RESEARCH CENTER
Sophia Antipolis - Méditerranée

FIELD

Activity Report 2015

Section Software

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ABS Project-Team

5. New Software and Platforms

5.1. The Structural Bioinformatics Library

5.1.1. Web site:

http://sbl.inria.fr

5.1.2. The SBL : Overview

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

For Biologists, the key advantages are:

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

For Developers, the striking facts are:

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

5.1.3. The SBL : Rationale and Design

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

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

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

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

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

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

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

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

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

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

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

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

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

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

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

5.1.7. Interoperability

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

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

5.1.8. Releases, Distribution, and License

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

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

ACUMES Team

5. New Software and Platforms

5.1. BuildingSmart

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

- Contact: Abderrahmane Habbal

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

5.2. Interoperability between Num3sis and Axel Platforms

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

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

AOSTE Project-Team

6. New Software and Platforms

6.1. SynDEx

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

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

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

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

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

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

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

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

6.2. TimeSquare

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

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

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

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

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

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

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

FUNCTIONAL DESCRIPTION

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

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

6.3. Lopht

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

SCIENTIFIC DESCRIPTION

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

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

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

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

6.4. EVT Kopernic

KEYWORD: Embedded systems

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

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

6.5. SAS

Simulation and Analysis of Scheduling
SCIENTIFIC DESCRIPTION

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

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

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

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

APICS Project-Team

5. New Software and Platforms

5.1. Dedale-HF

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

5.2. FindSources3D

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

ASCLEPIOS Project-Team

5. New Software and Platforms

5.1. MedInria

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

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

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

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

5.2. MUSIC

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

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

5.3. SOFA

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

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

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

5.4. VP2HF

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

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

5.5. LSVF

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

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

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

ATHENA Project-Team

5. New Software and Platforms

5.1. High Performance Diffusion MRI

KEYWORDS: Health - Neuroimaging - Medical imaging
FUNCTIONAL DESCRIPTION

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

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

5.2. DIPY

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

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

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

5.3. The White Matter Query Language

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

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

5.4. MedInria

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

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

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

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

5.5. Coadapt P300 Stimulator

KEYWORDS: Health - Brain-Computer Interface
FUNCTIONAL DESCRIPTION

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

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

5.6. FindSources3D

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

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

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

5.7. OpenMEEG

KEYWORDS: Health - Neuroimaging - Medical imaging

FUNCTIONAL DESCRIPTION

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

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

5.8. OpenVIBE

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

FUNCTIONAL DESCRIPTION

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

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

AYIN Team

6. New Software and Platforms

6.1. SAAD

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

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

6.2. ED

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

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

6.3. ET

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

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

6.4. ETK

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

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

6.5. CLESTO

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

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

6.6. CLERANK

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

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

6.7. Consulting for Industry

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

BIOCORE Project-Team

6. New Software and Platforms

6.1. In@lgae

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

FUNCTIONAL DESCRIPTION

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

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

6.2. Odin

KEYWORDS: Bioinformatics - Biotechnology
SCIENTIFIC DESCRIPTION

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

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

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

CASTOR Project-Team

4. New Software and Platforms

4.1. CEDRES++

FUNCTIONAL DESCRIPTION

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

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

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

4.2. Equinox

FUNCTIONAL DESCRIPTION

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

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

4.3. FBGKI (Full Braginskii)

FUNCTIONAL DESCRIPTION The Full Braginskii solver considers the equations proposed by Braginskii (1965), in order to describe the plasma turbulent transport in the edge part of tokamaks. These equations rely on a two fluid (ion - electron) description of the plasma and on the electroneutrality and electrostatic assumptions. One has then a set of 10 coupled non-linear and strongly anisotropic PDEs. FBGKI makes use in space of high order methods: Fourier in the toroidal periodic direction and spectral elements in the poloidal plane. The spectral vanishing viscosity (SVV) technique is implemented for stabilization. Static condensation is used to reduce the computational cost. In its sequential version, a matrix free solver is used to compute the potential. The parallel version of FBGKI presents two layers of parallelization: The first one corresponds to the

poloidal plane and the second one to the toroidal direction. In the poloidal plane, the domain decomposition is achieved using the software METIS. For the parallel linear algebra, one uses the software PETSC (Portable Extensible Toolkit for Scientific Computation). The time discretization makes use of a Strang splitting, that decouples the explicit treatment of the advection and Braginskii terms, from the implicit treatment of the Lorentz forces and the computation of the electric potential. Whereas the explicit part is easily parallelized, the implicit one requires solving a strongly anisotropic elliptic problem for the potential. In the parallel version of FBGKI the system matrix is assembled in sparse manner, in order to allow using the multigrid HYPRE preconditionner implemented in PETSC. Till now results have only been obtained for computations done on a few tens of processors. Both the weak and strong scalings look satisfactory. Numerical experiments are still required to go up to hundreds or thousands of processors.

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

4.4. FEEQS.M

FUNCTIONAL DESCRIPTION

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

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

4.5. Fluidbox

FUNCTIONAL DESCRIPTION

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

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

4.6. Jorek-Django

FUNCTIONAL DESCRIPTION

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

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

4.7. Plato

A platform for Tokamak simulation

FUNCTIONAL DESCRIPTION

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

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

4.8. VacTH

FUNCTIONAL DESCRIPTION

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

- Contact: Blaise Faugeras

COATI Project-Team

6. New Software and Platforms

6.1. Grph

Participants: Luc Hogie [Contact], Nathann Cohen, David Coudert.

FUNCTIONAL DESCRIPTION

GRPH is an open-source Java library for the manipulation of graphs. In 2015, the library has been maintained and augmented for users needs, especially with a new algorithm for iterating over the cycles of a given graph. This was requested by the EPI AOSTE for the TimeSquare tool.

URL: http://www.i3s.unice.fr/~hogie/grph/

6.2. JourneyPlanner

Participant: Marco Biazzini [Contact].

FUNCTIONAL DESCRIPTION

JourneyPlanner is a Java implementation of a recursive algorithm to solve a TSP problem on small dense graphs, where non-trivial constraints must be satisfied, that make commonly used paradigms (as dynamic programming) unfit to the task.
This work is done in collaboration with the R&D service of the "Train Transportation" division of Amadeus.

6.3. Sagemath

Participants: David Coudert [Contact], Nathann Cohen.

SCIENTIFIC DESCRIPTION

Sagemath is a free open-source mathematics software system initially created by William Stein (Professor of mathematics at Washington University). It builds on top of many existing open-source packages: NumPy, SciPy, matplotlib, Sympy, Maxima, GAP, FLINT, R and many more. Access their combined power through a common, Python-based language or directly via interfaces or wrappers.

OUR CONTRIBUTION

We contribute the addition of new graph algorithms to Sagemath, along with their documentation and the improvement of underlying data structures.

URL : http://www.sagemath.org/

6.4. TripPlanner

Participants: David Coudert [Contact], Stéphane Pérennes.

FUNCTIONAL DESCRIPTION

TripPlanner is a tool for computing a minimum cost trip across multiple cities when neither the order in which to visit the cities nor the sojourn duration in these cities are fully specified. The cost of a trip includes both the price of all airplane tickets necessarily for the trip plus the price of the hotels (both costs depend on the exact travel date) at which the user will sojourn. The trip planner is also able to compute the k cheapest trips.

TripPlanner is written in Python and uses the linear programming interface of Sagemath.

This work is done in collaboration with the R&D service of the "Train Transportation" division of Amadeus.

BNF Antepedia Deposit 2015-09-23-16-11-18

6.5. Platforms

6.5.1. BigGraphs

Participants: Luc Hogie [Contact], Nicolas Chleq [SED-SOP], Michel Syska [Coordinator], David Coudert, Paul Bertot, Flavian Jacquot, Arnaud Legout [DIANA], Fabrice Huet [SCALE], Éric Madelaine [SCALE].

FUNCTIONAL DESCRIPTION

The objective of BigGraphs is to provide a distributed platform for very large graphs processing. A typical data set for testing purpose is a sample of the Twitter graph with 3 millions of nodes and 200 millions of edges. Last year we started the project with the evaluation of existing middlewares (GraphX/Spark and Giraph/Hadoop). After having tested some useful algorithms (written in the BSP model) we decided to develop our own platform.

This platform is based on the existing BIGGRPH library and this year we have focused on the quality and the improvement of the code. In particular we have designed strong test suites and some non trivial bugs have been fixed. We also have implemented specific data structures for BSP and support for distributed debugging. This comes along with the implementation of algorithms such as BFS or strongly connected components that are run on the NEF cluster.

This project is a joint work of the three EPI COATI, DIANA and SCALE and is supported by an ADT grant.

URL: http://www.i3s.unice.fr/~hogie/software/index.php?name=grph

The following software are useful tools that bring basic services to the platform (they are not dedicated to BIGGRPH).

JAC-A-BOO: is a framework aiming at facilitating the deployment of distributed Java scientific applications over clusters and is used to start BIGGRPH. computers.

LDJO: (Live Distributed Java Objects) is a framework for the development and the deployment of Java distributed data structures

OCTOJUS: provides an object-oriented RPC (Remote Procedure Call) implementation in Java

Participants : Luc Hogie [Contact], Nicolas Chleq

URL : http://www.i3s.unice.fr/~hogie/ {jacaboo,ldjo,octojus}

COFFEE Project-Team

5. New Software and Platforms

5.1. NS2DDV

The code NS2DDV is developed jointly with the team SIMPAF, of the Inria Research Centre Lille Nord Europe. It is devoted to the simulation of non-homogeneous viscous flows, in two-dimensional geometries. The code is based on an original hybrid Finite Volume/Finite Element scheme; it works on unstructured meshes and can include mesh refinements strategies. Further details can be found in the research papers J. Comput. Phys., 227, 4671–4696, 2008 and J. Comput. Phys., 229 (17), 6027–6046, 2010. The code exists in two versions: a `Matlab` public version, a `C++` prototype version allowing more ambitious simulations. Both versions are still subject to developments. The current versions is restricted to incompressible flows but ongoing progress are concerned with the simulation of avalanches. The source code of the public version is downloadable and several benchmarks tests can be reproduced directly.

- Contact: Emmanuel Creusé
- URL: math.univ-lille1.fr/~simpaf/SITE-NS2DDV/home.html
- The code has been subject to an APP deposit many years ago, but we never received any registration number.

