastix.gforge.inria.fr

6.7. QR_Mumps

`qr_mumps` is a software package for the solution of sparse, linear systems on multicore computers. It implements a direct solution method based on the QR factorization of the input matrix. Therefore, it is suited to solving sparse least-squares problems and to computing the minimum-norm solution of sparse, under-determined problems. It can obviously be used for solving square problems in which case the stability provided by the use of orthogonal transformations comes at the cost of a higher operation count with respect to solvers based on, e.g., the LU factorization. `qr_mumps` supports real and complex, single or double precision arithmetic.

`qr_mumps` is mainly developed and maintained by the APO team of the IRIT laboratory of Toulouse. HIEPACS is an active contributor to this project.

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-3 (good quality middle-term maintenance).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Emmanuel Agullo
- URL: http://buttari.perso.enseeiht.fr/qr_mumps/

6.8. ScalFMM

`ScalFMM` is a library to compute N-body interactions using the Fast Multipole Method. This is a parallel kernel independent fast multipole method based on interpolation (Chebychev or equispaced grid points).

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 (fork-join and tasks models), MPI and runtime system (`StarPU`). The software architecture has been designed with two major objectives: being easy to maintain and easy to understand. There is two main parts:

- the management of the tree structure (hierarchical octree and Group-Tree) and the parallel algorithms ;
- the kernels (scalar, tensorial and multi-rhs). Classical kernels are available (Coulombic, Leonard-Jones, Gaussian, Stokes, ...)

This modular architecture allows us to easily add new FMM algorithms or kernels and new paradigm of parallelization. Today, we also proposed the FMM based on spherical harmonic expansion with Blas or rotation optimization for Coulombic potential) and all algorithms are designed to treat more complex kernels by adding multiple right-hand sides, tensorial structures, ...

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-4 (original software implementing a fair number of original ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-3 (good quality middle-term maintenance).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Olivier Coulaud
- URL: http://scalfmm-public.gforge.inria.fr/doc/

6.9. ViTE

ViTE is a trace explorer. It is a tool to visualize execution traces in Pajé or OTF format for debugging and profiling parallel or distributed applications. It is developed with C++ programming language with OpenGL and Qt technologies.

- Audience: A-4 (large audience, used by people outside the team).
- Software originality: SO-3 (original software reusing known ideas and introducing new ideas).
- Software maturity: SM-3 (well-developed software, good documentation, reasonable software engineering).
- Evolution and maintenance: EM-2 (basic maintenance to keep the software alive).
- Software distribution and licensing: SDL-4 (public source or binary distribution on the Web).
- Contact: Mathieu Faverge
- URL: http://vite.gforge.inria.fr

6.10. Platforms

6.10.1. PlaFRIM: Plateforme Fédérative pour la Recherche en Informatique et Mathématiques

PlaFRIM is an experimental platform for research 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.

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 1,000 cores (excluding GPU and Xeon Phi) that are available for all research teams of Inria Bordeaux, Labri and IMB. This computer is in particular used by all the engineers who work in HiePACS and are advised by F. Rue from the SED.

- Contact: Olivier Coulaud
- URL: https://www.plafrim.fr/en/home/

HYBRID Project-Team

6. New Software and Platforms

6.1. #FIVE

KEYWORDS: Virtual reality - Behaviour - 3D interaction
FUNCTIONAL DESCRIPTION

#FIVE (Framework for Interactive Virtual Environments) is a framework for the development of interactive and collaborative virtual environments. #FIVE was developed to answer the need for an easier and a faster design and development of virtual reality applications. #FIVE provides a toolkit that simplifies the declaration of possible actions and behaviours of objects in a VE. It also provides a toolkit that facilitates the setting and the management of collaborative interactions in a VE. It is compliant with a distribution of the VE on different setups. It also proposes guidelines to efficiently create a collaborative and interactive VE. The current implementation is in C# and comes with a Unity3D engine integration, compatible with MiddleVR framework. #FIVE contains software modules that can be interconnected and helps in building interactive and collaborative virtual environments. The user can focus on domain-specific aspects for his/her application thanks to #FIVE's modules. These modules can be used in a vast range of domains using virtual reality applications and requiring interactive environments and collaboration, such as in training for example.

- Participants: Bruno Arnaldi, Valerie Gouranton, Florian Nouviale, Guillaume Claude
- Contact: Valerie Gouranton and Florian Nouviale
- URL: https://bil.inria.fr/fr/software/view/2527/tab

6.2. #SEVEN

KEYWORDS: Virtual reality - Scenario - Training - Petri Net - 3D interaction
FUNCTIONAL DESCRIPTION

#SEVEN (Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environments) is a sensor effector based scenario engine that enables the execution of complex scenarios for driving Virtual Reality applications. #SEVEN's scenarios are based on an enhanced Petri net model which is able to describe and solve intricate event sequences. #SEVEN comes with an editor for creating, editing and remotely controlling and running scenarios. #SEVEN is implemented in C# and can be used as a stand-alone application or as a library. An integration to the Unity3D engine, compatible with MiddleVR, also exists.

- Participants: Bruno Arnaldi, Valerie Gouranton, Florian Nouviale, Guillaume Claude
- Contact: Valerie Gouranton and Florian Nouviale
- URL: https://bil.inria.fr/fr/software/view/2528/tab

6.3. OpenViBE

KEYWORDS: Neurosciences - Interaction - Virtual reality - Health - Real time - Neurofeedback - Brain-Computer Interface - EEG - 3D interaction
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, Jerome Chabrol, Charles Garraud, and Marsel Mano
- Partners: Inria teams POTIOC, ATHENA and NEUROSYS
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr
- URL: https://bil.inria.fr/fr/software/view/1194/tab

6.4. Platform: Immerstar

- Participants : Florian Nouviale, Ronan Gaugne

With the two platforms of virtual reality, Immersia and Immermove, grouped under the name Immerstar, the team has access to high level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform is granted by a Inria CPER funding for 2015-2019 that enables important evolutions of the equipment. In 2016, the first technical evolutions have been decided, with, for Immermove, the addition of a third face to the immersive space, and the extension of the Vicon tracking system, and for Immersia, the installation of WQXGA laser projectors and of a new tracking system.

HYCOMES Project-Team

6. New Software and Platforms

6.1. SunDAE

Structural analysis tool for multimode DAE systems
FUNCTIONAL DESCRIPTION

SunDAE is a multimode DAE (mDAE) structural analysis tool. Structural differentiation index is determined, impulsion analysis is performed and a BTF scheduling of the equations is performed, for each mode of a mDAE system. The input language consists in guarded equations. The output is a state-machine where states define continuous-time dynamics and transitions define resets. Both are defined by scheduled blocks of equations. SunDAE has been developed since 2016 by the Hycomes team and is distributed as an open-source software, under the CeCCIL Free Software Licensing Agreement.

- Contact: Benoit Caillaud

6.2. 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: Benoit Caillaud
- URL: http://tinyurl.com/oql6f3y

6.3. 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: Benoit Caillaud
- Contact: Benoit Caillaud
- URL: http://www.irisa.fr/s4/tools/mica/

I4S Project-Team

6. New Software and Platforms

6.1. Cloud2IR

KEYWORDS: Sensors - SHM (Structural Health Monitoring) - Sensors network - Open Geospatial Consortium - OGC

SCIENTIFIC DESCRIPTION

Cloud2IR is an helpful tool to build physicals models for the SHM of civil engineering structures.

In this context the software is deployed in the SenseCity-EQUIPEX driven by IFSTTAR (http://sense-city.ifsttar.fr/)

FUNCTIONAL DESCRIPTION

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.

- Partner: IFSTTAR
- Contact: Jean Dumoulin

This work has been developed during the ADT of Antoine Crinière, Cloud2SM.

6.2. PEGASE

KEYWORD: Sensors - SHM (Structural Health Monitoring)

SCIENTIFIC DESCRIPTION

PEGASE (Plate-forme Experte Générique pour Applications Sans-fil Embarquées) is a generic and high level wireless sensor platform. Currently, the setup of the new PEGASE 2 platform is finalized as the technological successor of the previous PEGASE platform developed by IFSTTAR. This PEGASE 1 platform is licensed and disseminated by the third party company A3IP since 2008 and has been sold in thousands of units.

Based on various feedback from monitoring applications of PEGASE, and due to the fast obsolescence of electronic devices, the design of the new PEGASE 2 platform has been launched in 2013. Some of the main functions of PEGASE are reinforced:

- Software genericity: use of a Linux embedded OS to make application development independent from the hardware, and to enable the user to manage the system without any 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) where each pluggable daughter board implements a specific function (sensing, 3G, Ethernet, communication, signal processing and relay control).
- Accurate time synchronization principle: based on an original GPS and PPS algorithm, PEGASE platform is one of the only boards able to time-stamp data from sensors or any event with high accuracy and in a deterministic way.

On PEGASE 2 platform, previous principles are maintained or extended. A full electronic design from scratch has been decided by the team in 2014 to maximize its capacities in terms efficiency, cost, energy consumption, etc. The main new characteristics of PEGASE 2 are:

- A “real” Linux kernel is now flashed inside the board based on a professional Debian 4.0 (or higher version) of Linux. This Linux branch is the only one validated by IEEE to suit embedded applications
- Previous SDK in C language has been ported and improved in C++ with a generalization of the signal/slot principle to offer end-users a full programing context based on “event driven developments”.
- Extended hardware capacities: GigaBytes of memory, multiple USB port, etc...
- PEGASE 2 board implements new hardware such as a on-board Battery Management System (BMS) to be able to manage an energy efficiency based on a battery and a solar cell; PEGASE 2 mother board integrates a MEMS Mpu9150 from Invenses company wich is a MEMS that provides Acceleration, Temperature and Gyroscope in 3D,...

In 2015 and 2016 various functional daughter boards have been designed to complete the PEGASE 2 panoply:

- 8 analog and 8 digital daughter boards
- LORA protocol Daughter Board
- 3G Daughter Board

Figure 6. PEGASE and PEGASE daughter board

In 2016, based on an industrial contract with the company SDEL-CC (subsidiary company of Vinci group) an important algorithm has been implemented in PEGASE 2 board to make it able to time stamp any physical event up to 10 nanoseconds (independently from the wireless protocol or the distances between the platform that could be some tens of kilometers). This time stamping ability is unique and makes PEGASE 2 the only wireless device in the world with such a time accuracy in a deterministic way and in universal time (based on its GSP/PPS principle).

The most significant development in the PEGASE 2 context is the development of a Generic Cloud Server Application:

- manage multiple instrumentation projects
- various sensors (based on PEGASE 1 or 2 or others) can be set up
- collect big data based on Mongo DB database
- visualize the graphs of data from sensors in f(t) on dynamic charts
- export data to files, through specific API, or to third-party software (Matlab, QT C++...)

In the last two years the Generic Supervisor became a professional software product that is transfered under industrial Licensing, e.g. to the companies Power Lan and Stimio. By the end of 2016, at least these 2 companies will be officially licensed by IFSTTAR to disseminate the Supervisor.

- 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

NAME
Application Portique

DESCRIPTION
Monitoring SSI du portique routier d'IFSTTAR.

6 accéléromètres :

- Acc 1x : x = 0; y = 0; z = 0;
- Acc 2z : x = 0; y = 0; z = +1505mm;
- Acc 3x : x = 0; y = +3740mm; z = -15mm;
- Acc 4y : x = 0; y = +3740mm; z = +25mm;
- Acc 5x : x = 0; y = +5665mm; z = -35mm;
- Acc 6x : x = 0; y = -5730mm; z = -5mm;

CREATED ON
18/04/2016 13:48:18

PROJECT STATUS
Running

Resources used in the project

Name	Profile	Last API Access	Actions
Boitier Pegase2 - SSI	PEGASE - SSI	13 minutes ago	

Documents
Attach files to this project, like descriptions about the site under test.

Images
Attach photos or schematics of the site under test.

Timeline
All important events of the project are listed here, from newer to older.

Map
View resources attached to this project on a map.

Storage metrics
Statistics and metrics about the storage used by this project.

Wednesday, Nov 30, 17:52:26.007
pegasePN_labo3 : Temperature: 6.77 °C (Average)

Figure 7. Supervisor

6.3. TrackingMecaSys

Keywords: Bayesian estimation - Monte-Carlo - GPGPU - Kalman filter - Particular filter - Vibrating system

Functional Description

Implementation of a method based on the use of Bayesian modal parameter recursive estimation based on a particular Kalman filter algorithm with decoupled distributions for mass and stiffness. Algorithm optimized for a GPGPU implementation. This work has been done during ADT of Antoine Crinière and will be updated during the postdoc of S. Sen.

- Contact: Laurent Mevel

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 a tool 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 8.7.2. In comparison with the previously distributed versions, GNA 8.7.2 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 Grenoble Alpes
- 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, Yannick Martin, Michel Page, Delphine Ropers, Valentin Zulkower
- Partners: Université Grenoble Alpes
- 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, Yannick Martin, Michel Page, Delphine Ropers, Valentin Zulkower
- Partners: Université Grenoble Alpes
- Contact: Hidde de Jong
- URL: https://team.inria.fr/ibis/wellinverter/

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 Grenoble Alpes
- Contact: Hidde de Jong
- URL: http://ibis.inrialpes.fr/article957.html

ILDA Project-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 developer can decide the types of widgets associated to pucks from the wall application side.

- Contact: Olivier Chapuis
- URL: http://smarties.lri.fr/

Smarties was used in the projects that led to the following publications this year: [7], [8], [22].

6.2. ZVTM

Zoomable Visual Transformation Machine

KEYWORDS: Information visualization - Data visualization - 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, Maria Jesus Lobo Gunther, Arnaud Prouzeau, Hande Ozaygen, Can Liu and Olivier Chapuis
- Contact: Emmanuel Pietriga
- URL: http://zvtm.sf.net

Smarties was used in the projects that led to the following publications this year: [7], [8], [22], [19], [21].

6.3. Platforms

6.3.1. Platform: WILDER

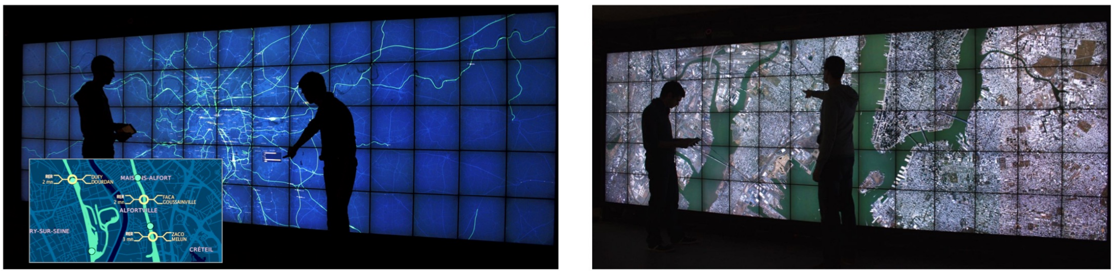


Figure 2. Geovisualization applications running on the WILDER platform. Real-time monitoring of railroad traffic in France (left), large-scale high-resolution orthoimagery visualization (right).

Ultra-high-resolution wall-sized displays [33] 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.

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).

WILDER was used in the projects that led to the following publications this year: [7], [8], [22], [19], [23].

6.3.2. Platform: ANDES

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).

ANDES was used in the projects that led to the following publications this year: [7].

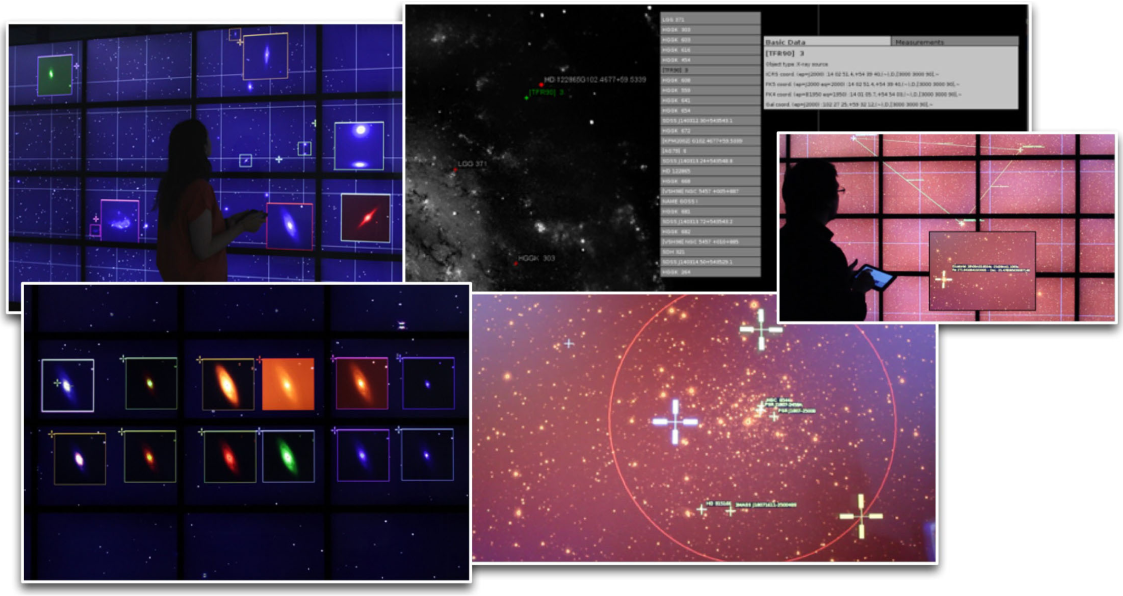


Figure 3. Visualization of high-dynamic-range FITS images and associated data catalogs in the domain of Astronomy on ANDES (collaboration with Inria Chile, Millenium Institute of Astrophysics, and Institut d'Astrophysique Spatiale).

IMAGINE Project-Team

5. New Software and Platforms

5.1. Expressive

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, Even Entem, Thomas Delame, Ulysse Vimont
- Contact: Marie Paule Cani

5.2. MyCF

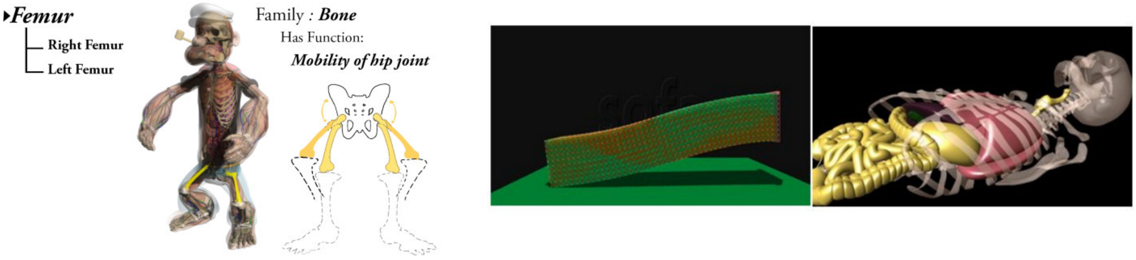


Figure 1. Left: My Corporis Fabrica is an anatomical knowledge database developed in our team. Right: SOFA is an open source simulator for physically based modeling.

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

5.3. SOFA

Simulation Open Framework Architecture

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.
Sofa is extensively used by Anatoscope, who add proprietary plugins and helps maintaining the public plugins.

- Participants: François Faure, Armelle Bauer, Matthieu Nesme, Romain Testylier.
- Contact: François Faure
- URL: http://www.sofa-framework.org

5.4. Natron

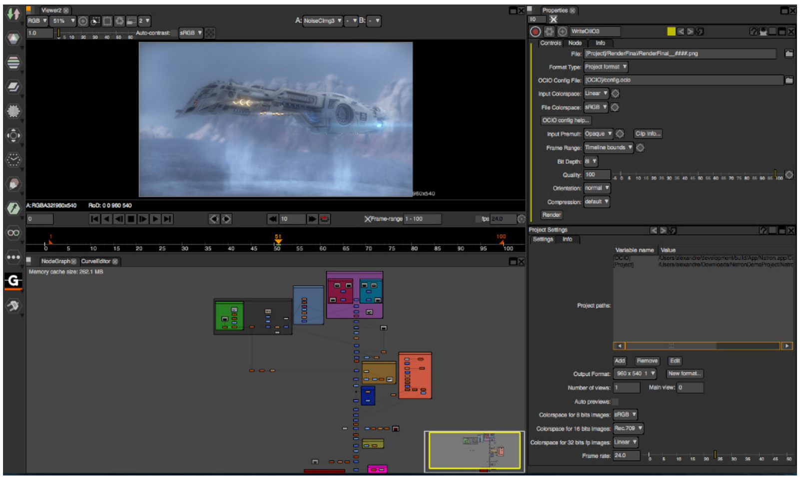


Figure 2. Video compositing using the Natron interface.

Natron (http://natron.fr) is a professional-quality video post-production software specialized in compositing and visual effects. Compositing is the combining of visual elements from separate sources into single images, often to create the illusion that all those elements are parts of the same scene. The math behind compositing was formalized by Porter & Duff (1984) after the preliminary work by Wallace (1981).

Typical examples of compositing are, for example:

- The superimposition of a character filmed on a green background over a scene shot in another place, at another time, or a computer-generated scene; - The manual detouring (also called rotoscopy) of an element in a video to embed it in another video, possibly with a different motion; - Artistic modifications of a video, after shooting a live-action scene or rendering a CGI scene, in order to modify its lighting, colors, depth of field, camera motion, or to remove noise or add film grain.

A video compositing software is not a 3D computer graphics software, like Blender or Maya, but it is perfectly suited for combining computer-generated elements produced by other software with live-action video or 2D animation. Rather than rendering a full 3D scene with the 3D software, which may cost many hours of computation, the video compositing software can assemble the elements produced separately with a much more reactive interface and an almost instantaneous visual feedback.

- Participants: Frédéric Devernay, Alexandre Gauthier-Foichat.
- Contact: Frédéric Devernay
- URL: http://natron.fr

INDES Project-Team

4. New Software and Platforms

4.1. Hop

KEYWORDS: Domotique - Web 2.0 - Iot - Functional language - Programming

SCIENTIFIC DESCRIPTION

Hop.js is a platform for web, cloud, and IoT applications. Its development environment is composed of:

- a programming language named HopScript, which is based on ECMAScript 262, //aka// JavaScript;
- an optimized web server;
- on-the-fly compilers for generating HTML, CSS, and client-side JavaScript;
- an ahead-of-time compiler for compiling JavaScript to native code;
- numerous APIs for networking, multimedia, robotics, IoT, etc.

The HopScript language extends JavaScript to consistently define the server and client part of web applications and IoT applications. HopScript supports syntactic forms that help creating HTML elements. It supports services that enable function calls over HTTP. Being at higher level than traditional Ajax programming, Hop.js services avoid the burden and pitfalls of URL management and explicit data marshalling. They combine the benefits of a high level RPC mechanism and low level HTTP compatibility.

Although Hop.js can be used to develop traditional web servers, it is particularly adapted to the development of web applications embedded into devices, where the server and client part of the application are intimately interoperating with each other. The programing model of Hop.js fosters the joint specification of server and client code, and allows the rapid development of web user interfaces, on the client, controlling the execution of the distributed application. By defining a single data model, providing functions that can run indifferently on both sides, and almost forgetting about client-server protocols, Hop.js seems well suited for agile development of web applications for this class of applications.

- Participants: Manuel Serrano and Vincent Prunet
- Contact: Manuel Serrano
- URL: http://hop.inria.fr

4.2. Mashic

FUNCTIONAL DESCRIPTION

The Mashic compiler is applied to mashups with untrusted scripts. The compiler generates mashups with sandboxed scripts, secured by the same origin policy of the browsers. The compiler is written in Bigloo.

- Contact: Tamara Rezk
- URL: http://web.ist.utl.pt/~ana.matos/Mashic/mashic.html

4.3. Webstats

Webstats is a follow-up of the internship on JavaScript constructs used in top Alexa sites, started in summer 2015 by Dolière Francis Some. He analyzed the top 10,000 Alexa sites, and provided statistics about them. Among those statistics, their are:

- the most popular JavaScript libraries
- the most recurrent JavaScript constructs
- the adoption of security features such as:
  - The Content Security Policy, a policy for defending against Cross-Site-Script attacks
  - HttpOnly and Secure cookies, that prevents attacks like session hijacking.

Starting from April, 2016, this study is performed periodically, at the end of each month. The results are accessible online at https://webstats.inria.fr.

- Contact: Francis Some
- URL: https://webstats.inria.fr

INFINE Project-Team

5. New Software and Platforms

5.1. RIOT

KEYWORDS: Internet of things - Operating system - Sensors - Iot - Wireless Sensor Networks - Internet protocols

SCIENTIFIC DESCRIPTION

While requiring as low as 1,5kB of RAM and 5kB or ROM, RIOT offers real time and energy efficiency capabilities, as well as a powerful API (partially POSIX compliant) that is consistent across heterogeneous low-end IoT hardware (8-bit, 16-bit and 32-bit architectures). This API is developer-friendly in that it enables multi-threading, standard C and C++ application programming (as well as scripting) and the use of standard debugging tools – all of which was not possible so far for such embedded programming. On top of this, RIOT supports a large number of software libraries (e.g. crypto, maths, drivers...) and aggregates in a simple manner a wide variety of third-party open source software packages. In particular, various network stacks are available with RIOT, 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 standard protocols for embedded systems. RIOT allows, for example, the development of applications that collect sensor data and transmit it to a central node (e.g. a server). This data can then be used for smart energy management for instance. Other use-cases include also IoT-enabled low-cost robots.

RIOT is specially designed for embedded systems, which are strongly constrained in memory and energy. Further, RIOT can easily be ported to different hardware devices and follows the latest evolution of IP standards.

RIOT applications can readily be tested in the FIT IoT-Lab, which provides a large-scale infrastructure facility with 3000 nodes for testing remotely small wireless devices.

- Participants: Emmanuel Baccelli, Oliver Hahm, Cedric Adjih, Francisco Acosta
- Partner: Freie Universität Berlin
- Contact: Emmanuel Baccelli
- URL: https://github.com/RIOT-OS/RIOT

5.2. MACACO

Mobile context-Adaptive CAching for COntent-centric networking

FUNCTIONAL DESCRIPTION

MACACOapp is developed in the context of the EU CHIST-ERA MACACO project. It consists in a mobile phone application that periodically samples phone's 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 users' phones location and/or from/to the wireless infrastructure closest to the users' 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. User's 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/

5.3. GardiNet (previously DragonNet)

FUNCTIONAL DESCRIPTION

GardiNet (previously known as DragonNet) is a generic framework for network coding in wireless networks. It is initially a 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: Cedric Adjih, Ichrak Amdouni, Hana Baccouch and Antonia Masucci
- Contact: Cedric Adjih
- URL: http://getrf.gforge.inria.fr/https://github.com/GardiNet/gardinet

INOCS Team (section vide)

IPSO Project-Team (section vide)

KERDATA Project-Team

6. New Software and Platforms

6.1. Týr

Title: Týr: Blob Storage Meets Built-In Transactions.

Keywords: Big Data; Transactions; Tyr; BlobSeer.

Scientific Description: Týr [25] is the first blob storage system to provide built-in, multi-blob transactions, while retaining sequential consistency and high throughput under heavy access concurrency.

Functional Description: Týr offers fine-grained random write access to data and in-place atomic operations. Large-scale experiments on Microsoft Azure with a production application from CERN LHC show Týr throughput outperforms state-of-the-art solutions by more than 75%. Týr leverages the approaches developed within BlobSeer, the reference data management system for large distributed blobs, developed over the past years in KerData.

Contact data:

Participants: Pierre Matri, Alexandru Costan and Gabriel Antoniu.

Partners: INSA Rennes, Universidad Politécnica de Madrid.

Contact: Gabriel Antoniu.

URL: http://tyr.io/.

6.2. Damaris

Title: Damaris: I/O and data management for large-scale, MPI-based HPC simulations.

Keywords: I/O; HPC; Data management; Visualization; Big Data; Exascale.

Scientific Description: Damaris is a middleware for multicore SMP nodes enabling them to efficiently handle data transfers for storage and visualization. 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 JLESC. The current version 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.

Damaris has been preliminarily evaluated at NCSA (Urbana-Champaign) with the CM1 tornado simulation code. CM1 is one of the target applications of the Blue Waters supercomputer in production at NCSA/UIUC (USA), in the framework of the JLESC. Damaris now has external users, including (to our knowledge) visualization specialists from NCSA, Big Data experts from the HDF group, 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, CROCO). Works are in progress to evaluate it in the context of several other simulation codes including HACC (cosmology) and GTC (fusion).

Damaris is the object of a *Technical Development Action* (ADT) supported by Inria.

Functional Description: Damaris targets large-scale HPC simulations: in situ data analysis by some dedicated cores of the simulation platform; asynchronous and fast data transfer from HPC simulations to Damaris; semantic-aware dataset processing through Damaris plug-ins.

Contact data:

Participants: Matthieu Dorier (ANL), Lokman Rahmani, Gabriel Antoniu, Orçun Yildiz, Hadi Salimi and Luc Bougé.

Partners: ENS Rennes, Argonne National Laboratory.

Contact: Gabriel Antoniu.

URL: http://damaris.gforge.inria.fr/.

6.3. Other software

6.3.1. JetStream

Title: JetStream: Enabling High-Performance Event Streaming across Cloud Data-Centers.

Keywords: Big Data, streaming, data transfer, multisite cloud.

Scientific Description. JetStream is a middleware solution for batch-based, high-performance streaming across cloud data centers. JetStream implements a set of context-aware strategies to optimize batch-based streaming, being able to self-adapt to changing conditions.

Functional Description. 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. JetStream is currently used at Microsoft Research ATLE Munich for the management of the Azure cloud infrastructure.

Participants: Ovidiu-Cristian Marcu, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan.

6.3.2. Omnisc'IO

Title: Omnisc'IO: a Grammar-Based Approach to Spatial and Temporal I/O Patterns Prediction.

Keywords: HPC, Input-Output, Prediction, Grammar.

Scientific Description. Omnisc'IO is a library that aims to be integrated into I/O middleware.

Functional Description. It traces I/O operations, models the stream of such operations using grammar-inference techniques, and predicts when new I/O operations will be performed, as well as where and how much data will be written.

Participants: Matthieu Dorier (ANL), Gabriel Antoniu, Shadi Ibrahim.

Contact: Gabriel Antoniu.

6.3.3. OverFlow

Title: OverFlow: Workflow Data Management as a Service for Multi-Site Applications.

Keywords: Small data; workflow; multi-site cloud.

Scientific Description. 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 performance for transfer cost and time, within and across sites.

Functional Description. 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. 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.

Participants: Paul Le Noac'h, Ovidiu-Cristian Marcu, Alexandru Costan and Gabriel Antoniu.

Contact: Alexandru Costan.

6.3.4. iHadoop

Title: iHadoop: A Hadoop Simulator Developed In Java on Top of SimGrid.

Keywords: Simulation, Map-Reduce, Hadoop, SimGrid.

Scientific Description. iHadoop is a Hadoop simulator developed in Java on top of SimGrid. It simulates the behavior of Hadoop and therefore accurately predicts the performance of Hadoop in normal scenarios and under failures. iHadoop is extended to (1) simulate the execution and predict the performance of multiple Map-Reduce applications; (2) simulate the execution of Map-Reduce applications under various data distributions and data skew models.

Functional Description. iHadoop is an internal software prototype, which was initially developed to validate our idea regarding the behavior of Hadoop under failures. iHadoop has preliminarily evaluated within our group and it has shown very high accuracy to predict the execution time of a Map-Reduce applications. We intend to integrate iHadoop within the SimGrid distribution and make it available to the SimGrid community.

Participants: Shadi Ibrahim and Tien-Dat Phan.

Contact: Shadi Ibrahim.

LACODAM Team

6. New Software and Platforms

6.1. EcoMata

FUNCTIONAL DESCRIPTION

The EcoMata tool-box provides means for qualitative modeling and ecosystem exploration and for assisting the design of 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

6.2. PaturMata

KEYWORDS: Bioinformatics - Biology
SCIENTIFIC 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.
FUNCTIONAL 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 .

- Participants: Christine Largouët, Marie-Odile Cordier, Yulong Zhao
- Contact: Christine Largouët

6.3. QTempIntMiner

KEYWORDS: Data mining - Health - Medical - Physiology - Temporal information
SCIENTIFIC DESCRIPTION

QTempIntMiner: the QTempIntMiner (Quantitative Temporal Interval Miner) data mining software implements several algorithms presented in [46] and [3] (QTIAPriori and QTIPrefixSpan). The software is mainly implemented in Matlab. It uses the Mixmod toolbox [33] 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 intervals 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 (care pathways).

- Participants: Thomas Guyet and René Quiniou
- Partner: AGROCAMPUS
- Contact: Thomas Guyet
- URL: http://people.irisa.fr/Thomas.Guyet/QTempIntMiner/

LAGADIC Project-Team

6. New Software and Platforms

6.1. DESlam

Dense Egocentric SLAM
KEYWORDS: Deph Perception - Robotics - Localization
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 types 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: Francois 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. It provides the functionalities to do image acquisition, semantic annotation, dense registration, localization and 3D mapping. The omnidirectional RGB-D sensors used within this software have been developed at Inria Sophia Antipolis.

- Participants: Eduardo Fernandez Moral, Renato José Martins and Patrick Rives
- Contact: Patrick Rives
- URL: https://team.inria.fr/lagadic

6.4. Sinatrack

KEYWORDS: Computer vision - Robotics
FUNCTIONAL DESCRIPTION

Sinatrack is a tracking software that performs the 3D localization (translation and rotation) of an object with respect to a monocular camera. It allows considering objects with complex shape. The underlying approach is a model-based tracking technique. It has been developed for satellite localization and on-orbit service applications but is also suitable for augmented reality purpose.

- Participants: Antoine Petit, Eric Marchand and Francois Chaumette
- Contact: Eric 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 and visual servoing based on ultrasound images. Written in C++, UsTk provides tools for ultrasound image acquisition, processing, and display, as well as control of ultrasound probe motion by ultrasound visual servoing. This year we started the development of a new version. The objective is first to consolidate existing developments, to improve the quality of the software, to add new state-of-the-art algorithms, and then to disseminate them within the community as an open-source software.

- Participants: Marc Pouliquen, Alexandre Krupa, Pierre Chatelain and Fabien Spindler
- Contact: Alexandre Krupa
- URL: https://team.inria.fr/lagadic/

6.6. ViSP

KEYWORDS: Computer vision - Robotics - Augmented reality - Visual servoing

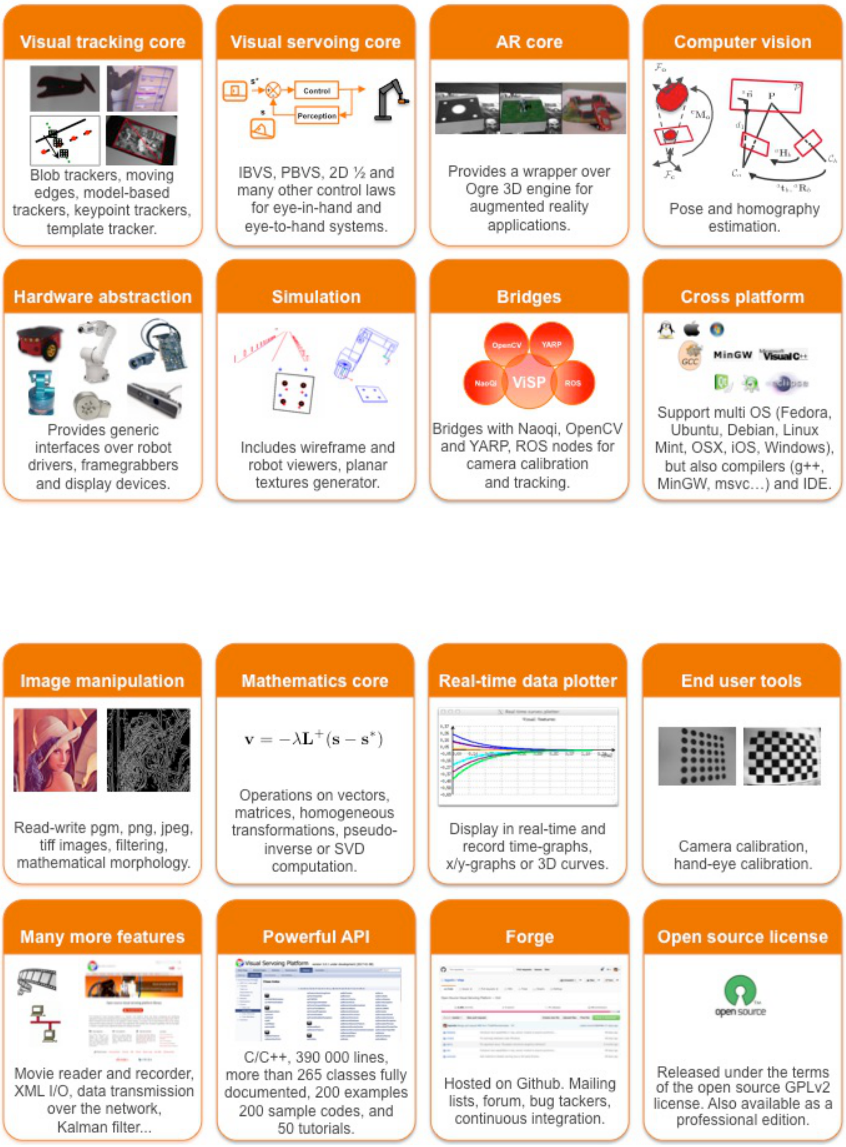
SCIENTIFIC DESCRIPTION

Since 2005, we have been developing and releasing 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, Eric Marchand, Fabien Spindler, Aurélien Yol and Souriya Trinh
- Partner: Inria, Université de Rennes 1
- 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 Naoqi, OpenCV and YARP, ROS nodes for camera calibration and tracking.

Cross platform
Support multi OS (Fedora, Ubuntu, Debian, Linux Mint, OSX, iOS, 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++, 390 000 lines, more than 265 classes fully documented, 200 examples 200 sample codes, and 50 tutorials.

Forge
Hosted on Github. Mailing lists, forum, bug tackers, continuous integration.

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 Github as an open source software under GPLv2 license.

In December 2015, ViSP 3.0.0 new modular architecture was released. The corresponding source code tarball was downloaded 2138 times, much more than the previous 2.10.0 release that was downloaded 1412 times. This confirms that ViSP popularity is increasing and motivates the efforts we are doing since more than 10 years to improve the software. ViSP 3.0.0 last release was packaged for Debian, Ubuntu 16.04 LTS, Arch Linux, OSX and ROS. ViSP 3.0.1 next release is in preparation and should be released at the beginning of 2017. This release will be also packaged for iOS devices. In this new version we introduced new wrapper for USB-3 or GigE PointGrey cameras, Haption haptic device, ATI force/torque sensors, Intel RealSense RGB-D devices. We also make an effort to optimize some critical code sections using SSE and make possible cross-compilation for Raspberry PI and iOS targets, and also Nao, Romeo and Pepper robots from SoftBank Robotics. We also introduce a new version of the 3D model-based tracker dedicated to stereo tracking, fixed some issues, improved the documentation by providing new tutorials and by updating the existing ones.

Concerning ROS community, all the existing packages in “`vision_visp`” ROS stack (see http://wiki.ros.org/vision_visp) were updated and ported to kinetic 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, Canada, Japan, Korea, India, China, Italy, Spain, Portugal, etc. 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. Last August, during the Intel Developer Forum opening keynote, Intel CEO Brian Krzanich introduced the Intel Joule compute module. Using an Intel Joule with glasses from French company PivotHead, Intel demonstrated an augmented reality application that was using ViSP (https://www.youtube.com/watch?v=QRBofzL4MDY).

6.7. WarpDriver

KEYWORDS: Crowd Simulation - Pedestrian Simulation - Collision Avoidance - Reactive Navigation

FUNCTIONAL DESCRIPTION

WarpDriver is a microscopic crowd simulation software, which simulates the collision-free locomotion of many individual agents among the obstacles of a given environment. The originality of the algorithm relies on motion prediction mechanism which allows each agent to predict the probability of colliding other agents with respect to their current motion, their past motion, and the presence of obstacles forcing agents to follow some paths in the environment. Agents then move to their goal whilst they minimize their probability of colliding obstacles.

- Participants: David Wolinski and Julien Pettré
- Contact: Julien Pettré
- URL: http://team.inria.fr/lagadic

6.8. 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: Eric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html

6.9. Platforms

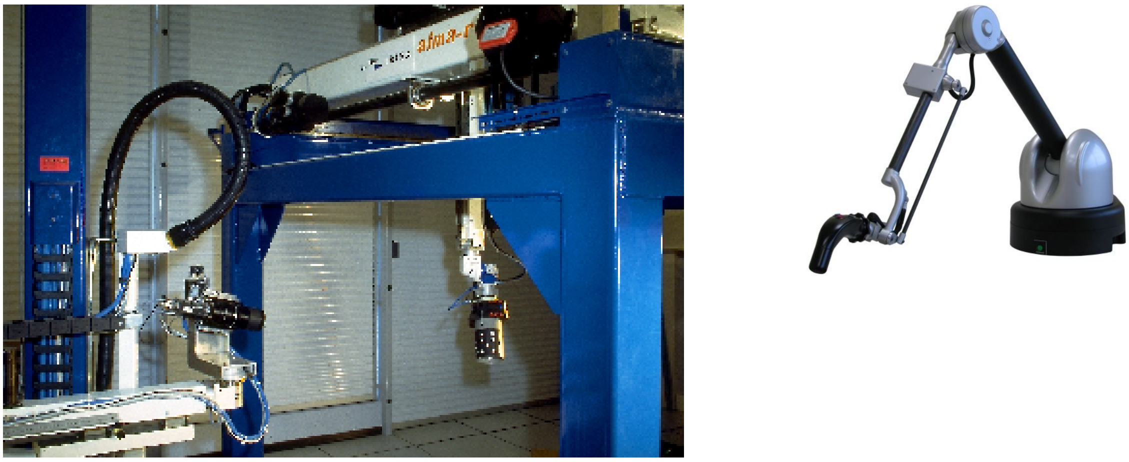
6.9.1. Robot vision platform

Participant: Fabien Spindler [contact].

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 .a). These robots are equipped with cameras. The Gantry robot also allows embedding grippers on its end-effector.

This year we completed the platform with a haptic Virtuose 6D device from Haption company (see Fig. 2 .b). This device is used for visual-based shared control (see Section 9.3.1.3).

Note that 3 papers published by Lagadic in 2016 enclose results validated on this platform [21][48][46].



(a) (b)

Figure 2. a) Lagadic robotics platform for vision-based manipulation, b) Virtuose 6D haptic device

6.9.2. Mobile robots

Participants: Fabien Spindler [contact], Marie Babel, Patrick Rives.

6.9.2.1. 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 Pioneer 3DX from Adept (see Fig. 3 .b). These platforms are equipped with various sensors needed for Slam purposes, autonomous navigation and sensor-based control.