5.2. Compass

for Computing Parallel Architecture to Speed up Simulation is a parallel code for the discretization of polyphasic flows by Finite Volumes methods. The code is mainly devoted to applications in porous media. It works on quite general polyhedral meshes. A first step in the code development has been made during the 2012 edition of CEMRACS and then pursued by C. Guichard, R. Masson and R. Eymard in 2013. A first version of the code has been deposited at the Agency for the Protection of Programs (APP). This current version of `ComPASS` has been tested on a gas storage two phase flow benchmark with GDFSuez using the Vertex Approximate Gradient spatial discretization. The results have shown a very good parallel scalability on the CICADA Cluster at UNS with a few millions of cells and up to 1024 cores. The objective is to develop a generic simulator for multiphase Darcy flows. This simulator will implement advanced finite volume methods on general 3D meshes and on heterogeneous anisotropic media, taking into account discrete fracture networks represented as interfaces of codimension one and coupled with the surrounding matrix. It will be able to treat a large range of multiphase Darcy flow models accounting for thermodynamical equilibrium and the coupling with an energy conservation equation. The simulator will run on massively parallel architectures with a few thousands of cores. It will be applied to several type of industrial applications starting with the simulation of high energy geothermal systems as a carbon-free source of power production.

- Participants: Roland Masson, Cindy Guichard, Feng Xing and Robert Eymard, Thierry Goudon,
- Contact: Roland Masson
- URL: math.unice.fr/~massonr/
- The code has been subject to an APP deposit a few years ago, but we never received any registration number.

5.3. SimBiof

We are developing numerical methods, currently by using Finite Differences approaches, for the simulation of biofilms growth. The underlying system of PDEs takes the form of multiphase flows equations with conservation constraints and vanishing phases. The numerical experiments have permitted to bring out the influence of physical parameters on the multidimensional growth dynamics.

- Contact: Magali Ribot

5.4. AP_PartFlow

We are developing experimental codes, mainly based on Finite Differences, for the simulation of particulate flows. A particular attention is paid to guaranty the asymptotic properties of the scheme, with respect to relaxation parameters.

- Contact: Thierry Goudon

DEMAR Project-Team

4. New Software and Platforms

4.1. Synergy Neurostimulation Software

Participants: Arthur Hiairrassary, David Andreu, David Guiraud.

We have developed a specific software environment called Synergy Neurostimulation Software (fig.1), allowing to remotely manage a stimulation architecture based on one controller piloting a set of distributed stimulation units, connected by means of a dedicated network. The controller embeds the set of FES functions according to which it controls stimulation units, in real-time.

This FES distributed architecture is based on our last version of stimulation units that embed stimulation sequencing and a more efficient modulation mechanism.

Synergy Neurostimulation Software has been registered at the french Agence de Protection des Programmes (APP).

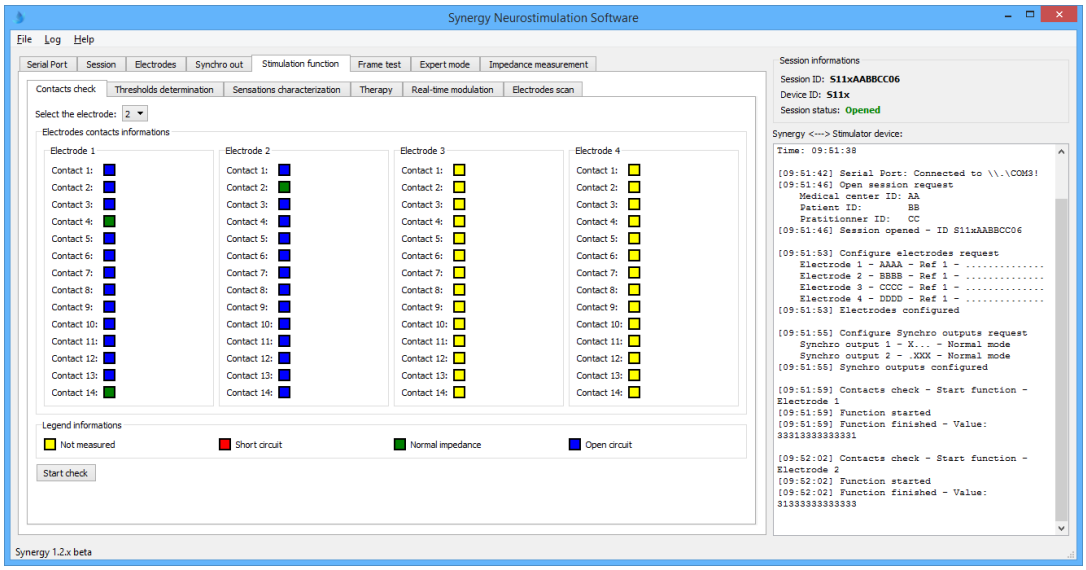


Figure 1. Synergy Neuromodulation Software

4.2. HILECOP

High Level hardware Component Programming
FUNCTIONAL DESCRIPTION

Our SENIS (Stimulation Electrique Neurale dIStribuee) based FES architecture relies on distributed stimulation units (DSU) which are interconnected by means of a 2-wire based network. A DSU is a complex digital system since its embeds among others a dedicated processor (micro-machine with a specific reduced instruction set), a monitoring module and a 3-layer protocol stack. To face the complexity of the units digital part and to ease its prototyping on programmable digital devices (e.g. FPGA), we developed an approach for high level hardware component programming (HILECOP). To support the modularity and the reusability of sub-parts of complex hardware systems, the HILECOP methodology is based on components. An HILECOP component has: a Petri Net (PN) based behavior (fig.2), a set of functions whose execution is controlled by the PN, and a set of variables and signals. Its interface contains places and transitions from which its PN model can be inter-connected as well as signals it exports or imports. The interconnection of those components, from a behavioral point out view, consists in the interconnection of places and/or transitions according to well-defined mechanisms: interconnection by means of oriented arcs or by means of the "merging" operator (existing for both places and transitions).

The Eclipse-based version of HILECOP (registered at the french Agence de Protection des Programmes (APP)) has been refactored: for instance, the application ECore model, a new Eclipse E4 architecture and a set of new features (new link types and new views to connect components) have been developed.

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

Specification of GALS systems (Globally Asynchronous Locally Synchronous) is also an ongoing work, the aim being to take into account deployment properties like connecting different clocks to HILECOP components within a same FPGA, or on a set of interconnected FPGAs (and thus interconnecting them by means of asynchronous signals).

- Participants: Baptiste Colombani, David Andreu, Thierry Gil, Robin Passama
- Contact: David Andreu

4.3. MOS2SENS

Model Optimization and Simulation To Selective Electrical Neural Stimulation
KEYWORDS: Neurosciences - Health - Physiology
FUNCTIONAL DESCRIPTION

This model can predict nerve fiber activation through multipolar electrode stimulation. Furthermore the models provide an optimal current configuration to activate accurately the targeted muscle or organ (indeed a targeted group of fiber).

The new software MOS2SENS is an adjustment support tool for neuroprosthetics devices. It models and optimizes the current injected by multipolar CUFF electrodes inside the nerve in order to activate selective fiber targets in terms of spatial criterion.

- Participants: Melissa Dali, Olivier Rossel and David Guiraud
- Contact: David Guiraud

4.4. PALGate

KEYWORDS: Health - Home care - Handicap

- Contact: David Daney

4.5. PersoBalance

PersoBalance: A Personalized Balance Assessment in Home Rehabilitation
KEYWORDS: Health - Home care - Handicap

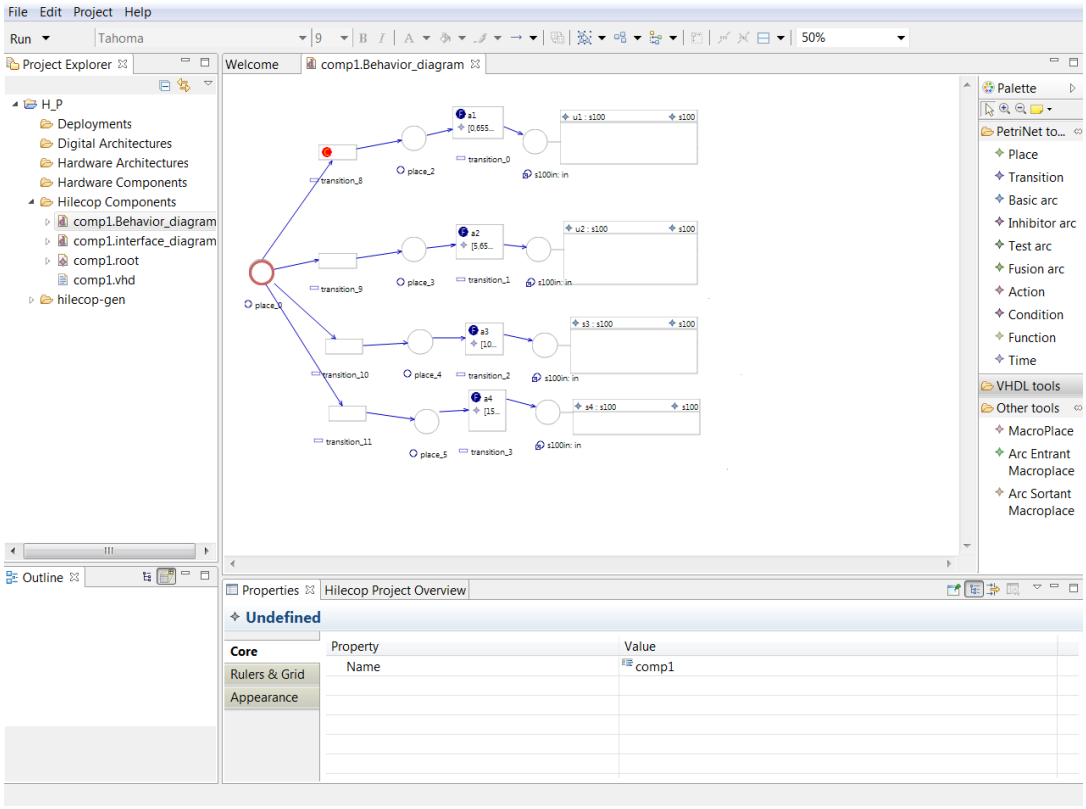


Figure 2. HILECOP screenshot

4.5.1. PersoBalance: A Personalized Balance Assessment in Home Rehabilitation

Participants: Mitsuhiro Hayashibe, Alejandro Gonzalez [Euromov], Philippe Fraisse.