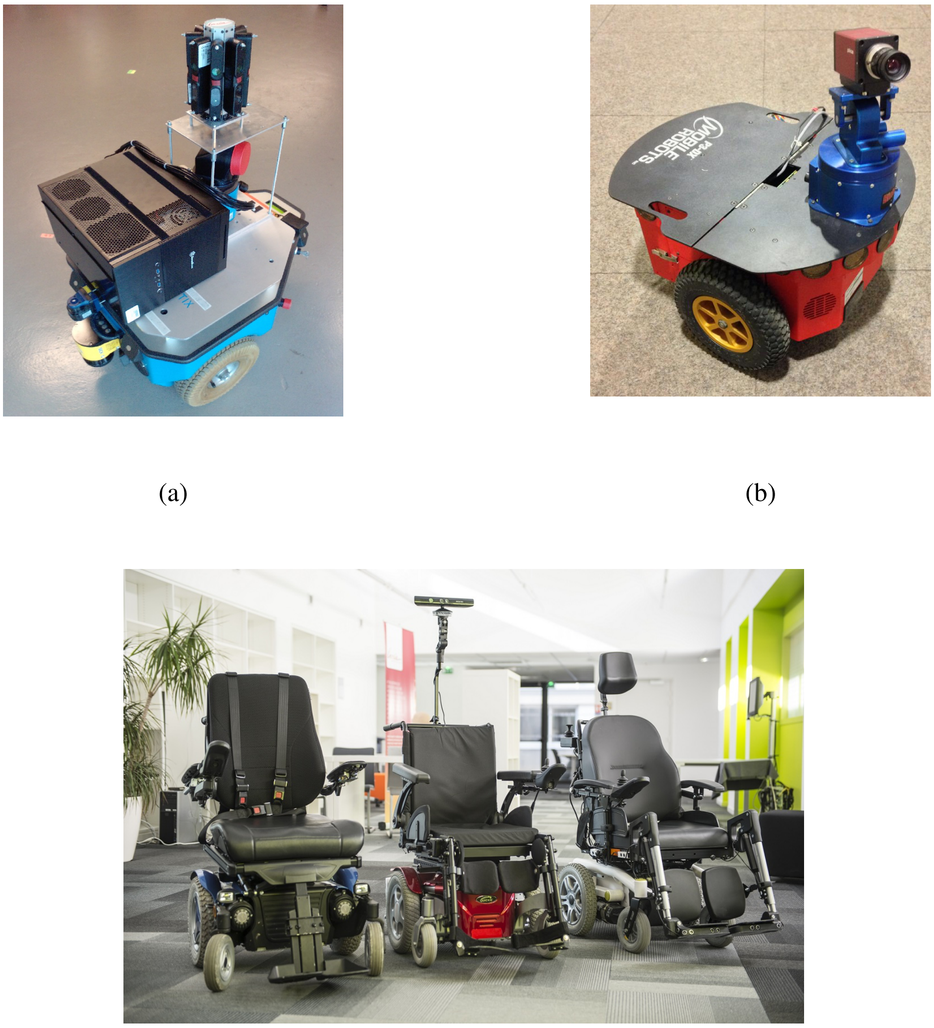
Moreover, to validate the researches in personally assisted living topic (see Section 7.4.5), we have three electric wheelchairs in Rennes, one from Permobil, one from Sunrise and the last from YouQ (see Fig. 3 .c). The control of the wheelchair is performed using a plug and play system between the joystick 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 ultrasound sensors to perform the required servoing for assisting handicapped people.

Note that 11 papers exploiting the indoors mobile robots were published this year [67][26][61][37][62][30][55][38][71][64][66].

6.9.2.2. Outdoor vehicles

A camera rig has been developed in Sophia Antipolis. It can 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 shown in the video http://www-sop.inria.fr/members/Renato-Jose.Martins/iros15.html.

Paper [68] contains experimental results obtained with this camera rig.



(a) (b)

(c)

Figure 3. a) Hannibal platform, b) Pioneer P3-DX robot, c) wheelchairs from Permobil, Sunrise and YouQ.

6.9.3. Medical robots

Participants: Fabien Spindler [contact], Alexandre Krupa.

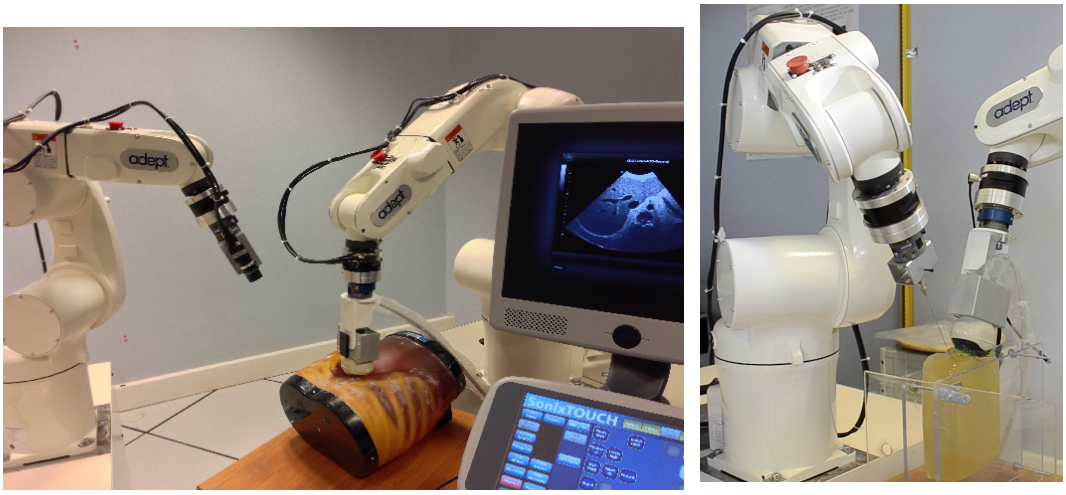
This testbed is of primary interest for researches and experiments concerning ultrasound visual servoing applied to probe positioning, soft tissue tracking or robotic needle insertion tasks (see Section 7.3).

Figure 4. Globeye stereo sensor and acquisition system.

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.

This year we replaced the F/T sensor attached to one of the Viper robot in order to use a DAQ acquisition board able to provide measures at a higher frame rate (up to 1 kHz). This feature is especially useful for flexible needle steering by ultrasound visual servoing (see Fig. 5 .b).

Notice that 10 papers published this year include experimental results obtained with this platform [40][31][34][58][57][70][52][59] [50][51].



(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.

6.9.4. Humanoid robots

Participants: Giovanni Claudio, Fabien Spindler [contact].

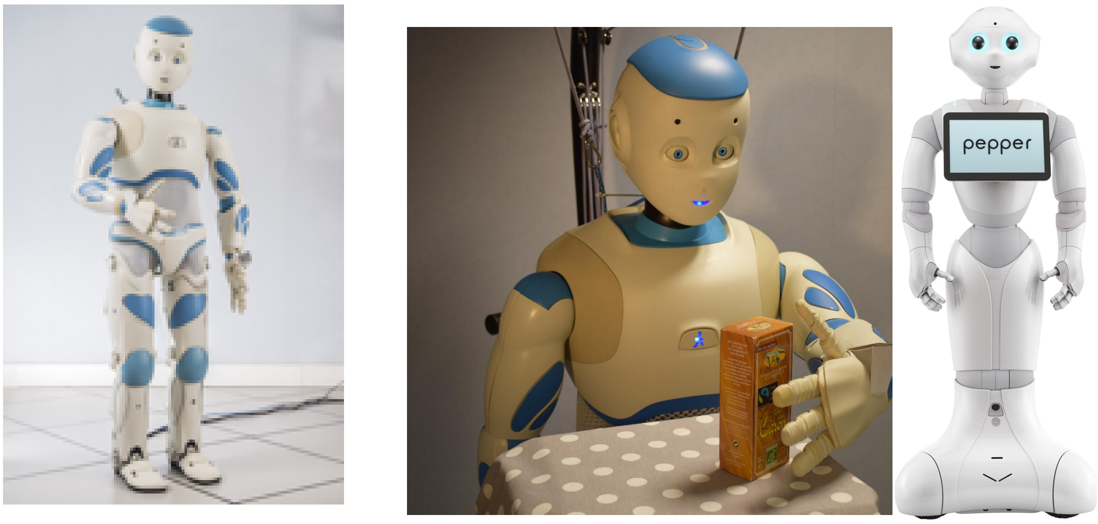
Romeo is a humanoid robot from SoftBank Robotics which is intended to be a genuine personal assistant and companion. For the moment only the upper part of the body (trunk, arms, neck, head, eyes) is working. This research platform is used to validate our researches in visual servoing and visual tracking for object manipulation (see Fig. 6 .a).

In July, this platform was extended with Pepper, another human-shaped robot designed by SoftBank Robotics to be a genuine day-to-day companion (see Fig. 6 .b). It has 17 degrees of freedom mounted on a wheeled holonomic base and a set of sensors (cameras, laser, ultrasound, inertial) that makes this platform interesting for researches in vision-based manipulation and navigation. Our first developments were devoted to visual servoing for controlling the gaze of the robot exploiting the redundancy of the head and mobile base and adding the capability to follow a person.

Note that 4 papers published this year include experimental results obtained with these platforms [53][81][65][20].

6.9.5. Unmanned Aerial Vehicles (UAVs)

Participants: Thomas Bellavoir, Paolo Robuffo Giordano [contact].

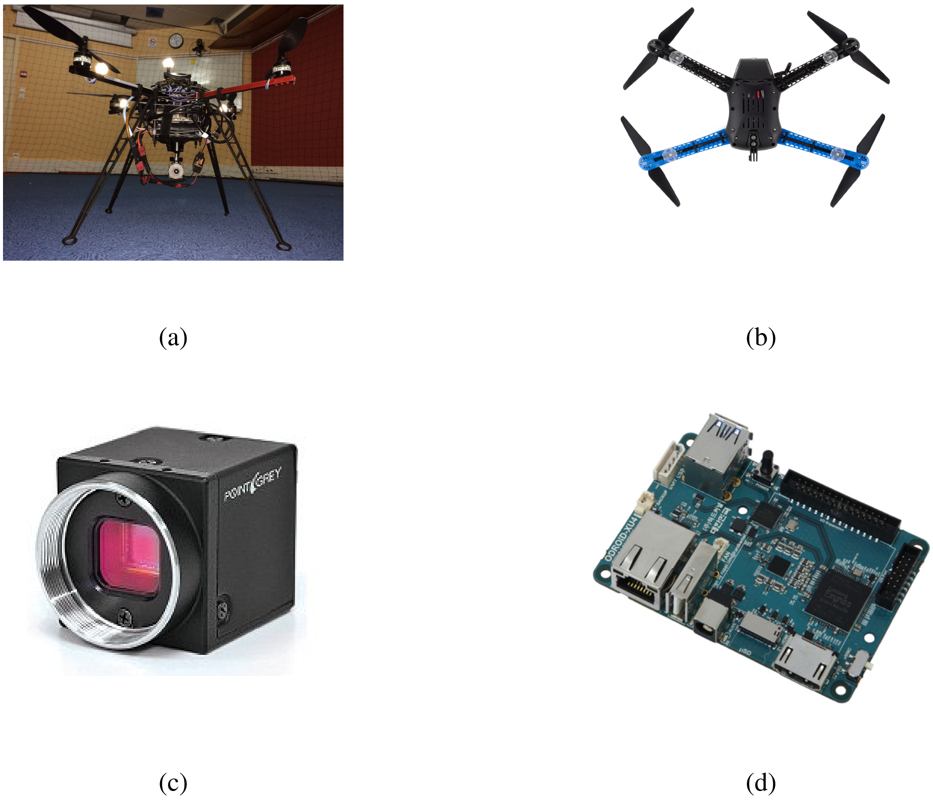


(a) (b)

Figure 6. a) Romeo experimental platform, b) Pepper human-shaped robot

From 2014, Lagadic 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 9.2.5). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (see Fig. 7 .a), and one quadrotor from 3DRobotics, USA (see 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 (see Fig. 7 .d) 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 (see Fig. 7 .c). The quadrotor group is 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.

Two papers published this year enclose experimental results obtained with this platform [72][64].



(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. Limbo

LIbrary for Model-based Bayesian Optimization
KEYWORDS: Black-box optimization - C++ - Global optimization - Machine learning - Policy Learning - Bayesian optimization
FUNCTIONAL DESCRIPTION

Limbo is an open-source C++11 library for Bayesian optimization which is designed to be both highly flexible and very fast. It can be used to optimize functions for which the gradient is unknown, evaluations are expensive, and where runtime cost matters (e.g., on embedded systems or robots). Benchmarks on standard functions show that Limbo is about 2 times faster than BayesOpt (another C++ library) for a similar accuracy.

- Partners: Imperial College London - UPMC
- Contact: Jean-Baptiste Mouret
- URL: http://www.resibots.eu/limbo

6.2. sferes2

A lightweight generic C++ framework for evolutionary computation
FUNCTIONAL DESCRIPTION

Sferes2 is a high-performance, multi-core, lightweight, generic C++98 framework for evolutionary computation. It is intently kept small to stay reliable and understandable.

Sferes2 relies heavily on template-based meta-programming in C++ to get both abstraction and execution speed.

- Partner: UPMC
- Contact: Jean-Baptiste Mouret
- URL: http://github.com/sferes2/sferes2/

6.3. xsensdriver

`xsens_driver`
FUNCTIONAL DESCRIPTION

This is a driver for the third and fourth generation of Xsens IMU devices. The driver is in two parts, a small implementation of most of the MT protocol in Python and a ROS node. It works both on serial and USB interfaces.

These MT* devices can store their configuration and will retrieve it at each boot and then stream data according to this configuration. The node only forwards the data streamed onto ROS topics. In order to configure a device, one can use the mtdevice.py script (or the vendor tool on Windows).

- Contact: Francis Colas
- URL: https://github.com/ethz-asl/ethzasl_xsens_driver

6.4. Platforms

6.4.1. iCub

iCub is a humanoid robot with the size of a 4 years old child. It is developed by the Italian Institute of Technology (Genoa, Italy), which is the coordinator of the EU project CoDyCo. The iCub robot was acquired thanks to the funding of this project.

Our version of iCub has a v2 head, v1 torso, v2.5 legs. It has 6 force/torque sensors, a distributed tactile skin, and inertial sensor in the head.

The robot is used in the context of the projects CoDyCo and Resibots. The software developed for the iCub is mostly published on the github page of our team:

https://github.com/inria-larsen

6.4.2. Pepper

Pepper is a humanoid mobile robot, produced by SoftBank Robotics (formerly Aldebaran). It is designed to engage humans in social interactions, entertain or communicate through gestures and visual animations on its front laptop.

The robot was acquired in the context of the CPER SCIARAT to study human-robot interaction for personal assistance.

LEMON Team

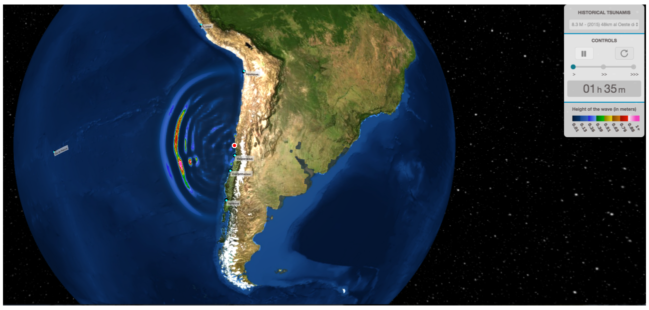
6. New Software and Platforms

6.1. TsunamiLab

Participant: Antoine Rousseau.

Tsunami-Lab is an educational platform enabling simulation and visualization of tsunami effects in real time, with several historical scenarios and the possibility to build your own one. The target of this project is to provide students as well as general audience with an educational tool, intended to reduce tsunamis impact in Chile and help sparing human lives.

Tsunami-Lab was initated by José Galaz, engineer in mathematics and civil ingeneering, when he was working at the National Research Center for Integrated Gestion of Natural Hazards (CIGIDEN). The app is born with the match of a need - teach general audience more efficient methods to decrease tsunamis impact and spare human lives - and the use of new technologies. Later, a collaboration came up between CIGIDEN, Inria Chile and Inria (team LEMON) in order to optimize this project development.



HISTORICAL TSUNAMIS

8.3 M - (2015) 48km al Oeste d

Figure 2. Propagation of a tsunami wave created by the a 8.3M earthquake in Chile (2015) using the TsunamiLab platform.

- Participant: Antoine Rousseau
- Contact: José Galaz, jdgalazm@gmail.com
- URL: https://tsunamilab.inria.fr/

6.2. 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
- three different closure relationships between the averaged flow variables and porosity-based fluxes
- 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.

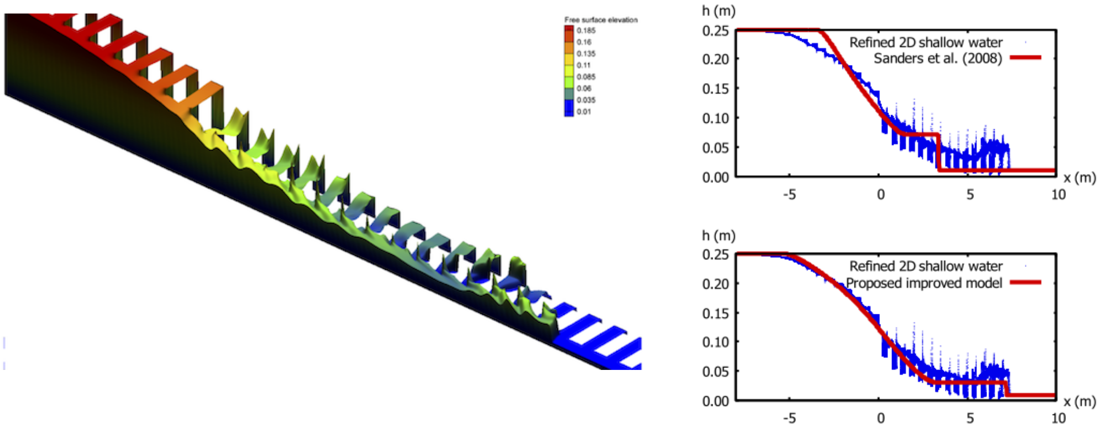


Figure 3. Propagation of a flood wave into a channel with lateral storage. Refined 2D simulation using the SW2D computational code

- Contact: Vincent Guinot
- URL: http://vincentguinot.free.fr

6.3. 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).

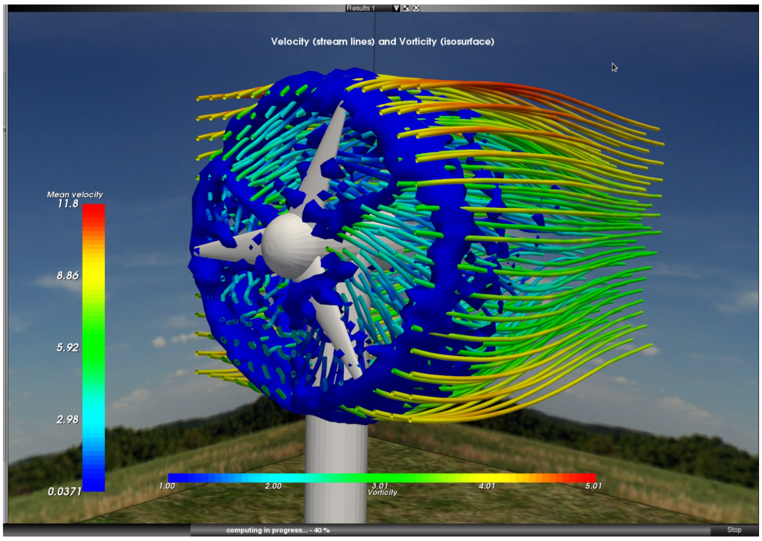


Figure 4. Velocity streamlines and vorticity around a wind mill (artistic view). WINDPOS Project.

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.

This is a joint work with Mireille Bossy from the team TOSCA.

- Contact: Mireille Bossy, mireille.bossy@inria.fr
- 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-1.3.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. FLINT

FUNCTIONAL DESCRIPTION FLINT is a C library for number theory and basic computer algebra, maintained by William Hart with code by William Hart, Sebastian Pancratz, Andy Novocin, Fredrik Johansson, Tom Bachmann, Mike Hansen, Martin Lee, David Harvey, and a large number of other authors.

FLINT is used as a back end library for polynomial arithmetic and number theory functionality in a large number of applications, including SageMath and Singular.

- Participant: Fredrik Johansson
- Contact: William Hart
- URL: http://flintlib.org/

5.9. 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 Theveny and Mickaël Gastineau
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/

5.10. 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

5.11. mpmath

FUNCTIONAL DESCRIPTION mpmath is a Python library for real and complex floating-point arithmetic with arbitrary precision. It has been developed by Fredrik Johansson since 2007, with help from many contributors.

As a dependency of the SymPy computer algebra system as well as SageMath, mpmath is a core component of the Python scientific software ecosystem.

- Participant: Fredrik Johansson
- Contact: Fredrik Johansson
- URL: http://mpmath.org/

5.12. 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

5.13. 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/

5.14. 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, Bill Allombert, Henri Cohen and Andreas Enge
- 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, performing static analyses, making simulations, specifying behaviors in temporal logic and searching parameter values in high dimension.

This year BIOCHAM has been completely rewritten with a modular architecture. The new version v4.0 will be released soon with new features for synthesizing biochemical reaction systems from input/output function specifications.

- Participants: François Fages, Guillaume Le Guludec, Thierry Martinez Sylvain Soliman
- Contact: François Fages
- URL: http://lifeware.inria.fr/biocham/

6.2. CellStar

KEYWORDS: Systems biology - Bioinformatics
FUNCTIONAL DESCRIPTION

In close collaboration with Kirill Batmanov, Cédric Lhoussaine and Cristian Versari (LIFL, CNRS/Lille Univ), with Szymon Stoma (Inria; now ETHZ), and with Pascal Hersen (MSC, CNRS/Paris7), 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 tools. 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 and Szymon Stoma
- Contact: Grégory Batt
- URL: http://cellstar-algorithm.org/

6.3. CLP2Zinc

KEYWORDS: Modeling language - Constraint programming - Search
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 was 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 and Sylvain Soliman
- Contact: Thierry Martinez
- URL: http://lifeware.inria.fr/~tmartine/clp2zinc/

LINKMEDIA Project-Team

6. New Software and Platforms

6.1. A||GO multimedia web services

Participants: Guillaume Gravier [correspondent], Gabriel Sargent.

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. Based on the A||GO infrastructure, LINKMEDIA has continued making available a number of web services related to multimedia content analysis. In 2016, we revamped the multimedia-related web service offer, making all serices interoperable and broadening the scope of services made available (silence detection, face detection, text-based fragmentation). We also made available short videos that demonstrate the usefulness of our web services.

LINKS Project-Team

6. New Software and Platforms

6.1. ShEx Validator

KEYWORDS: RDF Data management - RDF - Shape Expression
FUNCTIONAL DESCRIPTION

Shape Expression schemas is a formalism for defining constraints on RDF graphs. This software allows to check whether a graph satisfies a Shape Expressions schema.

- Participants: Iovka Boneva
- Contact: Iovka Boneva
- URL: https://gforge.inria.fr/projects/shex-impl

6.2. gMark

KEYWORDS: graph benchmark - Graph Database - Graph Query
FUNCTIONAL DESCRIPTION

gMark allow the generation of graph databases and an associated set of query from a schema of the graph. gMark is based on the following principles: great flexibility in the schema definition, ability to generate big size graphs, ability to generate recursive queries and queries with a desired selectivity .

- Participants: Aurélien Lemay
- Contact: Aurélien Lemay
- URL: https://github.com/graphMark/gmark

6.3. QuiXPath

KEYWORDS: XML Streams - XPath 3.0 Queries - Aggregation - Data Joins
FUNCTIONAL DESCRIPTION

QuiXPath is a streaming implementation that covers most of XPath 3.0. It was developed during the PhD thesis of T. Sebastian funded by our industrial transfer partner Innovimax.

- Participants: Tom Sebastian and Joachim Niehren
- Contact: Joachim Niehren
- URL: https://project.inria.fr/quix-tool-suite

6.4. 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 Project-Team

6. New Software and Platforms

6.1. FELiScE-branch HappyHeart

Finite Elements for Life SCiences and Engineering problems
KEYWORDS: Finite element modelling - Cardiac Electrophysiology - Cardiovascular and respiratory systems
SCIENTIFIC 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.

FUNCTIONAL DESCRIPTION

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: Gautier Bureau, Federica Caforio, Dominique Chapelle, Sébastien Gilles, Sébastien Imperiale, Philippe Moireau,
- 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 designed to perform both simulation and estimation of the heart mechanical behavior (based on various types of measurements, e.g. images).

FUNCTIONAL DESCRIPTION

The heartLab software is a library designed to perform both simulation and estimation of the heart mechanical behavior (based on various types of measurements, e.g. images).

Also included are 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.

- Participants: Gautier Bureau, 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 a free and 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.

- Participants: Gautier Bureau, Dominique Chapelle, Philippe Moireau
- Contact: Philippe Moireau
- URL: http://verdandi.gforge.inria.fr/

MADYNES Project-Team

5. New Software and Platforms

5.1. Distem

KEYWORDS: Large scale - Experimentation - Virtualization - Emulation
FUNCTIONAL DESCRIPTION

Distem is a distributed systems emulator. When doing research on Cloud, P2P, High Performance Computing or Grid systems, 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, or aiming at tolerating performance degradations or variations which are frequent in the Cloud or in other applications distributed at large scale (P2P for example).

- Participants: Luc Sarzyniec, Lucas Nussbaum and Tomasz Buchert
- Partners: CNRS - Grid'5000 - Inria - Loria - Université de Lorraine
- Contact: Lucas Nussbaum
- URL: http://distem.gforge.inria.fr

5.2. Grid'5000 testbed

FUNCTIONAL DESCRIPTION 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 Emile Morel
- Contact: Lucas Nussbaum
- URL: https://www.grid5000.fr/

5.3. Kadeploy

KEYWORD: Operating system provisioning
FUNCTIONAL DESCRIPTION

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, 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 - Grid'5000 - Inria - Loria - Université de Lorraine
- Contact: Lucas Nussbaum
- URL: http://kadeploy3.gforge.inria.fr

5.4. MECSYCO-RE-C++

Multi-agent Environment for Complex SYstems COsimulation. Cœur C++

KEYWORDS: Modeling - Simulation - Simulator - Multi-model - Multi-agent - Agent - Artefact

FUNCTIONAL DESCRIPTION

MECSYCO is a project 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). MECSYCO-RE-C++ is the C++ implementation of the central part (core) of MECSYCO. It can be complimente by mecsyco-com (a communication package for distributed exécution) and mecsyco-visu (a set of tools for vizualizing simulations).

- Participants: Vincent Chevrier, Laurent Ciarletta, Benjamin Camus, Julien Vaubourg, Yannick Presse, Victorien Elvinger, Benjamin Segault and Nicolas Kirchner
- Partners: Inria - Université de Lorraine
- Contact: Vincent Chevrier

5.5. MECSYCO-RE-java

Multi-agent Environment for Complex SYstems COsimulation. Coeur java

KEYWORDS: Modeling - Simulation - Simulator - Multi-model - Co-simulation - Multi-agent - Agent - Artefact

FUNCTIONAL DESCRIPTION

MECSYCO is a project 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). MECSYCO-RE-java is the Java implementation of the central part (core) of MECSYCO. It can be complimente by mecsyco-com (a communication package for distributed exécution) and mecsyco-visu (a set of tools for vizualizing simulations).

- Participants: Christine Bourjot, Vincent Chevrier, Laurent Ciarletta, Benjamin Camus, Julien Vaubourg, Yannick Presse, Victorien Elvinger and Julien Siebert
- Partners: Inria - Université de Lorraine
- Contact: Vincent Chevrier
- URL: http://www.mecsyco.com

5.6. NDNperf

KEYWORDS: Performance measure - Named-Data Networking

FUNCTIONAL DESCRIPTION

We designed NDNperf, an open source tool for NDN server-side performance evaluation and sizing purposes, in order to have an idea of the throughput a server can achieve when it has to generate and transmit NDN Data packets. It is very similar to iPerf and also needs a client and a server to perform the measurements while minimizing the number of instructions between Interest reception and Data emission. It has the following features: - Periodic report of performances: end-to-end throughput, latency, processing time, - Fresh NDN Data generation or NDN Data delivery from caches, - Multi-threaded (one main thread for event lookup and N threads for NDN Data generation), - Able to use all available signatures implemented in the NDN library, choose the size of the key, and the transmission size of Data packets.

- Contact: Thibault Cholez
- URL: http://madynes.loria.fr/software/

5.7. Ruby-cute

KEYWORDS: Experimentation - HPC - Cloud

FUNCTIONAL DESCRIPTION

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/

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 (Univ. Versailles Saint-Quentin)
- 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. We have also developed a generator of video traffic and objects that allow to generate easily simulation scenarios.

We have made available the code related to the communication based train control and the one generating video traffic. Some of our contribution to the ns-3 simulator and selected results illustrating some of the issues that can be addressed using our contribution are presented and discussed in [35].

- Participants: Sara Alouf, Giovanni Neglia and Alina Tuholukova
- Contact: Alina Tuholukova
- ns-3 codereview issue of the cbtc module: https://codereview.appspot.com/289110043
- ns-3 codereview issue of the video generator: https://codereview.appspot.com/286160043

MAGIQUE-3D Project-Team

5. New Software and Platforms

5.1. Elasticus

SCIENTIFIC DESCRIPTION Elasticus simulate acoustic and elastic wave propagation in 2D and in 3D, 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 to optimization of its performances. Developped 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.

- Participants: Simon Ettouati, Julien Diaz and Lionel Boillot
- 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. 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 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).

- Participants: Julien Diaz, Marie Bonnasse-Gahot 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, elasto-dynamic 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. For time-domain simulations, a wide range of ODE (Ordinary Differential Equation) solvers have been implemented : high-order explicit or implicit time schemes. Several applications are currently available : wave equation, elastodynamics, aero-acoustics, Maxwell's equations.

- Participants: Marc Duruflé, Juliette Chabassier, Mamadou N'Diaye and Michaël Leguèbe
- Contact: Marc Duruflé
- URL: http://montjoie.gforge.inria.fr/

5.4. TMBM-DG

Time-Marching Based Methods-Discontinuous Galerkin
SCIENTIFIC DESCRIPTION TMBM-DG simulate acoustic and elastic wave propagation in 2D and in 3D, 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 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.

- Participants: Julien Diaz, Lionel Boillot and Simon Ettouati
- Partner: TOTAL
- Contact: Julien Diaz

MAGNET Project-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 pre-processing, 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://team.inria.fr/magnet/software/

6.2. Magneto

Python toolbox for generating and evaluating vector space representations for Natural Language Processing
FUNCTIONAL DESCRIPTION

Version 1.0 of Magneto contains preprocessing methods for texts in french and english. It includes classical methods for generating vector space representations: count based models, dimensionality reduction based methods and predictive methods (word2vec and Glove). For version 1.0, vector space representations can be evaluated on dedicated evaluation tasks such as similarity and analogy.

- Participants: Pascal Denis, Rémi Gilleron, Mikaela Keller, François Noyer and Nathalie Vauquier
- Contact: Pascal Denis
- URL: https://team.inria.fr/magnet/software/

MAGRIT Project-Team

5. New Software and Platforms

5.1. Ltrack

The Inria development action (ADT) LTrack aims at developing an Android platform in order to facilitate the transfer of some of our algorithms onto mobile devices. For the moment, the tracking-by-synthesis algorithm has been implemented (up to our knowledge, for the first time on a mobile device) in order to rigidly track a real object in real time assuming that a CAD model of this object is available. The design and implementation of the platform have been guided by the need to enable easy integration of any tracking algorithm based on combining video data and other sensor information.

- 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. His contract ended at the end of September, 2016.

This year, the library was ported on Android, and Qt 5.7. Various diffusion media were also built: demos, e.g. linked with OpenCV; web site http://polar.inria.fr; detailed documentation with tutorials; and a paper was published at ISMAR'2016 conference [23].

PoLAR was made available to the public in October 2015, and can be used under Linux, Windows, MacOS and Android.

- Contact: Erwan Kerrien, Pierre-Frédéric Villard.
- URL: http://polar.inria.fr

5.3. Fast>VP

Fast>VP is a fast and effective tool to detect vanishing points in uncalibrated images of man-made environments and automatically orthorectify the involved planes. It is a Matlab implementation of the algorithm described in our Eurographics'2016 paper [25].

- Contact: Gilles Simon
- URL: https://members.loria.fr/GSimon/fastvp/

5.4. The GridMethod Toolbox

This Matlab toolbox implements several efficient and state-of-the art algorithms to estimate displacement and strain fields from grid images deposited on the surface of a specimen submitted to a loading or tensile test.

- Contact: Frédéric Sur
- URL:http://www.thegridmethod.net

MAMBA Project-Team

6. New Software and Platforms

6.1. TiQuant

Tissue Quantifier
KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology
Systems biology and medicine on histological scales require 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 hitherto has been little recognised. 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, permitting 3D reconstructions of liver lobules down to a resolution of less than a micrometer [72]. It is implemented in portable object-oriented ANSI C++. The GUI is based on QT and supports real-time visualisation using OpenGL. TiQuant is embedded in the tissue modelling framework CellSys and thus is tightly linked with TiSim, a versatile and efficient simulation environment for tissue models. TiQuant provides an interface to VolView and further complements its functionality by linking to the open-source libraries ITK and VTK (itk/vtk.org). The image/volume processing chains currently implemented in TiQuant for example include techniques to segment conduit and cell segmentation from 3D confocal micrographs of liver tissue based on the Adaptive Otsu Thresholding method and a number of morphological operators [75]. TiQuant is currently extended by a machine learning component.

FUNCTIONAL DESCRIPTION

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, permitting 3D reconstructions of liver lobules down to a resolution of less than a micrometer.

- Contact: Dirk Drasdo
- URL: http://www.msysbio.com

6.2. TiSim

Tissue Simulator
KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology
FUNCTIONAL DESCRIPTION

TiSim (Tissue Simulator) is a software for agent-based models of multicellular systems. It permits model development with centre-based models and deformable cell models; it contains modules for monolayer and multicellular spheroid simulations as well as for simulations of liver lobules. Besides agent-based simulations, the flow of blood and the transport of molecules can be modelled in the extracellular space; intracellular processes such as signal transduction and metabolism can be simulated, for example over an interface permitting integration of SBML-formulated ODE models.

TiSim is written in modern C++, keeping central model constituents in modules to be able to reuse them as building blocks for new models. For user interaction, the GUI Framework Qt is used in combination with OpenGL for visualisation. A non-interactive mode to use the software also exists, accepting a combination of XML and HDF5 (hierarchical data format v5) as input, which produces output data in VTP (VTK) and HDF5 format. SBML, SBML_ODESolver and sundials are deployed for the creation and solution of the differential equations of metabolic networks and signalling pathways presented in SBML data format. TiSim permits agent-based simulations of multicellular systems and can be directly fed by processed image data from TiQuant.

- Contact: Dirk Drasdo
- URL: (No url yet)

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 BRDFs. It provides a set of command line software to fit measured data to analytical forms, tools to understand models and data.

- 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, AVX, FMA, AVX512, AltiVec, VSX 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 2016, we released three revisions of the 3.2 branch, as well as the new 3.3 version that leverages numerous major novel features and improvements. Those include, a novel evaluation mechanism of expressions, support for AVX, FMA, AVX512, VSX and ZVector vector instructions, unaligned vectorization, nvcc/CUDA, more OpenMP parallelism, a fast divide and conquer SVD algorithm, a CompleteOrthogonalDecomposition class for fast minimal norm solving, a LS-CG solver, a fast reciprocal condition number estimators in LU and Cholesky factorizations, LU::transpose()/adjoint() API, support for inplace decompositions, support for matrix-free iterative solvers, new array functions, support for any BLAS/LAPACK libraries as backend, improved support for mixing scalar types, eigenvectors in GeneralizedEigenSolver, a complete rewrite of LinSpaced, a non officially supported but massively used Tensor module with CUDA and OpenCL support, and more.

- 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. 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/

MARELLE Project-Team

4. New Software and Platforms

4.1. Coq

The Coq Proof Assistant
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 Gregoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Dénès, Stephane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pedrot, Loic Pottier, Matthias Puech, Yann Regis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliatre
- Partners: CNRS - ENS Lyon - Université Paris-Diderot - Université Paris-Sud
- Contact: Matthieu Sozeau
- URL: http://coq.inria.fr/

The Marelle team, in collaboration with the pi.r2 team, plays an important role in the development of Coq. During this year, we contributed to the 8.6 version of Coq, released in December. As the *release manager*, Maxime Dénès led the implementation of a time-based release process, aiming at shorter and more predicitible release cycles. We successfully transitioned to 10-month cycles and hope to soon move to 6-month cycles, making it easier for users to benefit from the latest improvements.

At a more detailed level, members of the Marelle team attended the Coq developer meetings (organized in Paris by Maxime Dénès and Matthieu Sozeau) and contributed to the development of Coq concerning bug fixes for virtual machine execution (Benjamin Grégoire and Maxime Dénès), cleaning up the API for plug-in developers (Matej Košík), improving the State Transaction Machine (Enrico Tassi), setting up a package index based on OPAM (Enrico Tassi), introducing a system to discuss Coq Enhancement Proposals (Enrico Tassi), and implementing a new configurable system of warnings (Maxime Dénès).

We supervise of an engineer working at MIT on questions related to efficient proof construction and proof development environments, in cooperation with researchers from the pi.r2 team. The collaboration with MIT was also an occasion to reflect on the licence framework governing collaborations around the Coq system.

We also prepared the set-up of a consortium to gather intensive users and contributors to the development of Coq. This was an occasion to work with the promotors of the InriaSoft structure which is expected to host the consortium in the long run.

4.2. 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 Gregoire and Pierre-Yves Strub
- Contact: Benjamin Grégoire
- URL: https://www.easycrypt.info/trac/

This year, development on this software system concerned the development of new logical settings to work on differential privay problems: a Hoare logic based on union bound and a logic based on probabilistic couplings.

4.3. 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, Francois Garillot, Georges Gonthier, Stéphane Le Roux, Assia Mahboubi, Sidi Ould Biha, Ioana Pasca, Laurence Rideau, Alexey Solovyev, Enrico Tassi, Laurent Théry and Russell O'Connor
- Contact: Assia Mahboubi
- URL: http://www.msr-inria.fr/projects/mathematical-components-2/

This year we contributed to the library by adding a new module to cover finite sets within potentially infinite finite types, organizing tutorials and schools to teach its usage:

- in January in Sophia Antipolis (one-week format) https://team.inria.fr/marelle/en/advanced-coq-winter-school-2016/ (organized by Enrico Tassi, with contributions by Cyril Cohen, Laurence Rideau, Laurent Théry)
- in August in Nancy (one-day tutorial format, colocated with the ITP conference, organized by Assia Mahboubi and Enrico Tassi, with contributions by Yves Bertot, Cyril Cohen, and Laurent Théry) https://github.com/math-comp/wiki/wiki/tutorial-itp2016
- in November in Sophia Antipols https://team.inria.fr/marelle/en/advanced-coq-winter-school-2016-2017/ (organized by Enrico Tassi, with contributions by Yves Bertot, Cyril Cohen, Laurence Rideau).

4.4. 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, Laurent Thery, Assia Mahboubi and Georges Gonthier
- Contact: Yves Bertot
- URL: http://ssr.msr-inria.inria.fr/

This year we mainly performed maintenance operations on this software extension to the Coq system (Enrico Tassi).

4.5. 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 year, we extended the tool to be able to deal with schemes based on cyclic groups and bilinear maps.

- Participants: Benjamin Gregoire, Gilles Barthe and Pierre-Yves Strub
- Contact: Benjamin Grégoire
- 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

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.

- Contact: Gabriel Stoltz
- URL: https://gitlab.inria.fr/matherials/simol

MATHNEURO Team

4. New Software and Platforms

4.1. New Software

4.1.1. Julia library LSODA.jl

LSODA.jl is a Julia package that interfaces to the liblsoda library, developed by Simon Frost (University of Cambridge), thereby providing a way to use the LSODA algorithm from Linda Petzold and Alan Hindmarsh from Julia.

4.1.2. Julia library PDMP.jl

PDMP.jl This is a joint work of Romain Veltz and Simon Frost.

PDMP.jl is a Julia package that allows simulation of Piecewise Deterministic Markov Processes (PDMP); this encompasses hybrid systems, comprising of continuous and discrete components, as well as processes with time-varying rates. It is based on an implementation of the True Jump Method for performing stochastic simulations of PDMP, and requires solving stiff ODEs in an efficient manner. Sundials.jl is used, but other solvers could be easily added.

MATHRISK Project-Team

6. New Software and Platforms

6.1. PREMIA

KEYWORDS: Financial products - Computational finance - Option pricing

6.2. Scientific Description

Premia is a software designed for option pricing, hedging and financial model calibration.
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.

6.3. Functional Description

- Participants: Mathrisk project team and contributors
- Partners: Ecole des Ponts ParisTech - Inria - 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)
- OS/Middelware: Linux, Mac OS X, Windows
- APP: The development of Premia started in 1999 and 17 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++
- Documentation: scientific documentation of all the algorithm implemented. PNL has a 100 pages user documentation
- Size of the software: For the Src part of Premia : 337046 lines , that is 14 Mbyte of code, and 117 Mbyte of PDF files of documentation; For PNL: 747952 lines , that is 25 MO.
- interfaces : Nsp for Windows/Linux/Mac, Excel, binding Python, and a Web interface.
- Publications: [15], [68], [75], [83], [86], [56], [66].

6.4. Content

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.

- **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.

- **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.

- **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)

- **Hybrid products**

  A PDE solver for pricing derivatives on hybrid products like options on inflation and interest or change rates is implemented.

- **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.

6.5. PNL numerical library

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.

This year, Jérome Lelong has performed the following tasks on the development of PNL:
Releases 1.7.3 and 1.7.4. of the *PNL* library (http://pnl.gforge.inria.fr/).

1. Simplify the use of PNL under Visual Studio. It can either be compiled using CMake or added as an external library to an existing project.
2. Improve the construction of large `PnlBasis` objects and make it possible to deal with non tensor functions.
3. Add complex error functions.

6.6. Consortium Premia

The software Premia is supported by a Consortium of financial institutions created in 1999. The members of the Consortium give an annual financial contribution and receive every year a new version enriched with new algorithms. They participate to the annual meeting where future new developments are discussed.

6.7. Diffusion

All releases of the software Premia (18 in 2016) are registered at the French agency APP. The most recent is provided to the Consortium with an appropriate licence. An opensource version is also available for academic purposes. The software is thus used in many universities, with in France and abroad.

6.8. Algorithms implemented in Premia in 2016

Premia 18 has been delivered to the consortium members in March 2016.

It contains the following new algorithms:

6.8.1. Insurance, Risk Management, Optimal Trade Execution

- A Forward Solution for Computing Derivatives Exposure. M. Ben Taarit, B. Lapeyre.
- Monte Carlo Calculation of Exposure Profiles and Greeks for Bermudan and Barrier Options under the Heston Hull-White Model. Q. Feng, C.W. Oosterlee.
- Dynamic optimal execution in a mixed-market-impact Hawkes price model. A. Alfonsi, P. Blanc. *Finance & Stochastics*
- A Hamilton Jacobi Bellman approach to optimal trade execution. P. Forsyth, *Applied Numerical Mathematics 61, 2011.*

6.8.2. Equity Derivatives

- Value function approximation or stopping time approximation: a comparison of two recent numerical methods for American option pricing using simulation and regression. L. Stentoft, *Journal of Computational Finance, 18(1), 2014.*
- Pricing American-Style Options by Monte Carlo Simulation: Alternatives to Ordinary Least Squares. S. Tompaidis, C. Yang, *Journal of Computational Finance, 18(1), 2014,*
- Solving Optimal Stopping Problems using Martingale Bases. J.Lelong
- The Stochastic Grid Bundling Method: Efficient Pricing of Bermudan Options and their Greeks. S. Jain, C.W. Oosterlee.
- Two-dimensional Fourier cosine series expansion method for pricing financial options. C.W.Oosterlee M.J. Ruijter, *SIAM J. Sci. Comput., 34(5), 2012.*
- Estimation of the parameters of the Wishart process. A.Alfonsi, A.Kebaier, C.Rey, *Preprint*
- The 4/2 Stochastic Volatility Model. M. Grasselli, *Preprint.*
- Ninomiya Victoir Scheme and Multi Level Scheme. A. Al Gerbi, E. Clement, B. Jourdain.
- Importance Sampling for Multilevel Monte Carlo. A.Kebaier J.Lelong
- The evaluation of barrier option prices under stochastic volatility. C.Chiarella, B.Kang, G.H.Meyer, *Computers and Mathematics with Applications 64, 2012.*
- Volatility swaps and volatility options on discretely sampled realized variance. G.Lian, C.Chiarella, P.S.Kalev, *Journal of Economic Dynamics Control 47 2014*
- Efficient variations of the Fourier transform in applications to option pricing. S. Boyarchenko and S.Levendorski, *Journal of Computational Finance, 18(2), 2014.*
- Model-free implied volatility: from surface to index. M. Fukasawa et al., *Int. J. Theor. Appl. Finan. 14, 433, 2011*

- Stratified approximations for the pricing of options on average. N.Privault J.Yu *Journal of Computational Finance.*

Moreover, J. Lelong has ensured everyday maintenance to fix various bugs, especially related to Visual C++; and has get rid of the old bunch of scripts to generate the HTML documentation by implementing the required mechanism directly in TeX. This makes the system much more robust; He has also worked on the continuous integration process with Sébastien Hinderer. Moreover, part of Premia documentation is now generated directly from the source code. The 3000 lines of undocumented C code used so far had become unmaintainable. Now, it is replaced by a much more flexible and efficient Python script.

MAVERICK Project-Team

6. New Software and Platforms

6.1. 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: Joelle Thollot, Pascal Barla, Adrien Bousseau and Alexandrina Orzan
- Partners: CNRS - INP Grenoble - LJK - Université Joseph-Fourier
- Contact: Joelle Thollot
- URL: http://maverick.inria.fr/Publications/2008/OBWBTS08/index.php

6.2. 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 and Romain Vergne
- Partner: UJF
- Contact: Romain Vergne
- URL: http://gratin.gforge.inria.fr/

6.3. 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. Ongoing researches are addressing animation. GigaVoxels is currently used for the quality real-time exploration of the detailed galaxy in ANR RTIGE. Most of the work published by Cyril Crassin (and al.) during his PhD (see http://maverick.inria.fr/Members/Cyril.Crassin/) is related to GigaVoxels. GigaVoxels is available for Windows and Linux under the BSD-3 licence.

- Participants: Cyril Crassin, Fabrice Neyret, Prashant Goswami, Jérémy Sinoir, Pascal Guehl and Eric Heitz
- Contact: Fabrice Neyret
- URL: http://gigavoxels.inrialpes.fr

6.4. HQR

High Quality Renderer
KEYWORDS: Lighting simulation
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 developpement 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

6.5. MobiNet

KEYWORDS: Co-simulation - Education - Programmation
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). It is available in public domain for Linux,Windows and MacOS.

- Participants: Fabrice Neyret, Sylvain Lefebvre, Samuel Hornus, Joelle Thollot and Franck Hetroy-Wheeler
- Partners: Cies - CNRS - GRAVIR - INP Grenoble - Inria - IREM - LJK
- Contact: Fabrice Neyret
- URL: http://mobinet.imag.fr/index.en.html

6.6. 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. Most of the work published by Eric Bruneton and Fabrice Neyret (see http://evasion.inrialpes.fr/Membres/Eric.Bruneton/) has been done within Proland and integrated in the main branch. Proland is available under the BSD-3 licence.

- Participants: Antoine Begault, Eric Bruneton, Guillaume Piolet and Fabrice Neyret
- Contact: Fabrice Neyret
- URL: https://proland.inrialpes.fr/

6.7. ShwarpIt

KEYWORD: Warping
FUNCTIONAL DESCRIPTION ShwarpIt is a simple mobile app that allows you to manipulate the perception of shapes in images. Slide the ShwarpIt slider to the right to make shapes appear rounder. Slide it to the left to make shapes appear more flat. The Scale slider gives you control on the scale of the warping deformation.

- Contact: Georges-Pierre Bonneau
- URL: http://bonneau.meylan.free.fr/ShwarpIt/ShwarpIt.html

6.8. 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/

6.9. X3D TOOLKIT

X3D Development platform

FUNCTIONAL DESCRIPTION X3DToolkit is a library to parse and write X3D files, that supports plugins and extensions.

- Participants: Gilles Debunne and Yannick Le Goc
- Contact: Cyril Soler
- URL: http://artis.imag.fr/Software/X3D/

6.10. libylm

LibYLM

KEYWORD: Spherical harmonics

FUNCTIONAL DESCRIPTION This library implements spherical and zonal harmonics. It provides the means to perform decompositions, manipulate spherical harmonic distributions and provides its own viewer to visualize spherical harmonic distributions. It is available for linux on the Launchpad PPA of the author.

- Author: Cyril Soler
- Contact: Cyril Soler
- URL: https://launchpad.net/~csoler-users/+archive/ubuntu/ylm

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 an open-source software developed to solve optimal control problems by coupling shooting and homotopy methods. More generally, it can be used to solve general Hamiltonian boudary value problems. It also implements an efficient computation of Jacobi fields (allowing in particular second order optimality condition checks) based on the repeated use of automatic differentiation.

- Participants: Jean-Baptiste Caillau, Olivier Cots and Joseph Gergaud
- Contact: Oliver Cots
- URL: http://www.hampath.org

MEMPHIS Project-Team

6. New Software and Platforms

6.1. COCOFLOW

FUNCTIONAL DESCRIPTION

The code is written in fortran 95 with a MPI parallelization. It solves equations of conservation modeling 3D compressible flows with elastic models as equation of state.

- Contact: Florian Bernard
- URL: https://gforge.inria.fr/projects/cocoflow

6.2. KOPPA

Kinetic Octree Parallel PolyAtomic
FUNCTIONAL DESCRIPTION

KOPPA is a C++/MPI numerical code solving a large range of rarefied flows from external to internal flows in 1D, 2D or 3D. Different kind of geometries can be treated such as moving geometries coming from CAO files or analytical geometries. The models can be solved on Octree grids with dynamic refinement.

- Participant: Florian Bernard
- Contact: Florian Bernard
- URL: https://git.math.cnrs.fr/gitweb/?p=plm/fbernard/KOPPA.git;a=summary

6.3. NS-penal

Navier-Stokes-penalization
KEYWORDS: 3D - Incompressible flows - 2D
FUNCTIONAL DESCRIPTION

The software can be used as a black box with the help of a data file if the obstacle is already proposed. For new geometries the user has to define them. It can be used with several boundary conditions (Dirichlet, Neumann, periodic) and for a wide range of Reynolds numbers.

- Partner: Université de Bordeaux
- Contact: Charles-Henri Bruneau

6.4. NaSCar

Navier-Stokes Cartesian
KEYWORDS: HPC - Numerical analyse - Fluid mechanics - Langage C - PETSc
SCIENTIFIC DESCRIPTION

NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.
FUNCTIONAL DESCRIPTION

This code is devoted to solve 3D-flows in around 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's type. The code is written in C language and use Petsc 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.

- Participant: Michel Bergmann
- Contact: Michel Bergmann
- URL: https://gforge.inria.fr/projects/nascar/

MEPHYSTO Project-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/

MEXICO Project-Team

6. New Software and Platforms

6.1. DarkSider

FUNCTIONAL DESCRIPTION

DarkSider computes anti-alignments between a Petri net model and a log of observed traces, as described in [15], [25].

- Participant: Thomas Chatain
- Contact: Thomas Chatain
- URL: http://www.lsv.ens-cachan.fr/~chatain/darksider/

6.2. COSMOS

FUNCTIONAL DESCRIPTION

COSMOS is a statistical model checker for the Hybrid Automata Stochastic Logic (HASL). HASL employs Linear Hybrid Automata (LHA), a generalization of Deterministic Timed Automata (DTA), to describe accepting execution paths of a Discrete Event Stochastic Process (DESP), a class of stochastic models which includes, but is not limited to, Markov chains. As a result HASL verification turns out to be a unifying framework where sophisticated temporal reasoning is naturally blended with elaborate reward-based analysis. COSMOS takes as input a DESP (described in terms of a Generalized Stochastic Petri Net), an LHA and an expression Z representing the quantity to be estimated. It returns a confidence interval estimation of Z, recently, it has been equipped with functionalities for rare event analysis. COSMOS is written in C++

- Participants: Benoît Barbot, Hilal Djafri, Paolo Ballarini, Marie Duflot-Kremer and Serge Haddad
- Contact: Hilal Djafri
- URL: http://www.lsv.ens-cachan.fr/~barbot/cosmos/

6.3. CosyVerif

FUNCTIONAL DESCRIPTION

CosyVerif is a platform dedicated to the formal specification and verification of dynamic systems. It allows to specify systems using several formalisms (such as automata and Petri nets), and to run verification tools on these models.

- Participants: Serge Haddad, Fabrice Kordon, Laure Petrucci and Alban Linard
- Partners: LIP6 - LIPN (Laboratoire d'Informatique de l'Université Paris Nord) - LSV
- Contact: Serge Haddad
- URL: http://www.cosyverif.org/

6.4. Mole

FUNCTIONAL DESCRIPTION

Mole computes, given a safe Petri net, a finite prefix of its unfolding. It is designed to be compatible with other tools, such as PEP and the Model-Checking Kit, which are using the resulting unfolding for reachability checking and other analyses. The tool Mole arose out of earlier work on Petri nets.

- Participant: Stefan Schwoon
- Contact: Stefan Schwoon
- URL: http://www.lsv.ens-cachan.fr/~schwoon/tools/mole/

MIMESIS Team

4. New Software and Platforms

4.1. Simulation Open Framework Architecture

Keywords: Real time - Multi-physics simulation - Medical applications

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.

URL: http://www.sofa-framework.org

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 gait cycles. To this end it is based on analyzing the knee 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.

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 for ergonomics purposes. Kimea is able to manage most of the occultations that can occur on workstations (real working situations). To this end, Kimea relies on a database of examples/poses organized as a graph, in order to replace unreliable body segment reconstructions by poses that have already been measured on real subjects. 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

KEYWORDS: Behavioral animation - Virtual cities
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 pedestrians performing different kind of activities implying travels between different locations. However the generic aspect of the algorithm and underlying representations enables 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.
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.
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.
- Participants: Fabrice Lamarche and Carl-Johan Jorgensen
- Contact: Fabrice Lamarche

6.6. The Theater

KEYWORDS: Interactive Scenarios - 3D animation - Storytelling

SCIENTIFIC DESCRIPTION

The Theater is a software framework to develop interactive scenarios in virtual 3D environments. The framework provides means to author and orchestrate 3D character behaviors and simulate them in real-time. The tools provide 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

6.7. Immerstar Platform

Participants: Georges Dumont [contact], Ronan Gaugne, Anthony Sorel, Franck Multon.

With the two platforms of virtual reality, Immersia and Immermove, grouped under the name Immerstar, the team has access to high level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform is granted by a Inria CPER funding for 2015-2019 that enables important evolutions of the equipment. In 2016, the first technical evolutions have been decided, with, for Immermove, the addition of a third face to the immersive space, and the extension of the Vicon tracking system, and for Immersia, the installation of WQXGA laser projectors and of a new tracking system.

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], Siddhartha Dutta.

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, Things using CoAP [0]. 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 *GIDL*, 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 GIDL, 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;

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[0] https://tools.ietf.org/html/rfc7252

- VSB provides support for the client-server, publish/subscribe, tuple space and data streaming interaction paradigms;
- 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: we have developed related tools that support the automated generation of a BC for a service/Thing from its GIDL interface description.

VSB is being developed within the H2020 CHOReVOLUTION project (see § 8.2.1.1). It is also based on previous development carried out in the FP7 CHOReOS project [0]. VSB is available for download under open source license.

6.3. Ambiciti App & Platform: Monitoring the Exposure to Environmental Pollution

Participants: Valerie Issarny [contact], Cong Kinh Nguyen, Pierre-Guillaume Raverdy, Fadwa Rebhi.

URL: http://ambiciti.io

Is your exposure to noise too high on certain days? How is air pollution in your street? Will air quality improve in the next hours? Do you want to measure the noise pollution on the way between your home and your office? What pollution levels are considered harmful for your health? Ambiciti (previously SoundCity) provides answers to these questions and many others through dedicated Apps and Platforms that leverage Inria research results in the area of mobile distributed systems (from MiMove team) and data assimilation (from Inria CLIME team). The Ambiciti app is available for download on both the App and the Play stores. Starting December 2016, the Ambiciti software solutions are licensed to the Ambiciti start-up.

Monitoring exposure to noise pollution: Noise pollution is a major environmental health problem, with an estimated number of 10,000 premature deaths each year in Europe. The 2002 European environmental noise directive defines a common approach intended to avoid, prevent or reduce the harmful effects of noise. It requires the determination of exposure to environmental noise in major cities, through noise mapping. Until recently, this has been done solely through numerical simulation. Daytime, evening and nighttime averages are generally produced, without distinction between the different days of the year. Also, it is difficult to fill the gap between a noise map and the actual exposure of people where they live and stay. This motivates to monitor noise pollution where and when people are exposed. One promising direction is to make use of the noise sensors that people carry most of the time, i.e., the microphones embedded in their mobile phones.

Ambiciti (previously called SoundCity as it was initially focused on the monitoring of noise pollution) measures the actual noise levels to which individuals are exposed using such an approach, while taking into account the relatively low quality of the collected measurements. Ambiciti can then monitor noise levels throughout the day and inform users about their instantaneous, hourly and daily exposures.

In addition to the monitoring of the individual exposure to the noise pollution using mobile phones, the collective exposure may be derived from crowd-sensing. The adoption rate of mobile phones makes it possible to collect a huge amount of observational data about the noise pollution at the city scale. Recent studies have indeed highlighted the emergence of new environmental monitoring schemes leveraging the combination of mobile phones-embedded sensors and citizen participation. Ambiciti then leverages a mobile phone sensing middleware for collecting noise measurements at the urban scale, which are then assimilated toward the production of real-time pollution maps.

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[0] http://www.choreos.eu

Monitoring exposure to air pollution: The Ambiciti app delivers information about the exposure to air pollution, providing hourly air quality maps, which are computed using numerical simulation. Depending on the user's location, the user may have access to hourly air quality maps, at street resolution, in real time and for the next two days. Currently, only Paris (France) and the Bay area enjoy such high resolution maps, but other cities are on the way to be included.

Mobile app features: Ambiciti is easy to use, while featuring various functions to meet different levels of user engagement (from passive monitoring to citizen scientists):

- Measuring noise level, anytime on demand or automatically during the day,
- Providing air quality indexes (according to the EU definition), in the past, present and future hours or days, together with pollution levels for nitrogen dioxide, fine particulate matter and ozone,
- Displaying statistics on exposure to pollutions, hourly, daily, during daytime and nighttime, for both noise and air.
- Displaying maps with own's noise measurements and/or hourly NO2 levels (including street-level resolution for Paris and the San Francisco Bay area)
- Promoting citizen science where communities of users may engage into the intensive measurement of noise in order to analyze a given journey or to map neighborhoods.
- Providing pollution-aware routing.
- Calibration of the smartphone for noise monitoring, automatically with Ambiciti database or manually with a sound level meter,

Privacy: The Ambiciti app has been designed with privacy in mind, which especially holds in the case of noise pollution monitoring. It is in particular important to stress that actual sound samples are never stored on the phone or uploaded to the Ambiciti servers. Only the amplitude of the sound in dB(A) is calculated, and uploaded provided the user's permission. An anonymous identifier is further created for each device for distinguishing between the data sent by different users, while no identifying information is collected. Further detail may be found from the App information page.

The Ambiciti platform is developed in collaboration with the Inria CLIME team together with The Civic Engine and the NUMTECH SMEs in the context of CityLab@Inria and Inria@SiliconValley, and with the support of the EIT Digital Env&You activity.

6.4. AppCivist-PB: A Platform for Democratic Assembly Customized for Participatory Budgeting

Participants: Valérie Issarny [contact], Cristhian Parra Trepowski, Rafael Angarita.

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.

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, together with the support of the EIT Digital CivicBudget activity.

MINT Project-Team

5. New Software and Platforms

5.1. ControllAR

FUNCTIONAL DESCRIPTION

ControllAR is a novel system that facilitates the appropriation of rich visual feedback on control surfaces through remixing of graphical user interfaces and augmented reality display.

- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/ControllAR

5.2. GINA

- Participants: Nicolas Bremard and Laurent Grisoni
- Contact: Laurent Grisoni

5.3. Revil

FUNCTIONAL DESCRIPTION

Revil is an application for building and manipulating 3D SceneGraphs for Mixed-Reality Artistic Performances. It is based on OpenGL/GLSL(glfw, glm), OpenNI2, FLTK and is entirely controllable via OpenSoundControl messages. It relies on the approach of revealing virtual content in the physical space by intersecting it with performers and spectator's bodies and props.

- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/Revil

5.4. TaxtelOSC

FUNCTIONAL DESCRIPTION

TaxtelOSC is a software wich uses the concept of taxtel to reproduce rich and dense tactile feedback on

- Contact: Laurent Grisoni
- URL: http://forge.lifl.fr/ControllAR

MISTIS Project-Team

6. New Software and Platforms

6.1. BOLD model FIT

KEYWORDS: Functional imaging - FMRI - Health
FUNCTIONAL DESCRIPTION

This Matlab toolbox performs the automatic estimation of biophysical parameters using the extended Balloon model and BOLD fMRI data. It takes as input a MAT file and provides as output the parameter estimates achieved by using stochastic optimization

- Authors: Pablo Mesejo Santiago, Jan M Warnking and Florence Forbes
- Contact: Pablo Mesejo Santiago
- URL: https://hal.archives-ouvertes.fr/hal-01221115v2/

6.2. 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 generalization 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

6.3. 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, Aina Frau Pascual and Jaime Eduardo Arias Almeida
- Partners: CEA - NeuroSpin
- Contact: Florence Forbes
- URL: http://pyhrf.org

6.4. xLLiM

High dimensional locally linear mapping

KEYWORDS: Clustering - Regression

FUNCTIONAL DESCRIPTION

This is an R package available on the CRAN.

XLLiM provides a tool for non linear mapping (non linear regression) using a mixture of regression model and an inverse regression strategy. The methods include the GLLiM model (Deleforge et al (2015)) based on Gaussian mixtures and a robust version of GLLiM, named SLLiM (see [71]) based on a mixture of Generalized Student distributions.

- Participants: Emeline Perthame, Florence Forbes and Antoine Deleforge
- Contact: Florence Forbes
- URL: https://cran.r-project.org/web/packages/xLLiM/index.html

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 2016. Notable changes concern the migration of code on GitHub, the set up of continuous integration and the automated release of buildings for Windows, Linux and MacOS. libpointing can be easily installed using apt-get command on Linux and and Homebrew and Macport package installers on MacOS. New features like the estimation of the input frequency have been added and different demos have been developed. Code has been re-factored and various bugs fixed.

Web site: http://libpointing.org/

Software characterization: [A-3] [SO-3] [SM-2] [EM-2↑] [SDL-5]

6.3. Liblag

Participants: Géry Casiez [correspondent], Nicolas Roussel, Sébastien Poulmane.

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, Ubuntu and Windows) 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.

Sébastien Poulmane was recruited in May as an engineer on the TurboTouch project. He has been contributing to refactor the code, integrate new input devices and new prediction techniques and also develop associated demos and experiments.

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

6.4. Mouse-based lagmeter

Participants: Géry Casiez [correspondent], Stéphane Huot, Nicolas Roussel.

As part of the work reported in [46], 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) was made available in 2016 on a public git repository. The online interactive demo has been improved to collect anonymous latency measurement data from users and integrate libpointing in order to get information about the input and output devices connected. A native Android version has also been developed.

Web site: http://mjolnir.lille.inria.fr/turbotouch/lagmeter/

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

6.5. TAN

Participants: Fanny Chevalier [correspondent], Nicolas Roussel, Stéphane Huot.

TAN stands for *Transitions animées*, i.e. *Animated transitions*. This web site illustrates some of our past research on this topic. It combines videos and live demonstrations of Histomages, an image editing tool that associates pixel and color space; Diffamation, an animation tool to follow and understand the modifications made to a document over time; and Gliimpse, a markup language editor (e.g. HTML, LaTeX, Wiki) to instantly switch from source code to the document it produces and vice versa. The source code for the three demonstrators (about 87,000 lines of Java and JavaScript) is not distributed for the moment.

Web site: http://tan.lille.inria.fr/

Software characterization: [A-4] [SO-2] [SM-3] [EM-2] [SDL-4]

6.6. InspectorWidget

Participants: Christian Frisson [correspondent], Sylvain Malacria.

InspectorWidget [26] is an HTML5/nodejs/C++ software suite that can be used by an experimenter to track and analyze users' behaviors in closed interactive software. The suite has a *recording* module that records users' display and captures low-level events while she carries her task, and an *annotation* module that combines OCR and low-level inputs analysis so the experimenter post-annotate users' activity afterwards. InspectorWidget is cross-platform, open-source and publicly available under the GPLv3 license. New features, notably recording and exploiting accessibility API, are currently under development in order to be tested and added to the software suite.

Web site: https://github.com/InspectorWidget/InspectorWidget/

Software characterization: [A-2↑] [SO-3] [SM-3↑] [EM-3] [SDL-4]

MNEMOSYNE Project-Team

6. New Software and Platforms

6.1. Positioning

Our previous works in the domain of well-defined distributed asynchronous adaptive computations [55], [52], [57] have already made us define a library (DANA [51]), 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 [41], 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. ENAS

Event Neural Assembly Simulation
KEYWORDS: Neurosciences - Health - Physiology
SCIENTIFIC DESCRIPTION

As one gains more intuitions and results on the importance of concerted activity in spike trains, models are developed to extract potential canonical principles underlying spike coding. These methods shed a new light on spike train dynamics. However, they require time and expertise to be implemented efficiently, making them hard to use in a daily basis by neuroscientists or modelers. To bridge this gap, we developed the license free multiplatform software ENAS (https://enas.inria.fr) integrating tools for individual and collective spike analysis and simulation, with some specificities devoted to the retina. The core of ENAS is the statistical analysis of population codes. One of its main strength is to provide statistical analysis of spike trains using Maximum Entropy-Gibbs distributions taking into account both spatial and temporal correlations as constraints, allowing to introduce causality and memory in statistics. ENAS also generates simulated spike trains. On one hand, one can draw a population raster from an user-specified Gibbs distribution. On the other hand, we have integrated in ENAS our retina simulator VIRTUAL RETINA, extended here to include lateral connections in the IPL. We hope that ENAS will become a useful tool for neuroscientists to analyse spike trains and we hope to improve it thanks to user feedback. Our goal is to progressively enrich it with the latest research results, in order to facilitate transfer of new methods to the community.

FUNCTIONAL DESCRIPTION

As one gains more intuitions and results on the importance of concerted activity in spike trains, models are developed to extract potential canonical principles underlying spike coding. These methods shed a new light on spike train dynamics. However, they require time and expertise to be implemented efficiently, making them hard to use in a daily basis by neuroscientists or modelers. To bridge this gap, we developed the license free multiplatform software ENAS integrating tools for spike trains analysis and simulation. These tools are accessible through a friendly Graphical User Interface that avoids any scripting or writing code from the user. Most of them have been implemented to run in parallel to reduce the time and memory consumption. ENAS offers basic visualizations and classical analysis for statistics of spike trains analysis. It also proposes statistical analysis with Maximum Entropy-Gibbs distributions taking into account both spatial and temporal correlations as constraints, allowing to introduce causality and memory in statistics. ENAS also includes specific tools dedicated to the retina: Receptive Field computation and a virtual retina simulator. Finally, ENAS generates synthetic rasters, either from know statistics or from the VIRTUAL RETINA simulator. We expect ENAS to become a useful tool for neuroscientists to analyse spike trains and we hope to improve it thanks to users feedback. From our perspective, our goal is to progressively enrich ENAS with the latest research results, in order to facilitate transfer of new methods to the community.

- Participants: Bruno Cessac, Salim Kraria, Hassan Nasser, Thierry Viéville, Rodrigo Cofre Torres, Geoffrey Portelli, Pierre Kornprobst, Theodora Karvouniari and Daniela Pamplona
- Contact: Bruno Cessac
- URL: https://enas.inria.fr

6.4. Virtual Enaction

KEYWORDS: Neurosciences - Simulation - Health

FUNCTIONAL DESCRIPTION

VirtualEnaction: A Platform for Systemic Neuroscience Simulation. The computational models studied in our team 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 have deployed an existing open-source video game middleware (Minecraft) in order to be able to shape the survival situation to be studied and we have begun to revisit some models in order to be able to integrate them as an effective brainy-bot. This was made as a platform associated to a scenario that is the closest possible to a survival situation (foraging, predator-prey relationship, partner approach to reproduction). We could integrate in the platform 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 was corresponding to the major anatomical regions studied in the team.

Nevertheless, we have seen recently that a major entertainment company (Microsoft) bought Minecraft to make similar (but larger) adaptations to what was being targeted by our VirtualEnaction project. We are currently studying the resulting product (the Malmö project) in order to adapt our strategy.

- Participants: André Garenne, Frédéric Alexandre, Nicolas Rougier and Thierry Viéville
- Contact: Frédéric Alexandre
- URL: http://virtualenaction.gforge.inria.fr/

MODAL Project-Team

6. New Software and Platforms

6.1. BlockCluster

Block Clustering

KEYWORDS: Statistic analysis - Clustering package

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) (published in 2016) 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: Matthieu Marbac-Lourdelle
- 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

KEYWORDS: Bioinformatics - Data mining - Statistics - Genomics
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

High-Dimensional Penalized Regression
FUNCTIONAL DESCRIPTION

HDPenReg 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

Multi-Patient Analysis of Genomic markers
KEYWORDS: Segmentation - Genomics - Marker selection - Biostatistics
SCIENTIFIC DESCRIPTION

MPAgenomics 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

Meta-analysis for MicroArrays
KEYWORDS: Transcriptomics - Meta-analysis - Differential analysis - Microarrays - Biostatistics
FUNCTIONAL DESCRIPTION

MetaMA 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

KEYWORDS: Transcriptomics - Meta-analysis - Differential analysis - High throughput sequencing - Biostatistics
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

Clustering using Mixture Models
KEYWORDS: Clustering - Clustering package - Generative Models
FUNCTIONAL DESCRIPTION

MixAll 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 (http://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: Matthieu Marbac-Lourdelle
- URL: https://r-forge.r-project.org/R/?group_id=1939

6.14. Mixmod

Many-purpose software for data mining and statistical learning
KEYWORDS: Data mining - Classification - Mixed data - Data modeling - Big data
FUNCTIONAL DESCRIPTION

Mixmod is a free toolbox for data mining and statistical learning designed for large and high dimensional 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 - HEUDIASYC - Laboratoire Paul Painlevé - LIFL - LMB - Université Lille 1
- Contact: Gilles Celeux
- URL: http://www.mixmod.org

6.15. MixtComp

Mixture Computation
KEYWORDS: Clustering - Statistics - Missing data

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). A new advanced model concerning functional data is also available in 2016. 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://massiccc.lille.inria.fr/#/

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++

Statistical ToolKit
KEYWORDS: Statistics - Linear algebra - Framework
FUNCTIONAL DESCRIPTION

STK++ (Statistical ToolKit in C++) 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 published to an international journal dedicated to software: [24].

- 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

STK++ core library integration to R using Rcpp

KEYWORDS: C++ - Data mining - Clustering - Statistics - Regression

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 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

MOKAPLAN Project-Team

6. New Software and Platforms

6.1. 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 headlightsâŠ 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. Different solvers

- Participants: Simon Legrand, Jean-David Benamou, Quentin Merigot and Boris Thibert
- Contact: Jean-David Benamou
- URL: https://project.inria.fr/mokabajour/

6.2. Wasserstein Fisher Rao

Lenaic Chizat

https://github.com/lchizat/optimal-transport

This Julia toolbox provides several tools for solving optimal transport, the unbalanced extensions and related problems.

6.3. OT and Sparse Scaling

Bernhard Schmitzer

http://wwwmath.uni-muenster.de/num/wirth/people/Schmitzer/index.html?content=code

MONC Project-Team

6. New Software and Platforms

6.1. CADMOS

KEYWORDS: Health - Cancer - Partial differential equation - Cartesian grid

- Participants: Olivier Saut, Julien Jouganous, Annabelle Collin and Olivier Gallinato
- Partners: CNRS - INP Bordeaux - Université de Bordeaux
- Contact: Olivier Saut
- URL: https://team.inria.fr/monc/software/

6.2. Carcinom

Computer-Assisted Research about Cancer growth and INsights on Oncological Mechanisms
KEYWORDS: Cancer - Data modeling - Regression

- Participants: Vivien Pianet and Simon Evain
- Contact: Sébastien Benzekry
- URL: https://team.inria.fr/monc/software/

6.3. MetaPoumon

KEYWORDS: Health - Evolution - Cancer - Medical imaging
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.

- Participants: Olivier Saut, Thierry Colin, Marie Martin and Julien Jouganous
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Olivier Saut
- URL: https://team.inria.fr/monc/software/

6.4. Nenuphar

KEYWORDS: Modeling - Oncologie - Cancer - Partial differential equation - Medical - Medical imaging
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.

- Partners: CNRS - INP Bordeaux - Université Bordeaux 1
- Contact: Marie Martin
- URL: https://team.inria.fr/monc/software/

6.5. PapriK

- Contact: Cynthia Perier
- URL: https://team.inria.fr/monc/software/

6.6. SESAR

Monitor of the effect of RT on Retroperitoneal Sarcoma
KEYWORDS: Segmentation - Health - DICOM - Cancer - Medical imaging

- Partner: Institut Bergonié
- Contact: Cynthia Perier
- URL: https://team.inria.fr/monc/software/

6.7. SegmentIt

KEYWORDS: Health - Signal - Registration of 2D and 3D multimodal images - 3D - Image analysis - Image - Processing - Medical imaging
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).

- 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
- URL: https://team.inria.fr/monc/software/

MORPHEME Project-Team

4. New Software and Platforms

4.1. SPADE: Small PArticle DEtection

FUNCTIONAL DESCRIPTION SPADE is an algorithm primarily designed to detect objects whose size is smaller than a few pixels (particles) on fluorescence microscopy images. It is a simplified version of a marked point process based on a shape dictionnary.

- Participants: N. Cedilnik, E. Debreuve, and X. Descombes
- Contact: Xavier Descombes

MORPHEO Project-Team

6. New Software and Platforms

6.1. Kinovis: 4D repository

FUNCTIONAL DESCRIPTION

This website is now part of the Kinovis platform webiste. It 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: Edmond Boyer
- URL: http://kinovis.inrialpes.fr/4d-repository/

6.2. Lucy Viewer

KEYWORDS: Data visualization - 4D - Multi-Cameras
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 from the original real images.

- Participants: Mickaël Heudre, Jean-Sébastien Franco and Edmond Boyer
- Contact: Edmond Boyer
- URL: http://kinovis.inrialpes.fr/lucyviewer/

6.3. 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 directly compute resulting solids from an arbitrary number of inputs and for an arbitrary boolean combination function, with state of the art execution times.

- Participants: Matthijs Douze, Jean-Sébastien Franco and Bruno Raffin
- Partner: INP Grenoble
- Contact: Matthijs Douze
- URL: http://kinovis.inrialpes.fr/quickcsg/

6.4. 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 estimate the template deformations over the sequence that fit the observed 3D models.

- Contact: Edmond Boyer

6.5. 3DtLaplace

KEYWORDS: Laplace operator - Mesh sequence
FUNCTIONAL DESCRIPTION This software computes a discrete 3D+t Laplace operator for temporally mesh sequences.

- Participants: Victoria Fernández-Abrevaya, Franck Hétroy-Wheeler and Stefanie Wuhrer
- Partner: INP Grenoble
- Contact: Victoria Fernández-Abrevaya
- URL: http://3dtlaplace.gforge.inria.fr/

6.6. CVTGenerator

KEYWORDS: Mesh - Centroidal Voronoi tessellation - Implicit surface
FUNCTIONAL DESCRIPTION CVTGenerator is a program that builds Centroidal Voronoi Tessellations of any 3D meshes and implicit surfaces.

- Participants: Edmond Boyer, Franck Hétroy-Wheeler and Li Wang
- Partner: INP Grenoble
- Contact: Li Wang
- URL: http://cvt.gforge.inria.fr/

6.7. Platforms

6.7.1. 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. Mickaël Heudre and Julien Pansiot were managing the technical resources of both platforms.

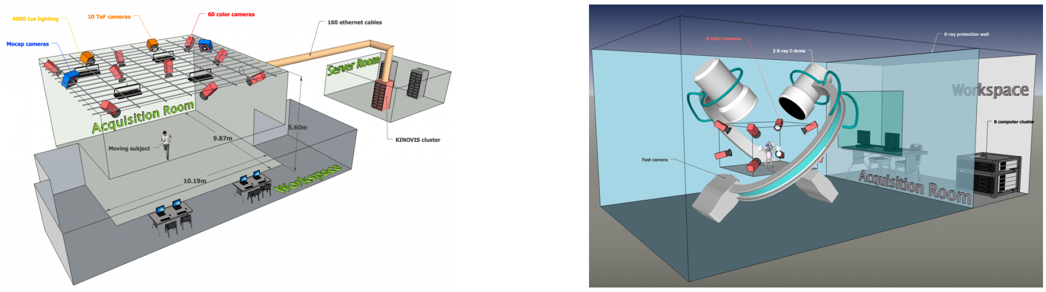


Figure 1. Kinovis platforms: on the left the Inria platform; on the right Grenoble Hospital platform.

MULTISPEECH Project-Team

6. New Software and Platforms

6.1. ASTALI

Automatic Speech-Text Alignment Software
KEYWORD: 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 possible 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. ASTALI is available through a web application, which makes the service easy to use, without requiring any software downloading. This year, the integration of the web application on the ORTOLANG platform has been finalized.

- Participants: Dominique Fohr, Odile Mella, Antoine Chemardin, Valérian Girard and Denis Jouvet
- Contact: Dominique Fohr
- URLs: https://www.ortolang.fr/market/tools/astali; http://astali.loria.fr/; and http://ortolang108.inist.fr/astali/

6.2. dnnsep

Multichannel audio source separation with deep neural networks
KEYWORDS: Audio - Source Separation - Deep learning
SCIENTIFIC DESCRIPTION

dnnsep is the only source separation software relying on multichannel Wiener filtering based on deep learning. Deep neural networks are used to initialize and reestimate the power spectrum of the sources at every iteration of an expectation-maximization (EM) algorithm. This results in state-of-the-art separation quality for both speech and music.

FUNCTIONAL DESCRIPTION

dnnsep is a new software that combines deep neural networks and multichannel signal processing for speech enhancement and separation of musical recordings.

- Participants: Aditya Nugraha, Antoine Liutkus and Emmanuel Vincent
- Contact: Emmanuel Vincent

6.3. 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. JSnoori can be used directly or via scripts written in Jython. This year, several approaches for computing the fundamental frequency have been added; and, JSnoori is now available through the ORTOLANG platform.

- Participants: Yves Laprie, Slim Ouni, Aghilas Sini and Ilef Ben Farhat
- Contact: Yves Laprie

6.4. KATS

Kaldi-based Automatic Transcription System
KEYWORD: Speech recognition
FUNCTIONAL DESCRIPTION

KATS 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. In this new software, the recognition engine is based on the Kaldi toolkit, and uses Deep Neural Network - DNN - based acoustic models. An extra processing pass is run in order to rescore the n-best hypotheses with a higher order language model.

- Participants: Odile Mella, Dominique Fohr and Denis Jouvet
- Contact: Dominique Fohr
- URL: Available online on the Allgo platform: https://allgo.inria.fr/app/loriasts_kaldi

6.5. PLAVIS

Sofware for audio-visual and multimodal data acquisition and processing
FUNCTIONAL DESCRIPTION

Within the ADT PLAVIS (cf. 9.2.12), we have developed a software for 3D audiovisual data acquisition and synthesis. The system incorporates an animation module of the talking head to reconstruct the animated face along with audio. The acquisition software handles one or several acquisition systems: motion-capture (Kinect-like), Vicon or EMA systems. The various acquisition channels are synchronized. The animation technique can exploit multimodal data to define blendshapes that controls the face; the advantage of using blendshapes is to be able to transfer the animation from one 3D human model to another. A semi-automatic acoustic boundary correction process is integrated in the corpus building process. The text-to-speech processing is driven by the Soja software.

- Participants: Vincent Colotte, Slim Ouni, Sara Dahmani
- Contact: Vincent Colotte

6.6. SOJA

Speech Synthesis platform in JAva
FUNCTIONAL DESCRIPTION

SOJA is a software for Text-To-Speech synthesis (TTS) which relies on a non uniform unit selection algorithm. It performs all steps from text input to speech signal output. A set of associated tools is available for elaborating a corpus for a TTS system (transcription, alignment. . .). Currently, the corpus contains about 3 hours of speech recorded by a female speaker. Most of the modules are in Java, some are in C. The SOJA software runs under Windows and Linux. It can be launched with a graphical user interface or directly integrated in a Java code or by following the client-server paradigm. During 2016, the part of code in C was reduced to go to a full-Java software in the future. The natural language processing can now be restarted from any step. This functionality is useful for instance during corpus processing when using semi-automatic boundaries correction.

- Participants: Vincent Colotte and Alexandre Lafosse
- Contact: Vincent Colotte

6.7. 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 coil trajectories 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. It is possible to generate a movie for any articulatory-acoustic sequence. During 2016, we have made a new version of VisArtico where the 3D view is now based on OpenGL. This allows a better quality rendering. It is possible to make measurement between sensors to compute the distance. Finally, we added the possibility to display the fundamental frequency on the spectrogram.

- Participants: Slim Ouni, Loic Mangeonjean, Ilef Ben Farhat and Bertrand Muller
- Contact: Slim Ouni
- URL: http://visartico.loria.fr

6.8. 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 when no software is available. 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 synthesizing speech from X-ray or 2D-MRI films.

During 2016, we developed a new version of the articulatory model which incorporates a more realistic model of the epiglottis and lips.

- Contact: Yves Laprie

6.9. Platforms

6.9.1. Platform MultiMod : Multimodal Acquisition Data Platform

FUNCTIONAL DESCRIPTION

Within a LORIA exploratory project (cf. 9.2.13), we have set up an acquisition hardware platform to acquire multimodal data in speech communication context. The system is composed of the articulograph Carstens AG501 (which was acquired as part of the EQUIPEX ORTOLANG - cf. 9.2.1), 4 Vicon cameras (a motion capture system), an Intel RealSense which is a depth camera (acquired as part of the project COREXp - cf. 9.1.1), a video camera and a microphone. With such heterogeneous hardware the synchronization is essential; this is achieved through a trigger device. All the data processing is performed with the PLAVIS software. This year, the system has been used to acquire multimodal data for the MCC project (cf. 9.4.2.1) and a first exploratory expressive multimodal corpus [40].

- Participants: Slim Ouni, Vincent Colotte, Valerian Girard, Sara Dahmani
- Contact: Slim Ouni

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 Stephane 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://team.inria.fr/muse/

5.3. Online HoA

Online implementation of home and access throughput bottleneck detection algorithm 'HoA'

FUNCTIONAL DESCRIPTION

"Home or Access" (HoA) is a system that localizes performance problems in home and access networks. Originally, we implement HoA as custom firmware that collect traces from off-the-shelf home routers. HoA uses timing and buffering information from passively monitored traffic at home routers to detect both access link and wireless network bottlenecks. HoA runs offline on a server to locate last-mile downstream throughput bottlenecks based on the analysis of packet traces collected from home routers. Our attempts to run HoA online on commodity home routers, however, revealed the challenges with performing per-packet analysis on such resource-constrained devices. The online HoA resolves this issue. We design an access bottleneck detector based on lightweight pings of the access link, and a wireless bottleneck detector based on a model of wireless capacity using metrics that are easily available in commodity home routers such as the wireless physical rate and the count of packets/bytes transmitted.

- 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: https://team.inria.fr/muse/

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://team.inria.fr/muse/

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

5. New Software and Platforms

5.1. Antescofo

Anticipatory Score Following and Real-time Language
FUNCTIONAL DESCRIPTION. Antescofo is a modular polyphonic Score Following system as well as a Synchronous Programming language for musical composition. The first 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 (DSL) within Antescofo allows flexible writing of time and interaction in computer music.

- Participants: Arshia Cont, Jean-Louis Giavitto, Florent Jacquemard and José Echeveste
- Contact: Arshia Cont
- URL: http://forumnet.ircam.fr/product/antescofo/

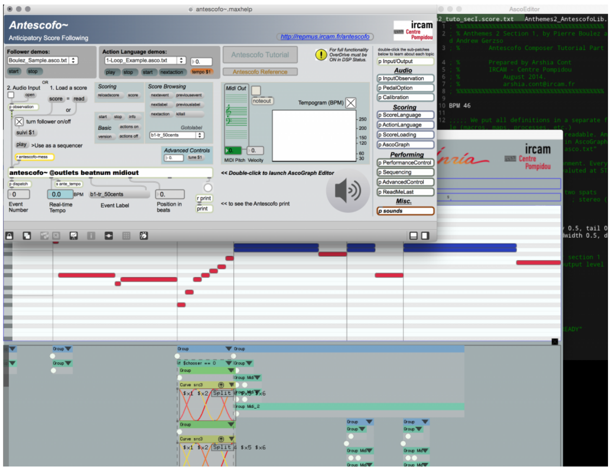


Figure 2. Antescofo and AscoGraph Screenshots

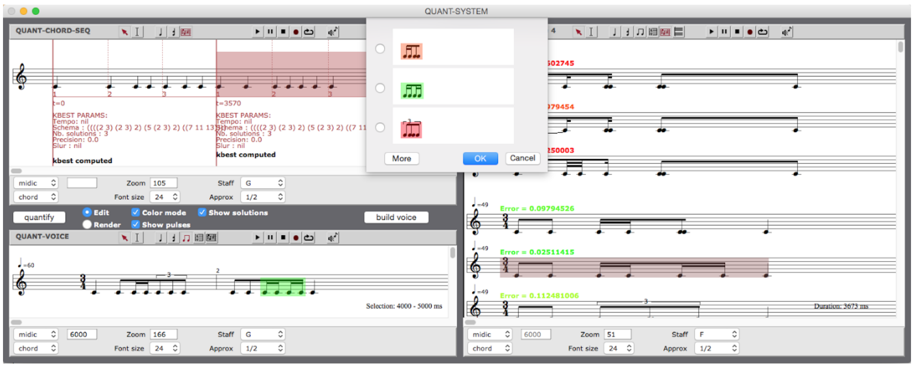
The design of the Antescofo DSL clearly benefits of a strong and continuous involvement in the production of world-class composer pieces and their continuous recreation throughout the world. These interactions motivate new developments, challenge the state of the art and in return, opens new creative dimensions for composers and musicians. The maturity of the system is assessed by the generalization of its use in a large proportion of Ircam new productions, and its use outside Ircam all around the world (Brasil, Chile, Cuba, Italy, China, US, etc.). Antescofo enjoys an active community of 150 active users: http://forumnet.ircam.fr/user-groups/antescofo/

5.2. OMRQ

Library for rhythm transcription integrated in the assisted composition environment OpenMusic.