The objective of this software is to realize a personalized evaluation of the postural balance to be used in home-based rehabilitation, by using portable sensors such as Kinect and wii board. After the one time of identification, the system provide us the personalized estimation of the center of mass (CoM) for the whole body only with Kinect information, through Statically Equivalent Serial Chain method.

The first function is the adaptive identification interface for the CoM parameters based on Kalman filter which allows a subject to provide different postures interactively with minimized time length. The second function is the balance measure visualization (stable or instable) based on the identified model for each subject considering subject-specific body differences on the segment mass distribution.

Recently, this software was demonstrated at the event of Rencontre Inria-Industrie 13/10/2015 at Bordeaux. https://www.inria.fr/centre/bordeaux/innovation/rii-sante/demonstrations2 It is also filed at Software Catalogue of Inria. https://www.inria.fr/centre/bordeaux/innovation/rii-sante/catalogue-logiciels

PersoBalance is registered with the Agency for the Protection of Programs (APP) and deposited at the BNF (Bibliotheque Nationale de France). Its registration number is Antepedia Deposit 20150710154654.

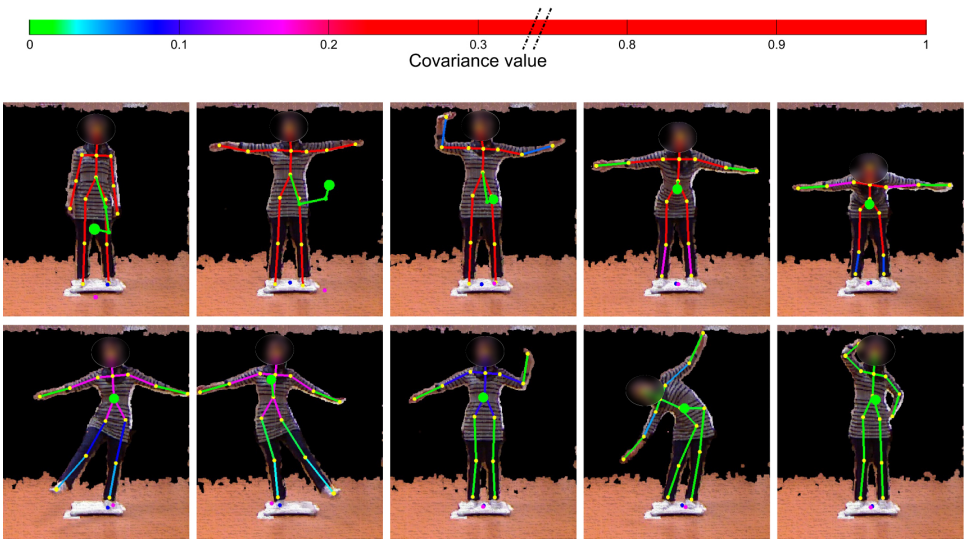


Figure 3. PersoBalance: A Personalized Balance Assessment in Home Rehabilitation: This scene shows the process how the CoM is being identified through different postures information with portable sensors.

4.6. SENISManager

Stimulation Electrique Neurale dIStribuee

FUNCTIONAL DESCRIPTION

SENISManager is a specific software environment allowing to remotely manage and control a network of DSUs, i.e. the distributed FES architecture. SENISManager performs self-detection of the architecture being deployed. This environment allows the manipulation of micro-programs from their edition to their remote control. It also allows the programming of control sequences executed by an external controller in charge of automatically piloting a stimulator.

- Participants: David Andreu and Robin Passama
- Contact: David Andreu

4.7. sensbiotk

KEYWORDS: Motion analysis - Sensors
SCIENTIFIC DESCRIPTION Sensbiotk is a toolbox in Python for the calibration, the acquisition, the analysis and visualization of motion capture Inertial Measurement Units (IMU). Motion and Gait parameter reconstruction algorithms are also available.
FUNCTIONAL DESCRIPTION

sensbiotk toolbox for Python. for the calibration, acquisition, analysis and visualization of motion capture using IMU

- Participants: Christine Azevedo Coste, Roger Pissard-Gibollet and Benoît Sijobert
- Contact: Roger Pissard Gibollet
- URL: http://sensbio.github.io/sensbiotk/

DIANA Project-Team

5. New Software and Platforms

5.1. ACQUA

Participants: Chadi Barakat [contact], Thierry Spetebroot, Nicolas Aguilera Miranda, Damien Saucez.

ACQUA is an Application for prediCting Quality of User experience at Internet Access. It was supported by the French ANR CMON project on collaborative monitoring and will be supported in 2016 by both the Inria ADT ACQUA and the ANR Project BottleNet. ACQUA presents a new way for the evaluation of the performance of Internet access. Starting from network-level measurements as the ones we often do today (bandwidth, delay, loss rates, etc), ACQUA targets the estimated quality of experience related to the different applications of interest to the user without the need to run them (e.g. estimated Skype quality, estimated video streaming quality). An application in ACQUA is a function that links the network-level measurements to the expected quality of experience. In its first version (the version available online), ACQUA was concentrating on delay measurements at the access and on the detection and estimation of the impact of delay anomalies (local problems, remote problems, etc). The current work is concentrating on using the ACQUA principle in the estimation and prediction of the quality of experience of main user's applications (see section 6.1.1 for more details). An Android version is under development supported by the Inria ADT ACQUA.

- URL: http://team.inria.fr/diana/acqua/
- Version: 1.1
- ACM: C.2.2, C.2.3
- Keywords: Internet measurement, Internet Access, Quality of Experience
- License: GPL (3)
- Type of human computer interaction: GUI for client, Web interface for experimentation
- OS/Middleware: MS Windows
- Required library or software: visual studio http://www.visualstudio.com/en-us/products/visual-studio-express-vs.aspx
- Programming language: C# for client, java for server, CGI and Dummynet for experimentation

5.2. ElectroSmart

Participants: Arnaud Legout [contact], Inderjeet Singh, Maksym Gabielkov.

The Internet and new devices such as smartphones have fundamentally changed the way people communicate, but this technological revolution comes at the price of a higher exposition of the general population to microwave electromagnetic fields (EMF). This exposition is a concern for health agencies and epidemiologists who want to understand the impact of such an exposition on health, for the general public who wants a higher transparency on its exposition and the health hazard it might represent, but also for cellular operators and regulation authorities who want to improve the cellular coverage while limiting the exposition, and for computer scientists who want to better understand the network connectivity in order to optimize communication protocols. Despite the fundamental importance to understand the exposition of the general public to EMF, it is poorly understood because of the formidable difficulty to measure, model, and analyze this exposition.

The goal of the ElectroSmart project is to develop the instrument, methods, and models to compute the exposition of the general public to microwave electromagnetic fields used by wireless protocols and infrastructures such as Wi-Fi, Bluetooth, or cellular. Using a pluri-disciplinary approach combining crowd-based measurements, in-lab experiments, and modeling using sparse and noisy data, we address challenges such as designing and implementing a measuring instrument leveraging on crowd-based measurements from mobile devices such as smartphones, modeling the exposition of the general public to EMF to compute the most accurate estimation of the exposition, and analyzing the evolution of the exposition to EMF with time. This technological breakthrough will have scientific, technical, and societal applications, notably on public health politics, by providing the scientific community and potential users with a unique measuring instrument, methods, and models to exploit the invaluable data gathered by the instrument.

This project has been supported by the Inria ADT ElectroSmart in 2014 and 2015 and will be supported by a Labex funding in the next two years.

In 2015, we released the first alpha version of the application for tests with real users (10 volunteers) and we published an associated Web site http://es.inria.fr.

- URL: http://es.inria.fr
- Version: 1.0alpha
- Keywords: background electromagnetic radiations
- License: Inria proprietary licence
- Type of human computer interaction: Android application
- OS/Middleware: Android
- Required library or software: Android
- Programming language: Java
- Documentation: javadoc

5.3. NEPI

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

NEPI, the Network Experimentation Programming Interface, is a framework to describe and orchestrate network experiments on a variety of network experimentation platforms, including simulators, emulators, live testbeds, and testbed federations. NEPI is capable of supporting arbitrary platforms through the use of a generic network experiment description model, based on abstracting network experiments as a collection of arbitrary resource objects, and through the generalization of the experiment life cycle for all resources. The common resource life cycle consists of the sequence of operations deploy, start, stop, and release. Different resource objects can implement specific versions of those operations to adapt to any platform. NEPI resolves experiment orchestration as an online scheduling problem.

In the context of Alina Quereilhac PhD, we generalized in 2015 the network experiments automation framework for arbitrary evaluation platforms, and for scenarios targeting any networking research domain. The proposed approach is based on abstracting the experiment life cycle for different platforms into generic steps that are valid for simulators, emulators, and testbeds. Based on these steps, a generic experimentation architecture was proposed and implemented, composed of an experiment model, an experimentation interface, and an orchestration algorithm. Three main aspects of the framework were evaluated: its extensibility to support heterogeneous platforms, its efficiency to orchestrate experiments, and its flexibility to support diverse use cases for different networking research domains, including education, platform management, and experimentation with testbed federations, and cross-platform and multi-platform scenarios. The results show that the proposed approach can be used to efficiently automate experimentation on heterogeneous evaluation platforms, for a wide range of scenarios.

On a much more practical level, NEPI is now available in a version numbered 6, that can run within both python2 and python3 environments.

- URL: http://nepi.inria.fr
- Version: 6.0
- ACM: C.2.2, C.2.4
- Keywords: networking experimentation, simulation, emulation
- License: GPL (3)
- Type of human computer interaction: python library
- OS/Middleware: Linux
- Required library or software: matplotlib - graphviz (both optional)
- Programming language: python2 or python3

5.4. ns-3

Participants: Walid Dabbous [contact], Thierry Turletti.

ns-3 is a discrete-event network simulator for Internet systems, targeted primarily for research and educational use. ns-3 includes a solid event-driven simulation core as well as an object framework focused on simulation configuration and event tracing, a set of realistic 802.11 MAC and PHY models, an IPv4, UDP, and TCP stack and support for nsc (integration of Linux and BSD TCP/IP network stacks). ns-3 is free software, licensed under the GNU GPLv2 license, and it is publicly available for research, development, and use. Our team has been involved in ns-3 project since 2006 and we are founding member of the ns-3 consortium including Washington University, Georgia Tech, CTTC, INESC PORTO as executive members. In 2015, using the NEPI framework, we worked on the automation of ns-3 experiments in multi-host scenarios with three example cases: a) running parallel simulations on a cluster of hosts, b) running distributed simulations spanning multiple hosts, and c) integrating live and simulated networks.