FUNCTIONAL DESCRIPTION. Rhythm transcription is the conversion of sequence of timed events into the structured representations of conventional Western music notation. Available as a graphical component of OpenMusisc, the library OMRQ privileges user interactions in order to search for an appropriate balance between different criteria, in particular the precision of the transcription and the readability of the musical scores produced.

This system follows a uniform approach, using hierarchical representations of timing notations in the form of rhythm trees, and efficient parsing algorithms for the lazy enumeration of solutions of transcription.



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

midic Zoom 105 Staff G
chord Font size 24 Approx 1/2

● Edit ☑ Color mode ☑ Show solutions
○ Render ☑ Show pulses

Selection: 4000 - 5000 ms

midic 6000 Zoom 166 Staff G
chord Font size 24 Approx 1/2

Error = 0.09794526
Error = 0.02511415
Error = 0.112481006
Duration: 3673 ms

midic 6000 Zoom 51 Staff F
chord Font size 24 Approx 1/2

Figure 3. Screenshot of the Open Music Rhythm Quantization library

Its implementation is carried out via a dedicated interface allowing interactive exploration of the solutions space, their visualization and local editing, with particular attention to the processing of grace notes and rests.

- Participants: Florent Jacquemard and Adrien Ycart
- Contact: Florent Jacquemard
- URL: http://repmus.ircam.fr/cao/rq, https://bil.inria.fr/fr/software/view/2904/tab

5.3. Antescofo Timed Test Platform

Timed testing plateform for Antescofo.

FUNCTIONAL DESCRIPTION. 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 [50], 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.

- Participants: Clément Poncelet, Florent Jacquemard, Pierre Donat-Bouillud
- Contact: Clément Poncelet

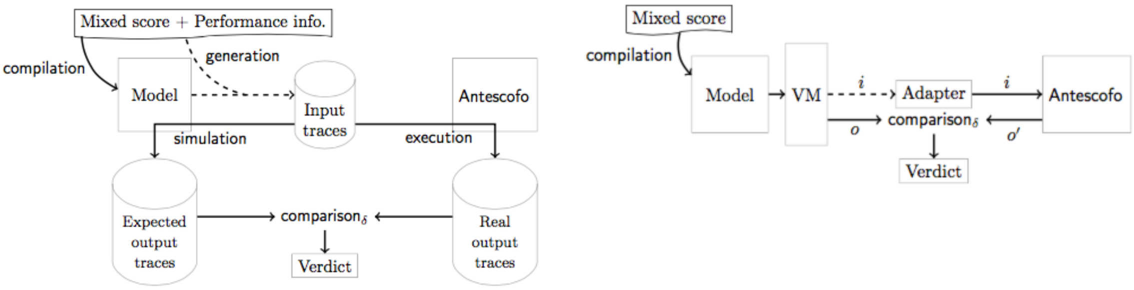


Figure 4. Offline and Online workflows for Antescofo Model Based Testing

These implementations have been conducted as a part of Clément Poncelet's PhD Thesis.

5.4. Ascograph

The Antescofo graphical score editor.

FUNCTIONAL DESCRIPTION. AscoGraph, 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 (Figure 5). 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.

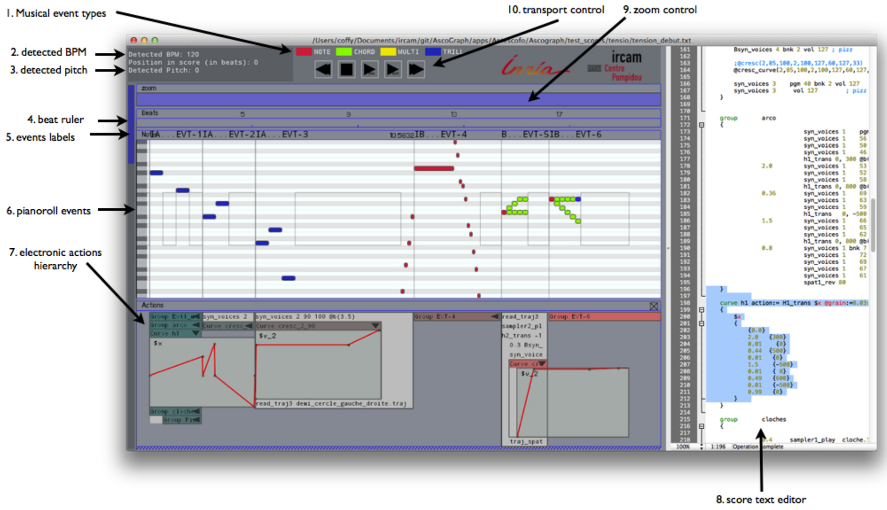


Figure 5. Screenshot of Ascograph, the Antescofo graphical score editor

MYCENAE Project-Team

6. New Software and Platforms

6.1. DynPeak

KEYWORDS: Biology - Health - Physiology
SCIENTIFIC DESCRIPTION

DynPeak is an algorithm for pulse detection and frequency analysis in hormonal time series. A new release of the DynPeak Scilab atom toolbox has been delivered in 2016 https://atoms.scilab.org/toolboxes/Dynpeak/2.1.0

- Participants: Frédérique Clement, Serge Steer, Thierry Martinez
- Partner: INRA
- Contact: Frédérique Clement
- URL: https://team.inria.fr/mycenae/en/software/

MYRIADS Project-Team

6. New Software and Platforms

6.1. ConPaaS

KEYWORDS: Cloud computing - PaaS
SCIENTIFIC DESCRIPTION ConPaaS [60] 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.
FUNCTIONAL DESCRIPTION

ConPaaS 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.

- Participants: Guillaume Pierre, Eliya Buyukkaya, Ancuta Iordache, Morteza Neishaboori, Dzenan Softic, Genc Tato and Teodor Crivat
- Contact: Guillaume Pierre
- URL: http://www.conpaas.eu/

6.2. GinFlow

KEYWORDS: Workflow - Distributed computing - Distributed - Distributed Applications - Framework
FUNCTIONAL DESCRIPTION GinFlow decentralizes the coordination of the execution of workflow-based applications. GinFlow relyies on an architecture where multiple service agents (SA) coordinate each others through a shared space containing the workflow description and current status. GinFlow allows the user to define several variants of a workflow and to switch from one to the other during run time.

- Participants: Matthieu Simonin, Cédric Tedeschi, Hector Fernandez, Javier Rojas Balderrama and Thierry Priol
- Partner: Université de Rennes 1
- Contact: Cédric Tedeschi
- URL: http://ginflow.inria.fr

6.3. Merkat

KEYWORDS: Resource management - Cloud - Elastic scaling - Market mechanisms - Service Level Objectives - HPC
FUNCTIONAL DESCRIPTION

Merkat is a platform that allows users of an organization to automatically manage and scale their applications while maximizing the infrastructure's utilization [12]. Merkat is generic and extensible, allowing users to automate the application deployment and management process. Users have the flexibility to control how many resources are allocated to their applications and to define their own resource demand adaptation policies. Merkat applies an unique approach to multiplex the infrastructure capacity between the applications, by implementing a proportional-share market and allowing applications to adapt autonomously to resource price and their given performance objectives. The price of the acquired resources acts as a control mechanism to ensure that resources are distributed to applications according to the user's value for them. Merkat was evaluated on Grid'5000 with several scientific applications.

- Participants: Stefania Costache, Christine Morin and Nikos Parlavantzas
- Contact: Nikos Parlavantzas
- URL: http://www.irisa.fr/myriads/software/Merkat/

6.4. Meryn

KEYWORDS: Resource management - PaaS - Cloud - Market mechanisms - Service Level Agreements
FUNCTIONAL DESCRIPTION

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. Meryn builds on the Snooze VM manager, and currently supports batch and MapReduce applications.

- Participants: Nikos Parlavantzas, Djawida Dib and Christine Morin
- Contact: Nikos Parlavantzas
- URL: http://www.irisa.fr/myriads/software/Meryn/

6.5. PaaSage Adapter

KEYWORDS: Cloud computing - Dynamic adaptation - Cloud applications management
FUNCTIONAL DESCRIPTION

The purpose of the Adapter is to transform the current configuration of a cloud application into a target configuration in an efficient and safe way. The Adapter is part of PaaSage, an open-source platform for modeling, deploying and executing applications on different clouds in an optimal manner. The Adapter has the following responsibilities: (1) validating reconfiguration plans, (2) applying the plans to the running system, and (3) maintaining an up-to-date representation of the current system state.

- Participants: Nikos Parlavantzas, Arnab Sinha, Manh Linh Pham, and Christine Morin
- Contact: Nikos Parlavantzas
- URL: https://team.inria.fr/myriads/software-and-platforms/paasage-adapter/

6.6. Resilin

KEYWORDS: Map Reduce - Parallel processing - Hadoop - Cloud - PaaS
FUNCTIONAL DESCRIPTION

Resilin is an open-source system for creating and managing MapReduce execution platforms over clouds. Resilin is compatible with the Amazon Elastic MapReduce (EMR) API, but it goes beyond Amazon's proprietary EMR solution in allowing users (e.g. companies, scientists) to leverage resources from one or more public and/or private clouds. This enables performing MapReduce computations over a large number of geographically-distributed and diverse resources. Resilin can be deployed across most of the open-source and commercial IaaS cloud management systems (e.g., OpenStack, OpenNebula, Amazon EC2). Once deployed, Resilin takes care of provisioning Hadoop clusters and submitting MapReduce jobs, allowing users to focus on writing their MapReduce applications rather than managing cloud resources. Resilin is implemented in the Python language and uses the Apache Libcloud library to interact with IaaS clouds. Resilin has been evaluated on multiple clusters of the Grid'5000 experimentation testbed. The results show that Resilin enables the use of geographically distributed resources with a limited impact on MapReduce job execution time.

- Participants: Ancuta Iodache, Christine Morin, Pierre Riteau, Nikos Parlavantzas and Matthieu Simonin
- Contact: Christine Morin
- URL: http://resilin.inria.fr

6.7. SAIDS

KEYWORDS: Cloud - Security
FUNCTIONAL DESCRIPTION SAIDS is a self-adaptable intrusion detection system for IaaS clouds. To maintain an effective level of intrusion detection, SAIDS monitors changes in the virtual infrastructure of a Cloud environment and reconfigures its components (security probes) accordingly. SAIDS can also reconfigure probes in the case of a change in the list of running services.

- Participants: Anna Giannakou, Jean-Léon Cusinato, Christine Morin, Jean-Louis Pazat, Louis Rilling and Fergal Martin-Tricot,
- Contact: Christine Morin
- URL: https://bil.inria.fr

6.8. SimGrid

KEYWORDS: Large-scale Emulators - Grid Computing - Distributed Applications
SCIENTIFIC DESCRIPTION SimGrid is a toolkit that provides core functionalities 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.

- Participants: Martin Quinson,
- Partners: Frédéric Suter, Arnaud Legrand, Adrien Lèbre, Luka Stanisic, Augustin Degomme.
- Contact: Martin Quinson
- URL: http://simgrid.gforge.inria.fr/

6.9. Snooze

KEYWORDS: Energy management - Fault-tolerance - Self-organization - Self-healing - Cloud computing - Consolidation - Virtualization

SCIENTIFIC DESCRIPTION

Snooze is a scalable, resilient and energy-aware virtual machine management framework for clouds. It is the result of Eugen Feller's PhD thesis which has been funded by the ANR EcoGrappe project (2008 - 2012).

The objectives of the Snooze ADT are threefold: (i) to distribute Snooze system as an open source software and to provide support to the user community (ii) to implement additional features to make it more user-friendly (iii) to integrate it with other open source software stacks and in public testbeds to favour its dissemination.

Snooze is a highly modular system for IaaS clouds. For the scientific community, it constitutes a unique framework for the experimentation of resource management policies in a real system. More generally, it allows any organization to operate a large-scale cluster as a resilient and energy-aware computing infrastructure enabling on demand provisioning of virtual clusters.

FUNCTIONAL DESCRIPTION

Snooze is a self-organizing and energy aware Cloud management framework.

Snooze 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 [59]), 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.

- Participants: Eugen Feller, Christine Morin, Jiajun Cao, Gene Cooperman, Yvon Jégou, David Margery and Matthieu Simonin
- Contact: Christine Morin
- URL: http://snooze.inria.fr/

6.10. VEP

KEYWORDS: Cloud - Security - Computing - IaaS - Standards - OVF - CIMI - SLA

SCIENTIFIC DESCRIPTION

Virtual Execution Platform (VEP) is a Contrail service that sits just above IaaS layer at the service provider end of the Contrail cloud federation. The VEP service provides a uniform interface for managing the whole lifecycle of elastic applications on the cloud and hides the details of the IaaS layer to the user. VEP applications are described in OVF (Open Virtualization Format) standard format. Resource usage is controlled by CEE (Constrained Execution Environment) rules which can be derived from SLAs (Service Level Agreement). The VEP service integrates a monitoring system where the major events about the application, mainly resource usage, are made available to the user.

The VEP service provides a RESTful interface and can be exploited directly by users on top of the provider IaaS. OpenNebula and OpenStack IaaS frameworks were initially supported. During the VEP-S EIT ICT Labs activity in 2014, VEP was extended with a new OCCI IaaS driver which allows to control any IaaS framework providing a standard OCCI API. Support for the new OCCI SLA proposition from OGF has also been added and allows to represent the VEP CEEs in a standard format. Finally, during this activity, the Zabbix open source distributed monitoring system was integrated to VEP.

FUNCTIONAL DESCRIPTION VEP is a management tool for IaaS clouds with a REST interface and simple GUI for administrator. It is an extensible and reusable software for easy deployment of distributed applications. It provides advance reservation, pro-active fault tolerance. It is SLA aware and manages elasticity.

- Participants: Yvon Jégou, Roberto Gioacchino Cascella, Florian Dudouet, Filippo Gaudenzi, Christine Morin and Arnab Sinha
- Contact: Christine Morin
- URL: https://project.inria.fr/vep/

NACHOS Project-Team

5. New Software and Platforms

5.1. DIOGENeS

DIscOntinuous GalErkin Nanoscale Solvers
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin - Computational nanophotonics
FUNCTIONAL DESCRIPTION

DIOGENeS is a software suite dedicated to the numerical modeling of light interaction with nanometer scale structures with applications to nanophotonics and nanoplasmonics. DIOGENeS relies on a two layer architecture. The core of the suite is a library of generic software components (data structures and algorithms) for the implementation of high order DG (Dicontinuous Galerkin) and HDG (Hybridizable Dicontinuous Galerkin) schemes formulated on unstructured tetrahedral and hybrid structured/unstructured (cubic/tetrahedral) meshes. This library is used to develop dedicated simulation software for time-domain and frequency-domain problems relevant to nanophotonics and nanoplasmonics, considering various material models.

- Contact: Stéphane Lanteri
- URL: http://www-sop.inria.fr/nachos/index.php/Software/DIOGENeS

5.2. GERShWIN

discontinuous GalERkin Solver for microWave INteraction with biological tissues
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin - Computational bioelectromagnetics
FUNCTIONAL DESCRIPTION

GERShWIN is based on a high order DG method formulated on unstructured tetrahedral meshes for solving the 3D system of time-domain Maxwell equations coupled to a Debye dispersion model.

- Contact: Stéphane Lanteri
- URL: http://www-sop.inria.fr/nachos/index.php/Software/GERShWIN

5.3. HORSE

High Order solver for Radar cross Section Evaluation
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin
FUNCTIONAL DESCRIPTION

HORSE is based on a high order HDG (Hybridizable Discontinuous Galerkin) method formulated on unstructured tetrahedral and hybrid structured/unstructured (cubic/tetrahedral) meshes for the discretization of the 3D system of frequency-domain Maxwell equations, coupled to domain decomposition solvers.

- Contact: Stéphane Lanteri
- URL: http://www-sop.inria.fr/nachos/index.php/Software/HORSE

NANO-D Project-Team

5. New Software and Platforms

5.1. SAMSON

Software for Adaptive Modeling and Simulation Of Nanosystems

KEYWORDS: Bioinformatics - Simulation - Nanosystems - Structural Biology - Chemistry

SCIENTIFIC DESCRIPTION

Please refer to https://www.samson-connect.net

FUNCTIONAL DESCRIPTION

SAMSON is a software platform for real-time modelling and simulation of natural or artificial nanosystems. The objective is to make SAMSON a generic application for computer-aided design of nanosystems, similar to existing applications for macrosystem prototyping (CATIA, SolidWorks, etc.).

- Contact: Stéphane Redon
- URL: http://www.samson-connect.net/

NECS Project-Team

6. New Software and Platforms

6.1. GTL

Grenoble Traffic Lab
FUNCTIONAL DESCRIPTION

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 the ramp-metering, the micro-simulator is a commercial software (developed by TSS AIMSUN ©). More details at http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php.

- Participants: Carlos Canudas De Wit, Iker Bellicot, Pascal Bellemain, Dominik Pisarski, Alain Kibangou, Hassen Fourati, Fabio Morbidi, Federica Garin, Andres Alberto Ladino Lopez, Pietro Grandinetti, Enrico Lovisari, Rohit Singhal, Anton Andreev, Remi Piotaix, Vadim Bertrand, Maria Laura Delle Monache and Paolo Frasca
- Contact: Carlos Canudas De Wit
- URL: 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

6.3. Wifi Scan Interval for Android application

Participants: T. Michel [contact person], H. Fourati, P. Geneves, N. Layaida.

This app records the wifi scan sampling rate on your phone. This application is available online: https://play.google.com/store/apps/details?id=fr.inria.tyrex.wifiscaninterval To contribute to a database: http://thibaud-michel.com/mobile/wifi-scan-interval.txt More information: https://github.com/ThibaudM/WifiScanIntervalhttp://stackoverflow.com/questions/37193175

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 is planned to 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.

- Participants: Axel Hutt and Laure Buhry
- Partner: University of Auckland
- Contact: Axel Hutt
- URL: https://gforge.inria.fr/projects/anasim/

6.2. BrianModel

Library of Brian Neuron Models
KEYWORDS: Spiking neural networks - Neurosciences - Numerical simulations
FUNCTIONAL DESCRIPTION

BrianModel is a library of neuron models and ionic currents for the BRIAN simulator. The purpose of BrianModel is to speed up simulation set-up 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, Hodgkin-Huxley pyramidal neuron with CAN receptors, Hodgkin-Huxley fast-spiking inhibitory hippocampal. 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 files, which are conveniently parsed by a Python library which acts as an interface to the BRIAN simulator API's.

- Contact: Francesco Giovannini
- URL: https://github.com/JoErNanO/brianmodel

6.3. MATCWT

continuous wavelet transform
KEYWORDS: Matlab - Visualization - Signal processing
FUNCTIONAL DESCRIPTION

This MATLAB script builds continuous wavelet transform (CWT) allowing to choose scales/frequencies and how to compute cone of influence (COI). It uses built-in MATLAB functions to calculate the transform (cwt.m and cwtft.m). This function returns scalogram, percentage energy for each coefficient of CWT. It also plots CWT (if such option is specified), all the values on the plot are linear ones. Plot function displays COI as hatched regions, to do so an additional function is required. Hatchfill function was used for that. I modifies this function slightly in order to control color of hatch lines and added to the repo for convenience. Otherwise, instead of using hatched regions, COI can be indicated by using MATLAB patch function with alpha set to a value less than 1.

- Contact: Mariia Fedotenkova
- URL: https://github.com/mfedoten/wavelets

6.4. MATSPECTRO

Spectrogram reassignment
KEYWORDS: Matlab - Visualization - Signal processing
FUNCTIONAL DESCRIPTION

This matlab function computes reassigned version of the conventional and multitaper spectrograms. The algorithm is based on Auger and Flandrin method, some parts are adopted from Fulop and Fitz. The idea is to first compute conventional spectrogram, then find optimal (in a sense of energy) time and frequency positions and reassigns values in the spectrogram to this new positions. The difference between conventional and multitaper spectrograms is that multitaper method computes additional spectrogram with each taper. Taper is a generic term for a window function but in this method tapers refer to Slepian sequences. As a result, generally multitaper spectrogram reveals less variance than conventional one.

- Contact: Mariia Fedotenkova
- URL: https://github.com/mfedoten/reasspectro

6.5. NFSimulator

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.

- Contact: Axel Hutt
- URL: https://gforge.inria.fr/projects/nfsimulator/

6.6. 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 and Nathanaël Foy
- Partners: CEA-List - GIPSA-Lab - INSERM
- Contact: Anatole Lécuyer, Hybrid/Inria Rennes-Bretagne Atlantique
- URL: http://openvibe.inria.fr

6.7. Platforms

6.7.1. EEG experimental room

A room at Inria Nancy - Grand Est is now dedicated to electroencephalographic recordings. An umbrella agreement and several additional experiment descriptions have been approved by the Inria Operational Legal and Ethical Risk Assessment Committee (COERLE).

Figure 1. Electroencephalographic Experimental room at Inria Nancy-Grand Est

NON-A Project-Team

6. New Software and Platforms

6.1. Blimp

FUNCTIONAL DESCRIPTION

Scientific research and development on the control of autonomous airship 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 airship 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
- URL: https://bil.inria.fr/fr/software/view/2279/tab

6.2. ControlHub

The driving idea is to interconnect a group of actors (researchers, engineers, etc.) around a control problem and grant them remote access to existing experimental facilities, thus allowing them to verify their theoretical results online, and finally share them with the project members.

The platform architecture relies on three key principles:

- Problem centric: The control problem to be solved is the core project, whereas the software resources, tools and online experiments are web services available to support experimental verification of the solutions.
- Separation of concerns: setup and maintenance of experiment facilities, installation of software tools, problem formulation and theoretical analysis, etc.
- Resource sharing: software packages, experimental facilities, open problems.
- Contact: R. Dagher, A. Polyakov, J.-P. Richard
- URL: https://bil.inria.fr/fr/software/view/2830/tab

6.3. 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: G. Zheng
- URL: https://bil.inria.fr/fr/software/view/2278/tab

NUMED Project-Team

5. New Software and Platforms

5.1. 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

5.2. 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

5.3. 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 et 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).

- Participants: Paul Vigneaux and Ehouarn Maguet
- Partner: ENS Lyon
- Contact: Paul Vigneaux

5.4. VAXSIMSTAB

KEYWORDS: Bioinformatics - Health - Drug development
FUNCTIONAL DESCRIPTION

VAXSIMSTAB is a modeler stability prediction of vaccine software.

- Participants: Benjamin Ribba, Emmanuel Grenier and Vincent Calvez
- Contact: Emmanuel Grenier

ORPAILLEUR Project-Team

6. New Software and Platforms

6.1. Symbolic KDD Systems

6.1.1. LatViz

- Contact: Thi Nhu Nguyen Le
- URL: http://latviz.loria.fr/latviz/
- KEYWORDS: Formal Concept Analysis, Pattern Mining, Concept Lattice, Implications, Visualization

FUNCTIONAL DESCRIPTION.

LatViz is a new tool which allows the construction, the display and the exploration of concept lattices. LatViz proposes some remarkable improvements over existing tools and introduces various new functionalities focusing on interaction with experts, such as visualization of pattern structures (for dealing with complex non-binary data), AOC-posets (the core elements of the lattice), concept annotations, filtering based on various criteria and a visualization of implications [28], [27]. This way the user can effectively perform interactive exploratory knowledge discovery as often needed in knowledge engineering.

The Latviz platform can be associated with the Coron platform and extends its visualization capabilities (see http://coron.loria.fr). Recall that the Coron platform includes a complete collection of data mining algorithms for extracting itemsets and association rules.

6.1.2. OrphaMine – Data mining platform for orphan diseases

- Partners: INSERM – MoDYCo CNRS – Greyc Université de Caen Basse Normandie
- Contact: Chedy Raïssi
- URL: http://orphamine.inria.fr/
- 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 at building 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.

6.1.3. POQEMON Analytics: Platform for Quality Evaluation of Mobile Networks

- Partners: Altran, DataPublica, GenyMobile, HEC, Inria Nancy-Grand Est, IP-Label, Next Interactive Media, Orange, Université Paris-Est Créteil
- Contact: Chedy Raïssi
- URL: https://members.loria.fr/poqemon/
- KEYWORDS: Data mining, data visualization.

FUNCTIONAL DESCRIPTION.

POQEMON is a quality evaluation platform for mobile phone networks developed in the Orpailleur team in the frameowrok of an FUI project (see 8.2.2). The quality measures which are studied 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.

6.1.4. Siren - Interactive and visual redescription mining

- Contact: Esther Galbrun
- URL: http://siren.gforge.inria.fr/main/
- KEYWORDS: Redescription mining, Interactivity, Visualization.

FUNCTIONAL DESCRIPTION.

Siren is a tool for interactive mining and visualization of redescriptions. Redescription mining aims to find distinct common characterizations of the same objects and, vice versa, to identify sets of objects that admit multiple shared descriptions. The goal is to provide domain experts with a tool allowing them to tackle their research questions using redescription mining. Merely being able to find redescriptions is not enough. The expert must also be able to understand the redescriptions found, adjust them to better match his domain knowledge and test alternative hypotheses with them, for instance. Thus, Siren allows mining redescriptions in an anytime fashion through efficient, distributed mining, to examine the results in various linked visualizations, to interact with the results either directly or via the visualizations, and to guide the mining algorithm toward specific redescriptions.

6.2. Stochastic systems for knowledge discovery and simulation

6.2.1. The CarottAge and ARPEnTAge Systems

- Contact: Jean-François Mari
- URL:http://carottage.loria.fr
- 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 [84]. CarottAge is currently used by INRA researchers interested in mining the changes in territory and landscape related to the loss of biodiversity (projects ANR BiodivAgrim and ACI Ecoger) and/or water contamination. CarottAge was also used for mining hydromorphological data and gave interesting results for that purpose.

ARPEnTAge, for "*Analyse de Régularités dans les Paysages : Environnement, Territoires, Agronomie*" is built on top of the CarottAge system to fully take into account the spatial dimension of input sequences. It can be used for analyzing spatio-temporal databases [85] and for space-time clustering of a landscape based on temporal land uses. Displaying tools and the generation of time-dominant shape files have also been defined. With agronomists, we are now focusing on the simulation of unknown spatial time sequences in order to explore various crop management scenarios.

CarottAge and ARPEnTAge are freely available under GPL license. A special effort is currently aimed at designing interactive visualization tools to provide the expert a user-friendly interface.

PACAP Project-Team

6. New Software and Platforms

6.1. ATMI

KEYWORDS: Analytic model - Chip design - 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.
FUNCTIONAL DESCRIPTION

ATMI is a library for modelling steady-state and time-varying temperature in microprocessors. ATMI uses a simplified representation of microprocessor packaging.

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

6.2. Heptane

KEYWORDS: Static analysis - Real time - Performance - WCET - IPET - Worst Case Execution Time
SCIENTIFIC DESCRIPTION

WCET estimation

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.

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.

For more information, please contact Damien Hardy or Isabelle Puaut.
FUNCTIONAL DESCRIPTION

In a hard real-time system, it is essential to comply with timing constraints, and Worst Case Execution Time (WCET) in particular. Timing analysis is performed at two levels: analysis of the WCET for each task in isolation taking account of the hardware architecture, and schedulability analysis of all the tasks in the system. Heptane is a static WCET analyser designed to address the first issue.

- Participants: Isabelle Puaut, Damien Hardy, Loïc Besnard
- Partner: Université de Rennes 1
- Contact: Isabelle Puaut
- URL: https://team.inria.fr/pacap/software/heptane/

6.3. Tiptop

KEYWORDS: HPC - Performance - CPU - Cache - Cycles - Instructions - Branch predictor
SCIENTIFIC DESCRIPTION

Tiptop is written in C. It can take advantage of libncurses when available for pseudo-graphic display.

Performance, hardware counters, analysis tool.

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 July 2015.

Tiptop has been integrated in major Linux distributions, such as Fedora, Debian, Ubuntu.

Tiptop is a new simple and flexible user-level tool that collects hardware counter data on Linux platforms (version 2.6.31+). 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
FUNCTIONAL DESCRIPTION

Today's microprocessors have become extremely complex. To better understand the multitude of internal events, manufacturers have integrated many monitoring counters. Tiptop can be used to collect and display the values from these performance counters very easily. Tiptop may be of interest to anyone who wants to optimise the performance of their HPC applications.

- Participant: Erven Rohou
- Contact: Erven Rohou
- URL: http://tiptop.gforge.inria.fr

6.4. 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/pacap/software/atc/

6.5. 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/

6.6. 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

6.7. 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.2015.000.10800.

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/pacap/software/Padrone/

6.8. 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/pacap/software/stimul/

6.9. 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: https://team.inria.fr/pacap/software/tpcalc/

6.10. Parasuite

Participants: Sylvain Collange, Imane Lasri, 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/

6.11. Simty

Participant: Sylvain Collange.

Simty: A Synthesizable General-Purpose SIMT Processor.

Simty is a massively multi-threaded processor core that dynamically assembles SIMD instructions from scalar multi-thread code. It runs the RISC-V (RV32-I) instruction set. Unlike existing SIMD or SIMT processors like GPUs, Simty takes binaries compiled for general-purpose processors without any instruction set extension or compiler changes. Simty is described in synthesizable VHDL.

Visit: http://team.inria.fr/pacap/simty

PANAMA Project-Team

6. New Software and Platforms

6.1. Audio Activity Detector

KEYWORD: Audio activity estimation

- Authors: Frédéric Bimbot, Ewen Camberlein, Romain Lebarbenchon and Vincent Soupe
- Contact: Frédéric Bimbot

6.2. Audio Breath Rhythm Estimator

KEYWORD: Breath rhythm estimation

- Authors: Frédéric Bimbot, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.3. Audio GMM Classifier

- Authors: Frédéric Bimbot, Vincent Soupe, Jérémy Paret, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.4. CSCbox

Compressive Spectral Clustering Toolbox
KEYWORD: Clustering
SCIENTIFIC DESCRIPTION

The Compressive Spectral Clustering Toolbox is a Matlab toolbox implementing routines to reproduce experiments from the paper "Compressive Spectral Clustering", by N. Tremblay, G. Puy, P. Vandergheynst and R. Gribonval.
FUNCTIONAL DESCRIPTION

Matlab toolbox implementing routines to reproduce experiments from the paper "Compressive Spectral Clustering"

- Authors: Nicolas Tremblay, Gilles Puy, Pierre Vandergheynst and Rémi Gribonval
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Rémi Gribonval
- URL: http://www.irisa.fr/panama/software

6.5. 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

6.6. FAuST

KEYWORDS: Learning - Sparsity - Fast transform - Multilayer sparse factorisation
FUNCTIONAL DESCRIPTION

C++ toolbox, designed to decompose a given dense matrix into a product of sparse matrices in order to reduce its computational complexity (both for storage and manipulation).

- Authors: Luc Le Magoarou, Rémi Gribonval, Adrien Leman, Nicolas Bellot and Thomas Gautrais
- Contact: Rémi Gribonval
- URL: http://faust.gforge.inria.fr/

6.7. 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/

6.8. SPADE

Sparse Audio Declipper
KEYWORDS: Audio - Sparse regularization - Declipping
SCIENTIFIC DESCRIPTION

Matlab routines to reproduce audio declipping experiments from the paper: - 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. <hal-00922497v3> - 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. <hal-01159700v2>

- Participants: Srdan Kitic, Nancy Bertin and Rémi Gribonval
- Contact: Rémi Gribonval
- URL: http://xspaad.gforge.inria.fr/

6.9. SPOD Audio

KEYWORDS: Audio source classification - Speaker verification - Breath rhythm estimation - Audio activity estimation

- Authors: Frédéric Bimbot, Vincent Soupe, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot
- URL: http://www.kerlink.fr/en/

6.10. SPOD Model Generation

KEYWORDS: Machine learning - Audio source classification - Statistical modeling - Speaker verification

- Authors: Frédéric Bimbot, Vincent Soupe, Jérémy Paret, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.11. SRP-PHAT

KEYWORD: Source localization

- Authors: Frédéric Bimbot, Nancy Bertin, Ewen Camberlein, Romain Lebarbenchon, Emmanuel Vincent, Charles Blandin and Alexey Ozerov
- Contact: Frédéric Bimbot

6.12. SketchMLBox

KEYWORD: Clustering

SCIENTIFIC DESCRIPTION

The SketchMLbox is a Matlab toolbox for fitting mixture models to large collections of training vectors using sketching techniques. The collection is first compressed into a vector called sketch, then a mixture model (e.g. a Gaussian Mixture Model) is estimated from this sketch using greedy algorithms typical of sparse recovery. The size of the sketch does not depend on the number of elements in the collection, but rather on the complexity of the problem at hand [2,3]. Its computation can be massively parallelized and distributed over several units. It can also be maintained in an online setting at low cost. Mixtures of Diracs ("K-means") and Gaussian Mixture Models with diagonal covariance are currently available, the toolbox is structured so that new mixture models can be easily implemented.

FUNCTIONAL DESCRIPTION

Matlab toolbox for fitting mixture models to large collections of feature vectors using sketching techniques.

- Authors: Nicolas Keriven, Rémi Gribonval and Nicolas Tremblay
- Partner: Université de Rennes 1
- Contact: Rémi Gribonval
- URL: http://sketchml.gforge.inria.fr

6.13. VoiceHome Corpus

KEYWORDS: Audio - Source Separation

FUNCTIONAL DESCRIPTION

This corpus includes reverberated, noisy speech signals spoken by native French talkers in a lounge and recorded by an 8-microphone device at various angles and distances and in various noise conditions. Room impulse responses and noise-only signals recorded in various real rooms and homes and baseline speaker localization and enhancement software are also provided.

- Contact: Nancy Bertin
- URL: http://voice-home.gforge.inria.fr/voiceHome_corpus.html

6.14. graphsamplingbox

- Authors: Nicolas Tremblay, Gilles Puy, Pierre Vandergheynst and Rémi Gribonval
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Rémi Gribonval
- URL: http://www.irisa.fr/panama/software

PARIETAL Project-Team

5. New Software and Platforms

5.1. 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/

5.2. Nilearn

NeuroImaging with scikit learn
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 and Virgile Fritsch
- Contact: Bertrand Thirion
- URL: http://nilearn.github.io/

5.3. 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

5.4. 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, Arthur Mensch
- Partners: CEA - Logilab - Nuxeo - Saint Gobain - Telecom Paris - Tinyclues
- Contact: Olivier Grisel
- URL: http://scikit-learn.org

PARKAS Project-Team

5. New Software and Platforms

5.1. Cmmtest

FUNCTIONAL DESCRIPTION

Cmmtest is a tool for hunting concurrency 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:

compiles the program using the compiler and compiler optimisations that are being tested,

runs the compiled program in an instrumented execution environment that logs all memory accesses to global variables and synchronisations,

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.

- Participants: Pankaj Pawan, Francesco Zappa Nardelli, Robin Morisset, Anirudh Kumar, Pankaj Prateek Kewalramani and Pankaj More
- Contact: Francesco Zappa Nardelli
- URL: http://www.di.ens.fr/~zappa/projects/cmmtest/

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

- Participants: Albert Cohen, Tobias Grosser, Feng Li, Riyadh Baghdadi 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 Gerard, Brice Gelineau, Gwenael Delaval and Eric Rutten
- Contact: Marc Pouzet

5.4. Lem

lightweight executable mathematics
FUNCTIONAL DESCRIPTION

Lem is a lightweight tool for writing, managing, and publishing large scale semantic definitions. It is also intended as an intermediate language for generating definitions from domain-specific tools, and for porting definitions between interactive theorem proving systems (such as Coq, HOL4, and Isabelle). As such it is a complementary tool to Ott. Lem resembles a pure subset of Objective Caml, supporting typical functional programming constructs, including top-level parametric polymorphism, datatypes, records, higher-order functions, and pattern matching. It also supports common logical mechanisms including list and set comprehensions, universal and existential quantifiers, and inductively defined relations. From this, Lem generates OCaml, HOL4, Coq, and Isabelle code.

- Participants: Scott Owens, Peter Sewell and Francesco Zappa Nardelli
- Contact: Francesco Zappa Nardelli
- URL: 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. Ott

FUNCTIONAL DESCRIPTION

Ott is a tool for writing definitions of programming languages and calculi. It takes as input a definition of a language syntax and semantics, in a concise and readable ASCII notation that is close to what one would write in informal mathematics. It generates output:

a LaTeX source file that defines commands to build a typeset version of the definition,

a Coq version of the definition,

an Isabelle version of the definition, and

a HOL version of the definition.

Additionally, it can be run as a filter, taking a LaTeX/Coq/Isabelle/HOL source file with embedded (symbolic) terms of the defined language, parsing them and replacing them by typeset terms.

The main goal of the Ott tool is to support work on large programming language definitions, where the scale makes it hard to keep a definition internally consistent, and to keep a tight correspondence between a definition and implementations. We also wish to ease rapid prototyping work with smaller calculi, and to make it easier to exchange definitions and definition fragments between groups. The theorem-prover backends should enable a smooth transition between use of informal and formal mathematics.

- Participants: Francesco Zappa Nardelli, Peter Sewell and Scott Owens
- Contact: Francesco Zappa Nardelli
- URL: http://www.cl.cam.ac.uk/~pes20/ott/

5.8. 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, Riyadh Baghdadi and Albert Cohen
- Contact: Sven Verdoolaege
- URL: http://freshmeat.net/projects/ppcg

5.9. 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, Louis Mandel and Cédric Pasteur
- Contact: Guillaume Baudart
- URL: http://rml.lri.fr

5.10. SundialsML

Sundials/ML
KEYWORDS: Simulation - Mathematics - Numerical simulations
SCIENTIFIC DESCRIPTION

Sundials/ML is an OCaml interface to the Sundials suite of numerical solvers (CVODE, CVODES, IDA, IDAS, KINSOL, ARKODE). It supports all features except for the Hypre and PETSC nvectors (which require additional libraries). 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.

FUNCTIONAL DESCRIPTION

Sundials/ML is an OCaml interface to the Sundials suite of numerical solvers (CVODE, CVODES, IDA, IDAS, KINSOL, ARKODE).

NEW PROGRESS

This year we updated our interface to work with versions 2.6.0 and 2.7.0 of the Sundials library. This included significant work to support the new ARKODE solver, sparse matrices and the KLU and SuperLU/MT linear solvers, OpenMP and Pthreads nvectors, and various new functions and linear solvers in existing solvers. The source files were completely reorganized. The OCaml types for nvectors were adapted to support multiple nvectors. Memory leaks were eliminated and the performance problems investigated. This work was presented at the ACM Workshop on ML [28].

- Participants: Marc Pouzet and Timothy Bourke
- Partner: UPMC, AIST (Jun Inoue)
- Contact: Timothy Bourke
- URL: http://inria-parkas.github.io/sundialsml/

5.11. Zélus

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.

- Participants: Marc Pouzet and Timothy Bourke
- Contact: Marc Pouzet

5.12. 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, Tobias Grosser and Albert Cohen
- Contact: Sven Verdoolaege
- URL: http://freshmeat.net/projects/isl

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.

- Participants: Dale Miller, Olivier Savary-Bélanger, Mary Southern, Yuting Wang, Kaustuv Chaudhuri, Matteo Cimini and Gopalan Nadathur
- Partner: Department of Computer Science and Engineering, University of Minnesota
- Contact: Kaustuv Chaudhuri
- URL: http://abella-prover.org/

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 that possibly contain 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.

- Participants: Quentin Heath, Roberto Blanco, and Dale Miller
- 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, Giselle Machado Nogueira Reis and Marco Volpe
- Contact: Tomer Libal
- URL: https://github.com/proofcert/checkers

6.4. Psyche

Proof-Search factorY for Collaborative HEuristics

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 trusted kernel interacts with plugins. The kernel offers an API of proof-search primitives, and plugins are programmed on top of the API to implement search strategies. This architecture is set up for pure logical reasoning as well as for theory-specific reasoning, for various theories.

The major effort in 2016 was the release of version 2.1 that allows the combination of theories, integrating and subsuming both the Nelson-Oppen methodology [79] and the *model constructing satisfiability* (MCSAT) methodology recently proposed by De Moura and Jovanovic [89], [65].

- Participants: Assia Mahboubi, Jean-Marc Notin and Stéphane Graham-Lengrand
- Contact: Stéphane Graham-Lengrand
- URL: http://www.lix.polytechnique.fr/~lengrand/Psyche/

PERCEPTION Project-Team

5. New Software and Platforms

5.1. ECMPR

Expectation Conditional Maximization for the Joint Registration of Multiple Point Sets
FUNCTIONAL DESCRIPTION

Rigid registration of two or several point sets based on probabilistic matching between point pairs and a Gaussian mixture model

- Participants: Florence Forbes, Radu Horaud and Manuel Yguel
- Contact: Patrice Horaud
- URL: https://team.inria.fr/perception/research/jrmpc/

5.2. Mixcam

Reconstruction using a mixed camera system
KEYWORDS: Computer vision - 3D reconstruction
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 2011-2014 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: Patrice Horaud, Pierre Arquier, Quentin Pelorson, Michel Amat, Miles Hansard, Georgios Evangelidis, Soraya Arias, Radu Horaud, Richard Broadbridge and Clement Menier
- Contact: Patrice Horaud
- URL: https://team.inria.fr/perception/mixcam-project/

5.3. NaoLab

Distributed middleware architecture for interacting with NAO
FUNCTIONAL DESCRIPTION

This software provides a set of librairies and tools to simply the control of NAO robot from a remote machine. The main challenge is to make easy prototuping applications for NAO ising C++ and Matlab programming environments. Thus NaoLab provides a prototyping-friendly interface to retrieve sensor date (video and sound streams, odometric data...) and to control the robot actuators (head, arms, legs...) from a remote machine.This interface is available on Naoqi SDK, developed by Aldebarab company, Naoqi SDK is needed as it provides the tools to acess the embedded NAO services (low-level motor command, sensor data access...)