- URL: http://www.nsnam.org
- Version: ns-3.21
- Keywords: networking event-driven simulation
- License: GPL (GPLv2)
- Type of human computer interaction: programmation C++/python, No GUI
- OS/Middleware: Linux, cygwin, osX
- Required library or software: standard C++ library: GPLv2
- Programming language: C++, python
- Documentation: doxygen

5.5. DCE

Participants: Thierry Turletti [contact], Walid Dabbous.

DCE enables developers and researchers to develop their protocols and applications in a fully controllable and deterministic environment, where tests can be repeated with reproducible results. It allows unmodified protocol implementations and application code to be tested over large and possibly complex network topologies through the ns-3 discrete-event network simulator. The single-process model used in the DCE virtualization core brings key features, such as the possibility to easily debug a distributed system over multiple simulated nodes without the need of a distributed and complex debugger. Examples of tested applications over DCE include Quagga, iperf, torrent, thttpd, CCNx and various Linux kernel versions (from 2.6.36 to 3.12 versions). DCE was initially developed by Mathieu Lacage during his PhD thesis and is maintained by engineers in the team in collaboration with Hajime Tazaki from University of Tokyo. Our effort on DCE was reduced in 2015 due to lack of resources, but DCE/ns-3 represents an important component of R2lab in particular for performance comparison and hybrid (real/simulation/emulation) experiments. DCE is free software, licensed under the GNU GPLv2 license, and is publicly available for research, development, and use.

- URL: https://www.nsnam.org/overview/projects/direct-code-execution/
- Version: DCE-1.7
- Keywords: emulation, virtualization, networking event-driven simulation
- License: GPL (GPLv2)
- Type of human computer interaction: programmation C/C++, No GUI
- OS/Middleware: Linux
- Required library or software: standard C++ library: GPLv2
- Programming language: C++, python
- Documentation: doxygen

5.6. OpenLISP

Participant: Damien Saucez [contact].

Among many options tackling the scalability issues of the current Internet routing architecture, the Locator/Identifier Separation Protocol (LISP) appears as a viable solution. LISP improves a network's scalability, flexibility, and traffic engineering, enabling mobility with limited overhead. As for any new technology, implementation and deployment are essential to gather and master the real benefits that it provides. We propose a complete open source implementation of the LISP control plane. Our implementation is deployed in the worldwide LISP Beta Network and the French LISP-Lab testbed, and includes the key standardized control plane features. Our control plane software is the companion of the existing OpenLISP dataplane implementation, allowing the deployment of a fully functional open source LISP network compatible with any implementation respecting the standards. As of 2015, OpenLISP is still used to provide connectivity between satellite sites of the LISP-Lab project and has been used as LISP implementation for PACAO, an overlay aiming at optimising Cloud access in distributed data-centers.

- http://www.lisp-lab.org/
- Version: 3.2
- ACM: C.2.1, C.2.2, C.2.6
- Keywords: routing, LISP, control-plane
- License: BSD
- Type of human computer interaction: XML, CLI
- OS/Middleware: POSIX
- Required library or software: Expat 2
- Programming language: C
- Documentation: Unix man
- Deployment: ddt-root.org

5.7. Platforms

5.7.1. Reproducible research laboratory ($\mathrm{R}^2\mathrm{LAB}$*)*

Scientific evaluation of network protocols requires that experiment results must be reproducible before they can be considered as valid. This is particularly difficult to obtain in the wireless networking domain, where characteristics of wireless channels are known to be variable, unpredictable and hardly controllable. We have built at Inria Sophia-Antipolis, in 2014, an anechoic chamber, with RF absorbers preventing radio waves reflections and with Faraday cage blocking external interferences. This lab, named $\mathrm{R}^2\mathrm{lab}$, represents an ideal environment for experiments reproducibility. $\mathrm{R}^2\mathrm{lab}$ has been announced for usage by the general public at the end of 2015. It was developed, and is now operated, in the context of the FIT 'Equipment of Excellence' project, and as such, it is now federated with the other testbeds that are part of the FIT initiative. This testbed is for the long-haul, and is scheduled to remain operational until at least 2020. Future work, in addition to regular operations, includes adding new hardware capabilities to the wireless nodes, such as USRP for running Software Defined Radio, as well as possibly OpenAirInterface for supporting 5G-like experiments.

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

ECUADOR Project-Team

5. New Software and Platforms

5.1. AIRONUM

SCIENTIFIC DESCRIPTION
Aironum is an experimental software that solves the unsteady compressible Navier-Stokes equations with k-, LES-VMS and hybrid turbulence modelling on parallel platforms, using MPI. The mesh model is unstructured tetrahedrization, with possible mesh motion.
FUNCTIONAL DESCRIPTION
Aironum was developed by Inria and University of Montpellier. It is used by Inria, University of Montpellier and University of Pisa (I). Aironum is used as an experimental platform for:

- Numerical approximation of compressible flows, such as upwind mixed element volume approximation with superconvergence on regular meshes.
- Numerical solution algorithms for the implicit time advancing of the compressible Navier-Stokes equations, such as parallel scalable deflated additive Schwarz algorithms.
- Turbulence modelling such as the Variational Multiscale Large eddy Simulation and its hybridization with RANS statistical models.
- Participant: Alain Dervieux
- Contact: Alain Dervieux
- URL: http://www-sop.inria.fr/tropics/aironum

5.2. TAPENADE

KEYWORDS: Static analysis - Optimization - Compilation - Gradients
SCIENTIFIC DESCRIPTION
Tapenade implements the results of our research about models and static analyses for AD. For a full specification and description, see [10]. AD produces analytical derivatives, that are exact up to machine precision. Adjoint AD computes gradients at a cost which is independent from the number of input variables. Tapenade performs sophisticated flow- and context-sensitive data-flow analysis on the complete source program to produce an efficient differentiated code. Analyses include Type-Checking, Read-Write analysis, Pointer analysis. AD-specific analyses include:

- Activity analysis: Detects variables whose derivative is either null or useless, to reduce the number of derivative instructions.
- Adjoint Liveness analysis: Detects the source statements that are dead code for the computation of derivatives.
- TBR analysis: In Adjoint AD, reduces the set of source variables that need to be recovered.

FUNCTIONAL DESCRIPTION
Tapenade transforms an original program into a new program that computes derivatives of the original program. Tapenade accepts source programs written in Fortran77, Fortran90, or C. Tapenade can differentiate in tangent, vector tangent, adjoint, and vector adjoint modes. Tapenade can be downloaded and installed on most architectures. Alternatively, it can be used as a web server. Higher-order derivatives can be obtained through repeated application.

- Participants: Laurent Hascoët, Valérie Pascual, Ala Taftaf
- Contact: Laurent Hascoët
- URL: http://www-sop.inria.fr/tropics/tapenade.html

FOCUS Project-Team

6. New Software and Platforms

6.1. AIOCJ

SCIENTIFIC DESCRIPTION

AIOCJ is an open-source choreography programming language for developing adaptive systems. It allows one to program adaptive distributed systems based on message passing. AIOCJ comes as a plugin for Eclipse, AIOCJ-ecl, allowing to edit descriptions of distributed systems as adaptive interaction-oriented choreographies (AIOC). From interaction-oriented choreographies the description of single participants can be automatically derived. Adaptation is specified by rules allowing to replace predetermined parts of the AIOC with a new behaviour. A suitable protocol ensures that all the participants are updated in a coordinated way. As a result, the distributed system follows the specification given by the AIOC under all changing sets of adaptation rules and environment conditions. In particular, the system is always deadlock free. AIOCJ can interact with external services, seen as functions, by specifying their URL and the protocol they support (HTTP, SOAP, ...). Deadlock-freedom guarantees of the application are preserved provided that those services do not block.

- Contact: Saverio Giallorenzo
- URL: http://www.cs.unibo.it/projects/jolie/aiocj.html

6.2. DF4ABS

Deadlock Framework for ABS
SCIENTIFIC DESCRIPTION

We have prototyped a framework for statically detecting deadlocks in a concurrent object-oriented language with asynchronous method calls and cooperative scheduling of method activations (the language is ABS, which has been developed in the EU project HATS and currently extended with primitives for cloud-computing in the EU project ENVISAGE. ABS is very similar to ASP, developed by the OASIS team.). Since this language features recursion and dynamic resource creation, deadlock detection is extremely complex and state-of-the-art solutions either give imprecise answers or do not scale. In order to augment precision and scalability we propose a modular framework that allows several techniques to be combined. The basic component of the framework is a front-end inference algorithm that extracts abstract behavioural descriptions of methods that retain resource dependency information. Then these behavioural descriptions are analysed by a back-end that uses a fix-point technique to derive in a deterministic way the deadlock information.

- Contact: Elena Giachino
- URL: http://df4abs.nws.cs.unibo.it/

6.3. HoCA

Higher-Order Complexity Analysis
SCIENTIFIC DESCRIPTION

Over the last decade, various tools for the static analysis of resource properties of programs have emerged. In particular, the rewriting community has recently developed several tools for the time complexity analysis of term rewrite systems. These tools have matured and are nowadays able to treat non-trivial programs, in a fully automatic setting. However, none of these automatic complexity analysers can deal with higher-order functions, a pervasive feature of functional programs.

Our tool HoCA (Higher-Order Complexity Analyser) overcomes this limitation by translating higher-order programs – in the form of side-effect free OCaml programs – into equivalent first-order rewrite systems. At the heart of our tool lies Reynold's defunctionalization technique. Defunctionalization however is not enough. Resulting programs have a recursive structure too complicated to be analysed automatically in all but trivial cases. To overcome this issue, HoCA integrates a handful of well established program transformation techniques, noteworthy dead-code elimination, inlining, instantiation and uncurrying. All these techniques have been specifically suited to the methods integrated in modern first-order complexity analysers. Of course, the complete transformation pipeline underlying our tool is not only proven semantically correct, but also to reflect the runtime behavior. This way, a complexity bound on the resulting first-order program can be relayed back reliably to the higher-order program of interest.
A detailed description of HoCA is available on http://arxiv.org/abs/1506.05043

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

6.4. JOLIE

Java Orchestration Language Interpreter Engine
SCIENTIFIC DESCRIPTION

Jolie is a service-oriented programming language. Jolie can be used to program services that interact over the Internet using different communication protocols.