- Authors: Quentin Pelorson, Fabien Badeig and Patrice Horaud
- Contact: Patrice Horaud
- URL: https://team.inria.fr/perception/research/naolab/

5.4. Stereo matching and recognition library

KEYWORD: Computer vision

FUNCTIONAL DESCRIPTION

Library providing stereo matching components to rectify stereo images, to retrieve faces from left and right images, to track faces and method to recognise simple gestures

- Participants: Jordi Sanchez-Riera, Soraya Arias, Jan Cech and Radu Horaud
- Contact: Soraya Arias
- URL: https://code.humavips.eu/projects/stereomatch

5.5. Platforms

5.5.1. Audio-Visual Head Popeye+

In 2016 we upgraded our audio-visual platform, from Popeye to Popeye+. Popeye+ has two high-definitions cameras with a wide field of view. We also upgraded the software libraries that perform synchronized acquisition of audio signals and color images. Popeye+ has been used for several datasets.
Website:
https://team.inria.fr/perception/projects/popeye/
https://team.inria.fr/perception/projects/popeye-plus/
https://team.inria.fr/perception/avtrack1/.

5.5.2. NAO Robots

The PERCEPTION team selected the companion robot NAO for experimenting and demonstrating various audio-visual skills as well as for developing the concept of a social robot that is able to recognize human presence, to understand human gestures and voice, and to communicate by synthesizing appropriate behavior. The main challenge of our team is to enable human-robot interaction in the real world.

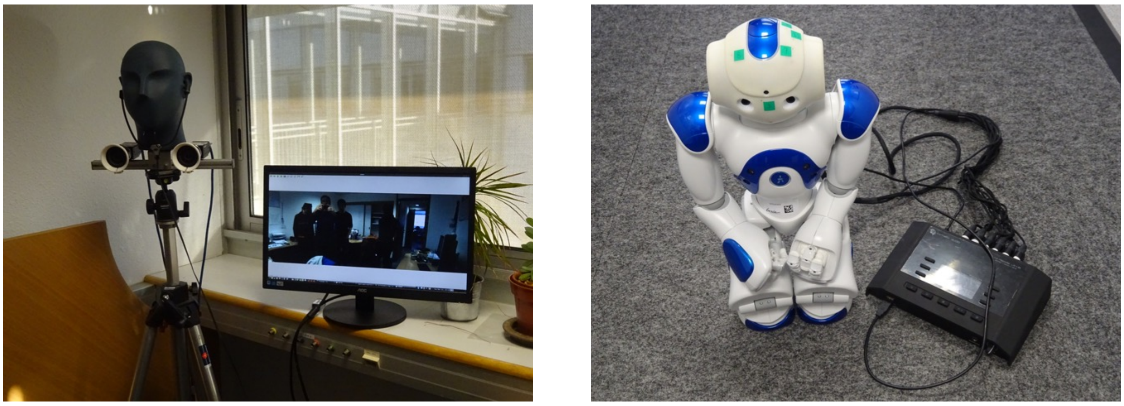


Figure 2. The Popeye+ audio-visual platform (left) delivers high-quality, high-resolution and wide-angle images at 30FPS. The NAO prototype used by PERCEPTION in the EARS STREP project has a twelve-channel spherical microphone array synchronized with a stereo camera pair.

The humanoid robot NAO is manufactured by Aldebaran Robotics, now SoftBank. Standing, the robot is roughly 60 cm tall, and 35cm when it is sitting. Approximately 30 cm large, NAO includes two CPUs. The first one, placed in the torso, together with the batteries, controls the motors and hence provides kinematic motions with 26 degrees of freedom. The other CPU is placed in the head and is in charge of managing the proprioceptive sensing, the communications, and the audio-visual sensors (two cameras and four microphones, in our case). NAO's on-board computing resources can be accessed either via wired or wireless communication protocols.

NAO's commercially available head is equipped with two cameras that are arranged along a vertical axis: these cameras are neither synchronized nor a significant common field of view. Hence, they cannot be used in combination with stereo vision. Within the EU project HUMAVIPS, Aldebaran Robotics developed a binocular camera system that is arranged horizontally. It is therefore possible to implement stereo vision algorithms on NAO. In particular, one can take advantage of both the robot's cameras and microphones. The cameras deliver VGA sequences of image pairs at 12 FPS, while the sound card delivers the audio signals arriving from all four microphones and sampled at 48 kHz. Subsequently, Aldebaran developed a second binocular camera system to go into the head of NAO v5.

In order to manage the information flow gathered by all these sensors, we implemented our software on top of the Robotics Services Bus (RSB). RSB is a platform-independent event-driven middleware specifically designed for the needs of distributed robotic applications. Several RSB tools are available, including real-time software execution, as well as tools to record the event/data flow and to replay it later, so that application development can be done off-line. RSB events are automatically equipped with several time stamps for introspection and synchronization purposes. RSB was chosen because it allows our software to be run on a remote PC platform, neither with performance nor deployment restrictions imposed by the robot's CPUs. Moreover, the software packages can be easily reused for other robots.

More recently (2015-2016) the PERCEPTION team started the development of NAOLab, a middleware for hosting robotic applications in C, C++, Python and Matlab, using the computing power available with NAO, augmented with a networked PC.

Websites:
https://team.inria.fr/perception/nao/
https://team.inria.fr/perception/research/naolab/

PERVASIVE INTERACTION Team

5. New Software and Platforms

5.1. DomiCube

- Participant: Rémi Pincent
- Contact: Rémi Pincent

5.2. EmoPRAMAD

KEYWORDS: Health - Home care
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.

- Contact: Dominique Vaufreydaz

5.3. Online Movie Director

- Participants: Patrick Reignier, Dominique Vaufreydaz and James Crowley
- Contact: Dominique Vaufreydaz

5.4. 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 curently 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

5.5. SmartServoFramework

- Participants: Dominique Vaufreydaz and Emeric Grange
- Contact: James Crowley

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 runs under 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.

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¬ª 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. Unix Interface for InfraRed Sensor

- Author: Pierre Baret
- Contact: James Crowley

5.8. Virtual Reality rehabilitation platform for Complex Regional Pain Syndrome

Participants: Charles-Henry Dufetel, Jing Tao Chen, Sabine Coquillart Design and development of a Virtual Reality rehabilitation platform for CRPS (Complex Regional Pain Syndrome). This application is aimed at studying the impact of visual feedback on the rehabilitation process of a patient. It focuses on the hand by allowing the physical therapist to perturb (amplify or decrease) the feedback that the patient gets from his/her hand movment. First pilot tests have been conducted.

5.9. EquipEx AmiQual4Home - Ambient Intelligence for Quality of Life

The AmiQual4Home Innovation Factory is an open research facility for innovation and experimentation with human-centered services based on the use of large-scale deployment of interconnected digital devices capable of perception, action, interaction and communication. The Innovation Factory is composed of a collection of workshops for rapid creation of prototypes, surrounded by a collection of living labs and supported by an industrial innovation and transfer service. Creation of the Innovation Factory has been made possible by a grant from French National programme Investissement d'avenir, together with substantial contributions of resources by Grenoble INP, Univ Joseph Fourier, UPMF, CNRS, Schneider Electric and the Communaute de Communes of Montbonnot. The objective is to provide the academic and industrial communities with an open platform to enable research on design, integration and evaluation of systems and services for smart habitats.

The AmiQual4Home Innovation Factory is a unique combination of three different innovation instruments:

1. Workshops for rapid prototyping of devices that embed perception, action, interaction and communication in ordinary objects based on the MIT FabLab model,
2. Facilities for real-world test and evaluation of devices and services organized as open Living Labs,
3. Resources for assisting students, researchers, entrepreneurs and industrial partners in creating new economic activities.

The AmiQual4Home Innovation Factory works with the Inovallee TARMAC technology incubator as well as the SAT Linksium to proved innovation and transfer services to enable students, researchers and local entrepreneurs to create and grow new commercial activities based on smart objects and services.

PESTO Project-Team

6. New Software and Platforms

6.1. 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 includes the possibility for checking everlasting indistinguishability properties [32].

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.

6.2. 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.

6.3. Belenios

In collaboration with the Caramba 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 us 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 (SED Team). Since 2015, it is used by CNRS for remote election among its councils and since 2016, it used by Inria to elect representatives in the “comités de centre” of each Inria center. It has also been used to elect the leader of the GdR-IM working groups C2 and Calcul Formel. It has also been used in smaller elections (e.g., to choose an invited speaker).

6.4. Tamarin

The *TAMARIN* prover is a security protocol verification tool that supports both falsification and unbounded verification of security protocols specified as multiset rewriting systems with respect to (temporal) first-order properties and a message theory that models Diffie-Hellman exponentiation combined with a user-defined subterm-convergent rewriting theory.

Its main advantages are its ability to handle stateful protocols and its interactive proof mode. Moreover, it has recently been extended to verify equivalence properties.

The tool is developed jointly by the PESTO team, the Institute of Information Security at ETH Zurich, and the University of Oxford.

TAMARIN is freely available at http://tamarin-prover.github.io/. In a joint effort, the partners wrote and published a user manual in 2016, available from the same website.

6.5. 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. *TAMARIN* has also bee extended with dedicated heuristics that exploit the form of translated rules and favour termination.

SAPIC offers support for 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 also allows us to verify liveness properties and a recent extension adds a notion of location and reporting used for modelling trusted execution environments. It has been successfully applied on several case studies including the Yubikey authentication protocol, extensions of the PKCS#11 standard and fair exchange protocols.

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

PHOENIX Project-Team

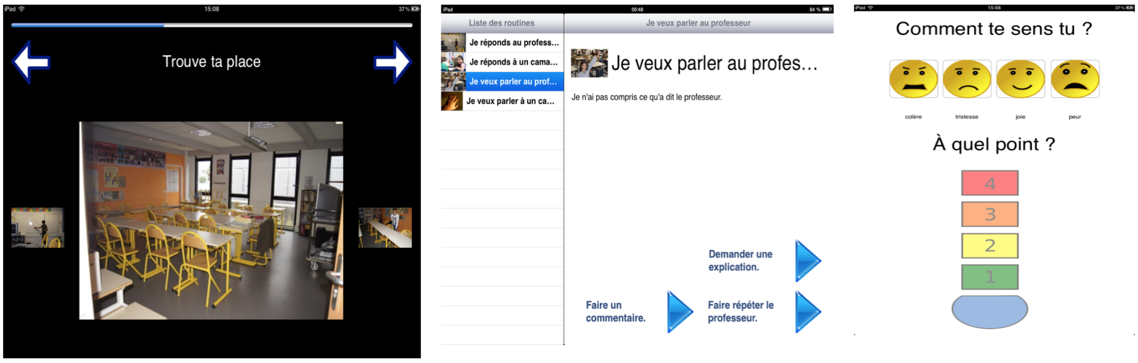
6. New Software and Platforms

6.1. College +

KEYWORDS: Neurosciences - Health - Autism - Mobile application

School+ (or College+ in french) 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.

6.1.1. Assistive applications



Je n'ai pas compris ce qu'a dit le professeur.

Figure 2. Assistive applications

6.1.1.1. 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.

6.1.1.2. Communication application

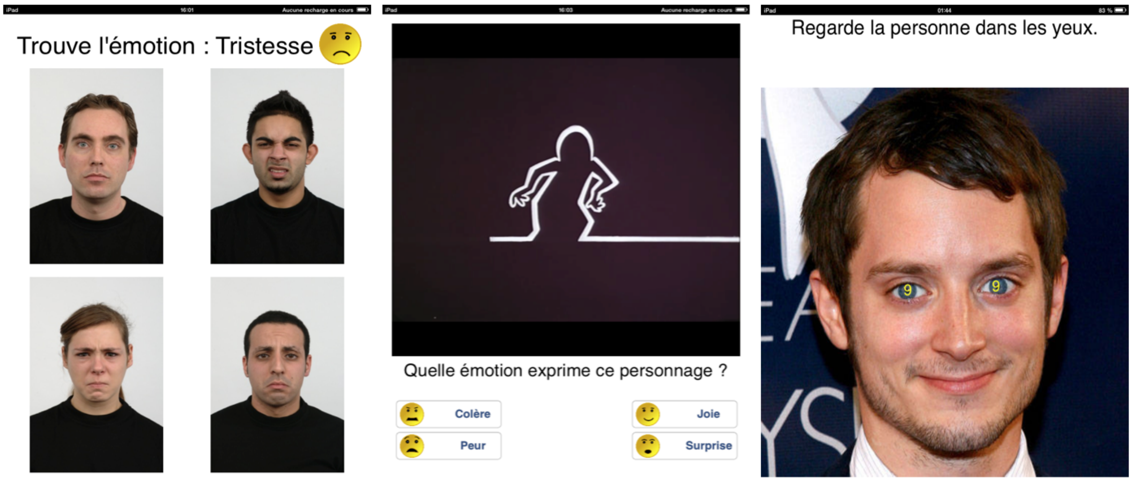
With the same design, the assistance provided by this application targets to communicating situations inside the classroom. The application covers four scenarios addressing two interaction situations (initiating and answering the interaction) and two types of interlocutors (professor and classmate). For each scenario, different slideshows guide the child, depending on the goal of the interaction.

6.1.1.3. 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.

6.1.2. Training applications

These three applications are serious games with increasing levels of difficulties, reachable after a ratio of good answers has been attained.



Trouve l'émotion : Tristesse

Quelle émotion exprime ce personnage ?

Regarde la personne dans les yeux.

Figure 3. Training applications

6.1.2.1. 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.

6.1.2.2. 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.

6.1.2.3. 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.

- Participants: Damien Martin Guillerez, Charles Fage, Helene Sauzeon and Alexandre Spriet
- Contact: Charles Consel

6.2. DiaSuite

SCIENTIFIC DESCRIPTION

DiaSuite is a suite of tools covering the development life-cycle of a pervasive computing application:

6.2.1. *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.

6.2.2. *Designing an application*

Given a taxonomy, the architect can design and structure applications. To do so, the DiaSpec language provides an application design layer. This layer is dedicated to an architectural pattern commonly used in the pervasive computing domain. Describing the architecture application allows to further model a pervasive computing system, making explicit its functional decomposition.

6.2.3. *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.

6.2.4. *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.

6.2.5. *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 .

FUNCTIONAL DESCRIPTION

DiaSuite is developed as a research project by the Inria/LaBRI Phoenix research group. The DiaSuite approach covers the development life-cycle of a pervasive computing application. It takes the form of a methodology, supported by (1) a high-level design language and (2) a suite of tools covering the development life-cycle of a pervasive computing application. Specifically, we have developed a design language dedicated to describing pervasive computing systems and a suite of tools providing customized support for each development stage of a pervasive computing system, namely, implementation (e.g., programming support), testing (e.g., unit test, 2D simulator), and deployment (e.g., distribution platforms like SIP and Web Services).

- Participants: Charles Consel, Milan Kabac, Paul Van Der Walt, Adrien Carteron and Alexandre Spriet
- Contact: Charles Consel

6.3. DiaSuiteBOX

KEYWORDS: Health - Smart home - Open application store - Development tool suite - Application certification - Home care

FUNCTIONAL DESCRIPTION

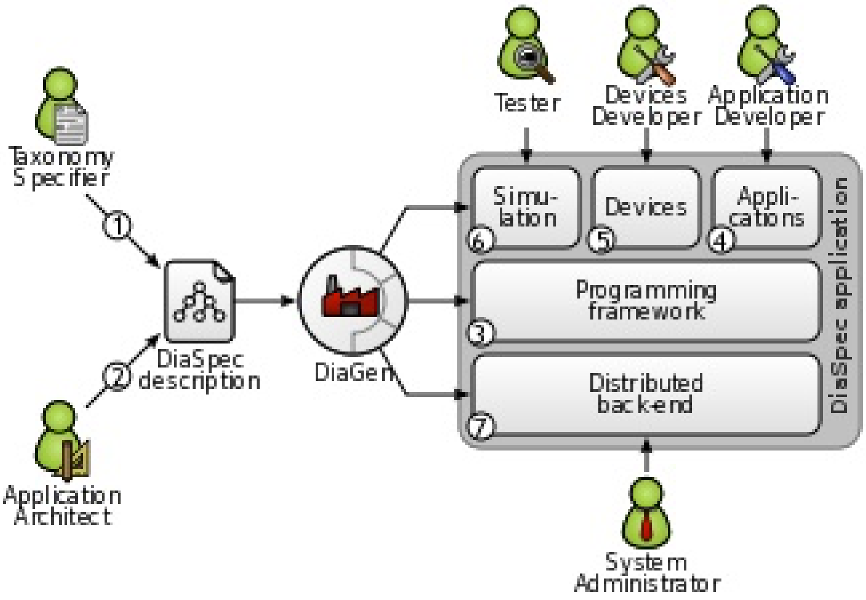


Figure 4. DiaSuite Development Cycle

DiaSuiteBOX proposes an application store that gathers the devices deployed at home. This store is open and available online such as an application store for Smartphone.

- Participants: Bertran Benjamin, Bruneau Julien, Consel Charles, Quentin Enard, Milan Kabac, Damien Martin Guillerez, Emilie Balland, Damien Cassou, Amelie Marzin, Julien Durand, Quentin Barlas, Ludovic Fornasari, Joan Rieu, Adrien Carteron, Eugene Volanschi and Helene Sauzeon
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Charles Consel
- URL: https://diasuitebox.inria.fr/

6.4. DomAssist

KEYWORDS: Health - Mobile application - Persons attendant - Home care

The HomeAssist platform (or DomAssist in french) 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.

6.4.1. 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.

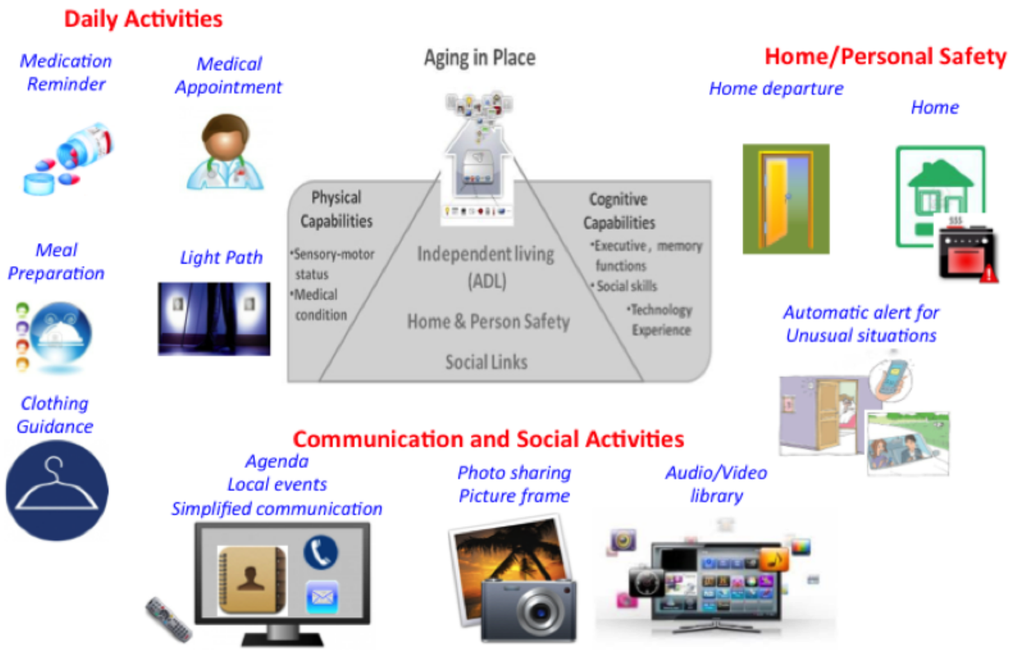


Figure 5. The HomeAssist platform and applications

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.

6.4.2. 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

FUNCTIONAL DESCRIPTION

3 mobile applications for assistive living : (1) DiAndroid : Interface for the main tablet with the DiaSuiteBox applications including those for the daily activities, the meetings scheduling, etc. and for home and personal safety; (2) Accueil : home screen restraining the use of a secondary tablet and offering communications and social activities applications with simplified communication means (ie. eMail), collaborative games, etc.; (3) eMail : mail client made for older people.

- Participants: Alexandre Spriet, Charles Consel, Helene Sauzeon and Julien Durand
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Charles Consel
- URL: http://phoenix.inria.fr/research-projects/homeassist

PI.R2 Project-Team

4. New Software and Platforms

4.1. 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, ...

- Closest participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Courtieu, Maxime Dénès, Hugo Herbelin, Matej Košík, Pierre Letouzey, Assia Mahboubi, Cyprien Mangin, Guillaume Melquiond, Jean-Marc Notin, Pierre-Marie Pédrot, Yann Régis-Gianas, Matthieu Sozeau, Arnaud Spiwack, Théo Zimmermann.
- Partners: CNRS - ENS Lyon - Université Paris-Diderot - Université Paris-Sud
- Contact: Matthieu Sozeau
- URL: http://coq.inria.fr/

4.1.1. Coq 8.6

The 8.6 version of Coq was released in December 2016. It initiates a time-based release cycle and concentrates on a smaller set of features than Coq 8.5 for which compatibility and testing were done more intensively. In the πr^2 team, Hugo Herbelin, Cyprien Mangin, Théo Zimmermann and Matthieu Sozeau contributed to the coordination of the development, to the discussion of the roadmap, to the implementation of the features, and to many bugfixes.

Matthieu Sozeau followed up his work on universe polymorphism making the explicit annotation system more accessible and resolving issues in the minimization algorithm used during refinement, resulting in a more predictable system. These improvements were used in the Coq/HoTT library for Homotopy Type Theory, which is described in an upcoming article [26].

Matthieu Sozeau implemented a new variant of the proof-search tactic for typeclasses that is set to replace the existing auto and eauto tactics in the following version. The new variant fully benefits from the features of the underlying proof engine, and allows much more control on proof-search (patterns used consistently, modes for triggering hints, ...). It is at the basis of the work of Théo Zimmermann described below.

4.1.2. The Equations plugin

Cyprien Mangin and Matthieu Sozeau continued work on the Equations plugin, modularizing it so that the use of axioms can be minimized, and making it compatible with developments in Homotopy Type Theory. To achieve this, it has moved to a simplification engine in ML based on telescopes and is able to produce axiom-free proofs of the examples that were previously implicitly using them. This work will be presented at the POPL workshop Type-Theoretic Tools (TTT), next January 2017.

4.1.3. Maintenance

Among other contributions, Hugo Herbelin, Pierre Letouzey, Matej Košík and Matthieu Sozeau worked at the maintenance of the system.

In particular, Pierre Letouzey vastly reworked the build mechanism of Coq, taking advantage of code evolutions driven by Pierre-Marie Pédrot. Pierre Letouzey also administrated (and improved) several machines or systems that are critical for the Coq community (web server, build test server, git repositories ...), in coordination with Inria's SIC support team.

Matej Košík developed a new benchmarking infrastructure based on Jenkins and continuous integration (http://ci.inria.fr). It allows easily testing any developer branch on the benchmark suite prior to integration to the main archive.

4.1.4. Coordination and animation

After 10 years coordinating the Coq development team, Hugo Herbelin handed over the coordination to Matthieu Sozeau.

A Coq working group is organised every two months (5 times a year). Discussions about the development happen, in particular, on `coq-dev@inria.fr`, Coq's GitHub http://github.com/coq and http://coq.inria.fr/bugs. This year, a week-long working group organized in Sophia-Antipolis was devoted to the 8.6 roadmap discussion.

4.1.5. Documentation and stabilization of Coq's programming interface

Matej Košík worked on the programming interfaces of Coq, starting to isolate a subset of key functions to be used by Coq plugin developers.

4.2. 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. Yann Régis-Gianas develops a reference implementation of a syntactic analyzer for the POSIX shell programming language. This analyzer is used by the Colis project to analyze the scripts embedded in the packages of the Debian GNU/Linux distribution. 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.

Yves Guiraud has updated the Catex tool for Latex, whose purpose is to automatise the production of string diagrams from algebraic expressions http://www.irif.fr/~guiraud/catex/catex.zip. Yves Guiraud collaborates with Samuel Mimram (LIX) to develop the prototype Rewr that implements several algorithms developed in the "Effective higher-dimensional algebra" research direction, including the homotopical completion-reduction procedure of [10]. An online version is available at http://www.lix.polytechnique.fr/Labo/Samuel.Mimram/rewr.

PLEIADE Team

6. New Software and Platforms

6.1. Magus

KEYWORDS: Bioinformatics - Genomic sequence - Knowledge database
FUNCTIONAL DESCRIPTION

Comparative genomics requires efficient and scalable tools for managing knowledge about genomes, genes, and the high-dimensional relations between them.

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.
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.

- Participants: David Sherman, Pascal Durrens
- Partners: CNRS - INRA - Université de Bordeaux
- Contact: David James Sherman
- URL: http://magus.gforge.inria.fr

6.2. 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/

6.3. 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/

6.4. 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/

6.5. Declic

Metabarcoding relies on mapping large sets of reads on reliable databases, with taxonomically annotated sequences. Declic facilitates data analyses for metabarcoding.

FUNCTIONAL DESCRIPTION

Declic is a Python library that provides several tools for data analysis in the domains of multivariate data analysis, machine learning, and graph based methods. It can be used to study in-depth the accuracy of the dictionary between molecular based and morphological based taxonomy.

Declic includes an interpreter for a Domain Specific Language (DSL) to make its Python library easy to use for scientists familiar with environments such as R.

- Partner: INRA
- Contact: Alain Franc

6.6. Platforms

6.6.1. 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.

6.6.2. 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.

6.6.3. Team Platform

PLEIADE maintains a dedicated computing platform for software development and experimentation by the team, comprised of a private cloud, storage, and a Project Atomic cluster for hosting Docker containers

POEMS Project-Team

6. New Software and Platforms

6.1. 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

6.2. 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 (v1.5) has been released in November 2016. This year, many bugs have been fixed and many improvements have been done. The main new features are: introduction of hierarchical matrix, new development for BEM computation (2D Helmholtz is now available), re-engineering of the automatic installation and compilation and connection to a Jenkins test platform. Two training days gathering thirty people have been organized in June 2016.

- Contact: Eric Lunéville and Nicolas Kielbasiewicz
- URL: http://uma.ensta-paristech.fr/soft/XLiFE++/

POLARIS Team

5. New Software and Platforms

5.1. 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: Guillaume Huard
- URL: http://soctrace-inria.github.io/framesoc/

5.2. 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 aim of GameSeer is a) to provide a numerical integration kernel for phase portrait and equilibrium set generation; and b) to provide a graphical user interface that allows the user to employ said capabilities from a simple and intuitive front-end.

- Contact: Panayotis Mertikopoulos
- URL: http://mescal.imag.fr/membres/panayotis.mertikopoulos/publications.html

5.3. Moca

Memory Organization Cartography and Analysis

MOCA is an efficient tool for the collection of complete spatiotemporal memory traces. Its objective is twofold, namely to *a*) avoid missuses of the memory hierarchy (such as false sharing of cache lines or contention); and *b*) to take advantage of the various cache levels and the memory hardware prefetcher. It is based on a Linux kernel module and provides a coarse-grained trace of a superset of all the memory accesses performed by an application over its addressing space during the time of its execution.

KEYWORDS: High-Performance Computing - Performance analysis

- Contact: Guillaume Huard
- URL: https://github.com/dbeniamine/MOCA

5.4. 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/

5.5. 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: Jean-Marc Vincent
- URL: http://psi.gforge.inria.fr/

5.6. SimGrid

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

SimGrid is a toolkit that provides core functionalities 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.

- Participants: Frederic Suter, Martin Quinson, Arnaud Legrand, Adrien Lebre, Jonathan Pastor, Mario Sudholt, Luka Stanisic, Augustin Degomme, Jean-Marc Vincent, Florence Perronnin and Jonathan Rouzaud-Cornabas
- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson
- URL: http://simgrid.gforge.inria.fr/

5.7. Tabarnac

Tool for Analyzing the Behavior of Applications Running on NUMA ArChitecture
KEYWORDS: High-Performance Computing - Performance analysis - NUMA

- Contact: David Beniamine
- URL: https://dbeniamine.github.io/Tabarnac/

5.8. 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, Jean-Marc Vincent, Benjamin Briot, Jean-Michel Fourneau and Franck Quessette
- Partner: UVSQ
- Contact: Alain Jean-Marie
- URL: http://marmotecore.gforge.inria.fr/

POLSYS Project-Team

5. New Software and Platforms

5.1. Epsilon

FUNCTIONAL DESCRIPTION

Epsilon is a library of functions implemented in Maple and Java for polynomial elimination and decomposition with (geometric) applications.

- Contact: Dongming Wang
- URL: http://wang.cc4cm.org/epsilon/index.html

5.2. 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

5.3. FGb Light

FUNCTIONAL DESCRIPTION

Gröbner basis computation modulo p (p is a prime integer of 16 bits).

- Participant: Jean-Charles Faugère
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/Software/FGb/

5.4. 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: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/Software/index.html

5.5. HFEBoost

FUNCTIONAL DESCRIPTION

Public-key cryptography system enabling an authentification of dematerialized data.

- Authors: Jean-Charles Faugère and Ludovic Perret
- Partner: UPMC
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/Links/hfeboost.html

5.6. RAGlib

Real Algebraic Geometry library

FUNCTIONAL DESCRIPTION

RAGLib is a powerful library, written in Maple, dedicated to solving over the reals polynomial systems. It is based on the FGb library for computing Grobner bases. It provides functionalities for deciding the emptiness and/or computing sample points to real solution sets of polynomial systems of equations and inequalities. This library provides implementations of the state-of-the-art algorithms with the currently best known asymptotic complexity for those problems.

- Contact: Mohab Safey El Din
- URL: http://www-polsys.lip6.fr/~safey/RAGLib/

5.7. 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

5.8. SPECTRA

Semidefinite Programming solved Exactly with Computational Tools of Real Algebra

FUNCTIONAL DESCRIPTION

SPECTRA is a Maple library devoted to solving exactly Semi-Definite Programs. It can handle rank constraints on the solution. It is based on the FGb library for computing Grobner bases and provides either certified numerical approximations of the solutions or exact representations of them.

- Contact: Mohab Safey El Din
- URL: http://homepages.laas.fr/henrion/software/spectra/

POSET Team

6. New Software and Platforms

6.1. T-calculus

Sketched in [10], 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], [9]. Its definition has been refined a number of times (see e.g. [10], [8]). A prototype implementation of its reactive kernel has eventually been achieved in Haskell on top of the Euterpea libraries during the spring 2016 [15], [21], [19], [23]

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[0] See [30] for an early note by Hudak about the notion of Domain Specific Language, and see [29], [32] for application of this notion is computer music.

POTIOC Project-Team

6. New Software and Platforms

6.1. PapARt

PapARt is a software development kit (SDK) that enables the creation of interactive projection mapping (See https://project.inria.fr/papart). This year, we focused on making this toolkit widely available. We created a set of examples and created tutorials. The PapARt code is now Open Source, our objective being to favor a wide appropiration by artists, teachers, or students.

Participants: Jeremy Laviole, Martin Hachet

URL: https://github.com/poqudrof/Papart-examples/wiki

6.2. Helios

Helios is a software tool (Unity3D) we have developed in collaboration with Stéphanie Fleck from Université de Lorraine. It is dedicated to the learning of astronomy at school. It bases on augmented reality and tangible interaction. See Section 7.4 .

Participants: Robin Gourdel, Jérémy Laviole, Benoit Coulais, Martin Hachet.

Partners: Université de Loraine - SATT Nancy Grand-Est.

6.3. Aïana

We have developped Aïana, a MOOC player, with the support of the Inria MOOC Lab. Aïana offers original interaction features in order to enable a wide spectrum of users including persons with disabilities. The first version of Aïana has been used by the 3700 participants of the Digital Accessibility MOOC we have produced on the national MOOC platform FUN. See Section 7.9 .

Participants: Pierre-Antoine Cinquin, Pascal Guitton

Partners: LearningLab Inria

6.4. HOBIT

Along with the project HOBIT (see Section 7.1), we continue enhancing the platform that is dedicated to the simulation and augmentation of optics experiments. In particular, this year, we did a major evolution that consists in making the system reconfigurable. Various optical components be plugged in, and the simulation and augmentations are updated accordingly.

Participants: Benoit Coulais, David Furio, Martin Hachet.

Partners: Université de Bordeaux - IUT de Bordeaux, LaBRI, IMS, CELIA

https://project.inria.fr/hobit

PRIVATICS Project-Team

5. New Software and Platforms

5.1. FECFRAME

FEC Framework following RFC 6363 specifications (https://datatracker.ietf.org/doc/rfc6363/)
KEYWORDS: Error Correction Code - Content delivery protocol - Robust transmission
FUNCTIONAL DESCRIPTION

This sofware implements the FECFRAME IETF standard (RFC 6363) co-authored by V. ROCA, and is compliant with 3GPP specifications for mobile terminals. It enables the simultaneous transmission of multimedia flows to one or several destinations, while being robust to packet erasures that happen on wireless networks (e.g., 4G or Wifi). This software relies on the OpenFEC library (the open-source http://openfec.org version or the commercial version) that provides the erasure correction codes (or FEC) and thereby offer robustness in front of packet erasures.

- Author: Vincent Roca
- Contact: Vincent Roca
- URL: http://openfec.org/

5.2. 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/mobilitics/

5.3. MyTrackingChoices

KEYWORDS: Privacy - User control
FUNCTIONAL DESCRIPTION

This extension lets you control how you are being tracked on the Internet. It allows you to choose the categories (e.g., health, adult) of the websites where you don't want to be tracked on. When you browse the web, your visited webpages will be categorized on the fly and, depending on your choices, the extension will block the trackers (webpage by webpage) or not.

Existing anti-tracking (Ghostery, Disconnect etc.) and ad-blocking (AdBlock Plus etc.) tools block almost ALL trackers and as a result, ads. This has a negative impact on the Internet economy because free services/content on the Internet are fuelled by ads. As a result, websites are starting to block access to their content if they detect use of Ad-blockers or they ask users to move to a subscription-based model (where users have to pay to get access to the website).

This extension is testing another approach: It is trying to find a trade-off between privacy and economy, that would allow users to protect their privacy while still accessing to free content.

It is based on the assumption that most people are not against advertisements, but want to keep control over their data. We believe that some sites are more sensitive than others. In fact, most people don't want to be tracked on "sensitive" websites (for example related to religion, health,. . .), but don't see any problem to be tracked on less sensitive ones (such as news, sport,. . .). This extension allows you to take control and specify which on which categories of sites you don't want to be tracked on! Furthermore, the extension also gives you the option to block the trackers on specific websites.

- Contact: Claude Castelluccia
- URL: https://addons.mozilla.org/FR/firefox/addon/mytrackingchoices/

5.4. 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

5.5. 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/

PROSECCO Project-Team

6. New Software and Platforms

6.1. ProVerif

Participants: Bruno Blanchet [correspondant], Xavier Allamigeon [April–July 2004], Vincent Cheval [Sept. 2011–Dec. 2014], Benjamin Smyth [Sept. 2009–Feb. 2010], Marc Sylvestre [Oct. 2016–].

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–Dec. 2013].

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], Cedric Fournet [Microsoft Research], Markulf Kohlweiss [Microsoft Research], Antoine Delignat-Lavaud [Microsoft Research], Nikhil Swamy [Microsoft Research], Santiago Zanella-Béguelin [Microsoft Research], Jean Karim Zinzindohoué, Benjamin Beurdouche, Alfredo Pironti.

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.

Papers describing the miTLS library was published at IEEE S&P 2013, CRYPTO 2014, and IEEE S&P Journal 2016. miTLS is now being developed on GitHub with dozens of contributors and regular updates. The miTLS team was awarded the Levchin prize for contributions to Real-World Cryptography in 2016. The software and associated research materials are available from http://mitls.org.

6.4. F*

Participants: Alejandro Aguirre, Danel Ahman [University of Edinburgh], Benjamin Beurdouche, Karthikeyan Bhargavan, Antoine Delignat-Lavaud [Microsoft Research], Cédric Fournet [Microsoft Research], Catalin Hritcu, Chantal Keller [Université Paris-Sud], Kenji Maillard, Guido Martínez, Gordon Plotkin, Samin Ishtiaq [Microsoft Research], Markulf Kohlweiss [Microsoft Research], Jonathan Protzenko [Microsoft Research], Tahina Ramananandro [Microsoft Research], Aseem Rastogi [Microsoft Research], Nikhil Swamy [Microsoft Research], Peng Wang [MIT], Santiago Zanella-Béguelin [Microsoft Research], Jean Karim Zinzindohoué.

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 [44]. 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.

6.5. HACL*

Participants: Karthikeyan Bhargavan, Jean Karim Zinzindohoué, Marina Polubelova, Benjamin Beurdouche, Jonathan Protzenko [Microsoft Research].

HACL* is a verified cryptographic library written in F*. It implements modern primitives, including elliptic curves like Curve25519, symmetric ciphers like Chacha20, and MAC algorithms like Poly1305. These primitives are then composed into higher-level constructions like Authenticated Encryption with Additional Data (AEAD) and the NaCl API. All the code in HACL* is verified for memory safety, side channel resistance, and where applicable, also for functional correctness and absence of integer overflow. HACL* code is used as the basis for cryptographic proofs for security in the miTLS project.

HACL* code can be compiled to OCaml using the standard F* compiler, or to C, using the Kremlin backend of F*. The generated C code is as fast as state-of-the-art cryptographic libraries written in C. HACL* is being actively developed on Github; see https://github.com/mitls/hacl-star

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 Signal and TLS 1.3 protocols in JavaScript.

The ProScript compiler and various libraries written in ProScript are being developed on Github and will be publicly released in 2017.

6.7. QuickChick

Participants: Maxime Dénès [Inria Sophia-Antipolis], Catalin Hritcu, John Hughes [Chalmers University], Leonidas Lampropoulos [University of Pennsylvania], Zoe Paraskevopoulou [Princeton University], Benjamin Pierce [University of Pennsylvania].

QuickChick is a verified plugin that integrates property-based testing and proving in the Coq proof assistant. This integration is aimed at reducing the cost of formal verification and at providing stronger, formal foundations to property-based testing. https://github.com/QuickChick/QuickChick

6.8. Luck

Participants: Leonidas Lampropoulos [University of Pennsylvania], Diane Gallois-Wong [ENS and Inria Paris], Catalin Hritcu, John Hughes [Chalmers University], Benjamin Pierce [University of Pennsylvania], Li-Yao Xia [ENS and Inria Paris].

Property-based random testing a la QuickCheck requires building efficient generators for well-distributed random data satisfying complex logical predicates, but writing these generators can be difficult and error prone. We propose a domain-specific language in which generators are conveniently expressed by decorating predicates with lightweight annotations to control both the distribution of generated values and the amount of constraint solving that happens before each variable is instantiated. This language, called Luck, makes generators easier to write, read, and maintain. https://github.com/QuickChick/Luck

6.9. Privacy-preserving federated identity

Participants: Harry Halpin, George Danezis [University College London].

security protocols, secure messaging, decentralization, blockchain

Working with the partners in the NEXTLEAP project, we helped design a protocol for decentralized and privacy-preserving identity and key management, creating both a fix privacy vulnerabilities in OAuth (UnlimitID) and on generic versions of blockchain for usages such as key management (ClaimChain). While this software has been prototyped in 2016 using Python working with NEXTLEAP project partner University College London (George Danezis), we expected either formal analysis using ProVerif or verified implementations using Fstar in 2017, as well and integrate this work with formal verification work done in Prosecco on end-to-end secure messaging.

QUANTIC Project-Team (section vide)

RAP Project-Team (section vide)

RAPSODI Team

6. New Software and Platforms

6.1. New Software

6.1.1. NS2DDV-M: a code for the simulation of inhomogeneous fluid flow

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.

6.1.2. A scientific computing software for fast simulation of large systems of interacting particles

Benoît Merlet and Thomas Rey have developed a set of numerical codes for the numerical simulation of large systems of interacting particles. For a system of N particles, the number of interactions is a quadratic functions of N, leading to a quadratic cost of a brut force implementation. This fact limits simulations by “naïve” methods to systems with “only” tenth of thousands of particles. In order to treat larger systems (involving millions of particles), the team has implemented a method based on the Non Uniform Fast Fourier Transform which reduces the computation cost of the interactions to $O(N \log N)$. The NUFFT is used to handle the long range smooth interactions. To treat the possibly singular short range interactions (involving only neighboring particles) a quadtree-like method is used. The method is applied to two kind of problems : computations of the dynamics of interacting particles where a standard ordinary differential equation is used; numerical optimization of the energy of a system of interacting particles thanks to a Nonlinear Conjugate Gradient method.

As an illustration of the efficiency of the code, the team has performed numerical experiments which support the following crystallization conjecture : in 2D, a large number of identical charged particles tend to arrange themselves into a regular triangular lattice.

A user friendly version will be released to the public in 2017.

6.1.3. The Fast Spectral Kinetic Scheme

The Fast Spectral Kinetic Scheme (FSKS), has been jointly developed by researchers from the universities of Ferrara, Toulouse, and Lille, and is the first high-order 7-dimensional deterministic numerical method capable of dealing with the complete physics of rarefied gas dynamics. The FSKM indeed solves the Boltzmann equation in 1 dimension of time, 3 of physical space and 3 of velocity space, and has been used to model accurately aerospace engineering problems such as space shuttle re-entry in the atmosphere or very rarefied gas flow in microscopic devices (Knudsen pump).

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, Romain Leguay, Artur Alves Pessoa, Boris Detienne, Franck Labat, François Clautiaux, Pierre Pesneau, Eduardo Uchoa Barboza, Michael Poss and Halil Sen
- Partners: CNRS - IPB - Universidade Federal Fluminense - Université de Bordeaux
- Contact: François Vanderbeck
- URL: https://wiki.bordeaux.inria.fr/realopt/pmwiki.php/Project/BaPCod

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 [23] , for elastic version management, for adaptive replication, for partial replication, and for reconfigurable sharding.

- Participants: Tyler Crain, Marc Shapiro 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 and Masoud Saeida Ardekani
- 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: Lokesh Gidra
- URL: http://gforge.inria.fr/projects/transgc/

REO Project-Team

6. New Software and Platforms

6.1. cardioXcomp

KEYWORDS: Cardiac Electrophysiology - Safety Pharmacology
FUNCTIONAL DESCRIPTION

cardioXcomp is a software dedicated to the safety pharmacology industry. It is developed in the framework of the joint laboratory (LabCom) “cardioXcomp” with the software company Notocord. Its purpose is to model the electrical potential of cardiomyocytes measured by a microelectrode array (MEA), and to model the effect of drugs on this signal. It was registered in November 2015 at the Agence pour la Protection des Programmes under the Inter Deposit Digital Number IDDNFR.001.480003.000.S.P.2015.000.31230.

- Participants: Jean-Frédéric Gerbeau, Fabien Raphel, Nejib Zemzemi
- Contact: Jean-Frédéric Gerbeau

6.2. FELiScE

Finite Elements for Life SCiences and Engineering problems
KEYWORDS: Finite element modeling - 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 Ángel Fernández Varela, Jean-Frédéric Gerbeau, Philippe Moireau, Marina Vidrascu, Sebastien Gilles, Benoit Fabreges, Axel Fourmont, Mikel Landajuela Larma, Damiano Lombardi, Matteo Aletti, Irene Vignon-Clementel and Faisal Amlani
- Contact: Jean-Frédéric Gerbeau
- URL: http://felisce.gforge.inria.fr

6.3. MODULEF

FUNCTIONAL DESCRIPTION

MODULEF is a legacy finite element library developed at Inria since the 1980’s. Here, we limit ourselves to recent developments done within this library.

A numerical method to approximate the constitutive laws for rubber elasticity derived from polymer physics are implemented in 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/

6.4. 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

5. New Software and Platforms

5.1. 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.