Differently from other Web Services programming languages such as WS-BPEL, Jolie is based on a user-friendly C/Java-like syntax (more readable than the verbose XML syntax of WS-BPEL) and, moreover, the language is equipped with a formal operational semantics. This language is used for the *proof of concepts* developed around Focus activities. For instance, contract theories can be exploited for checking the conformance of a Jolie program with respect to a given contract.
Developments in 2015: Jolie has transitioned from version 1.1 to version 1.4.1. The releases are the result of more than 400 commits with hundreds of bug fixes and enhancements. Highlights include: a new web site and documentation, a new pre-compiled installer, 2 new IDEs as plugins for the editors Sublime Text and Atom, a transition from SouceForge to GitHub, introduction of new behavioural and architectural constructs, structured support for the development of REST applications, introduction of the construct of internal services: embedded Jolie services defined directly within the embedder program (internal services offer a convenient way of reusing code as in procedural programming, without breaking the principle that such code should be easily exported to an external microservice), increased compliance with protocol standards (foremost HTTP, SSL), enhanced stability and performances. Moreover, 2015 has seen the development of Jolie Redeployment Optimiser (JRO), a tool for the automatic and optimised deployment of microservices written in Jolie. JRO uses Zephyrus, a state-of-the-art tool that automatically generates configurations starting from partial and abstract descriptions of the target application. Given the output configuration from Zephyrus, JRO interacts with Jolie Enterprise, an administrative tool for the deployment of Jolie services on remote nodes, to deploy the wanted architecture.

- Contact: Fabrizio Montesi, Saverio Giallorenzo
- URL: http://www.jolie-lang.org/

6.5. SRA

Static Resource Analyzer for ABS
SCIENTIFIC DESCRIPTION

We prototype a static analysis technique that computes upper bounds of virtual machine usages in a concurrent language with explicit acquire and release operations of virtual machines. In our language it is possible to delegate other (ad-hoc or third party) concurrent code to release virtual machines (by passing them as arguments of invocations, a feature that is used by Amazon Elastic Cloud Computing or by the Docker FiWare). Our technique is modular and consists of (i) a type system associating programs with behavioural descriptions that record relevant information for resource usage (creations, releases, and concurrent operations), (ii) a translation function that takes behavioural types and returns cost equations, and (iii) an automatic off-the-shelf solver for the cost equations.

- Contact: Elena Giachino
- URL: http://sra.cs.unibo.it/

6.6. SUNNY-CP

SCIENTIFIC DESCRIPTION

Within the Constraint Programming paradigm, a portfolio solver combines different constraint solvers in order to create a globally better solver. Sunny-cp is a parallel parallel portfolio solver capable of solving Constraint (Satisfaction/Optimization) Problems defined in the MiniZinc language. It essentially implements the SUNNY algorithm introduced in the team. Sunny-cp is built on top of state-of-the-art constraint solvers, including: Choco, Chuffed, CPX, G12/LazyFD, G12/FD, G12/Gurobi, G12/CBC, Gecode, HaifaCSP, iZplus, MinisatID, Opturion, OR-Tools
SUNNY-CP is a portfolio solver for solving both Constraint Satisfaction Problems and Constraint Optimization Problems. The goal of SUNNY-CP is to provide a flexible, configurable, and usable CP portfolio solver that can be set up and executed just like a regular individual CP solver.

- Contact: Roberto Amadini
- URL: https://github.com/CP-Unibo/sunny-cp

6.7. Blender

SCIENTIFIC DESCRIPTION

The various tools developed in the Aeolus project (Zephyrus, Metis, Armonic) have been combined in this software which represents an integrated solution for the declarative specification of cloud applications, and its subsequent automatic deployment on an OpenStack cloud system. In particular, a web-based interface is used to specify the basic software artifacts to include in the application, indicate their level of replication, and specify co-installability conflicts (i.e. when two components cannot be installed on the same virtual machines). The tool Zephyrus is then used to synthesize the final architecture of the application, the tool Metis indicates the plan of configuration actions, and the Armonic platform provides the library of components and the low-level scripts to actually install and configure the entire application.

- Partners: IRILL - Mandriva
- Contact: Gianluigi Zavattaro
- URL: https://github.com/aeolus-project/blender

GALAAD2 Team

5. New Software and Platforms

5.1. AXEL

KEYWORDS: CAO - Algebraic geometric modeler
SCIENTIFIC DESCRIPTION

Axel is an algebraic geometric modeler that aims at providing "algebraic modeling" tools for the manipulation and computation with curves, surfaces or volumes described by semi-algebraic representations. These include parametric and implicit representations of geometric objects. Axel also provides algorithms to compute intersection points or curves, singularities of algebraic curves or surfaces, certified topology of curves and surfaces, etc. A plugin mechanism allows to extend easily the data types and functions available in the plateform.
FUNCTIONAL DESCRIPTION

Axel is a cross platform software to visualize, manipulate and compute 3D objects. It is composed of a main application and several plugins. The main application provides atomic geometric data and processes, a viewer based on VTK, a GUI to handle objects, to select data, to apply process on them and to visualize the results. The plugins provides more data with their reader, writer, converter and interactors, more processes on the new or atomic data. It is written in C++ and thanks to a wrapping system using SWIG, its data structures and algorithms can be integrated into C# programs, as well as Python. The software is distributed as a source package, as well as binary packages for Linux, MacOSX and Windows.

- Participants: Nicolas Douillet, Anaïs Ducoffe, Valentin Michelet, Bernard Mourrain, Meriadeg Perrinel, Stéphane Chau and Julien Wintz
- Contact: Bernard Mourrain
- URL: http://axel.inria.fr/

Collaboration with Elisa Berrini (MyCFD, Sophia), Tor Dokken (Gotools library, Oslo, Norway), Angelos Mantzaflaris (GISMO library, Linz, Austria), Laura Saini (Post-Doc GALAAD/Missler, TopSolid), Gang Xu (Hangzhou Dianzi University, China).

5.2. Mathemagix

SCIENTIFIC DESCRIPTION

The project aims at building a bridge between symbolic computation and numerical analysis. It is structured by collaborative software developments of different groups in the domain of algebraic and symbolic-numeric computation.

In this framework, we are working more specifically on the following components:

realroot: a set of solvers using subdivision methods to isolate the roots of polynomial equations in one or several variables, continued fraction expansion of roots of univariate polynomials, Bernstein basis representation of univariate and multivariate polynomials and related algorithms, exact computation with real algebraic numbers, sign evaluation, comparison, certified numerical approximation.

shape: tools to manipulate curves and surfaces of different types including parameterized, implicit with different type of coefficients, algorithms to compute their topology, intersection points or curves, self-intersection locus, singularities, ...

These packages are integrated from the former library Synaps (SYmbolic Numeric APplicationS) dedicated to symbolic and numerical computations. There are also used in the algebraic-geometric modeler axel .
FUNCTIONAL DESCRIPTION

Mathemagix is a free computer algebra system which consists of a general purpose interpreter, which can be used for non-mathematical tasks as well, and efficient modules on algebraic objects. It includes the development of standard libraries for basic arithmetic on dense and sparse objects (numbers, univariate and multivariate polynomials, power series, matrices, etc., based on FFT and other fast algorithms). These developments, based on C++, offer generic programming without losing effectiveness, via the parameterization of the code (template) and the control of their instantiations.

- Participants: Bernard Mourrain, Grégoire Lecerf, Philippe Trebuchet and Joris Van Der Hoeven
- Contact: Bernard Mourrain
- URL: http://www.mathemagix.org/

GEOMETRICA Project-Team

6. New Software and Platforms

6.1. GUDHI

Geometric Understanding in Higher Dimensions

SCIENTIFIC DESCRIPTION

The GUDHI open source library will provide the central data structures and algorithms that underly applications in geometry understanding in higher dimensions. It is intended to both help the development of new algorithmic solutions inside and outside the project, and to facilitate the transfer of results in applied fields.

FUNCTIONAL DESCRIPTION

The current release of the GUDHI library includes: – Data structures to represent, construct and manipulate simplicial complexes. – Algorithms to compute persistent homology and multi-field persistent homology. – Simplification methods via implicit representations. - A graphical user interface and several examples and datasets.
It also has improved performance, portability and documentation.

- Participants: Jean-Daniel Boissonnat, Marc Glisse, Anatole Moreau, Vincent Rouvreau and David Salinas
- Contact: Jean-Daniel Boissonnat
- URL: https://project.inria.fr/gudhi/software/

6.2. CGAL dD Triangulations

CGAL module: Triangulations in any dimension

KEYWORDS: Triangulation - Delaunay triangulation
FUNCTIONAL DESCRIPTION

This package of CGAL (Computational Geometry Algorithms Library, http://www.cgal.org) allows to compute triangulations and Delaunay triangulations in any dimension. Those triangulations are built incrementally and can be modified by insertion or removal of vertices.

- Participants: Samuel Hornus, Olivier Devillers and Clément Jamin
- Contact: Clément Jamin
- URL: http://doc.cgal.org/4.6/Triangulation/

6.3. CGAL Kernel_d

CGAL module: High-dimensional kernel Epick_d

FUNCTIONAL DESCRIPTION

Several functions were added in release 4.7 in preparation for a future alpha-complex implementation.

- Participants: Marc Glisse
- Contact: Marc Glisse
- URL: http://doc.cgal.org/4.7/Kernel_d/

6.4. R package TDA

Topological Data Analysis package for the R software

FUNCTIONAL DESCRIPTION

the R package TDA provides some tools for Topological Data Analysis. In particular, it includes implementations of functions that, given some data, provide topological information about the underlying space, such as the distance function, the distance to a measure, the kNN density estimator, the kernel density estimator, and the kernel distance.

- Participants: Clément Maria, Vincent Rouvreau
- Contact: Vincent Rouvreau
- URL: https://cran.r-project.org/web/packages/TDA/index.html

6.5. cgal Periodic Triangulations and Meshes

The CGAL library offers a package to compute the 3D periodic Delaunay triangulation of a point set in $\mathbb{R}^3$, more precisely the Delaunay triangulation of a point set in the 3-dimensional flat torus with cubic domain [49]. The package has been used in various fields. [0]

We have been extending this package in three directions:

First, a few new small functions have been added to the Delaunay triangulation class and integrated in CGAL 4.7.

We have developed and documented some new classes allowing to compute *weighted* periodic Delaunay triangulations. They have been submitted to the CGAL editorial board and accepted for inclusion in CGAL. The code still needs some polishing, and the testsuite must be completed, before a public distribution in CGAL.

We have continued our work to use this package together with the 3D mesh generation package of CGAL [48], in order to propose a construction of meshes of periodic volumes. Although last year's preliminary results were already convincing [50], [51], the work is not ready yet for being submitted to CGAL: the code requires to be completed, documented, and extensively tested.

- Participant : Aymeric Pellé
- Contact: Monique Teillaud (Vegas project-team)
- This work was done in the framework of the Inria ADT *(Action de Développement Technologique)* OrbiCGAL http://www.loria.fr/~teillaud/ADT-OrbiCGAL/

[0] see http://www.cgal.org/projects.html

GRAPHDECO Project-Team

6. New Software and Platforms

6.1. SWARPI

SWARPI (for Superpixel Warp for Image-based rendering)
FUNCTIONAL DESCRIPTION

This software package is the implementation of the publication and it was developed previously at REVES and now maintained by GRAPHDECO with public funding. The LINUX main software consists of two components: the depth synthesis step and the image-based runtime rendering step : a. depth synthesis step reads 3D points coming from the automated 3D reconstruction pipeline, together with images and calibrated cameras, and produces the superpixel decomposition and the depth synthesis algorithm. This package is provided as a set of C++ sources (for superpixel and depth) and matlab sources for depthSynth. b. The runtime rendering step is a C++ program (sources provided) which takes the result of the first step as input to allow interactive 3D navigation from pictures. The code uses multi-pass deferred shading with pixel and fragment shaders to perform the rendering.

- Participants: George Drettakis, Gaurav Chaurasia, Sylvain François Duchene and Olga Sorkine-Hornung
- Contact: George Drettakis

6.2. SWARPI-Unity

SWARPI-Unity (for Superpixel Warp for Image-based rendering for Unity)
This software package is the Unity port of the SWARPI used in the context of the CR-PLAY project.

- Participants: Jérôme Esnault, George Drettakis and Gaurav Chaurasia
- Contact: George Drettakis

6.3. SWARPI2-IBR-COMMON

SWARPI2-IBR-COMMON (for Superpixel Warp for Image-based rendering and common Image Based Rendering features)
This is the second version of SWARPI which is used internally for the research projects developed for Image-Based Rendering ([15]).

- Participants: George Drettakis, Gaurav Chaurasia, Jérôme Esnault and Sylvain François Duchene
- Contact: George Drettakis

6.4. CrossShade

CrossShade is an algorithm to estimate surface normals over a design sketch composed of vector curves representing silhouettes, boundaries and cross-sections. This algorithm has been developed in collaboration with U. of Toronto (Karan Singh) and U. British Columbia (A. Sheffer). We filed a patent on this technology and we have contacts with several companies about a potential transfer.

- Participants: Adrien Bousseau
- Contact: Adrien Bousseau

6.5. True2Form

True2Form is a sketch-based modeling system that reconstructs 3D curves from typical design sketches. This algorithm has been developed in collaboration with U. of Toronto (Karan Singh) and U. British Columbia (A. Sheffer). We filed a patent on this technology and we have contacts with several companies about a potential transfer.

- Participants: Adrien Bousseau
- Contact: Adrien Bousseau

GRAPHIK Project-Team

6. New Software and Platforms

6.1. DLGP 2.0

- Participants: Jean-François Baget, Michel Chein, Alain Gutierrez, Michel Leclère, Marie-Laure Mugnier, Swan Rocher and Clément Sipieter
- URL: http://graphik-team.github.io/graal/

DLGP (for Datalog+) is our textual format for the existential rules framework. This year, we extended it to ensure compatibility with Semantic Web languages. This required to include web notions such as IRIs and literals. A new parser was implemented, and is used in both Cogui (6.2) and Graal (6.3).

6.2. Cogui

Cogui is a tool for building and verifying knowledge bases. It is a freeware written in Java (version 1.6). Currently, it supports Conceptual Graphs and import/export in RDFS and Datalog+.

- Participants: Alain Gutierrez, Michel Leclère, Michel Chein, Marie-Laure Mugnier and Madalina Croitoru
- Contact: Michel Leclère (scientific contact) and Alain Gutierrez (technical contact)
- URL: http://www.lirmm.fr/cogui/

Objectives: Cogui is a visual tool for building conceptual graph knowledge bases (KB). It allows to create a KB, to edit its structure and content, and to control it. The KB can be serialized in the XML. Imports and exports from and to RDFS are also provided, as well as from and to the *Datalog+ (DLGP)* format that we defined for existential rules. Wizards allow to analyze and check facts with respect to some constraints, as well as to query them while taking into account inferences enabled by the ontology.

Users community:*Research:* MIMOS (National R&D center in information and communication technology, Malaysia http://www.mimos.my/), Defence R&D Canada, our partners in INRA, CIRAD, as well as a new collaboration with the Inria team Imagine. *Education:* Used in knowledge engineering in universities of Nice, Strasbourg, Montpellier, Sheffield, as well as in the engineering school of Tarbes.

Impact: internal use in several EU or National projects. We expect a broader audience by using Cogui as a graphical ontology modeling tool for our other software Graal, the communication being done through our DLGP format http://www.lirmm.fr/~mugnier/graphik/kiabora/downloads/datalog-plus_en.pdf.

State of the art: To the best of our knowledge, Cogui is the only ontology editing tool able to do reasoning with conceptual graph rules (equivalent to existential rules). Many tools exist for DLs and Semantic Web languages (e.g. Protégé http://protege.stanford.edu mainly designed for description logics and TopBraid Composer http://www.topquadrant.com/ designed for RDF and SPIN rules, which are rules without existential variables).

Misc.: Cogui is written in Java and has been part time developed since 2005 by Alain Gutierrez (approx. 50 man months). First developed as an interface communicating with the conceptual graph reasoner Cogitant http://cogitant.sourceforge.net/, it has become a standalone tool, integrating more and more reasoning features.

New features: This year, we mainly focused on improving the compatibility with the semantic web languages. The main improvements are the following:

- integration of the parser using our new textual format DLGP 2.0 (6.1).
- a new repository is available to store the projects. It facilitates collaborative work combined with a version control software (a feature developed for Qualinca combined with GIT).
- ergonomics: rule engine and query assistants have been redesigned, several graphical editor behaviors have been improved.
- A backward chaining rule evaluation algorithm, with lazy computation of rule bodies, has been developed for the kind of Datalog rules used in the system SudoQual.

6.3. GRAAL

In its current state, Graal allows storage of data via a generic interface in different storage paradigms and systems. Currently, the relational database management systems MySQL, PostgreSQL, Sqlite, and InMemory graph and LinkedList structures are implemented. The triple store Jena TDB and the graph database system Sparksee are coming soon. Graal also allows us to query this database taking into account an ontology represented by a set of existential rules. It provides forward chaining and query rewriting algorithms (building up on Mélanie König's PhD thesis) and a tool for the analysis of the properties of a set of rules which is an integration of Swan Rocher's tool Kiabora. The input and output of this software can be expressed in our Datalog-inspired format DLGP 2.0 (6.1), and can be translated from the semantic web language OWL2 or to RuleML. This software is designed in a modular way, hence it is possible to use only a subpart of Graal without embedding it all or to easily replace an implementation of a module by another.

FUNCTIONAL DESCRIPTION

Graal is intended to be a generic platform for ontology-based query answering with existential rules.

- Participants: Clément Sipieter, Swan Rocher, Jean-François Baget, Marie-Laure Mugnier, Michel Leclère
- Partner: LIRMM
- Contact: Marie-Laure Mugnier (scientific contact) and Clément Sipieter (technical contact)
- URL: http://graphik-team.github.io/graal/

Objectives: Graal is a generic platform for query answering under existential rules. It will integrate all algorithms designed in the team, and our ambition is to make it a reference platform in the research community, allowing for the integration of algorithms designed by other teams.

Users community: Graal is intended for use in research and education.

Impact: Due to the recent release of the first stable version, Graal has only been used for now in our projects. A related paper received the RuleML 2015 challenge award http://2015.ruleml.org/.

State of the art: To the best of our knowledge, the only other tool for reasoning with existential rules is Nyaya [0], a joint development from teams in Rome, Oxford, and Milan. It has been renamed IRIS+/- https://bitbucket.org/giorsi/nyaya.

Misc.: Graal is written in Java (around 30k lines of code, 30 man/months effort). It is mainly developed by Clément Sipieter (2 years Inria ADT funding) under the CeCILL licence (GPL compatible, see http://www.cecill.info/licences.fr.html). The development started 1.5 years ago from a prototype realized during Bruno Paiva's PhD thesis, and integrates work carried out by other PhD students (Mélanie König and Swan Rocher). Graal has been first presented at RuleML 2015 [23], [33], where it received a best paper award.

New features: Main features integrated in 2015 are query rewriting algorithms, projection algorithms, and translations to and from other languages (OWL2, RuleML).

Note that we do not detail here other software developments internal to our current projects and not publicly available.

[0] De Virgilio, R.; Orsi, G.; Tanca, L.; Torlone, R., "NYAYA: A System Supporting the Uniform Management of Large Sets of Semantic Data," in Data Engineering (ICDE), 2012 IEEE 28th International Conference on , vol., no., pp.1309-1312, 1-5 April 2012

HEPHAISTOS Project-Team

6. New Software and Platforms

6.1. ALIAS

Algorithms Library of Interval Analysis for Systems
FUNCTIONAL DESCRIPTION

The ALIAS library whose development started in 1998, is a collection of procedures based on interval analysis for systems solving and optimization.

ALIAS is made of two parts:

ALIAS-C++ : the C++ library (87 000 code lines) which is the core of the algorithms

ALIAS-Maple : the Maple interface for ALIAS-C++ (55 000 code lines). This interface allows one to specify a solving problem within Maple and get the results within the same Maple session. The role of this interface is not only to generate the C++ code automatically, but also to perform an analysis of the problem in order to improve the efficiency of the solver. Furthermore, a distributed implementation of the algorithms is available directly within the interface.