- Authors: Raoul de Charette, Fawzi Nashashibi and Evangeline Pollard
- Contact: Fawzi Nashashibi

5.2. 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: Joshue Perez Rastelli and Vicente Milanés
- Contact: Fawzi Nashashibi

5.3. 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: Fawzi Nashashibi

5.4. PML-SLAM

- Participants: Zayed Alsayed and Fawzi Nashashibi
- Contact: Fawzi Nashashibi

5.5. Platools

KEYWORD: Telecommunications

- Participant: Marios Makassikis
- Contact: Thierry Ernst

5.6. 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

5.7. 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

5.8. Taxi-col

KEYWORD: Mobile Computing, Transportation

- Participant: Eugenie Lioris
- Contact: Fawzi Nashashibi

5.9. V2Provue

Vehicle-to-Pedestrian
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

5.10. SimConVA

Participants: Pierre Merdrignac, Oyunchimeg Shagdar, Jean-Marc Lasgouttes.

This software was developed during the SINETIC FUI project. It aims at interfacing the network simulator ns-3 and the prototyping software RTMaps.

The source code of is software is a library to generate an RTMaps component that triggers and controls ns-3. The component handle emission and reception of data packets between RTMaps and ns-3 for every vehicle. It can also deal with the mobility of vehicles in ns-3 based on the localization known in ns-3.

This software was used with the communication stack developed in RITS. It has been shown during the SINETIC project how this it can be used for simulating and emulating cooperative driver assistance systems. Particularly, the software has been tested on cooperative platoons. The tests were conducted on both simulation and real platforms to prove how the such software can be used during the development phase and that it is fully compatible with the architecture already present in the experimental vehicles.

- Contact: Fawzi Nashashibi

RMOD Project-Team

6. New Software and Platforms

6.1. 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. In 2016, we released a new version Pharo (Pharo 5.0) completely revisited with fundamental changes in the VM (object representation, compiler, ...)

- Participants: Marcus Denker, Damien Cassou, Stephane Ducasse, Esteban Lorenzano, Damien Pollet, Igor Stasenko, Camillo Bruni, Camille Teruel and Clement Bera
- Partners: BetaNine - Debris publishing - École des Mines de Douai - HR Works - MAD - Pleiad - Sensus - Synectique - Université de Berne - Uqbar foundation Argentina - Vmware - Yesplan
- Contact: Marcus Denker
- URL: http://www.pharo.org

6.2. 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: Stephane Ducasse, Muhammad Bhatti, Andre Cavalcante Hora, Nicolas Anquetil, Anne Etien, Guillaume Larcheveque and Alexandre Bergel
- Partners: Pleiad - Sensus - Synectique - Université de Berne - USI - Vrije Universiteit Brussel - Feenk
- Contact: Stephane Ducasse
- URL: http://www.moosetechnology.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 is developed by INPT(ENSEEIHT)-IRIT, Inria, CERFACS, University of Bordeaux, CNRS and ENS Lyon. In 2014, a consortium of industrial users has been created (http://mumps-consortium.org).

- 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, François-Henry Rouet, Philippe Combes and Gilles Moreau
- Partners: CERFACS - CNRS - ENS Lyon - INPT - IRIT - LIP - Université de Bordeaux - Université de Lyon - Université de Toulouse
- Latest public release: MUMPS 5.0.2 (July 2016)
- Contact: Jean-Yves L'Excellent
- URL: http://mumps-solver.org/
- Next MUMPS User Days: we have started organizing the next MUMPS User days, which will be hosted by Inria on June 1 and 2, 2017 near Grenoble, France (see http://mumps.enseeiht.fr/ud_2017.php)

In the context of the MUMPS consortium (see Section 8.1 and http://mumps-consortium.org), we had scientific exchanges and collaborations with industrial members and released two versions in advance for the consortium (in July 2016 and November 2016), containing major improvements for large-scale problems and many other improvements. Much effort was also put on developing features and algorithms to improve the quality and performance of MUMPS, especially in the context of problems offering potential for low-rank compression. This work is done in close collaboration with the partners who co-develop MUMPS, in particular in Toulouse.

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 (XtremLogic SAS)
- Contact: Christophe Alias

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 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

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 the algorithm “Counter-example based generation of ranking functions”. 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 the algorithm “An encoding of array verification problems into array-free Horn clauses”. 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
- Demo page : http://laure.gonnord.org/pro/demopage/vaphor/index.php

SECRET Project-Team

6. New Software and Platforms

6.1. CFS

FUNCTIONAL DESCRIPTION

Reference implementation of parallel CFS (reinforced version of the digital signature scheme CFS). Two variants are proposed, one with a « bit-packing » finite field arithmetic and an evolution with a « bit-slicing » finite-field arithmetic (collaboration with Peter Schwabe). For 80 bits of security the running time for producing one signature with the « bit-packing » variant is slightly above one second. This is high but was still the fastest so far. The evolution with the « bit-slicing » arithmetic produces the same signature in about 100 milliseconds.

- Participants: Nicolas Sendrier and Gregory Landais
- Contact: Nicolas Sendrier
- URL: https://gforge.inria.fr/projects/cfs-signature/

6.2. Collision Decoding

KEYWORDS: Algorithm - Binary linear code

FUNCTIONAL DESCRIPTION

Collision Decoding implements two variants of information set decoding : Stern-Dumer, and MMT. To our knowledge it is the best full-fledged open-source implementation of generic decoding of binary linear codes. It is the best generic attack against code-based cryptography.

- Participants: Nicolas Sendrier and Gregory Landais
- Contact: Nicolas Sendrier
- URL: https://gforge.inria.fr/projects/collision-dec/

6.3. ISDF

FUNCTIONAL DESCRIPTION

Implementation of the Stern-Dumer decoding algorithm, and of a varaint of the algorithm due to May, Meurer and Thomae.

- Participants: Nicolas Sendrier and Gregory Landais
- Contact: Anne Canteaut
- URL: https://gforge.inria.fr/projects/collision-dec/

SELECT Project-Team

5. New Software and Platforms

5.1. BlockCluster

Block Clustering

KEYWORDS: Mixture model - Block cluster analysis

SCIENTIFIC DESCRIPTION

Blockcluster is software devoted to model-based block clustering. It is developed in partnership 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 also been provided. This non-asymptotic criterion appears to be more relevant than the BIC-like approximation of ICL.

FUNCTIONAL DESCRIPTION

BlockCluster is an R package for co-clustering of binary, contingency and continuous data based on mixture models.

- Participants: Gilles Celeux, Christine Keribin, Christophe Biernacki and Serge Iovleff
- Contact: Gilles Celeux
- URL: http://cran.r-project.org/web/packages/blockcluster/index.html

5.2. Mixmod

Multi-purpose software for model-based clustering and classification with continuous and categorical variables.

KEYWORDS: Mixture model - cluster analysis - discriminant analysis

FUNCTIONAL DESCRIPTION

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.

Josselin Demont and Benjamin Auder have contributed to software improvement in MIXMOD. They have implemented an interface to test any mathematical library (Armadillo, Eigen, etc.) to replace NEWMAT. They have contributed to the continuous integration setup using Jenkins tools, and prepared an automated testing framework for unit and non-regression tests.

Jonas Renault, an engineer, is in charge of developing a web version of MIXMOD.

- Participants: Christophe Biernacki, Gilles Celeux, Gérard Govaert, Florent Langrognet and Benjamin Auder
- Partners: CNRS - HEUDIASYC - Laboratoire Paul Painlevé - LIFL - LMB - Université Lille 1
- Contact: Gilles Celeux
- URL: http://www.mixmod.org

5.3. MASSICCC

Massive Clustering with Cloud Computing
KEYWORDS: Statistic analysis - Big data - Machine learning - Web Application
SCIENTIFIC DESCRIPTION

The web application let users use several software packages developed by Inria directly in a web browser. Mixmod is a classification library for continuous and categorical data. MixtComp allows for missing data and a larger choice of data types developed by MODAL team (Inria Lille). BlockCluster is a library for co-clustering data. When using the web application, the user can first upload a data set, then configure a job using one of the libraries mentioned and start the execution of the job on a cluster. The results are then displayed directly in the browser allowing for rapid understanding and interactive visualisation.

FUNCTIONAL DESCRIPTION

The MASSICCC web application offers a simple and dynamic interface for analysing heterogeneous data with a web browser. Various software packages for statistical analysis are available (Mixmod, MixtComp, BlockCluster) which allow for supervised and supervised classification of large data sets.

- Participants: Christophe Biernacki, Gilles Celeux, Benjamin Auder, Josselein Demont, Jonas Renault
- Contact: Jonas Renault
- URL: https://massiccc.lille.inria.fr

SEMAGRAMME Project-Team

5. New Software and Platforms

5.1. ACGtk

Abstract Categorial Grammar Development Toolkit
KEYWORDS: Natural language processing - NLP - Syntactic analysis - Semantics
FUNCTIONAL DESCRIPTION

ACGtk provides softwares for developing and using Abstract Categorial Grammars (ACG).

- Contact: Sylvain Pogodalla
- URL: http://www.loria.fr/equipes/calligramme/acg/

5.2. Grew

Graph Rewriting
FUNCTIONAL DESCRIPTION

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).

In 2016, Grew was used in different applications. The Graph Rewriting System presented in [1] was improved and is used in the preprocessing of data in the ZombiLingo project (see 6.3.1). It was also extensively used in the Universal Dependencies project for improving the French sub-corpus.

- Contact: Bruno Guillaume
- URL: http://grew.loria.fr

5.3. ZombiLingo

FUNCTIONAL DESCRIPTION

ZombiLingo is a GWAP (Game With A Purpose) where gamers have to give linguistic information about the syntax of natural language sentence.

During 2016, the main evolutions of the application were:

- New game modes: for instance the duel mode where two players can compare their results on a set on sentence.
- Integration of data preprocessing, data postprocessing to the back-office.
- Integration of evaluation methods [15] in the back-office.

The current version is used for the French language and it is planned to use it with other languages (English and low-resourced languages).

- Authors: Nicolas Lefebvre, Karën Fort, Bruno Guillaume and Valentin Stern
- Contact: Bruno Guillaume
- Application URL: http://zombilingo.org/
- Code URL: https://github.com/zombilingo

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 (disfluences) and MElt (POS and lemma). The tool was reimplemented in order to propose generic treatments for the different corpora.

- Contact: Maxime Amblard
- URL: http://slam.loria.fr

SEQUEL Project-Team

6. New Software and Platforms

6.1. BAC

Bayesian Policy Gradient and Actor-Critic Algorithms
KEYWORDS: Machine learning - Incremental learning - Policy Learning
FUNCTIONAL DESCRIPTION

To address this issue, we proceed to supplement our Bayesian policy gradient framework with a new actor-critic learning model in which a Bayesian class of non-parametric critics, based on Gaussian process temporal difference learning, is used. Such critics model the action-value function as a Gaussian process, allowing Bayes' rule to be used in computing the posterior distribution over action-value functions, conditioned on the observed data. Appropriate choices of the policy parameterization and of the prior covariance (kernel) between action-values allow us to obtain closed-form expressions for the posterior distribution of the gradient of the expected return with respect to the policy parameters. We perform detailed experimental comparisons of the proposed Bayesian policy gradient and actor-critic algorithms with classic Monte-Carlo based policy gradient methods, as well as with each other, on a number of reinforcement learning problems.

- Contact: Michal Valko
- URL: https://team.inria.fr/sequel/Software/BAC/

6.2. Collaborative Filtering Network

KEYWORDS: Recommender system - Neural networks - Deep learning
FUNCTIONAL DESCRIPTION

Recommendation systems advise users on which items (movies, musics, books etc.) they are more likely to be interested in. A good recommendation system may dramatically increase the amount of sales of a firm or retain customers. For instance, 80% of movies watched on Netflix come from the recommender system of the company. Colaborative Filtering (CF) aims at recommending an item to a user by predicting how a user would rate this item. To do so, the feedback of one user on some items is combined with the feedback of all other users on all items to predict a new rating. For instance, if someone rated a few books, CF objective is to estimate the ratings he would have given to thousands of other books by using the ratings of all the other readers.

The following module tackles Collaborative Filtering tasks by using a novel approach based on neural networks (sparse denoising autoencoders). In a few words, the module lets the user train neural networks to predict unknown entries in a history files.

The input files are classic csv files. The output files can either be the full matrix of ratings and/or the network weights. The root mean square error is computed to assess the quality of the training.

This module is based on Lua/Torch Framework. It works on both CPU/GPU and it is multithreaded.

- Contact: Florian Strub
- URL: https://github.com/fstrub95/Autoencoders_cf

SERENA Team

5. New Software and Platforms

5.1. GEOFRACFLOW

GEOFRACFLOW
SCIENTIFIC DESCRIPTION GEOFRACFLOW is a Matlab software for the simulation of steady state single phase flow in Discrete Fracture Networks (DFNs) using the Mixed Hybrid Finite Element (MHFEM) method for conforming and non conforming discretizations.

- Participants: Géraldine Pichot, Jocelyne Erhel, and Jean-Raynald De Dreuzy
- Contact: Géraldine Pichot
- URL: https://bil.inria.fr/fr/software/view/2653/tab

5.2. SBM

Skew Brownian Motion
SCIENTIFIC 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.

- Participants: Antoine Lejay, Géraldine Pichot
- Contact: Antoine Lejay
- URL: https://gforge.inria.fr/projects/sbm

5.3. Sklml

The OCaml parallel skeleton system
SCIENTIFIC DESCRIPTION Writing parallel programs is not easy, and debugging them is usually a nightmare. To cope with these difficulties, the skeleton programming approach uses a set of predefined patterns for parallel computations. The skeletons are higher-order functional templates that describe the program underlying parallelism. Sklml is a new framework for parallel programming that embeds an innovative compositional skeleton algebra into the OCaml language. Thanks to its skeleton algebra, Sklml provides two evaluation regimes to programs: a regular sequential evaluation (merely used for prototyping and debugging) and a parallel evaluation obtained via a recompilation of the same source program in parallel mode. Sklml was specifically designed to prove that the sequential and parallel evaluation regimes coincide.
FUNCTIONAL DESCRIPTION Sklml is a functional parallel skeleton compiler and programming system for OCaml programs. Slogan is “easy coarse grain parallelization”.

- Participants: Pierre Weis and François Clément
- Contact: François Clément
- URL: http://sklml.inria.fr

SERPICO Project-Team

6. New Software and Platforms

6.1. TMA-Lib

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The TMA-LIB enables to jointly detect (adaptive wavelet transform), segment (parametric active contours) and restore (artifact correction and deconvolution) TMA (Tissue MicroArrays) images.

- **Participants**: Hoai Nam Nguyen, Charles Kervrann.
- **Partner:** INNOPSYS Company.
- **Contact:** Charles Kervrann.
- **Languages:** C/C++, Matlab.

6.2. QuantEv

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The QUANTEV software is dedicated to the analysis of the spatial distribution of intracellular events represented by any static or dynamical descriptor (e.g. detected points, segmented regions, trajectories...), provided that the descriptors are associated with spatial coordinates. QuantEv first computes 3D histograms of descriptors in a cylindrical coordinate system with computational cell shape normalization, enabling comparisons between cells of different shape. Densities are obtained via adaptive kernel density estimation, and we use the Circular Earth Mover's Distance to measure the dissimilarity between densities associated to different experimental conditions. A statistical analysis on these distances reliably takes into account the biological variability over replicated experiments.

- **Participants**: Thierry Pécot, Charles Kervrann, Jean Salamero.
- **Contact:** Thierry Pécot, Charles Kervrann.
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::...
- **Languages:** C/C++ and JAVA (plug-in ICY: http://icy.bioimageanalysis.org).

6.3. 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:** [12]

6.4. ATLAS

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The ATLAS software enables to detect spots in 2D fluorescence 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:** [1]

6.5. 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 shape-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/).

6.6. 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/).

6.7. 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) [5]. 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:** [5]

6.8. 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++.

6.9. 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.

- **Participants:** Denis Chrétien, Charles Kervrann, Sophie Blestel.
- **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/).

6.10. 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/).

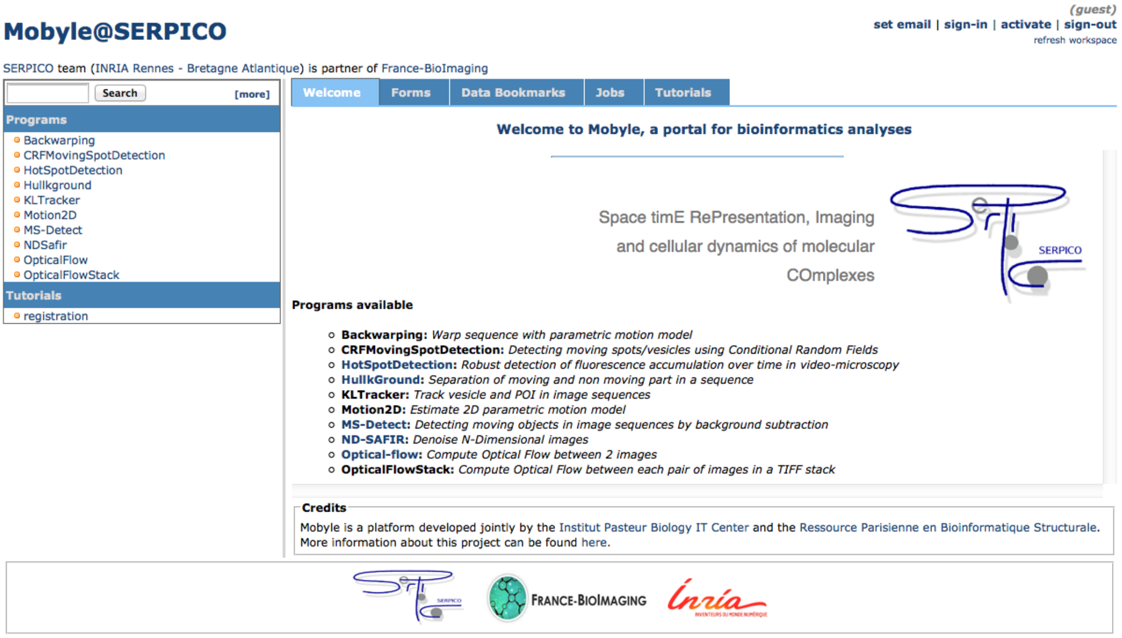
6.11. Platforms

6.11.1. Mobyle@Serpico plateform and software distribution

The objective is to disseminate the distribution of SERPICO image processing software for biologists:

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: QUANTEV, C-CRAFT[12], ATLAS[1], HOTSPOTDETECTION[56], HULLKGROUND[45], KLTRACKER[55], MOTION2D[54], MS-DETECT[47], ND-SAFIR[5], OPTICALFLOW and FLUX ESTIMATION [12]. The web interface makes our image processing methods available for biologists 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).



Welcome to Mobyle, a portal for bioinformatics analyses

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.*

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 [5], HULLKGROUND [45], MOTION2D [54], HOTSPOTDETECTION [56], STLAS [1]. The C-CRAFT algorithm [12] 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.

6.11.2. 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

5. New Software and Platforms

5.1. DICA : Discrete Independent Component Analysis

FUNCTIONAL DESCRIPTION

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.

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

5.2. LinearFW: Implementation of linearly convergent versions of Frank-Wolfe

FUNCTIONAL DESCRIPTION

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, 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

5.3. cnn_head_detection: Context-aware CNNs for person head detection

FUNCTIONAL DESCRIPTION

Code for ICCV 2015 paper "Context-aware CNNs for person head detection": 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

5.4. Lightning: large-scale linear classification, regression and ranking in Python

FUNCTIONAL DESCRIPTION

Lightning is a Python library for large-scale machine learning. More specifically, the library focuses on linear models for classification, regression and ranking. Lightning is the first project to integrate scikit-learn-contrib, a repository of high-quality projects that follow the same API conventions as scikit-learn. Compared to scikit-learn, the main advantages of lightning are its scalability and its flexibility. Indeed, lightning implements cutting-edge optimization algorithms that allow to train models with millions of samples within seconds on commodity hardware. Furthermore, lightning can leverage prior knowledge thanks to so-called structured penalties, an area of research that has recently found applications in domains as diverse as biology, neuroimaging, finance or text processing. Lightning is available under the 3-clause BSD license at http://contrib.scikit-learn.org/lightning/.

- Contact: Fabian Pedregosa
- URL: http://contrib.scikit-learn.org/lightning/

SIROCCO Project-Team

6. New Software and Platforms

6.1. 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

6.2. VideoInpainting

KEYWORDS: Video Inpainting - Motion informations - Loss concealment - BMFI (Bilinear Motion Field Interpolation)
SCIENTIFIC DESCRIPTION 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.

- Participants: Ronan Le Boulch and Olivier Le Meur
- Contact: Olivier Le Meur

6.3. Visual Fixation Analysis

SCIENTIFIC 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
- Partner: Université de Rennes 1
- Contact: Olivier Le Meur

6.4. Saccadic model

SCIENTIFIC DESCRIPTION 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. A presentation of this model is available on the following link: http://fr.slideshare.net/OlivierLeMeur/saccadic-model-of-eye-movements-for-freeviewing-condition. 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) under the number IDDN.FR.001.240029.000.S.P.2016.000.10000.

- Participants: Olivier Le Meur
- Partner: Université de Rennes 1
- Contact: Olivier Le Meur

6.5. ADT-ATep

The scientific and industrial community is nowadays exploring new multimedia applications using 3D data (beyond stereoscopy). In particular, Free Viewpoint Television (FTV) has attracted much attention in the recent years. In those systems, the user can choose in real time the view angle from which he wants to observe the scene. Despite the great interest for FTV, the lack of realistic and ambitious datasets penalizes the research effort. The acquisition of such sequences is very costly in terms of hardware and working effort, which explains why no multi-view videos suitable for FTV has been made available yet.

A project founded by Inriahub has recently started in the SIROCCO team. Called ATeP for “Acquisition, Traitement et Partage" (Acquisition, Processing and Sharing), it targets the acquisition of such dataset. Another interesting aspect of this project is that the acquisition system relies on omnidirectional cameras. The dataset will thus interest all the industries and scientists currently working on the development of efficient processing and coding tools for 360 videos.

- Participants: Cédric Le Cam, Thomas Maugey
- Partner: Inria
- Contact: Thomas Maugey

SISTM Project-Team

6. New Software and Platforms

6.1. New software

6.1.1. clogitLasso

Lasso Estimation of Conditional Logistic Regression Models for Case-Crossover and Matched Case-Control Studies

- KEYWORDS: Classification , Statistics , Cluster , Machine learning , Regression
- FUNCTIONAL DESCRIPTION Fit a sequence of conditional logistic regression models with lasso, for small to large sized samples.
- Contact: Marius Kwémou
- URL: https://github.com/robingenuer/

6.1.2. COVVSURF

Combination of Clustering Of Variables and Variable Selection Using Random Forests

- KEYWORDS: Classification , Statistics , Cluster , Machine learning , Regression
- FUNCTIONAL DESCRIPTION This package implements a two stage strategy, where first we use ClustOfVar package to perform a clustering of variables and second we use VSURF package to select features (i.e. synthetic variables built in the first step).
- Contact: Robin Genuer
- URL: https://github.com/robingenuer/CoVVSURF

6.1.3. NPflow

Bayesian Nonparametrics for Automatic Gating of Flow-Cytometry Data

- KEYWORDS: Bayesian estimation , Bioinformatics , Biostatistics
- FUNCTIONAL DESCRIPTION Dirichlet process mixture of multivariate normal, skew normal or skew t-distributions modeling oriented towards flow-cytometry data pre-processing applications.
- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/NPflow/

6.1.4. tcgsaseq

Time-Course Gene Set Analysis for RNA-Seq Data

- KEYWORDS: Genomics , Biostatistics , Statistical modeling , RNA-seq , Gene Set Analysis
- FUNCTIONAL DESCRIPTION Gene set analysis of longitudinal RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights.
- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/tcgsaseq/

6.1.5. CD4 Shiny

Reference curves for CD4 response to antiretroviral therapy in HiV infected patients

- KEYWORDS: HIV infection, antiretroviral therapy, cd4 response, reference curves, quantile regression
- FUNCTIONAL DESCRIPTION References curves for CD4 response to antiretroviral therapy in HIV infected patients derived from large cohorts and estimated according to known factors associated with the response to antiretroviral therapy.
- Contact: Rodolphe Thiébaut
- URL: http://shiny.isped.u-bordeaux.fr/CD4refcurves/

6.2. Older software still maintained by SISTM

6.2.1. NIMROD

Normal approximation Inference in Models with Random effects based on Ordinary Differential equations

- KEYWORDS: Biostatistics - Optimization
- FUNCTIONAL DESCRIPTION We have written a specific program called NIMROD for estimating parameter of ODE based population models.
- Contact: Rodolphe Thiebaut
- URL: http://etudes.isped.u-bordeaux2.fr/BIOSTATISTIQUE/NIMROD/documentation/html/index.html

6.2.2. R2GUESS

Graphical processing Unit Evolutionary Stochastic Search

- KEYWORDS: Bioinformatics - Biostatistics
- FUNCTIONAL DESCRIPTION R2GUESS package is a wrapper of the GUESS (Graphical processing Unit Evolutionary Stochastic Search) program. GUESS is a computationally optimised C++ implementation of a fully Bayesian variable selection approach that can analyse, in a genome-wide context, single and multiple responses in an integrated way. The program uses packages from the GNU Scientific Library (GSL) and offers the possibility to re-route computationally intensive linear algebra operations towards the Graphical Processing Unit (GPU) through the use of proprietary CULA-dense library.
- Contact: Rodolphe Thiebaut
- URL: https://cran.r-project.org/web/packages/R2GUESS/index.html

6.2.3. 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. Under development, and soon to be 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

6.2.4. 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: https://cran.r-project.org/web/packages/VSURF/index.html

6.2.5. marqLevAlg

Function optimization (minimization or maximization)

- KEYWORDS: Optimization - Biostatistics
- FUNCTIONAL DESCRIPTION An R package for function optimization. Available on CRAN, this package performs a minimization of function based on the Marquardt-Levenberg algorithm. This package is really useful when the surface to optimize is non-strictly convex or far from a quadratic function. A new convergence criterion, the relative distance to maximum (RDM), allows the user to have a better confidence in the stopping points, other than basic algorithm stabilization.
- Contact: Melanie Prague
- URL: https://cran.r-project.org/web/packages/marqLevAlg/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) [4]. 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. We also recently set up an educational platform on top of PlugDB, named SIPD (Système d'Information privacy-by-Design) and used at ENSIIE, INSA CVL and UVSQ through the Versailles Sciences Lab fablab, 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 and Aydogan Ersoz
- Contact: Nicolas Anciaux
- URL: https://project.inria.fr/plugdb/

5.2. Privacy Preserving Mobile Laboratory

FUNCTIONAL DESCRIPTION: We have started to design a privacy preserving mobile laboratory used as an experimental platform for multidisciplinary research launched 'in vivo'. The goal is to conduct reliable surveys and avoid the privacy paradox (what users declare on their privacy behavior is far from what they effectively do). The platform, built on top of PlugDB, includes two android applications, a "server" which takes as input a questionnaire description and broadcast it on demand to the client applications. Users interact with the questionnaire on the client applications, storing the detailed answers in their PlugDB personal server. Then a secure distributed computation takes place (between users' PlugDB servers) and computes non-sensitive global statistics based on potentially sensitive raw answers. A beta-version of this platform was developed during the PhD of Athanasia Katsouraki and was used for a pre-experimentation targeting 140 students. While the experiment was successful, it showed the limitation and complexity of the initial setting (laptops, required Internet access, complexity in the questionnaire deployment). We designed and implement a second platform running on android tablets with a local router and automatic questionnaire deployment. The platform has been demonstrated in several forums and very recently at the Sénat in Paris. This platform represents a backing for two PhD theses on privacy (the first one in economics, the second one in our team) funded in 2016 by the interdisciplinary doctoral program at UPSay (IDI 2016).

- Participants: Nicolas Anciaux, Luc Bouganim, Aydogan Ersoz, Athanasia Katsouraki, Riad Ladjel, Benjamin Nguyen, Remy Pasquion, Paul Tran Van
- Contact: Luc Bouganim
- URL: https://project.inria.fr/plugdb/en/PPML

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 Dupont De Dinechin, Nicolas Brunie, Matei Istoan and Antoine Martinet
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - UPVD
- Contact: Florent Dupont De Dinechin
- URL: http://flopoco.gforge.inria.fr/

5.2. WSNet

KEYWORD: Network simulator
FUNCTIONAL DESCRIPTION

WSNet 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. We still hope to find the proper resource to make WSNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem, Quentin Lampin, Alexandre Mouradian and Fabrice Valois
- Partner: CEA-LETI
- Contact: Guillaume Chelius
- URL: https://gforge.inria.fr/projects/wsnet-3/

5.3. 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 Jean-Marie 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
- URL: https://bil.inria.fr

5.4. 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

5.5. 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

5.6. 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 IoT test-beds (IoT-Lab), 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 int 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.

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[0] http://www.inria.fr/centre/grenoble/actualites/inauguration-reussie-de-la-plateforme-cortexlab-equipex-fit

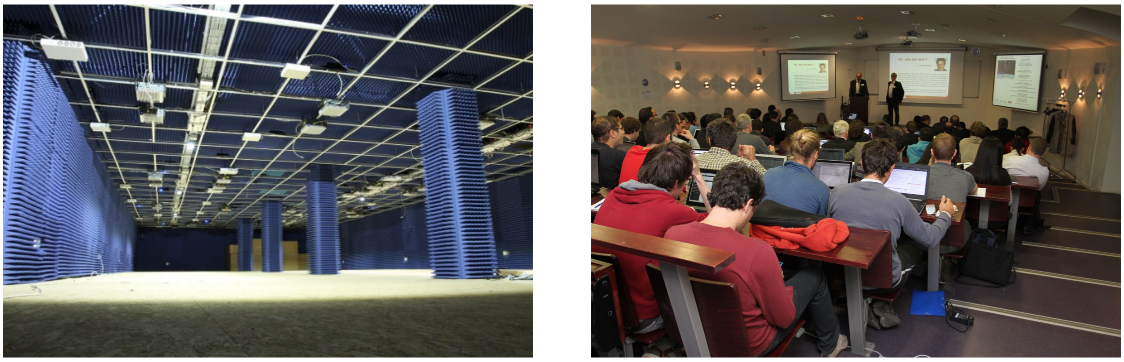

Figure 5. Photo of the FIT/CortexLab experimentation room installed and a snaptshot of the inauguration meeting

SPADES Project-Team

5. New Software and Platforms

5.1. 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, Zain Hammadeh (TU Braunschweig) and Leonie Ahrendts (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. This year, pyCPA_TWCA has been extended to task chains but remains limited to uniprocessor systems, scheduled according to static priority scheduling. A public release is planned but has not yet taken place.

- Authors: Zain Hammadeh and Leonie Ahrendts and Sophie Quinton.
- Contact: Sophie Quinton.

SPECFUN Project-Team

5. New Software and Platforms

5.1. DDMF

Dynamic Dictionary of Mathematical Functions
FUNCTIONAL DESCRIPTION

Web site consisting of interactive tables of mathematical formulas on elementary and special functions. The formulas are automatically generated by OCaml and computer-algebra routines. Users can ask for more terms of the expansions, more digits of the numerical values, proofs of some of the formulas, etc.
This year, Maxence Guesdon started to port DDMF to the new DynaMoW. To this end, a special environment has been set up to be able to use the Inria continuous-integration platform.

- Participants: Alexandre Benoit, Frédéric Chyzak, Alexis Darrasse, Stefan Gerhold, Thomas Grégoire, Maxence Guesdon, Christoph Koutschan, Marc Mezzarobba and Bruno Salvy
- Contact: Frédéric Chyzak
- URL: http://ddmf.msr-inria.inria.fr/1.9.1/ddmf

5.2. DynaMoW

Dynamic Mathematics on the Web
FUNCTIONAL DESCRIPTION

DynaMoW is a programming tool for controlling the generation of mathematical websites that embed dynamical mathematical contents generated by computer-algebra calculations. Implemented in OCaml.
After a complete redesign and rewrite last year, to get more reactiveness and configurability, the implementation of DynaMoW was made more robust this year while porting ECS to this new library. It was next further enhanced, in particular in order have informative and reliable traces of execution, to help with the debugging of asynchronous parallel executions of services.

- 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

ECS is an online 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.
This year, we finalized the port of ECS to the last evolutions of DynaMoW. A new website was setup, and ECS is now again online, after a few years of discontinuation for technical reasons.

- Participants: Stéphanie Petit, Alexis Darrasse, Frédéric Chyzak and Maxence Guesdon
- Contact: Frédéric Chyzak
- URL: http://ecs.inria.fr/

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.
This year we experimented the maintenance of the library using the public repository stored on the github platform since December 2015. This allowed for merging several contributions from external users and improved significantly the communication with the community of users. A new website has also been set up, which includes pointers to various teaching and documentation resources.

- Participants: Andrea Asperti, Jeremy Avigad, Yves Bertot, Cyril Cohen, Francois 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. Ssreflect

FUNCTIONAL DESCRIPTION

Ssreflect is a tactic language extension to the Coq system, developed by the Mathematical Components team.
This year we improved the manual of the language, in order to document new features and to clarify some older parts of the document.

- Participants: Cyril Cohen, Yves Bertot, Laurence Rideau, Enrico Tassi, Laurent Thery, Assia Mahboubi and Georges Gonthier
- Contact: Yves Bertot
- URL: http://ssr.msr-inria.inria.fr/

SPHINX Project-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 compute 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. μ-diff

μ-diff is a Matlab toolbox developed with B. Thierry (UPMC, France) for solving 2D multiple scattering problems by a random collection of circular cylinders.

- Contact: Xavier Antoine
- URL: http://mu-diff.math.cnrs.fr/mu-diff/

6.4. Platforms

6.4.1. A software for the efficient assignment of L-INP students

Each year, the 1500 students of the L-INP Collégium (gathering most of the engineering students in Lorraine) have to choose one or several among the 70+ courses. J-F. Scheid, a member of our team, is a faculty member of TELECOM Nancy and developed a solver giving a fair, fast and reliable assignment of the students to the courses. The solver works with integer linear optimization and is written in Python and CBC/COIN-OR.

SPIRALS Project-Team

6. New Software and Platforms

6.1. APISENSE

KEYWORDS: Mobile sensing - Crowd-sensing - Crowd-sourcing - Android
FUNCTIONAL DESCRIPTION

APISENSE platform is a software solution to collect various contextual information from Android devices (client application) and automatically upload collected data to a server (deployed as a SaaS). APISENSE is based on a Cloud computing infrastructure to facilitate datasets collection from significant populations of mobile users for research purposes.

- Participants: Nicolas Haderer, Romain Rouvoy, Christophe Ribeiro, Julien Duribreux and Antoine Veuiller
- Partner: Université Lille 1
- Contact: Romain Rouvoy
- URL: http://www.apisense.io

6.2. Nopol

KEYWORD: Automatic software repair
FUNCTIONAL DESCRIPTION

Nopol is an automatic software repair tool for buggy conditional statements (i.e., if-then-else statements) in Java programs. Nopol takes a buggy program as well as a test suite as input and generates a patch with a conditional expression as output. The test suite is required to contain passing test cases to model the expected behavior of the program and at least one failing test case that reveals the bug to be repaired. The process of Nopol consists of three major phases. First, Nopol employs angelic fix localization to identify expected values of a condition during the test execution. Second, runtime trace collection is used to collect variables and their actual values, including primitive data types and objected-oriented features (e.g., nullness checks), to serve as building blocks for patch generation. Third, Nopol encodes these collected data into an instance of a Satisfiability Modulo Theory (SMT) problem, then a feasible solution to the SMT instance is translated back into a code patch.

- Contact: Martin Monperrus
- URL: https://github.com/SpoonLabs/nopol/

6.3. PowerAPI

KEYWORD: Energy management
FUNCTIONAL DESCRIPTION

PowerAPI is a library for monitoring the energy consumption of software systems.

PowerAPI differs from existing energy process-level monitoring tool in its software orientation, with a fully customizable and modular solution that let the user to precisely define what he/she wants to monitor. PowerAPI is based on a modular and asynchronous event-driven architecture using the Akka library. PowerAPI offers an API which can be used to define requests about energy spent by a process, following its hardware resource utilization (in term of CPU, memory, disk, network, etc.).

- Participants: Romain Rouvoy, Adel Noureddine, Loic Huertas and Maxime Colmant
- Contact: Romain Rouvoy
- URL: http://www.powerapi.org

6.4. SPOON

KEYWORDS: Java - Code analysis
FUNCTIONAL DESCRIPTION

Spoon is an open-source library that enables you to transform (see below) and analyze Java source code (see example) . Spoon provides a complete and fine-grained Java metamodel where any program element (classes, methods, fields, statements, expressions…) can be accessed both for reading and modification. Spoon takes as input source code and produces transformed source code ready to be compiled.

- Participants: Nicolas Petitprez, Martin Monperrus, Lionel Seinturier and Gérard Paligot
- Contact: Martin Monperrus
- URL: http://spoon.gforge.inria.fr

6.5. Saloon

KEYWORDS: Feature Model - Software Product Line - Cloud computing - Model-driven engineering - Ontologies
FUNCTIONAL DESCRIPTION

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.

- Participants: Clement Quinton, Daniel Romero Acero, Laurence Duchien, Lionel Seinturier and Romain Rouvoy
- Partner: Université Lille 1
- Contact: Lionel Seinturier
- URL: https://gitlab.irisa.fr/drome00A/saloon

STARS Project-Team

5. New Software and Platforms

5.1. 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 Gaffe and Annie Ressouche
- Contact: Annie Ressouche
- URL: http://www-sop.inria.fr/teams/pulsar/projects/Clem/

5.2. 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, Francois Bremond and Vasanth Bathrinarayanan
- Contact: Francois Bremond

5.3. 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 Francois Bremond
- Contact: Francois Bremond

5.4. 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, Anais Ducoffe, Sofia Zaidenberg, Annunziato Polimeni and Julien Gueytat
- Partner: Neosensys
- Contact: Anais Ducoffe

5.5. 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 and Francois Bremond
- Contact: Francois Bremond

5.6. 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, Francois Bremond, Annunziato Polimeni and Yves Pichon
- Partner: Neosensys
- Contact: Francois Bremond

5.7. 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 - I2R - Université de Hamburg - USC Californie
- Contact: Francois Bremond
- URL: https://team.inria.fr/stars/software

5.8. 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 Francois Bremond
- Contact: Francois Bremond
- URL: http://www-sop.inria.fr/teams/pulsar/EvaluationTool/ViSEvAl_Description.html

5.9. py_ad

py action detection

FUNCTIONAL DESCRIPTION

Action Detection framework Allows user to detect action in video stream. It uses model trained in py_ar.

- Participants: Michal Koperski and Francois Bremond
- Contact: Michal Koperski

5.10. 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 Francois Bremond
- Contact: Michal Koperski

5.11. 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

5.12. 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 Francois Bremond
- Contact: Michal Koperski

5.13. 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 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 Francois Bremond
- Contact: Michal Koperski

STEEP Project-Team

6. New Software and Platforms

6.1. Comptabilité Ecologique

FUNCTIONAL DESCRIPTION

Databases, database handling tools and data visualization tools (on the website). Databases include socio-economic and environmental datasets. Visualization tools include interactive piecharts, maps and Sankey diagrams.

- Participants: Jean-Yves Courtonne and Pierre-Yves Longaretti
- Contact: Jean-Yves Courtonne
- URL: http://www.eco-data.fr

6.2. InterfacesTRANUS

FUNCTIONAL DESCRIPTION

This software contains two interfaces dedicated to facilitating the usage of the TRANUS integrated land use and transport model+software. The first interface is dedicated to enabling the execution of the TRANUS binary programs without the need to use the console or the TRANUS GUI. The second interface provides an aid for calibrating a TRANUS model, by interactively exploring ranges of different parameters of a TRANUS model and visualising model outputs across these ranges.

- Participants: Peter Sturm, Julien Armand and Thomas Capelle
- Contact: Peter Sturm
- URL: http://gitlab.inria.fr/tranus/TRANUS_Interfaces

6.3. LUM_OSM

Land Use Mix calculation from OpenStreepMap data

FUNCTIONAL DESCRIPTION

The software uses Mapzen Metro Extracts to retrieve the OpenStreetMap data of a given region in the PostgreSQL format. Afterwards, a continuous representation of residential and activity land uses is created. Finally, a GIS output containing the degree of land use mixture is calculated by means of using the land uses maps. The implemented approach is documented in [9].

- Participants: Martís Bosch Padros, Luciano Gervasoni, Serge Fenet and Peter Sturm
- Partners: EPFL - Ecole Polytechnique Fédérale de Lausanne - LIRIS
- Contact: Peter Sturm
- URL: http://github.com/martibosch/landusemix

6.4. QGIS_Tranus_Reports

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 – 2D or 3D – 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.

- Participants: Patricio Inzaghi, Peter Sturm, Huu Phuoc Nguyen, Fausto Lo Feudo and Thomas Capelle
- Contact: Peter Sturm
- URL: https://gitlab.inria.fr/tranus/QGIS_Tranus_Reports

6.5. 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: Emmanuel Prados, Patrick Criqui, Constantin Ilasca, Olivier Boucher and Hélène Benveniste
- Partners: EDDEN - IPSL
- Contact: Emmanuel Prados
- URL: http://redem.gforge.inria.fr/

6.6. REDEM web

REDEM Web is a reimplementation of the REDEM soft as a web application. The main library which contains the code corresponding to REDEM model is written in Python and the web part uses Javascript.

KEYWORDS: Benchmarking - Climate change - Global warming - Greenhouse gas emissions

- Participants: Emmanuel Prados, Patrick Criqui, Constantin Ilasca, Olivier Boucher, Hélène Benveniste and Nicolas Assouad
- Partners: EDDEN - UPMC
- Contact: Emmanuel Prados
- URL: http://redem.inria.fr/

6.7. 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 ans website is to automatize most of the work of standard input-output analysis and to visualize the resultes in a user-friendly way in order to efficently adress related key environmental questions.

- Participants: Julien Alapetite and Jean-Yves Courtonne
- Contact: Jean-Yves Courtonne

STORM Team

5. New Software and Platforms

5.1. 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.

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: Emmanuel Agullo, Mathieu Faverge, Cédric Castagnede and Florent Pruvost
- 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/

5.2. KLANG-OMP

The KStar OpenMP Compiler
KEYWORDS: Compilers - Task scheduling - OpenMP - Source-to-source compiler - Data parallelism
FUNCTIONAL DESCRIPTION

The Klang-Omp compiler, now renamed KStar following the recommendation of the local experimentation and development service, is a source-to-source OpenMP compiler for languages C and C++. The KStar compiler translates OpenMP directives and constructs into API calls from the StarPU runtime system or the XKaapi runtime system. The KStar compiler is virtually fully compliant with OpenMP 3.0 constructs. The KStar 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

5.3. 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

5.4. MORSE

- Contact: Emmanuel Agullo
- URL: http://icl.cs.utk.edu/morse/

5.5. AFF3CT

A Fast Forward Error Correction Tool (previously named P-Edge).

KEYWORDS: Code generation - Error Correction Code
FUNCTIONAL DESCRIPTION

The AFF3CT 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.