- Participants: Odile Pourtallier and Jean-Pierre Merlet
- Contact: Jean-Pierre Merlet
- URL: http://www-sop.inria.fr/hephaistos/developpements/main.html

INDES Project-Team

5. New Software and Platforms

5.1. Web programming

Participants: Yoann Couillec, Colin Vidal, Vincent Prunet, Manuel Serrano [correspondant].

5.1.1. The HOP web programming environment

HOP is a higher-order language designed for programming interactive web applications such as web agendas, web galleries, music players, etc. It exposes a programming model based on two computation levels. The first one is in charge of executing the logic of an application while the second one is in charge of executing the graphical user interface. HOP separates the logic and the graphical user interface but it packages them together and it supports strong collaboration between the two engines. The two execution flows communicate through function calls and event loops. Both ends can initiate communications.

The HOP programming environment consists in a web *broker* that intuitively combines in a single architecture a web server and a web proxy. The broker embeds a HOP interpreter for executing server-side code and a HOP client-side compiler for generating the code that will get executed by the client.

An important effort is devoted to providing HOP with a realistic and efficient implementation. The HOP implementation is *validated* against web applications that are used on a daily-basis. In particular, we have developed HOP applications for authoring and projecting slides, editing calendars, reading RSS streams, or managing blogs.

HOP has won the software *open source contest* organized by the ACM Multimedia Conference 2007. It is released under the GPL license. It is available at http://hop.inria.fr.

- Participants: Manuel Serrano
- Contact: Manuel Serrano
- URL: http://hop.inria.fr

5.1.2. The Bigloo compiler

The programming environment for the Bigloo compiler [7] is available on the Inria Web site at the following URL: http://www-sop.inria.fr/teams/indes/fp/Bigloo. The distribution contains an optimizing compiler that delivers native code, JVM bytecode, and .NET CLR bytecode. It contains a debugger, a profiler, and various Bigloo development tools. The distribution also contains several user libraries that enable the implementation of realistic applications.

BIGLOO was initially designed for implementing compact stand-alone applications under Unix. Nowadays, it runs harmoniously under Linux and MacOSX. The effort initiated in 2002 for porting it to Microsoft Windows is pursued by external contributors. In addition to the native back-ends, the BIGLOO JVM back-end has enabled a new set of applications: Web services, Web browser plug-ins, cross platform development, etc. The new BIGLOO .NET CLR back-end that is fully operational since release 2.6e enables a smooth integration of Bigloo programs under the Microsoft .NET environment.

- Participants: Manuel Serrano
- Contact: Manuel Serrano
- URL: http://www-sop.inria.fr/teams/indes/fp/Bigloo

LAGADIC Project-Team

6. New Software and Platforms

6.1. DESlam

Dense Egocentric SLAM
KEYWORDS: Deph Perception - Robotics - Localisation
FUNCTIONAL DESCRIPTION

This software proposes a full and self content solution to the dense Slam problem. Based on a generic RGB-D representation valid for various type of sensors (stereovision, multi-cameras, RGB-D sensors...), it provides a 3D textured representation of complex large indoor and outdoor environments and it allows localizing in real time (45Hz) a robot or a person carrying out a mobile camera.

- Participants: Maxime Meilland, Andrew Ian Comport and Patrick Rives
- Contact: Patrick Rives
- URL: http://team.inria.fr/lagadic

6.2. HandiViz

KEYWORDS: Health - Persons attendant - Handicap
FUNCTIONAL DESCRIPTION

The HandiViz software proposes a semi-autonomous navigation framework of a wheelchair relying on visual servoing.

It has been registered to the APP ("Agence de Protection des Programmes") as an INSA software (IDDN.FR.001.440021.000.S.P.2013.000.10000) and is under GPL license.

- Participants: François Pasteau and Marie Babel
- Contact: Marie Babel
- URL: https://team.inria.fr/lagadic/

6.3. Perception360

Robot vision and 3D mapping with omnidirectional RGB-D sensors.
KEYWORDS: Depth Perception - 3D rendering - Computer vision - Robotics - Image registration - Sensors - Realistic rendering - 3D reconstruction - Localization
FUNCTIONAL DESCRIPTION

This software is a collection of libraries and applications for robot vision and 3D mapping with omnidirectional RGB-D sensors or standard perspective cameras. This project provides the functionality to do image acquisition, semantic annotation, dense registration, localization and 3D mapping. The omnidirectional RGB-D sensors used within this project have been developed in Inria Sophia-Antipolis by the team LAGADIC.

- Contact: Patrick Rives
- URL: https://team.inria.fr/lagadic/software-eng.html

6.4. Sinatrack

KEYWORDS: Computer vision - Robotics
FUNCTIONAL DESCRIPTION

Sinatrack is a tracking software that allows the 3D localization (translation and rotation) of an object with respect to a monocular camera. It allows to consider object with complex shape. The underlying approach is a model-based tracking techniques. It has been developed for satellite localization and on-orbit service applications but is also suitable for augmented reality purpose.

- Participants: Antoine Guillaume Petit, Éric Marchand and François Chaumette
- Contact: Éric Marchand
- URL: http://team.inria.fr/lagadic

6.5. UsTk

Ultrasound Toolkit
KEYWORDS: Echographic imagery - Image reconstruction - Active contours - Medical robotics
FUNCTIONAL DESCRIPTION

UsTk, standing for Ultrasound Toolkit, is a cross-platform library for two- and three-dimensional ultrasound image processing. Written in C++, UsTk provides tools for ultrasound image acquisition, processing and display of these images. Combined with the UsSimulator software that simulates a virtual ultrasound probe interacting with a 3D ultrasound volume and the UsGraphCut library that allows real-time segmentation of ultrasound images, it can serve as an useful framework for developing and testing new visual servoing approaches based on ultrasound images.

- Participants: Alexandre Krupa, Pierre Chatelain and Christophe Collewet
- Partners: Université de Rennes 1 - IRSTEA
- Contact: Alexandre Krupa
- URL: https://team.inria.fr/lagadic/

6.6. ViSP

KEYWORDS: Augmented reality - Computer vision - Robotics - Visual servoing (VS)
SCIENTIFIC DESCRIPTION

Since 2005, we develop and release ViSP [5] , an open source library available from http://visp.inria.fr. ViSP standing for Visual Servoing Platform allows prototyping and developing applications using visual tracking and visual servoing techniques at the heart of the Lagadic research. ViSP was designed to be independent from the hardware, to be simple to use, expandable and cross-platform. ViSP allows to design vision-based tasks for eye-in-hand and eye-to-hand visual servoing that contains the most classical visual features that are used in practice. It involves a large set of elementary positioning tasks with respect to various visual features (points, segments, straight lines, circles, spheres, cylinders, image moments, pose...) that can be combined together, and image processing algorithms that allow tracking of visual cues (dots, segments, ellipses...) or 3D model-based tracking of known objects or template tracking. Simulation capabilities are also available.

FUNCTIONAL DESCRIPTION

ViSP provides simple ways to integrate and validate new algorithms with already existing tools. It follows a module-based software engineering design where data types, algorithms, sensors, viewers and user interaction are made available. Written in C++, ViSP is based on open-source cross-platform libraries (such as OpenCV) and builds with CMake. Several platforms are supported, including OSX, Windows and Linux. ViSP online documentation allows to ease learning. More than 250 fully documented classes organized in 16 different modules, with more than 200 examples and 35 tutorials are proposed to the user. ViSP is released under a dual licensing model. It is open-source with a GNU GPLv2 license. A professional edition license that replaces GNU GPLv2 is also available.

- Participants: François Chaumette, Éric Marchand, Fabien Spindler, Aurélien Yol and Souriya Trinh
- Partners: Université de Rennes 1 - CNRS
- Contact: Fabien Spindler
- URL: http://visp.inria.fr

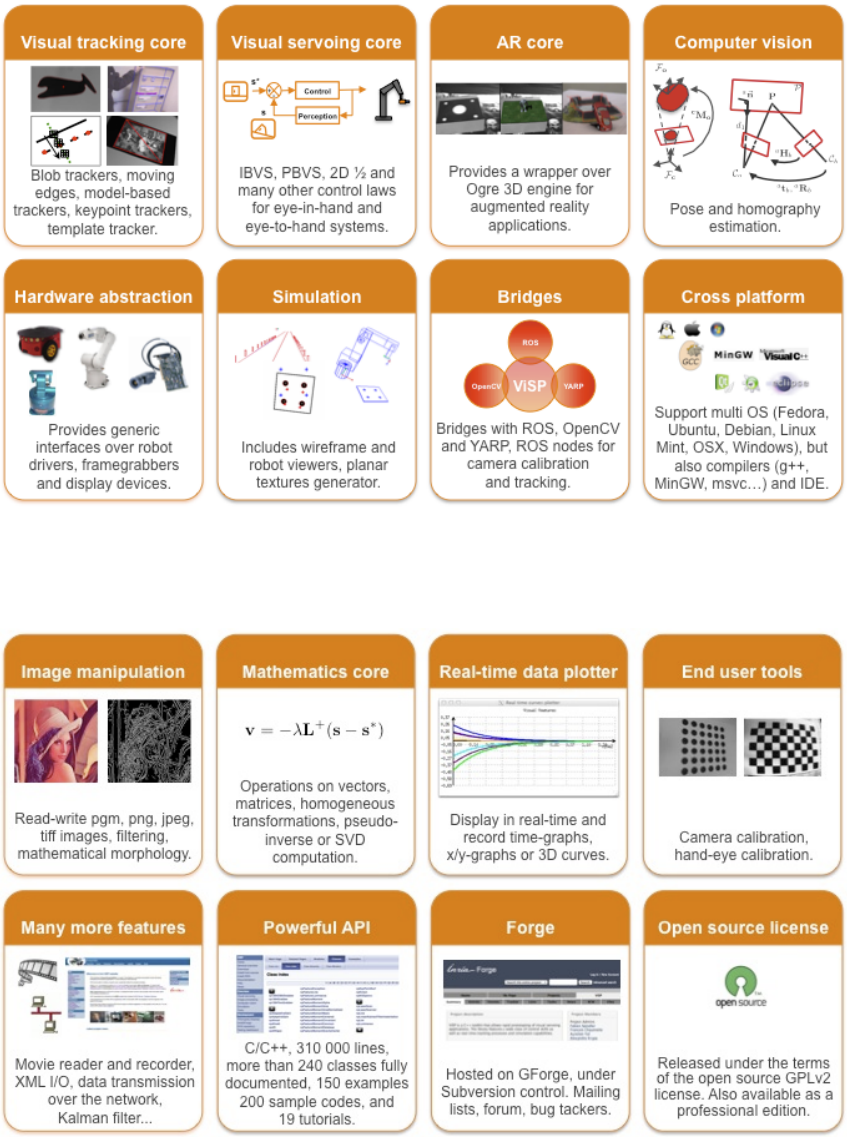


Figure 1. This figure highlights ViSP main capabilities for visual tracking, visual servoing, and augmented reality that may benefit from computer vision algorithms. ViSP allows controlling specific platforms through hardware abstraction or in simulation. ViSP provides also bridges over other frameworks such as OpenCV and ROS. All these capabilities are cross-platform. Moreover, for easing the prototyping of applications, ViSP provides tools for image manipulation, mathematics, data plotting, camera calibration, and many other features. ViSP powerful API is fully documented and available on Inria's forge as an open source software under GPLv2 license.