- Previous name: P-Edge
- Authors: Adrien Cassagne, Olivier Aumage, Bertrand Le Gal, Camille Leroux and Denis Barthou
- Partner: IMS
- Contact: Adrien Cassagne
- URL: https://aff3ct.github.io/

5.6. 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 (eg. 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 (eg. 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 (eg. 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: Cédric Augonnet, Samuel Thibault, Nathalie Furmento, Simon Archipoff, Jérôme Clet-Ortega, Nicolas Collin, Ludovic Courtes, Mehdi Juhoor, Xavier Lacoste, Benoît Lize, Ludovic Stordeur, Cyril Roelandt, Corentin Salingue, Chiheb Sakka, Samuel Pitoiset, François Tessier, Pierre-André Wacrenier, Andra Hugo, Terry Cojean, Raymond Namyst, Olivier Aumage and Marc Sergent
- Contact: Olivier Aumage
- URL: http://starpu.gforge.inria.fr/

5.7. hwloc

Hardware Locality

KEYWORDS: HPC - Topology - Open MPI - Affinities - GPU - Multicore - NUMA - 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 applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

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
- Partners: AMD - Intel - Open MPI consortium
- Contact: Brice Goglin
- URL: http://www.open-mpi.org/projects/hwloc/

SUMO Project-Team

6. New Software and Platforms

6.1. Active Workspaces

KEYWORDS: Guarded attribute grammar - Active workspace - Artifact centric workflow system

SCIENTIFIC DESCRIPTION

Tool for computer supported cooperative work where a user's workspace is given by an active structured repository containing the pending tasks together with information needed to perform the tasks. Communication between active workspaces is asynchronous using message passing. The tool is based on the model of guarded attribute grammars [44]. Late in 2015 Éric Badouel produced in Haskell a software prototype implementing active workspaces based on Guarded Attribute Grammars (GAGs).

Concurrently, Christophe Morvan was beginning a startup project consisting in making on-line collective decision making tools: *Open Agora*. This project included collaboration workspaces for people participating in constructing possible decisions. There was a natural connection between the prototype, and the startup project.

In order to make industrial use of the GAG prototype, Olivier Bache (already involved in the Open agora project) applied to a 6 month InriaHub program (between April and September 2016). During these 6 months he bundeled the prototype into an API (also programmed in Haskell) and developped a web infrastructure, based on the PHP framework, to allow the interaction with Active Workspaces in a browser. This developpement will be licenced to Open Agora SAS after its creation expected in January 2017.

FUNCTIONAL DESCRIPTION

Prototype in Haskell of user's active workspaces based on Guarded Attribute Grammars.

- Author: Eric Badouel
- Contact: Eric Badouel
- URL: http://people.rennes.inria.fr/Eric.Badouel/Research/ActiveWorkspaces.html

6.2. SIMSTORS

SIMSTORS is a simulator for regulated stochastic timed Petri nets. These Petri nets are a variant of stochastic and timed nets, whose 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. This year, the software has been extended to consider headway management.

- Participants: Loïc Hélouët and Karim Kecir
- Contact: Loïc Hélouët
- URL: http://www.irisa.fr/sumo/Software/SIMSTORS/

TACOMA Team

5. New Software and Platforms

5.1. THEGAME: data fusion for Smart Home and Smart Building

KEYWORDS: Smart home - Smart building

- Participants: Yoann Maurel and Frédéric Weis
- Partner: Université de Rennes 1
- Contact: Frédéric Weis
- URL: https://github.com/bpietropaoli/THEGAME/ (C-version)
- URL: https://bitbucket.org/TACOMA-irisa/java-bft (Java-version)

SCIENTIFIC 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 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. Platform Pervasive_RFID

KEYWORDS: Composite objects - RFID

- Participants: Paul Couderc and Anthony Blair
- Partner: Université de Rennes 1 (IETR)
- Contact: Paul Couderc

SCIENTIFIC DESCRIPTION

In 2016 we completed the RFID experiment testbed realized in 2014-2015 in collaboration with IETR (see Figure 2). This system allows both interactive testing as well as long running experiments of RFID reading protocols. It comprises a software platform 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).

5.3. Metamorphic Housing platform and Software

KEYWORDS: Smart Home - Metamorphic House

- Partner: Université de Rennes 1
- Partner: Université de Rennes 1 (Fondation Rennes 1)
- Contact: Michele Dominici and Frédéric Weis

SCIENTIFIC DESCRIPTION- SOFTWARE

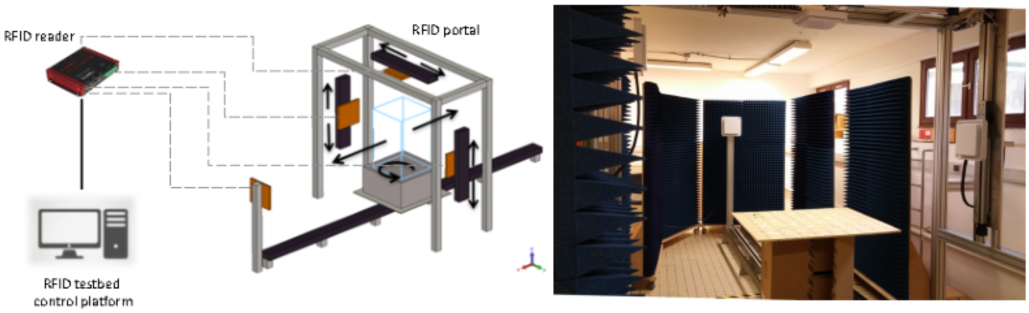

Figure 2. RFID testbed

As part of the experimentation of the On-demand room see 6.6 , we have developed a software system that will be used to manage the room and provide functionalities to end users and building managers (access control, electrical and time consumption monitoring and report, room state display...). The software is expected to be deployed in the building that hosts the experimentation. This software is co-developed by Michele Dominici (University of Rennes 1), Guillermo Andrade (SED Inria) and Ghislain Nouvel (MobBI platform). Contributions might be provided by members of the Diverse project-team. Intellectual protection is expected to be applied on such software.

SCIENTIFIC DESCRIPTION- PLATFORM

In 2015, we realized a prototype of the on-demand room as an immersive interactive virtual-reality application, leveraging the Immersia platform (see https://raweb.inria.fr/rapportsactivite/RA2015/tacoma/uid29.html), with real domestic appliances connected to Immersa. In 2016, the experimentation of the On-demand room is organized in the following steps: modification of the original building to create a common, On-demand room between two apartments; deployment of the computer and hardware and software that we are developing; rental of the apartments to two households, for an estimated duration of one year. The building that will host the experimentation is showed in Figure 3 . During the rental of the apartments, data will be collected and stored about the use of the room by households. Data will include time of occupation, mode (private or shared), consumptions, errors etc. The On-demand room will thus constitute an experimentation platform, where real people live and produce data that can be analyzed for statistical purposes. Produced data could also be used in combination with interviews of the occupants to improve the functionalities of the On-demand room, evaluate acceptance and appropriation.

5.4. ISO/IEC 15118-2 Open source Implementation

KEYWORDS: Smart Grid - Intelligent Transport System

- Partner: Telecom Bretagne
- Contact: Jean-Marie Bonnin

SCIENTIFIC DESCRIPTION

The ISO/IEC 15118 standard, named "Road vehicles ? Vehicle-to-Grid Communication Interface", defines how an electric vehicle and a charging station should communicate. It enables the Smart Charging of electric vehicles by allowing them to plan their charging sessions. As we want to be able to manage the charge of electric vehicles in our micro Smart Grid systems, we decided to implement the protocol defined by this standard. The goal is also to participate actively in the design of the new version of this protocol. During a charging session the charging station provides the vehicle with the status of the electric power grid. The vehicle

Figure 3. On-demand room real experimentation

is then able to plan its sharing session accordingly. It sends back its charge plan to the charging station, so that the Smart Grid is aware of it. The protocol also provides security and authentication features.

This software platform was implemented onto small PCs, and was used to control the charge in a small and portable demonstration platform, to demonstrate how it is possible to interconnect this high level decision and communication software with low level components, such as a Battery Management System (BMS), and a battery charger. In 2016, in the context of the Greenfeed project our software has been demonstrated to control the charge of the electric vehicle during the final demonstration of the project. The integration work has been done in collaboration with VeDeCom.

TADAAM Team

6. New Software and Platforms

6.1. NetLoc

Network Locality
FUNCTIONAL DESCRIPTION

NETLOC (Network Locality) is a library that extends HWLOC to network topology information by assembling HWLOC knowledge of server internals within graphs of inter-node fabrics such as Infiniband, Intel OmniPath or Cray networks. NETLOC builds a software representation of the entire cluster so as to help application properly place their tasks on the nodes. It may also help communication libraries optimize their strategies according to the wires and switches. NETLOC targets the same challenges as HWLOC but focuses on a wider spectrum by enabling cluster-wide solutions such as process placement. NETLOC is distributed within HWLOC releases starting with HWLOC 2.0.

- Participants: Cyril Bordage and Brice Goglin
- Contact: Brice Goglin
- URL: http://www.open-mpi.org/projects/netloc/

6.2. NewMadeleine

KEYWORDS: High-performance calculation - 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, Nathalie Furmento, Raymond Namyst and Clement Foyer
- Contact: Alexandre Denis
- URL: http://pm2.gforge.inria.fr/newmadeleine/

6.3. PaMPA

Parallel Mesh Partitioning and Adaptation
KEYWORDS: Dynamic load balancing - Unstructured heterogeneous meshes - Parallel remeshing - Subdomain decomposition - Parallel numerical solvers
SCIENTIFIC DESCRIPTION

PAMPA is a parallel library for handling, redistributing and remeshing unstructured meshes on distributed-memory architectures. PAMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes. It provides solver writers with a distributed mesh abstraction and an API to:

- describe unstructured and possibly heterogeneous meshes, on the form of a graph of interconnected entities of different kinds (e.g. elements, faces, edges, nodes);
- attach values to the mesh entities;
- distribute such meshes across processing elements, with an overlap of variable width;
- perform synchronous or asynchronous data exchanges of values across processing elements;
- describe numerical schemes by means of iterators over mesh entities and their connected neighbors of a given kind;
- redistribute meshes so as to balance computational load;
- perform parallel dynamic remeshing, by applying adequately a user-provided sequential remesher to relevant areas of the distributed mesh.

PAMPA runs concurrently multiple sequential remeshing tasks to perform dynamic parallel remeshing and redistribution of very large unstructured meshes. E.g., it can remesh a tetrahedral mesh from 43 millio elements to more than 1 billion elements on 280 Broadwell processors in 20 minutes.

FUNCTIONAL DESCRIPTION

Parallel library for handling, redistributing and remeshing unstructured, heterogeneous meshes on distributed-memory architectures. PAMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes.

- Participants: Cedric Lachat, François Pellegrini and Cécile Dobrzynski
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Cedric Lachat
- URL: http://project.inria.fr/pampa/

6.4. SCOTCH

KEYWORDS: High-performance computing - Graph algorithms - Domain decomposition - Static mapping - Mesh partitioning - Sparse matrix ordering

SCIENTIFIC DESCRIPTION

SCOTCH is a software package and libraries for sequential and parallel graph partitioning, static mapping and clustering; sequential mesh and hypergraph partitioning; and sequential and parallel sparse matrix block ordering.

Its main use is to subdivise a scientific problem, expressed as a graph, into a set of subproblems as independent as possible from each other (in terms of connecting edges).

FUNCTIONAL DESCRIPTION

SCOTCH takes the form of a set of libraries, plus additional standalone programs. The sequential and parallel libraries provide a set of interfaces to describe centralized and distributed graphs to partition, the target architectures to map onto, the resulting centralized and distributed mapping and ordering structures, etc. SCOTCH takes advantage of Posix threads, and its parallel version, PT-SCOTCH, uses the MPI interface.

- Participants: François Pellegrini, Cédric Lachat, Rémi Barat and Cédric Chevalier
- Partners: CNRS - IPB - Region Aquitaine
- Contact: François Pellegrini
- URL: http://www.labri.fr/~pelegrin/scotch/

6.5. TreeMatch

KEYWORDS: Intensive parallel computing - High-Performance Computing - Hierarchical architecture - Placement
SCIENTIFIC DESCRIPTION

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 and MPICH2.
FUNCTIONAL DESCRIPTION

TreeMatch is a library for performing process placement based on the topology of the machine and the communication pattern of the application.

- Participants: Emmanuel Jeannot, François Tessier, Adele Villiermet, Guillaume Mercier and Pierre Celor
- Partners: CNRS - IPB - Université de Bordeaux
- Contact: Emmanuel Jeannot
- URL: http://treematch.gforge.inria.fr/

6.6. hwloc

Hardware Locality
KEYWORDS: HPC - Topology - Open MPI - Affinities - GPU - Multicore - NUMA - 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 applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

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
- Partners: AMD - Intel - Open MPI consortium
- Contact: Brice Goglin
- URL: http://www.open-mpi.org/projects/hwloc/

TAMIS Team

6. New Software and Platforms

6.1. MHD

GNU libmicrohttpd
KEYWORDS: Embedded - Web 2.0
SCIENTIFIC DESCRIPTION

We are providing a standards compliant and complete implementation of the HTTP server protocol that allows developers to easily write correct HTTP servers. Key challenges include code size minimization (for IoT devices), performance (zero copy, scalability to 100k concurrent connections), portability and security. MHD is already widely used in production by both academic and industrial users. Ongoing research challenges include formal verification.

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.

- Participants: Evgeny Grin, Christian Grothoff and Sree Hrsha Totakura
- Partner: The GNU Project
- Contact: Christian Grothoff
- URL: http://www.gnu.org/software/libmicrohttpd/

6.2. PLASMA Lab

KEYWORDS: Model Checking - Statistical - Model Checker - Runtime Analysis - Security - Code analysis - Statistics - Energy - Aeronautics
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 compact, efficient and flexible platform for statistical model checking of stochastic models. PLASMA Lab demonstrates the following advances: -Use your own simulator and checker via our plugin system. -Build your software around Plasma Lab using our API. -Prism (Reactives Modules Language-RML) and Biological languages supported. -Matlab and SytemC plugins. -Distributed architecture. Whether you plan to use several computers on a local area network or a grid, you can run PLASMA Lab in an easy way. -Fast algorithms. -Efficient data structure, low memory consumption. -Developed with Java for compatibility.

- Participants: Axel Legay, Sean Sedwards, Benoit Boyer, Louis-Marie Traonouez, Kevin Corre and Matthieu Simonin
- Contact: Axel Legay
- URL: http://plasma-lab.gforge.inria.fr/plasma_lab_doc/1.4.0/html/introduction.html#

6.3. Quail

FUNCTIONAL DESCRIPTION

Privacy is a central concern 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/

6.4. GNUnet

SCIENTIFIC DESCRIPTION

The GNUnet project seeks to answer the question what a modern Internet architecture should look like for a society that care about security and privacy. We are considering all layers of the existing well-known Internet, but are also providing new and higher-level abstractions (such as voting protocols, Byzantine consensus, etc.) that are today solved in application-specific ways. Research questions include the desired functionality of the overall stack, protocol design for the various layers as well as implementation considerations, i.e. how to implement the design securely.

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: Christian Grothoff, Florian Dold, Jeffrey Paul Burdges, Gabor Toth, Sree Hrsha Totakura and Alvaro Garcia Recuero
- Partner: The GNU Project
- Contact: Christian Grothoff
- URL: https://gnunet.org/

6.5. Taler

GNU Taler

KEYWORD: Privacy

SCIENTIFIC DESCRIPTION

Taler is a Chaum-style digital payment system that enables anonymous payments while ensuring that entities that receive payments are auditable. In Taler, customers can never defraud anyone, merchants can only fail to deliver the merchandise to the customer, and payment service providers can be fully audited. All parties receive cryptographic evidence for all transactions, still, each party only receives the minimum information required to execute transactions. Enforcement of honest behavior is timely, and is at least as strict as with legacy credit card payment systems that do not provide for privacy.

The key technical contribution underpinning Taler is a new refresh protocol which allows fractional payments and refunds while maintaining untraceability of the customer and unlinkability of transactions. The refresh protocol combines an efficient cut-and-choose mechanism with a link step to ensure that refreshing is not abused for transactional payments.

We argue that Taler provides a secure digital currency for modern liberal societies as it is a flexible, *libre* and efficient protocol and adequately balances the state's need for monetary control with the citizen's needs for private economic activity.

FUNCTIONAL DESCRIPTION

Taler is a new electronic payment system. It includes an electronic wallet for customers, a payment backend for merchants and the main payment service provider logic called the exchange. Taler offers Chaum-style anonymous payments for citizens, and income-transparency for taxability.

- Participants: Jeffrey Paul Burdges, Marcello Stanisci, Florian Dold, Gabor Toth and Christian Grothoff
- Partner: The GNU Project
- Contact: Christian Grothoff
- URL: http://taler.net/

6.6. VITRAIL - Visualisation Tool

Real-Time, Advanced, Immersive Visualization of Software / Visualizer
KEYWORD: Visualization of software
SCIENTIFIC DESCRIPTION

It is difficult for developers to explore and understand the source code of large programs, for example in objet-oriented languages programs featuring thousands of classes. Visualization methods based on daily life metaphors have thus been proposed. The VITRAIL Visualization tool (or VITRAIL Vizualizer) makes it possible to display, visualize and explore Java programs in a metaphorical way, using the city metaphor. An execution trace of the Java (byte)code provided by VITRAIL JBInstrace tool, is provided as input to VITRAIL Visualizer which displays a city-like metaphorical world showing the static structure of the code as well as some dynamic elements (calls).
This program may be used in Tamis as a basis for tools for the visualization of security events in programs.

FUNCTIONAL DESCRIPTION

This program makes it possible to displays, visualizes and explores Java programs in a metaphorical way (using the city metaphore). Useful for complex application developers/architects.

- Participants: Damien Bodenes, Olivier Zendra and Olivier Demengeon
- Contact: Olivier Zendra

6.7. VITRAIL 6 JBInsTrace

Real-Time, Advanced, Immersive Visualization of Software / Java Bytecode Instrumenter and Tracer
KEYWORDS: Java - Bytecode - Instrumentation - Profiling - Execution trace - Basic block
SCIENTIFIC DESCRIPTION

VITRAIL JBInsTrace is a program to instrument Java bytecode to trace its execution. The trace contains both static and dynamic information (calls). It is produced by intercepting the JVM class loader and replacing it by ours. Thus Java bytecode file are not modified, since instrumentation is performed on the fly, in memory. This makes it possible to instrument the whole program code, including libraries. Java source code is not needed. The trace which is then fed into our program VITRAIL Visualizer is an XML-like file.
This program may be used in Tamis as a basis for tools to instrument Java bytecode for security.

FUNCTIONAL DESCRIPTION

VITRAIL JBInsTrace is a program to instrument Java bytecode files to trace their execution. The trace is then fed into our VITRAIL Visualizer tool.

- Participants: Pierre Caserta and Olivier Zendra
- Contact: Olivier Zendra

6.8. Platforms

6.8.1. Malware'o'Matic

This LHS platform is dedicated to the collect, the categorization and the analyze of malware. We are currently interested in a specific kind of malware the ransomware. The platform grabs periodically samples of public data bases, executes the ransomware without virtualization on a victim PC and evaluate the implemented detection mechanisms. Once a ransomware has been executed the image of the OS is automatically restored and a new sample is evaluated. The platform is fully automatic and target Windows platforms (seven, W10) in both 32 bits and 64 bits versions.

6.8.2. Faustine

This LHS platform is dedicated to the EM fault injection experiments. It is composed of a motion table (XY), a pulse generator, an amplifier and a control PC. It injects EM pulses in a controlled way on a targeted device using an EM probe. It controls with a high precision the timing and the edges of the pulse. A recent development consists in adding a FPGA board to control the trigger in a more convenient and precise way. Then, the pulse can be triggered while a specific information is sent to the board under attack.

6.8.3. EMA

This last LHS platform is dedicated to side channel analysis (SCA) for evaluating the capabilities of dynamic countermeasure developed in the ANR Cogito. This platform uses a low cost oscilloscope, an EM probe and a set of software developed to perform the analysis. An additional oscilloscope, more performant has been added to the platform to target faster devices. We use the Julia language platform and custom developments to control the target and to analyze the EM traces.

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) [65] 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, Python) which allows to run and log experiments on a suite of test functions. Several testbeds are provided. (ii) a Python tool for generating figures and tables that can be browsed in `html` or used in LaTeX templates.

FUNCTIONAL DESCRIPTION

The COCO platform provides the functionality to automatically benchmark optimization algorithms for bounded or unbounded, (yet) 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, 140+ 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. A new test suite of bi-objective problems [74] has been used for the BBOB-2016 workshop at GECCO.

- Participants: Dimo Brockhoff, Arnaud Liefooghe, Thanh-Do Tran, Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara, Asma Atamna, Tea Tusar and Dejan Tusar
- Partners: Université technique de Dortmund - Université technique de Prague
- Contact: Dimo Brockhoff
- URL: https://github.com/numbbo/coco

6.3. Cartolabe

FUNCTIONAL DESCRIPTION

The goal of Cartolabe is to build a visual map representing the scientific activity of an institution/university/domain from published articles and reports. Using the HAL Database and building upon the AnHALytics processing chain, Cartolabe provides the user with a map of the thematics, authors and articles and their dynamics along time. ML techniques are used for dimensionality reduction, cluster and topics identification; visualisation techniques are used for a scalable 2D representation of the results.

- Participants: Felix Louistisserand, Philippe Caillou, Michèle Sebag, Jean-Daniel Fekete (AVIZ)
- Partners: AVIZ (Inria)
- Contact: Philippe Caillou
- URL: https://cartolabe.lri.fr

6.4. 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. A main further work is the introduction of generic tools for stochastic dynamic programming into the platform, for comparison and hybridization with other tools from the UCT-SIG.

- Participants: Olivier Teytaud, Jeremie Decock, Jean-Joseph Christophe, Vincent Berthier, Marie Liesse Cauwet and Sandra Cecilia Astete Morales
- Partner: Artelys
- Contact: Olivier Teytaud
- URL: https://www.lri.fr/~teytaud/metis.html

6.5. io.datascience

FUNCTIONAL DESCRIPTION

This Data as a Service (DaaS) platform 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 [41], [73]. A related specific software is the Tester for Triplestore (TFT) software suite, which benchmarks the compliance of sparql databases wrt the RDF standard and publishes the results through the SparqlScore service. The io.datascience platform has been selected for presentation at numerous venues, see section 10.3 for details.

- Contact: Cécile Germain
- URL: https://io.datascience-paris-saclay.fr/

6.6. CodaLab

KEYWORDS Benchmarking, competitions.

FUNCTIONAL DESCRIPTION

Challenges in machine learning and data science are competitions running over several weeks or months to resolve problems using provided datasets or simulated environments. Challenges can be thought of as crowdsourcing, benchmarking, and communication tools. They have been used for decades to test and compare competing solutions in machine learning in a fair and controlled way, to eliminate “inventor-evaluator" bias, and to stimulate the scientific community while promoting reproducible science.

Codalab Competitions (http://competitions.codalab.org) is a project that was started by Microsoft Research in 2013 in which Isabelle Guyon has taken an active part, to promote the use of challenges in Machine Learning and Data Science. The TAO team has been selected to take over the project under Isabelle Guyon’s leadership. The transfer has been successfully completed in the fall 2016. New features are being implemented, including developing a Wizard http://staging.chalab.eu/.

With already over 50 public competitions (including this year the Data Science Game, a student Olympiad co-organized by our PhD. student Benjamin Donnot http://www.datasciencegame.com/, the AutoML challenge http://automl.chalearn.org/ [42] and a new contest in the LAP challenge series http://chalearnlap.cvc.uab.es/ [47], co-organized by Isabelle Guyon), Codalab is taking momentum in medical imaging, computer vision, time series prediction, text mining, and other applications. TAO is going to continue expanding Codalab to accommodate new needs. For example, two competitions in preparation – TrackML competition (in High Energy Physics) [72] and the See.4C competition (spatio-temporal time series in collaboration with RTE) [48] – will require code submission, permitting to benchmark methods in a controlled environment. We are re-designing the backend of CodaLab to allow organizers to add more servers to satisfy on-the-fly demands of new competitions. Other features coming soon will be the possibility of interacting with a data generating model (rather than analyzing “canned” data), which enables the organization of reinforcement learning competitions and the possibility of organizing “coopetitions” (a mix of competition and collaboration). Other existing challenge platforms are too restrictive to simulate collaboration between participants and implement “coopetitions”. Our starting PhD. student Lisheng Sun designed and implemented a first prototype of coopetition “Beat AutoSKLearn", which was run at the NIPS Challenges in Machine Learning workshop (CiML 2016 http://ciml.chalearn.org/).

- Contact: Isabelle Guyon
- URL: http://competitions.codalab.org

TAPDANCE Team (section vide)

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 behaviors (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

KEYWORDS: Constraint Programming - Scheduling - Optimisation - Operational research - Financial analysis - Planning
SCIENTIFIC DESCRIPTION

or second consecutive year, CHOCO has participated at the MiniZinc Challenge , an annual competition of constraint programming solvers. In concurrency with 16 other solvers, CHOCO has won three 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 (v3.3.0, Dec. 17th) has the particularity to be promoted on Maven Central Repository. The major modifications were related to a simplification of the API but also improvement of the overall solver.

Within the context of the PhD thesis of Charles Prud'homme, a domain specific language that allows prototyping propagation engines was integrated within CHOCO, A paper appears at Constraints.

Within the context of the PhD thesis of Charles Prud'homme, a generic strategy based on explanations for large neighborhood search was designed and integrated within CHOCO. A corresponding paper appears at Constraints.

Within the context of the PhD thesis of Jean-Guillaume Fages, a documented package for graph variables was designed and integrated within CHOCO .
FUNCTIONAL DESCRIPTION

CHOCO is a Java discrete constraints library for describing hard combinatorial problems in the form of Constraint Satisfaction Problems and solving them with Constraint Programming techniques. Choco can be used to solve a broad range of real combinatorial problems. It is easy to use and offers excellent performance. This technique enables non-specialists to tackle strategic or operational problems, for instance, problems related to planning, scheduling, logistics, financial analysis and bio-informatics.

- Participants: Charles Prud'homme, Nicolas Beldiceanu, Jean-Guillaume Fages, Xavier Lorca, Thierry Petit and Rémi Douence
- Partner: Ecole des Mines de Nantes
- Contact: Julien Prud'homme
- URL: http://www.choco-solver.org/

6.3. GCCat

Global Constraint Catalog
KEYWORDS: Constraint Programming - Graph - Global constraint
FUNCTIONAL DESCRIPTION

The global constraint catalog presents and classifies global constraints and describes different aspects with meta data.

- Participants: Nicolas Beldiceanu and Sophie Demassey
- Contact: Nicolas Beldiceanu
- URL: http://sofdem.github.io/gccat/gccat/index.html

6.4. GCCat on time series

Global Constraint Catalog, Volume II, time-series constraints
KEYWORDS: Constraint Programming - Sequence - Transducer - Global constraint
FUNCTIONAL DESCRIPTION

The second volume of the Global Constraint Catalogue is devoted to time-series constraints. Within the context of Constraint Programming, time-series constraints go back to the work of Goldin and Kanellakis. This volume contains 626 constraints, which are explicitly described in terms of automata with accumulators. Checkers and propagators for all these constraints were synthesised from 22 transducers.

As in the first volume, the global constraints described in this second volume are not only accessible to humans, who can read the catalogue when searching for some information. It is also available to machines, which can read and interpret it. This is why there also exists an electronic version of this catalogue where one can get, for all time-series constraints, a complete description in terms of meta-data used in the first volume. In fact, unlike the first volume, *all the meta-data* of the electronic version as well as *all text and figures* of this second volume were automatically generated. While this second volume is by no means supposed to contain all possible time-series constraints, it contributes in the context of time-series constraints to the *systematic reconstruction* of the Global Constraint Catalogue that we have previously advocated. This reconstruction is based on the following methodology:

- First reuse, adapt or come up with abstractions, which allow to concisely represent structures and properties of time series as abstract combinatorial objects. In our context these abstractions essentially correspond to:
    1. Transducers where letters of the output alphabet are interpreted as semantic letters indicating how to recognise pattern occurrences.
    2. Transducers glue matrices expressing the relationship between the prefix, the suffix and the full sequence passed to a transducer.
    3. Properties associated to regular expressions corresponding to fragments of the input language of our transducers.
- Second, create from these abstract combinatorial objects a data base of concrete combinatorial objects.
- Third, synthesise concrete code for various technologies, languages, tasks from this data base of concrete combinatorial objects. In this context, correctness and efficiency of the synthesised code are essentially side product of:
    - The correctness of the formulae of our data base which is itself based on the wellformedness of our abstractions.
    - The generality behind our abstract combinatorial objects.

The time-series catalogue is done in the following way:

- All time-series constraints are now defined in a *compositional way* from a few basic constituents, i.e., patterns, features, aggregators, and predicates, which completely define the meaning of a constraint, where patterns are defined using regular expressions.
- Constraint names are now constructed in a systematic way as the *concatenation* of pattern name, feature name, and aggregation or predicate name.
- Given a pattern p, checkers and constraints are now *systematically synthesised* from a transducer that, given an input sequence over the input alphabet $\{<,=,>\}$, compares two adjacent values of a time-series and determines an output sequence over a output semantic alphabet describing how to recognise the occurrences of p.
- For each time-series constraint associated with a pattern p, the generation of an automaton with accumulators is completely driven by the transducer associated with pattern p as well as by *decoration tables* describing for each semantic letter of the output alphabet of the transducers how to generate accumulator updates. Code optimisation is ensured by using decoration tables that depend on properties of the pattern, of the feature, and of the aggregator associated with the time-series constraint.
- Lower and upper bounds of characteristics of time-series that appear in the restriction slot of a time-series constraint are synthesised from a *few parameterised formulae* that only depend on a restricted set of characteristics of the regular expression associated with the pattern.
- Parametrised glue matrices are provided for each transducer that corresponds to reversible time-series constraints. A concrete glue matrix is given for each reversible time-series constraint.
- Linear invariants are systematically obtained by applying the Farkas Lemma to the automata with accumulators that were synthesised. They consist of *linear constraints typically linking consecutive accumulator values*, e.g., see the legend of the second automaton of the constraints, which are generated even with non-linear accumulator updates. Missing linear invariants will be completed later on.
- Last but not least, time-series constraints were used for generating time-series verifying a conjunction of constraints both in the context of Constraint Programming and in the context of Linear Programming.
- In the context of sequential pattern mining, time-series constraint checkers can be used to identify and extract patterns from fixed sequences. While the time-series catalogue may need to be extended in order to capture more patterns, having a possibly large set of fixed time-series constraints is a natural safeguard to prevent overfitting when dealing with few sequences, at a price of not finding patterns that are not covered by the catalogue.
- Finally, both SICStus and MiniZinc code are synthesised. The later allows using time series constraints on many plate forms such as Choco, Gecode, ORtools, Cplex or Gurobi and is available Electronic Constraint Catalogue.
- Participants: Ekaterina Arafailova, Nicolas Beldiceanu, Rémi Douence, Mats Carlsson, Pierre Flener, Maria Andreina Francisco Rodriguez, Justin Pearson, Helmut Simonis
- Contact: Nicolas Beldiceanu
- URL: https://arxiv.org/abs/1609.08925

6.5. GHOST

General meta-Heuristic Optimization Solving Tool

FUNCTIONAL DESCRIPTION

GHOST 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

6.6. TorchCraft

Machine learning framework for games

FUNCTIONAL DESCRIPTION

TorchCraft is a library that enables deep learning research on Real-Time Strategy (RTS) games such as StarCraft: Brood War, by making it easier to control these games from a machine learning framework, here Torch. This white paper argues for using RTS games as a benchmark for AI research, and describes the design and components of TorchCraft.

- Participants: Gabriel Synnaeve, Nantas Nardelli, Alex Auvolat, Soumith Chintala, Timothe´e Lacroix, Zeming Lin, Florian Richoux, Nicolas Usunier
- Contact: Florian Richoux
- URL: https://arxiv.org/abs/1611.00625

TEA Project-Team

6. New Software and Platforms

6.1. ADFG: Affine data-flow graphs scheduler synthesis

Participants: Alexandre Honorat, Jean-Pierre Talpin, Thierry Gautier, Loïc Besnard.

We proposed [2], and implemented [0], a new data-flow design model: ADFG, initially to synthesize schedulers for SCJ/L1 applications. The principle of ADFG is to perform a linear abstraction of complex cyclo-static scheduling problems followed by the exploration of a concrete solution extracted from the abstract solution space, hence the name: abstract affine data-flow scheduling. ADFG guarantees schedules that ordinary (e.g. RTJ, SCJ) task-sets do not cause overflows or underflows. ADFG objectives are to maximize the throughput (the processors utilization) while minimizing buffering storage space needed between actors. ADFG supports EDF and fixed-priority scheduling policies for uni-, multi-processors and distributed systems.

The data-flow design model of ADFG 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. Abstract affine scheduling is first applied on the data-flow 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.

In the case of safety-critical Java, and through a model-to-text transformations using Acceleo, 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.

6.2. The Eclipse project POP

Participants: Loïc Besnard, Thierry Gautier, Jean-Pierre Talpin.

The distribution of project POP 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 finalized 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.

Project POP is composed of the Polychrony tool set, under GPL license, and its Eclipse framework, under EPL license. SSME (Syntactic Signal-Meta under Eclipse), is the meta-model 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 meta-model 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 tool-chain. Polychrony now comprises the

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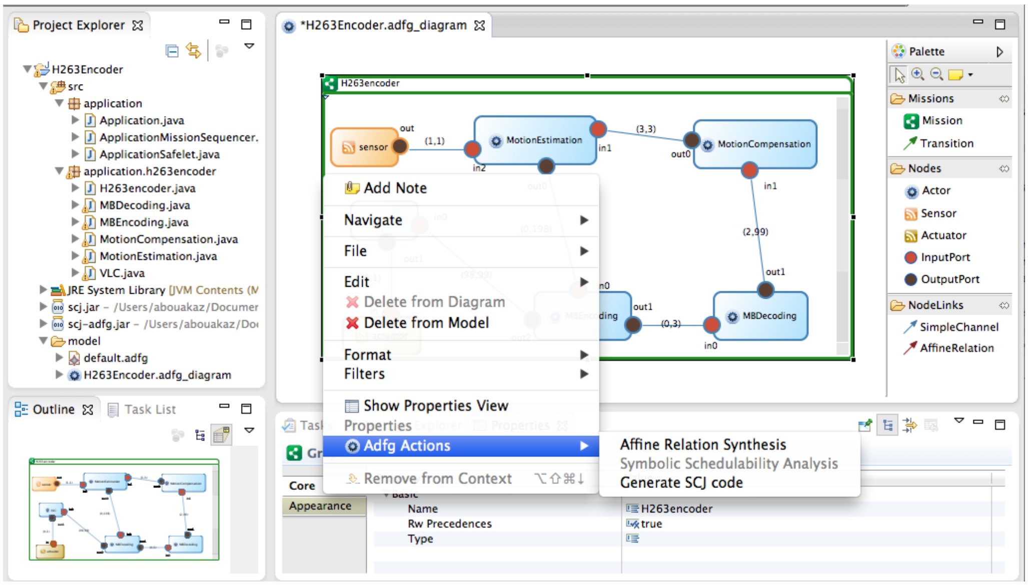
[0] *The ADFG tool*, Adnan Bouakaz, http://people.irisa.fr/Adnan.Bouakaz/software.htm

[0]

SIGNAL V4-Inria version: Reference Manual. Besnard, L., Gautier, T. and Le Guernic, P. http://www.irisa.fr/espresso/Polychrony, 2010



Name: H263encoder
Rw Precedences: true
Type:

Figure 1. The ADFG tool

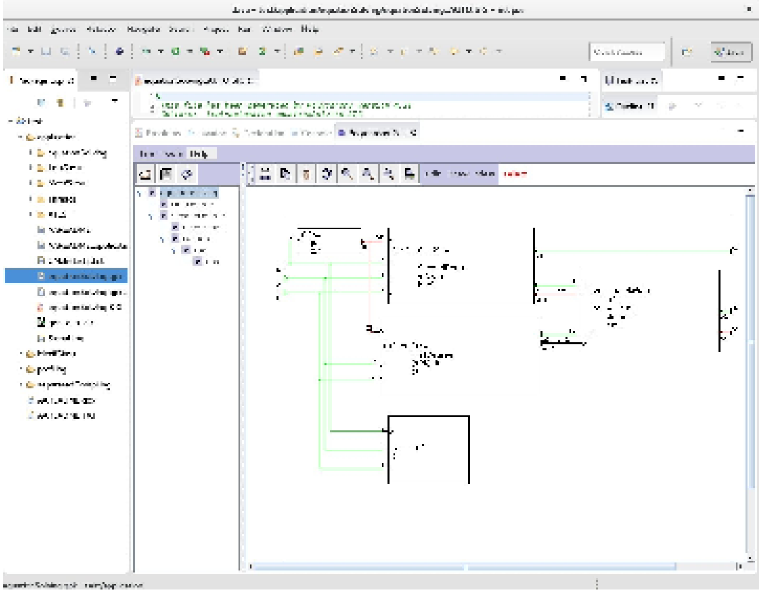


Figure 2. The Eclipse POP Environment

capability to directly import and export Ecore models instead of textual Signal programs, in order to facilitate interaction between components within such a tool-chain. 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.

6.3. The Polychrony toolset

Participants: Loïc Besnard, Thierry Gautier, 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 data-flow 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 tool-set 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; compose heterogeneous components (bottom-up with COTS); generate executable code for various architectures. The Polychrony tool-set 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.

As part of its open-source release, the Polychrony tool-set 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 tool-set. The Polychrony tool-set 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 tool-set can be freely downloaded from http://polychrony.inria.fr/. This site, intended for users and for developers, contains executable and source versions of the software for different 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 contains the whole source of the environment and its documentation. It is intended for developers.

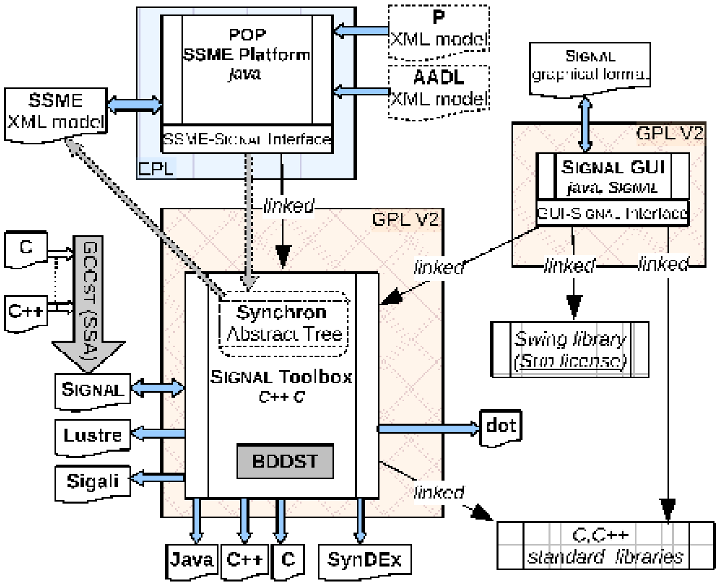


Figure 3. The Polychrony toolset high-level architecture

THOTH Project-Team

6. New Software and Platforms

6.1. CoNFab: COnvolutional Neural FABric

Participants: Shreyas Saxena, Jakob Verbeek.

Despite the success of convolutional neural networks, selecting the optimal architecture for a given task remains an open problem. Instead of aiming to select a single optimal architecture, we propose Convolutional Neural Fabrics [20] that embed an exponentially large class of CNN architectures. The fabric consists of a 3D trellis that connects response maps at different layers, scales, and channels with a sparse homogeneous local connectivity pattern. The only hyper-parameters of the model (nr. of channels and layers) are not critical for performance. While individual CNN architectures can be recovered as paths in the trellis, the trellis can in addition ensemble all embedded architectures together, sharing their weights where their paths overlap. By the non-cyclic property of the trellis, its parameters can be efficiently learned using methods based on error back-propagation. The trellis parameters can be learned using standard methods based on back-propagation, at a cost that scales linearly in the fabric size. This software implements Convolutional Neural Fabrics by means of wrappers on top of the Caffe library to specify and learn such models.

6.2. Modl

Participants: Julien Mairal, Arthur Mensch [Parietal], Gael Varoquaux [Parietal], Bertrand Thirion [Parietal].

Modl is a new Python library written by Arthur Mensch for factorizing huge matrices. It implements the method presented in [25], [17], which targets matrices of several terabytes that do not fit into the main computer's memory.

6.3. M-CNN: Weakly-Supervised Semantic Segmentation using Motion Cues

Participants: Pavel Tokmakov, Cordelia Schmid, Karteek Alahari.

This is a public implementation of the method described in [23]. It includes a framework for integrating motion cues into training a deep network for weakly-supervised semantic segmentation, code for data preprocessing and trained models that correspond to the results reported in the paper. Our code is built on top of DeepLab https://bitbucket.org/aquariusjay/deeplab-public-ver2 extension of the Caffe deep learning framework http://caffe.berkeleyvision.org.

6.4. DALY: Daily Action Localization in Youtube

Participants: Philippe Weinzapfael, Xavier Martin, Cordelia Schmid.

DALY is a video dataset with spatial and temporal annotation of 10 everyday human actions in 31 hours of Youtube videos, which allows to train and benchmark methods for action recognition and localization in videos. It is available at http://thoth.inrialpes.fr/daly/. We developed the dataset jointly with a new action localization technique. Both are described in [33].

6.5. GUN-71

Participant: Gregory Rogez.

This dataset consist of 12,000 RGB-D images of object manipulation scenes (captured from a chest-mounted camera) that were labeled with one of 71 fine-grained grasps. We considered 28 objects per grasp, resulting in a total of 1988 different hand-object configurations with 5-6 views for each. The data were captured with 8 different subjects (4 males and 4 females) in 5 different houses, see http://www.gregrogez.net/research/egovision4health/gun-71/.

6.6. Synthetic human 3D pose dataset

Participants: Gregory Rogez, Cordelia Schmid.

Participants: Gregory Rogez, Cordelia Schmid This large-scale dataset consists of 2,000,000 artificial RGB images of humans and associated 2D and 3D pose annotations. This dataset was generated using the image-based rendering algorithm presented in [19] and has been used to train state-of-the-art Convolutional Neural Networks (CNN) for in-the-wild 3D human pose estimation, see http://www.gregrogez.net/research/human-pose-data-synthesis-for-cnn/.

TITANE Project-Team

6. New Software and Platforms

6.1. CGAL Barycentric_coordinates_2

This CGAL software component offers an efficient and robust implementation of two-dimensional closed-form generalized barycentric coordinates defined for simple two-dimensional polygons.

- Participants: Pierre Alliez
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Barycentric_coordinates_2/index.html#Chapter_2D_Generalized_Barycentric_Coordinates

6.2. MeshMantics

This software component implements an approach that reconstructs 3D urban scenes in the form of levels of detail (LODs). Starting from raw data sets such as surface meshes generated by multi-view stereo systems, the algorithm proceeds in three main steps: classification, abstraction and reconstruction. From geometric attributes and a set of semantic rules combined with a Markov random field, we classify the scene into four meaningful classes. The abstraction step detects and regularizes planar structures on buildings, fits icons on trees, roofs and facades, and performs filtering and simplification for LOD generation. The abstracted data are then provided as input to the reconstruction step which generates watertight buildings through a min-cut formulation on a set of 3D arrangements.

- Participants: Florent Lafarge and Pierre Alliez
- Contact: Pierre Alliez
- URL: https://bil.inria.fr

6.3. Module CGAL : Point Set Processing

This CGAL 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 and Clément Jamin
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Point_set_processing_3/index.html#Chapter_Point_Set_Processing

6.4. Module CGAL : Scale space surface reconstruction

This method allows to reconstruct 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
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Scale_space_reconstruction_3/index.html#Chapter_Scale_space_reconstruction

6.5. Skeleton-Blockers

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/

6.6. APP Deposits

WALLEMME is a software for classifying large-scale urban areas from dense textured 3D meshes in a supervised manner.

- Participants: Mohammad Rouhani, Florent Lafarge and Pierre Alliez.

DIMUVIC is a software for reconstructing in 3D a polyline-sketch using contextual knowledge contained in multiview stereo images.

- Participants: Jean-Dominique Favreau, Florent Lafarge and Adrien Bousseau.

ROOFEXTRACTOR is a software for reconstructing roofs from dense defect-laden meshes as compact piecewise-planar surface representations.

- Participants: Sven Oesau and Florent Lafarge.

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, Evelyne Contejean, Mohamed Iguernelala, Stephane 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 Chargueraud
- 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 Gregoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Denes, Stephane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pedrot, Loic Pottier, Matthias Puech, Yann Regis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliatre
- Partners: CNRS - ENS Lyon - Université Paris-Diderot - Université Paris-Sud
- 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, Erik Martin Dorel, Nicolas Brisebarre, Miora Maria Joldes, Micaela Mayero, Jean Michel Muller, Laurence Rideau and Laurent Thery
- 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 Filliatre, Claude Marche, Guillaume Melquiond, Andriy Paskevych, François Bobot, Martin Clochard and Levs Gondelmans
- Partners: CNRS - Université Paris-Sud
- Contact: Claude Marche
- URL: http://why3.lri.fr/

TONUS Team

5. New Software and Platforms

5.1. SCHNAPS - KIRSCH

Participants: Emmanuel Franck, Pierre Gerhard, Philippe Helluy, Michel Massaro, Malcolm Roberts, David Coulette, Laura Mendoza, Bruno Weber.

SCHNAPS: Solveur pour les lois de Conservation Hyperboliques Non-linéaires Appliqué aux PlasmaS
SCIENTIFIC DESCRIPTION

The 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 or Xeon Phi). When designing new algorithms, it is important to adapt them to this kind of architecture. Practically, we use the MPI library for managing the coarse grain parallelism, while the OpenCL library 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 kernel 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.
Since the middle of the year a specific version of SCHNAPS (called KIRSCH for Kinetic Representation of SChnaps) has been developed to handle Lattice Boltzmann schemes for MHD and fluid simulations.

FUNCTIONAL DESCRIPTION

SCHNAPS and KIRSCH are a generic Discontinuous Galerkin solver and an implicit Lattice Boltzmann solver, written in C, based on the OpenCL, MPI and StarPU frameworks.

- Partner: AxesSim
- Contact: Philippe Helluy
- URL: http://schnaps.gforge.inria.fr/

5.2. Selalib

Participants: Sever Adrian Hirstoaga, Michel Mehrenberger, Pierre Navaro, Laurent Navoret, Thi Trang Nhung Pham, Christophe Steiner.

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/

5.3. 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 physicists have obtained some important results. However to run larger and more complex test cases it is necessary to extend the numerical methods used.
  In 2014, the DJANGO code has been created, the aim of this code is twofold: 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 2008 with a Basic MPI framework.
- 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:
  Mustafa Gaja, Jalal Lakhlili, Matthias Hoelzl and Eric Sonnendrücker (Max Planck Institut of Plasma Physic, Garching, Germany), Ayoub Iaagoubi (ADT Inria Nice), Hervé Guillard (University of Nice and Inria Sophia-Antipolis, France), Virginie Grandgirard, Guillaume Latu (CEA Cadarache, France)
- Year 2016:
  Between the years 2015 and 2016 the code has been partially rewritten using Fortran 2008 to prepare the implementation of new methods (compatible finite element spaces, 3D B-Splines meshes). The different models, hyperbolic, parabolic and elliptic introduced in the previous version of the code have been rewritten and validated. Actually, we will begin to introduce the Maxwell equations for the coupling with kinetic equations and the nonlinear fluid models (first step for the MHD simulations). A large effort of optimization and parallelization in the matrices assembly has been made and new preconditioning for elliptic models has been introduced.
  - Partners: Max Planck Institute - Garching - IRMA, Université de Strasbourg - Inria Nice Sofia- Antipolis
  - Contact: Emmanuel Franck

TOSCA Project-Team

5. New Software and Platforms

5.1. AGH

FUNCTIONAL DESCRIPTION

AGH (for Analysis of Galton-Watson Harris paths) is a Matlab toolbox providing methods for statistical analysis of ordered trees from their Harris paths in a user-friendly environment. More precisely it allows to easily compute estimators of the relative scale of trees which share the same shape. These estimators have been introduced for Galton-Watson trees conditioned on their number of nodes but may be computed for any ordered tree.

- Participants: Romain Azaïs, Alexandre Genadot, Benoît Henry
- Contact: Benoît Henry
- URL: http://agh.gforge.inria.fr/

5.2. 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.

- Participants: Madalina Deaconu and Antoine Lejay
- Contact: Antoine Lejay
- URL: http://exitbm.gforge.inria.fr/

5.3. SDM-WindPoS

Stochastic Downscaling Method and Wind Power Simulation
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-windpos 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.

The ability of SDM-WindPoS to regamma the wind computation in the horizontal scale but also in the vertical scale is of particular interest for wind farm power production assessment. WindPoS couples direct actuator disk approach and SDM Atmospheric Boundary Layer (ABL) model for wind farm simulation.

This year we start to introduce more accurate ABL convection models in SDM. Moreover, we start to add the possibility to introduce more accurate topography when SDM is running with some coarse scale atmospheric input data. Our dedicated GUI was also improved (better rendering for the 2D and 3D views).

- Participants: Mireille Bossy
- Contact: Mireille Bossy
- URL: http://windpos.inria.fr

TROPICAL Team

6. New Software and Platforms

6.1. New Software

6.1.1. Coq-Polyhedra

Coq-Polyhedra is a library which aims at formalizing convex polyhedra in Coq. A description of the associated contributions can be found in Section 7.3.1 . Coq-Polyhedra is distributed under the CeCILL-B licence, and can be found at https://github.com/nhojem/Coq-Polyhedra.

TYREX Project-Team

5. New Software and Platforms

5.1. Benchmarks Attitude Smartphones

KEYWORDS: Experimentation - Motion analysis - Sensors - Performance analysis - Smartphone
SCIENTIFIC DESCRIPTION

We investigate the precision of attitude estimation algorithms in the particular context of pedestrian navigation with commodity smartphones and their inertial/magnetic sensors. We report on an extensive comparison and experimental analysis of existing algorithms. We focus on typical motions of smartphones when carried by pedestrians. We use a precise ground truth obtained from a motion capture system. We test state-of-the-art attitude estimation techniques with several smartphones, in the presence of magnetic perturbations typically found in buildings. We discuss the obtained results, analyze advantages and limits of current technologies for attitude estimation in this context. Furthermore, we propose a new technique for limiting the impact of magnetic perturbations with any attitude estimation algorithm used in this context. We show how our technique compares and improves over previous works.

- Participants: Thibaud Michel, Hassen Fourati, Pierre Geneves and Nabil Layaida
- Partner: GIPSA-Lab
- Contact: Pierre Genevès, Thibaud Michel
- URL: http://tyrex.inria.fr/mobile/benchmarks-attitude/

5.2. 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

- Participants: Pierre Geneves, Nabil Layaida and Marti Bosch Padros
- Contact: Pierre Geneves
- URL: http://tyrex.inria.fr/websolver/

5.3. RDFHive

KEYWORDS: Hadoop - RDF - SPARQL
SCIENTIFIC DESCRIPTION

SPARQL is the W3C standard query language for querying data expressed in RDF (Resource Description Framework). The increasing amounts of RDF data available raise a major need and research interest in building efficient and scalable distributed SPARQL query evaluators.

In this context, we propose and share RDFHive: a simple implementation of a distributed RDF datastore benefiting from Apache Hive. RDFHive is designed to leverage existing Hadoop infrastructures for evaluating SPARQL queries. RDFHive relies on a translation of SPARQL queries into SQL queries that Hive is able to evaluate.

Technically, RDFHive directly evaluates SPARQL queries i.e. there is no preprocessing step, indeed an RDF triple file is seen by Hive as a three-column table. Thus, the bash translator simply translates SPARQL queries according to this scheme. This method has two advantages: first, creating a database is very fast, second, since the upfront investment is light, RDFHive is an interesting tool to evaluate a few SPARQL queries at once.

- Participants: Damien Graux, Nabil Layaida and Pierre Geneves
- Contact: Pierre Genevès, Damien Graux
- URL: https://github.com/tyrex-team/rdfhive

5.4. Tree Reasoning Solver

SCIENTIFIC DESCRIPTION

The tree reasoning solver is a software tool which implements research advances in tree logics, and in the analysis of query and programming languages for the web. The core algorithm is a satisfiability solver of an expressive tree logic. The underlying logic is very expressive: it is a μ-calculus variant for finite trees, which is MSO-complete, and equipped with additional features (converse modalities, nominals, logical combinators...)

The decision procedure has an optimal worst-case complexity, and its implementation performs quite well in practice. This allows efficient reasoning with tree structures. In particular, it opens the way for solving a wide variety of problems that require reasoning with very large sets of trees.

Initially developed for the analysis of XML/XPath queries, this tool has been extended by the team to support more general query analysis, reasoning with schema constraints, with functions, and with domain specific languages such as cascading style sheets.

- Participants: Pierre Geneves, Nabil Layaida and Nils Gesbert
- Contact: Pierre Geneves
- URL: http://tyrex.inria.fr/websolver/

5.5. XQuery Type-Checker

SCIENTIFIC DESCRIPTION

This prototype implements a sound static type-system for an XQuery core. The type language supported is a large subset of RelaxNG+Schematron, which is novel in static type checking. It also supports the static typing of backward axes, which is not supported by any other system nor the XQuery recommendation. 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.

- Participants: Pierre Geneves, Nabil Layaida and Nils Gesbert
- Contact: Pierre Geneves
- URL: http://tyrex.inria.fr/websolver/

5.6. SPARQLGX

KEYWORDS: RDF - SPARQL - Distributed computing

SCIENTIFIC DESCRIPTION

SPARQL is the W3C standard query language for querying data expressed in RDF (Resource Description Framework). The increasing amounts of RDF data available raise a major need and research interest in building efficient and scalable distributed SPARQL query evaluators.

In this context, we propose and share SPARQLGX: our implementation of a distributed RDF datastore based on Apache Spark. SPARQLGX is designed to leverage existing Hadoop infrastructures for evaluating SPARQL queries. SPARQLGX relies on a translation of SPARQL queries into executable Spark code that adopts evaluation strategies according to (1) the storage method used and (2) statistics on data. Using a simple design, SPARQLGX already represents an interesting alternative in several scenarios.

- Participants: Damien Graux, Louis Jachiet, Nabil Layaida and Pierre Geneves
- Contact: Pierre Genevès, Damien Graux
- URL: https://github.com/tyrex-team/sparqlgx

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: Razvan Stanica and Hervé Rivano.
- 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 and Razvan Stanica.
- Contact: Razvan Stanica
- URL: http://kolntrace.project.citi-lab.fr/

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

6.3.2. Extention of the FIT IoT Lab Equipex in Tech La Doua Campus

This testbed is located in an experimentation room which belongs to the CITI laboratory and the Telecommunications Department of INSA Lyon, Villeurbanne. The target usages of this room are quite diverse: practical works with students, robots/drones testing, wireless sensor networks experimentation, Wi-Fi security evaluation, services deployment, etc. During an experimentation, this room could be shared with others practical works. Basically, we claim that this room is useful to observe the behavior of nodes with this dense interactivity. 18 M3 open nodes, 11 A8 nodes and 12 mobile on robots are available for experimentation.

- Participants: Romain Pujol, Hervé Rivano, Fabrice Valois.
- Contact: Fabrice Valois
- URL: https://www.iot-lab.info/deployment/lyon/

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. 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]. This version is not yet distributed.

Via the Inria ADT FastTrack funding, Eric Biagioli has joined the project in November 2016 for 6 months. He is porting the maple code to C code and enhancing the visualization. This work will prepare for a better diffusion of the software via a webserver and a transfert to Maplesoft with which Inria has signed a contract in April 2016.

- 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.

The software has been improved and a technical report published [28].

- Contact: Rémi Imbach
- URL: https://bil.inria.fr/fr/software/view/2605/tab

VERIDIS Project-Team

6. New Software and Platforms

6.1. The Nunchaku Higher-Order Model Finder

FUNCTIONAL DESCRIPTION

Nunchaku is a model finder for higher-order logic, with dedicated support for various definitional principles. It is designed to work as a backend for various proof assistants and to use state-of-the-art model finders and other solvers as backends.

In 2016, the first three versions of the tools were released (0.1 through 0.3). The Isabelle2016-1 release includes Nunchaku as well as the frontend that bridges the gap between the proof assistant and the model finder. Work has commenced on a Coq frontend [28] and a TLA$^+$ frontend. Currently, the backends CVC4, Kodkod, and Paradox are supported.

- Participants: Jasmin Blanchette and Simon Cruanes
- Contact: Jasmin Blanchette
- URL: https://github.com/nunchaku-inria

6.2. 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 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.

In 2016 there was significant progress with the generation of models for real satisfiability problems [15]. When obtained via quantifier elimination by virtual substitutions, such models contain in general non-standard numbers like positive infinitesimal and infinite values. In an efficient post-processing step Redlog now generates standard models.

- Participants: Thomas Sturm and Marek Kosta
- Contact: Thomas Sturm
- URL: http://www.redlog.eu/

6.3. The SPASS automated theorem prover

FUNCTIONAL DESCRIPTION

The classic SPASS is an automated theorem prover based on superposition that handles first-order logic with equality and several extensions for particular classes of theories. With version SPASS 3.9 we have stopped the development of the classic prover and have started the bottom-up development of SPASS 4.0 that will actually be a workbench of automated reasoning tools.

In 2016 we have made available for the first time our LIA solver SPASS-IQ. Furthermore, we have developed a state-of-the-art SAT solver SPASS-SATT that will be available in 2017.

- Contact: Christoph Weidenbach
- URL: http://www.spass-prover.org/

6.4. TLAPS, 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 is ongoing. Its objectives are a cleaner interaction with the standard TLA$^+$ front-ends, in particular SANY, the standard parser and semantic analyzer. This is necessary for extending the scope of the fragment of TLA$^+$ that is handled by TLAPS, such as full temporal logic and module instantiation.

TLAPS has been used in several case studies, including the proof of determinacy of PharOS [21] and the verification of the Pastry routing protocol [22]. These case studies feed back into the development of the proof system and of its standard library.

- Contact: Stephan Merz
- URL: https://tla.msr-inria.inria.fr/tlaps/content/Home.html

6.5. The veriT Solver

SCIENTIFIC DESCRIPTION

veriT comprises a SAT solver, a congruence closure based decision procedure for uninterpreted symbols, a simplex-based decision procedure for linear arithmetic, and instantiation-based quantifier handling.

FUNCTIONAL DESCRIPTION

VeriT is an open, trustable and efficient SMT (Satisfiability Modulo Theories) solver, featuring efficient decision procedure for uninterpreted symbols and linear arithmetic, and quantifier reasoning.

Efforts in 2016 have been focused on non-linear arithmetic reasoning and quantifier handling. The reasoning capabilities of veriT have been significantly improved along those two axes, but non-linear arithmetic reasoning is not yet stable.

The veriT solver participated in the SMT competition SMT-COMP 2016 with good 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, it is integrated within the Atelier B.

- Participants: Pascal Fontaine, 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, 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 study plant morphogenesis at the scale of the 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 provides a framework for the visualization, exploration, 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, Grégoire Malandain, Christophe Pradal, Christophe Godin.
- Contact: Christophe Godin
- URL: https://github.com/virtualplants/tissuelab

5.3. Draco-Stem

KEYWORDS: 3D Reconstruction - Triangular Mesh - Biomechanical Simulations

FUNCTIONAL DESCRIPTION

A computational tool called DRACO-STEM (Dual Reconstruction by Adjacency Complex Optimization - SAM Tissue Enhanced Mesh) has been made available, with the aim of bridging the gap between experimental data and tissue biomechanics models. It provides the necessary tools to generate a FEM-ready, topologically accurate, complete 3D triangular mesh of meristematic tissue, based on a segmented image obtained from a confocal microscopy acquisition. The produced meshes proved to be useable as an input for computational simulations of biomechanical and physiological cellular processes.

- Participants: Guillaume Cerutti, Christophe Godin, Olivier Ali
- Contact: Guillaume Cerutti
- URL: https://github.com/VirtualPlants/draco_stem/

5.4. 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 disappear) which enables powerful post-correction based on the study of the resulting tracking.

- Participants: Léo Guignard, Emmanuel Faure, Grégoire Malandain, Patrick Lemaire, Christophe Godin
- Contact: Christophe Godin
- URL: https://gforge.inria.fr/projects/marsalt/

5.5. AutoWIG

KEYWORDS: Syntaxic Analysis
FUNCTIONAL DESCRIPTION

High-level programming languages, such as Python and R, are popular among scientists. They are concise, readable, lead to rapid development cycles, but suffer from performance drawback compared to compiled languages. However, these languages allow to interface C, C++ and Fortran code. In this way, most of the scientific packages incorporate compiled scientific libraries to both speed up the code and reuse legacy libraries. While several semi-automatic solutions and tools exist to wrap these compiled libraries, the process of wrapping a large library is cumbersome and time consuming. We developped AutoWIG [40], [47], a Python library that wraps automatically compiled libraries into high-level languages. Our approach consists in parsing C++ code using the LLVM/Clang technologies and generating the wrappers using the Mako templating engine. Our approach is automatic, extensible, and applies to very complex C++ libraries, composed of thousands of classes or incorporating modern meta-programming constructs. The usage and extension of AutoWIG have been illustrated on a set of statistical libraries (StructureAnalysis).

- Participants: Pierre Fernique, Christophe Pradal
- Contact: Pierre Fernique
- URL: https://github.com/VirtualPlants/AutoWIG

5.6. Phenomenal

KEYWORDS: Image Analysis, Phenotyping
FUNCTIONAL DESCRIPTION

Phenomenal [65] is a Python library dedicated to the analysis of high throughput phenotyping data and models. It has been developed in the frame of the Phenome high throughput phenotyping infrastructure. It is based on the OpenAlea platform [76], [77] that provides methods and softwares for the modelling of plants, together with a user-friendly interface for the design and execution of scientific workflows. OpenAlea is also part of the InfraPhenoGrid infrastructure that allows high throughput computation and recording of provenance during the execution [26].

- Participants: Simon Artzet, Jérôme Chopard, Tsu-Wei Chen, Nicolas Brichet, Christian Fournier, Christophe Pradal
- Contact: Christian Fournier, Christophe Pradal
- URL: https://gitlab.inria.fr./phenome/phenomenal

5.7. Platforms

5.7.1. 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.).

New methodological developments around scientific workflows in *OpenAlea* have been done recently.

5.7.2. 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: Olivier Commowick, Rene-Paul Debroize, Florent Leray and Renaud Hédouin
- Contact: Olivier Commowick
- APP number: IDDN.FR.001.460020.000.S.P.2015.000.31230
- URL: https://github.com/Inria-Visages/Anima-Public/wiki

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.

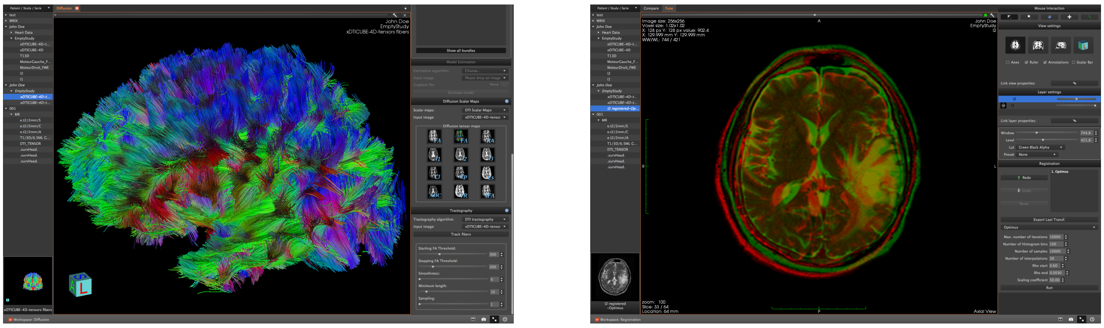


Figure 2. The medInria software platform: Tractography overlapped with 3D image (left), and Fused view of registered images (right).

FUNCTIONAL DESCRIPTION: MedInria is a free software platform dedicated to medical data visualization and processing as illustrated in Fig. 2 .

- Participants: Olivier Commowick and Rene-Paul Debroize
- 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. Shanoir

SHAring NeurOImaging Resources

KEYWORDS: Shanoir - Webservices - Data base - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS - Nifti - Data Sharing - Web Application

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 Fig. 3).

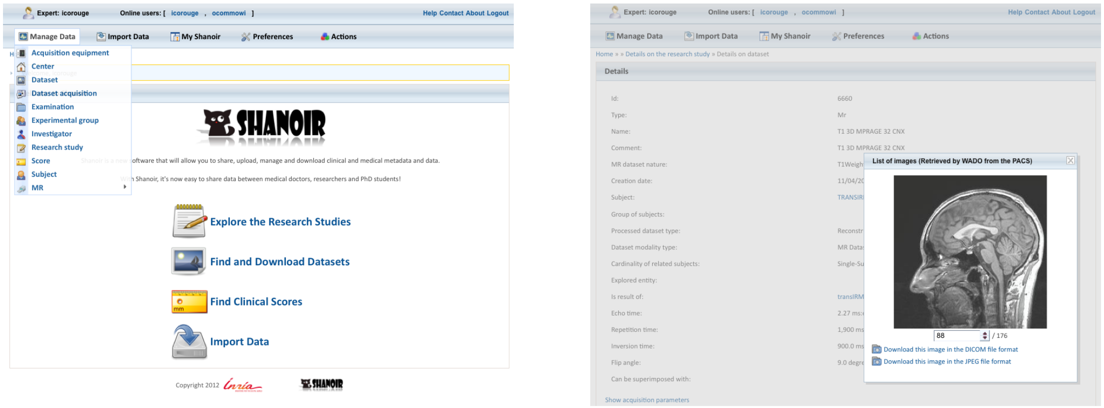
Shanoir is a secured J2EE application running on a JBoss server, reachable via graphical interfaces in a browser or by third party programs via web services. It behaves as a repository of neuroimaging files coupled with a relational database hoding meta-data. The data model, based on OntoNeurolog, an ontology devoted to the neuroimaging field, is structured around research studies where of involved patients have examinations which 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 files 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 an 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.



oftware that will allow you to share, upload, manage and download clinical and medical metadata and data.

n 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:

88 / 176

Figure 3. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

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, Christian Barillot, Anthony Baire, Mathieu Simon, Julien Louis, Isabelle Corouge, Élise Bannier, Aneta Morawin and Yao Chi
- Partners: CNRS - INSERM - Université de Rennes 1
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.520021.003.S.A.2008.000.31230 (2014/08/20)

6.4. 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.
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.

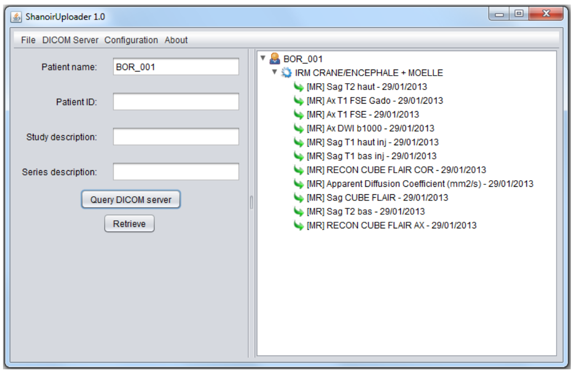
- Participants: Olivier Commowick and Florent Leray
- Contact: Christian Barillot
- URL: http://qtshanoir.gforge.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230 (2012/02/08)

6.5. 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 Fig. 4 . 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.



Patient name: BOR_001

- 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

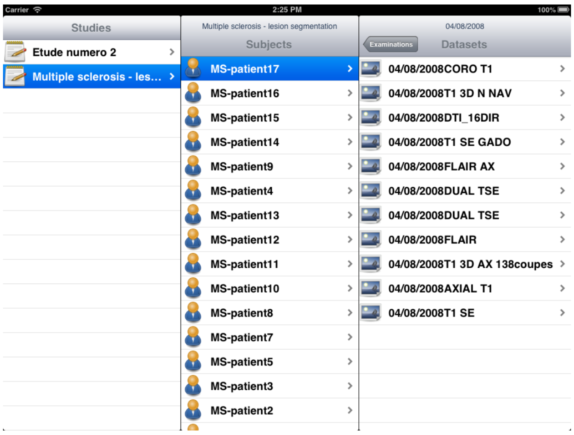
Figure 4. The ShanoirUploader software is a desktop application designed to interact with a PACS to query and retrieve the data stored on any PACS.

- Participants: Michael Kain, Inès Fakhfakh and Christian Barillot
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.380026.000.S.P.2015.000.31230 (2015/09/11)

6.6. 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 as illustrated in Fig. 5 . For this the Shanoir SOAP web-services are called. 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 corresponding viewer, the user already has to have installed on his device.



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 5. The iShanoir interface, showing the browsing tabs within the research studies stored in the Shanoir database.

- Participants: Michael Kain and Christian Barillot
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr

6.7. autoMRI

KEYWORDS: FMRI - MRI - ASL - FASL - SPM - Automation

SCIENTIFIC DESCRIPTION: Automri is an analysis pipeline to process morphological, perfusion, BOLD fMRI, relaxometry and neurovascular data. 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, to relaxometry data to detect deviations from a template, 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.

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).

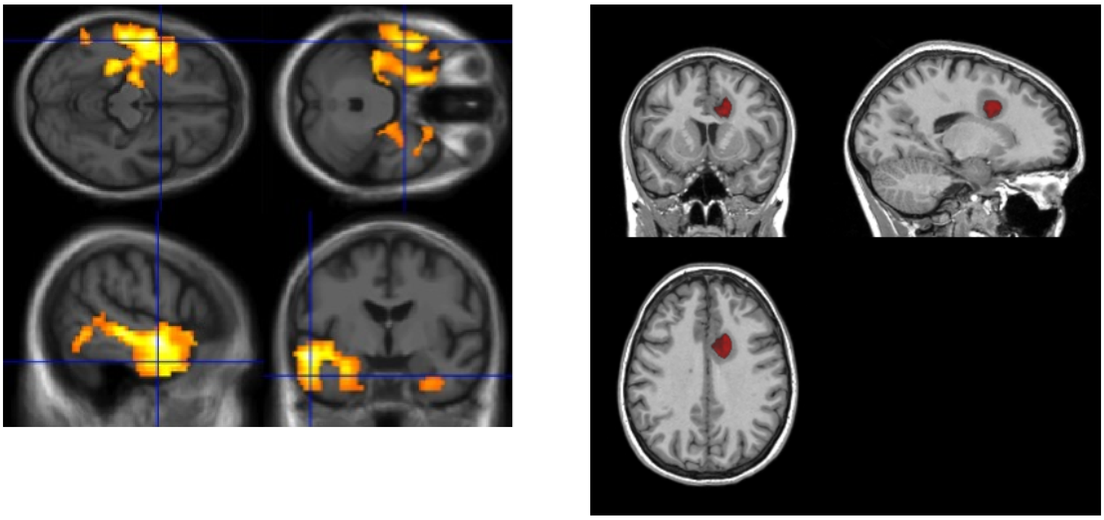


Figure 6. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (left) and detection of relaxometry defect in an MS patient (right).

- Participants: Isabelle Corouge, Quentin Duché, Cédric Meurée, Pierre Maurel and Élise Bannier.
- Contact: Isabelle Corouge
- URL: http://www.irisa.fr/visages/
- APP number: Part in IDDN.FR.001.130017.000.S.A.2012.000.31230

6.8. Integration of EEG and fMRI

KEYWORDS: medical imaging - EEG - fMRI

FUNCTIONAL DESCRIPTION: 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).

- Participants: Marsel Mano, Lorraine Perronnet, Anatole Lecyuer, Christian Barillot.
- Contact: Marsel Mano
- International Patent Number: PCT/EP2016/1652279

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 [0]. This platform has been supported under the “Contrat de Projets Etat-Région” (Christian 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 4 010 k€ (600 k€ for the infrastructures, 2 850 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 U650 - 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.

In 2016, VisAGeS has been awarded by IBISA as a “Plateforme d’excellence”.

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[0] http://www.neurinfo.org

WHISPER Project-Team

6. New Software and Platforms

6.1. Prequel

KEYWORDS: Code quality - Evolution - Infrastructure software

FUNCTIONAL DESCRIPTION

The commit history of a large, actively developed code base such as the Linux kernel is a gold mine of information on how evolutions should be made, how bugs should be fixed, etc. Nevertheless, the high volume of commits available and the rudimentary filtering tools provided imply that it is often necessary to wade through a lot of irrelevant information before finding example commits that can help with a specific software development problem. To address this issue, we have developed Prequel (Patch Query Language) [20]. Prequel builds on the semantic patch lamguage SmPL developed for Coccinelle, which is now well known to the Linux kernel developer community, to allow developers to scan the changes in a source code development history, taking into account not only the specific changes made, but also the context in which these changes occur. As the history of a code base under active development quickly becomes large, with the Linux kernel incorporating around 13,000 commits on each 2-3 month release cycle, a particular goal in the development of Prequel has been to provide reasonable performance. Currently, most queries in our experiments complete in under minute when running on a single core on a standard laptop. So far, we have applied Prequel to the problem of understanding how to eliminate uses of deprecated functions [20], and are investigating how it may be useful in a systematic driver porting methodology.

Prequel is publicly available under GPLv2. The development of Prequel is supported by OSADL, and Julia Lawall presented Prequel at the 2016 OSADL networking day (https://www.osadl.org/OSADL-Networking-Day-2016.networking-day-2016.0.html).

- Participants: Julia Lawall and Gilles Muller
- Partners: IRILL - LIP6
- Contact: Julia Lawall
- URL: http://prequel-pql.gforge.inria.fr/

6.2. Coccinelle

KEYWORDS: Code quality - Evolution - Infrastructure software

FUNCTIONAL DESCRIPTION

Coccinelle is a tool for C code program matching and transformation that has been developed by members of the Whisper team over the last 10 years [8]. Coccinelle is widely used by the Linux kernel developer community and for other C software projects. Over the last three years, Coccinelle has benefited from the support of an engineer from the SED. Major improvements in 2016 include support for Python 3, independence from a no-longer-supported interface between Python and OCaml, better support for parallelism, and better support for integrating arbitrary predicates into the matching process. These features significantly improve performance and improve the uniformity of the rule specification language, thus providing a better experience for users. Coccinelle is at the foundation of much of our research work, including the ANR ITrans project, and these improvements will enhance and facilitate our research, accordingly.

Coccinelle is publicly available under GPLv2. In 2016, Julia Lawall presented Coccinelle in an invited keynote at the Linux Security Summit (http://events.linuxfoundation.org/events/archive/2016/linux-security-summit) and at a “birds of a feather” session at Linuxcon Europe (http://events.linuxfoundation.org/events/LinuxCon-europe).

- Participants: Julia Lawall, Gilles Muller, and Thierry Martinez
- Partners: IRILL - LIP6
- Contact: Julia Lawall
- URL: http://coccinelle.lip6.fr

6.3. Hector (BtrLinux)

KEYWORDS: Code quality - Evolution - Infrastructure software

FUNCTIONAL DESCRIPTION

A major source of errors in systems code is resource-release omission, which can lead to memory leaks and to crashes, if the system ends up in an inconsistent state. Currently, many tools exist that detect common patterns in software and detect faults as deviations from those patterns, but most suffer from high rates of false positives. Hector takes the novel approach of detecting inconsistencies local to a single function, and thus has been able to find over 300 faults in Linux kernel code and other C infrastructure software, with a rate of false positives of only 23%. Hector was originally the subject of the PhD thesis of Suman Saha [75]. Over the past two years, improving the robustness of the implementation of Hector has been the focus of ADT (young engineer position) BtrLinux supported by Inria, with the goal of making Hector publicly available and popularizing its use in the Linux kernel developer community. Some Linux kernel patches based on the use of Hector have been integrated into the Linux kernel, and the public release of Hector is in progress. The ADT position also involved the creation and maintenance of the website https://btrlinux.inria.fr/ as a showcase for the work of the Whisper team around Linux kernel development tools.

Building on his experience acquired in the ADT position, Quentin Lambert has recently been offered a position as an engineer at Wolfram MathCore AB.

- Participants: Quentin Lambert, Julia Lawall, and Gilles Muller
- Partners: IRILL - LIP6
- Contact: Julia Lawall
- URL: https://btrlinux.inria.fr/

6.4. ssrbit

FUNCTIONAL DESCRIPTION

ssrbit is a Coq library offering an efficient formalization of bit vectors, a refinement framework for abstractly reasoning about bitsets, and a trustworthy extraction of bit vectors to OCaml integers. Initially developed by Whisper members (Pierre-Évariste Dagand, Julia Lawall), the development has attracted an external contributor (Emilio Jesús Gallego Arias, postdoctoral researcher in CRI Mines-ParisTech), which led to significant improvements. We plan to improve the overall support and documentation so as to provide a full-featured library.

- Participants: Pierre Évariste Dagand, Julia Lawall, and Emilio Jesús Gallego Arias
- Contact: Pierre Évariste Dagand
- URL: https://github.com/ejgallego/ssrbit/

WILLOW Project-Team

6. New Software and Platforms

6.1. 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" [9]. 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/.

6.2. Unsupervised learning from narrated instruction videos

Open source release of the software package for our paper "Unsupervised learning from narrated instruction videos" . It provides a full implementation of the method, including code for weakly supervised training from instruction video, as well as trained models. Links to all of these are available at our project page http://www.di.ens.fr/willow/research/instructionvideos/.

6.3. ContextLocNet: Context-aware deep network models for weakly supervised localization

Open source release of code reproducing the results in our "ContextLocNet: Context-aware deep network models for weakly supervised localization" [11]. It provides code for training models, testing on standard datasets and trained models. It can be found online at https://github.com/vadimkantorov/contextlocnet.

6.4. Long-term Temporal Convolutions for Action Recognition

Open source release of the software package for our paper "Long-term Temporal Convolutions for Action Recognition" [20]. It provides code for training models, testing on standard datasets and trained models. Links are available at our project page http://www.di.ens.fr/willow/research/ltc/.

WIMMICS Project-Team

6. New Software and Platforms

6.1. Corese

COnceptual REsource Search Engine
KEYWORDS: Semantic Web - Web of Data - Search Engine - RDF - SPARQL
FUNCTIONAL DESCRIPTION

Corese is a Semantic Web Factory that implements W3C RDF, RDFS, SPARQL 1.1 Query and Update. Furthermore, Corese query language integrates original features such as approximate search. It provides a SPARQL Template Transformation Language for RDF, a SPARQL based Inference Rule Language for RDF and a Linked Data Script Language. Corese also provides distributed federated query processing, a Semantic Web server and a SPARQL endpoint. Corese development is supported by an Inria grant (ADT).

- Participants: Olivier Corby, Erwan Demairy, Catherine Faron-Zucker, Fabien Gandon. Alumni: Virginie Bottollier, Olivier Savoie, and Fuqi Song.
- Partners: I3S - Mnemotix
- Contact: Olivier Corby
- URL: http://wimmics.inria.fr/corese, http://corese.inria.fr

6.2. DBpedia.fr

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 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. In addition, Wimmics extended the open source DBpedia platform with new capabilities and in particular DBpedia Historic to extract the entire edition history of a chapter as linked data.

- Participants: Fabien Gandon and Raphaël Boyer
- Contact: Fabien Gandon
- URL: http://dbpedia.fr

6.3. Discovery Hub

Discovery Hub Exploratory Search Engine
KEYWORD: Search Engine
FUNCTIONAL DESCRIPTION

Discovery Hub is an exploratory search engine built on top of linked data sources and, in particular, DBpedia. The exploratory search is a new way to search the web to find new topics the users were not aware of but which may be interesting for them. It allows users performing queries in an innovative way and helps them navigate rich results. As a hub, it proposes redirections to others platforms to let users benefit from their discoveries. It relies on an extension of spreading activation algorithms over linked data to recommend and explain results.

- Participants: Nicolas Marie, Fabien Gandon, Emilie Palagi and Alain Giboin
- Partner: Alcatel-Lucent
- Contact: Fabien Gandon
- URL: http://discoveryhub.co/

6.4. Licentia

License you Data

KEYWORDS: Licenses - Normative Reasoning - Semantic Web - RDF

FUNCTIONAL DESCRIPTION

Licentia is a web service application with the aim to support users in licensing data. Our goal is to provide a full suite of services to help in the process of choosing the most suitable license depending on the data to be licensed. The core technology used in our services is powered by the SPINdle Reasoner and the use of Defeasible Deontic Logic to reason over the licenses and conditions. The dataset of RDF licenses we use in Licentia is the RDF licenses dataset where the Creative Commons Vocabulary and Open Digital Rights Language (ODRL) Ontology are used to express the licenses.

- Participants: Serena Villata, Fabien Gandon. Alumni: Cristian Cardellino
- Partners: I3S
- Contact: Serena Villata
- URL: http://licentia.inria.fr/

6.5. Qakis

Question-Answening wiki framework based system

FUNCTIONAL DESCRIPTION

The QAKiS system (figure 2) 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, Julien Cojan, Amine Hallili, Alessio Palmero Aprosio, Fabien Gandon and Serena Villata.
- Contact: Elena Cabrio
- URL: http://www.qakis.org/

6.6. KNEWS

Versatile Text-to-Knowledge Pipeline

KEYWORD: NLP

FUNCTIONAL DESCRIPTION

KNEWS is a versatile text-to-knowledge pipeline for machine reading, configurable to use different external modules for word sense disambiguation and entity linking. KNEWS works by running these components separately on a text, then it aligns the output of a semantic parser (Boxer) to the output of the other two modules, to produce complete semantic structures linked to DBpedia and Wordnet and represented as RDF graphs. KNEWS provides different kind of outputs: frame instances (based on the FrameBase scheme), word-aligned frames, and first-order logic formulas.

- Participants: Valerio Basile, Elena Cabrio and Fabien Gandon.
- Contact: Valerio Basile & Elena Cabrio
- URL: https://github.com/valeriobasile/learningbyreading

XPOP Team

6. New Software and Platforms

6.1. mlxR

A R package for the simulation and visualization of longitudinal data. The models are encoded using the model coding language ’Mlxtran’, automatically converted into C++ codes, compiled on the fly and linked to R using the ’Rcpp’ package. That allows one to implement very easily complex ODE-based models and complex statistical models, including mixed effects models, for continuous, count, categorical, and time-to-event data.

6.2. FactoMineR

A R package dedicated to principal component methods (PCA, Correspondence Analysis for contingency tables, Multiple Correspondence Analysis for categorical data, MFA for multi-blocks data). Google users group and you-tube videos available.

6.3. missMDA

A R package to perform principal component methods (PCA, MCA, MFA) with missing values and to impute continuous, categorical and mixed data. Multiple imputation is available.

6.4. denoiseR

A R package that approximates a low-rank matrix from noisy data (Gaussian and Poisson Noise). Singular values shrinkage methods are implemented.

ZENITH Project-Team

6. New Software and Platforms

6.1. Pl@ntNet

Participants: Antoine Affouard, Jean-Christophe Lombardo, Hervé Goëau, Alexis Joly [contact].

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 Inria, CIRAD, INRA, IRD and Tela Botanica. 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. Since its first release in march 2013 on the apple store, the application has been downloaded by 3M users in more than 170 countries, with between 15,000 and 50,000 active users daily. 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 300K images covering more than 10K species in the world (and about 60% of the West European flora).

6.2. The Plant Game: crowdsourced plants identification

Participants: Maximilien Servajean, Alexis Joly [contact], Antoine Affouard.

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 objective is to learn botany with fun and participate to a large citizen sciences project in biodiversity. The game relies on consistent research contributions in scalable crowdsourcing models and algorithms that can deal with thousands of complex classes such as plant species. One major contribution 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. As of today, about 22K players are registered and produce hundreds of new validated plant observations per day. The accuracy of the produced taxonomic tags is about 94%, which is quite impressive considering the fact that a majority of users are beginners when they start playing.

6.3. Smart'Flore

Participants: Antoine Affouard [contact], Alexis Joly, Hervé Goëau.

URL: http://otmedia.lirmm.fr/

Smart'Flore is an Android mobile application for the discovery of the surrounding vegetal biodiversity. It has three main features: (i) the geo-based exploration of the world's largest repository of biodiversity occurrences (GBIF, http://www.gbif.org/), (ii) the exploration of virtual botanical trails (created offline through a dedicated web application hosted by TelaBotanica NGO) and (iii) the access to a variety of information about the plants. Smart'Flore is the first mobile app in the world making use of the GBIF web services which makes it a remarkable and possibly highly visible realization. The first public version of the application was released in may 2016. Since then, it has been downloaded by more than 22K users and the daily number of sessions is about 250.

6.4. 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 vector hashing, approximate k-nearest neighbors search and Hamming embedding. Snoop is a refactoring of a previous library called PMH developed jointly with INA. SnoopIm is a content-based image search engine built on top of Snoop that allows retrieving small visual patterns or objects in large collections of pictures. The software is used as the visual search engine of the Pl@ntNet applications and it is used in several other contexts, including a logo retrieval application in collaboration with INA, a whale's individuals matching application in collaboration with the CetaMada NGO, and a hieroglyph recognition application in collaboration with the Egyptology department of University Montpellier 3.

6.5. 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.

6.6. 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)

6.7. LogMagnet

Participant: 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.

6.8. FP-Hadoop

Participants: Reza Akbarinia, 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.

6.9. 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 has been validated on relational, document and graph data stores, as well as Spark/HDF in the context of the CoherentPaaS European project.

6.10. AgroLD

Participants: Pierre Larmande, Patrick Valduriez.

URL: http://www.agrold.org

Agronomic Linked Data (AgroLD) is a portal to help bioinformatics and domain experts exploiting the homogenized data models towards efficiently generating research hypotheses. AgroLD is an RDF knowledge base that is designed to integrate data from various publicly available plant centric data sources and ontologies, using Web Ontology Language (OWL) and the SPARQL Query Language (SPARQL).

6.11. SciFloware

Participants: Benjamin Billet, 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.