This year, a new ViSP 2.10 release was produced in February. The corresponding source code tarball was downloaded 1290 times. With the help of the community, this release was packaged for Debian and Ubuntu 14.04. We also designed a new modular software architecture where ViSP capabilities are grouped in several modules (core, io, gui, vision...). As a result, the user will find several shared or static libraries, one for each module. In the mean time we continued our efforts to improve the software by ensuring the compatibility with third-party libraries that continue also to evolve like CMake and OpenCV. We also fixed some issues, allowed the markerless 3D model-based hybrid tracker to consider cylinders and introduce a new algorithm to determine face visibility. Moreover, we improve the object detection algorithm based on keypoints that is able to return the pose of a learned object. We improved the documentation by providing new tutorials and by updating the existing ones. ViSP 3.0.0 will be released these days.

Concerning ROS community, all the existing packages in "`vision_visp`" ROS stack (see http://wiki.ros.org/vision_visp) were updated and ported to jade build system. To ease ViSP usage in the ROS framework, the releases of the year were packaged for ROS.

ViSP is used in research labs in France, USA, Japan, Korea, India, China, Lebanon, Italy, Spain, Portugal, Hungary, Canada. For instance, it is used as a support in graduate courses at IFMA Clermont-Ferrand, University of Picardie in Amiens, Télécom Physique in Strasbourg and ESIR in Rennes.

6.7. bib2html

FUNCTIONAL DESCRIPTION

The purpose of this software is to automatically produce html pages from BibTEX files, and to provide access to the BibTEX entries by several criteria: year of publication, category of publication, keywords, author name. Moreover cross-linking is generating between pages to provide an easy navigation through the pages without going back to the index.

- Contact: Éric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html

6.8. Robot vision platform

Participant: Fabien Spindler [correspondant].

We exploit two industrial robotic systems built by Afma Robots in the nineties to validate our researches in visual servoing and active vision. The first one is a Gantry robot with six degrees of freedom, the other one is a cylindrical robot with four degrees of freedom (see Fig. 2). These robots are equipped with cameras. The Gantry robot allows also to embed grippers on its end-effector.

Five papers published by Lagadic in 2015 enclose results validated on this platform [30][53][29][31][50].

6.9. Mobile robotics platforms

Participants: Fabien Spindler [correspondant], Marie Babel, Patrick Rives.

6.9.1. Indoor mobile robots

For fast prototyping of algorithms in perception, control and autonomous navigation, the team uses Hannibal in Sophia Antipolis, a cart-like platform built by Neobotix (see Fig. 3 .a), and, in Rennes, a Robotino from Festo (see Fig. 3 .b) and a Pioneer 3DX from Adept (see Fig. 3 .c). These platforms are equipped with various sensors needed for Slam purposes, autonomous navigation and sensor-based control.

Moreover, to validate the researches in personally assisted living topic (see 7.3.3), we have in Rennes a six wheel electric wheelchair from Penny and Giles Drives Technology (see Fig. 3 .d) and a five wheel electric wheelchair from You-Q (see Fig. 3 .e). The control of the wheelchair is performed using a plug and play system between the joystick and the low level control of the wheelchair. Such a system lets us acquire the user intention through the joystick position and control the wheelchair by applying corrections to its motion. The wheelchairs have been fitted with cameras and eleven ultrasound sensors to perform the required servoing for assisting handicapped people.

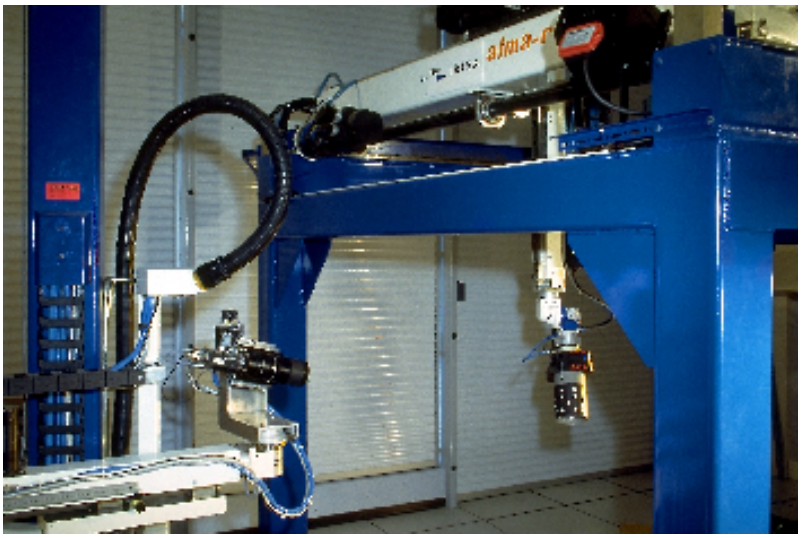


Figure 2. Lagadic robotics platform for vision-based manipulation

Note that 5 papers exploiting the indoors mobile robots were published this year [14][22][28][56][27].

6.9.2. Outdoor vehicles

The team exploits also Cycab urban electrical cars (see Figs. 3 .f and 3 .g). Two vehicles in Sophia Antipolis and one in Rennes are instrumented with cameras and range finders to validate researches in the domain of intelligent urban vehicle. Cycabs were used as experimental testbeds in several national projects in the past. This year we decided to donate the Cycab in Rennes to the INSA engineer school were it started a second live.

The camera rig can also be fixed to a standard car (see Fig. 4), which is driven at a variable speed depending on the road/traffic conditions, with an average of 30 km/h and a maximum speed of 80 km/h. The sequences are recorded at a frame rate of 20 Hz, where the six global shutter cameras of the stereo system are synchronized, producing spherical images with a resolution of 2048x665 (see fig. 4). Such sequences are fused offline to obtain maps that can be used later for localization or for scene rendering. (in a similar fashion to Google Street View) as we show in the accompanying video [0].

Four papers published by Lagadic in 2015 enclose experimental results obtained with these outdoor vehicles [20][37][10][42].

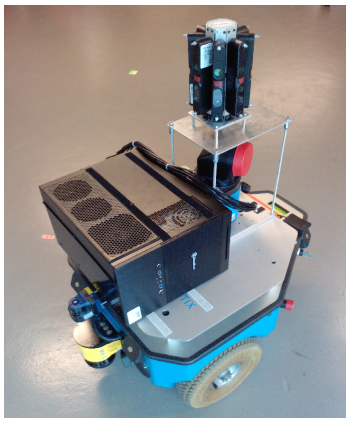
6.10. Medical robotics platform

Participants: Fabien Spindler [correspondant], Alexandre Krupa.

This testbed is of primary interest for researches and experiments concerning ultrasound visual servoing applied to probe positioning, soft tissue tracking or robotic needle insertion tasks described in Section 7.6 .

This platform is composed by two Adept Viper six degrees of freedom arms (see Fig. 5 .a). Ultrasound probes connected either to a SonoSite 180 Plus or an Ultrasonix SonixTouch imaging system can be mounted on a force torque sensor attached to each robot end-effector.

[0] video url:(www-sop.inria.fr/members/Renato-Jose.Martins/iros15.html)



(a)

(b)

(c)

(d)

(e)

(f)

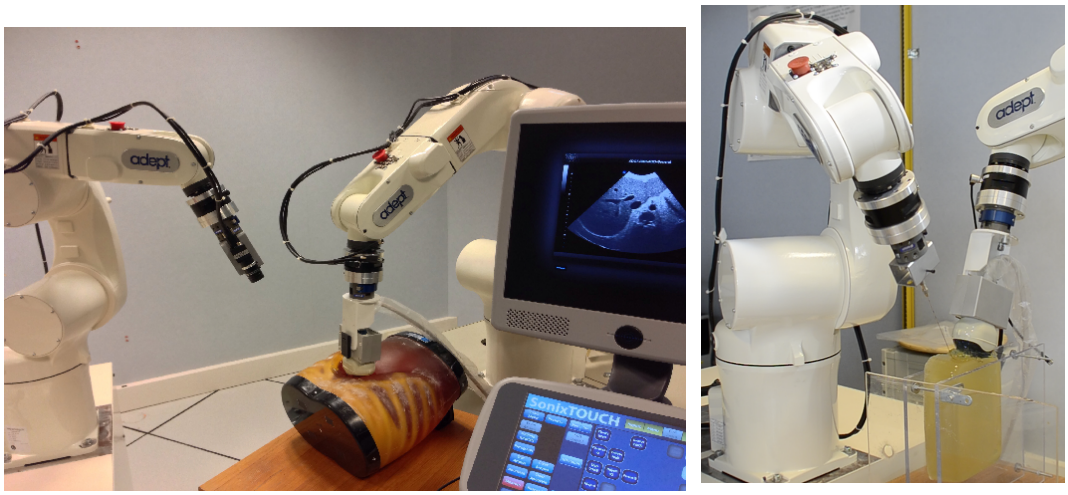
(g)

Figure 3. a) Hannibal platform, b) Robotino, c) Pioneer P3-DX robot, d) wheelchair from Penny and Giles Drives Technology, e) wheelchair from You-Q , f) Cycab available in Rennes, g) one of the Cycabs available in Sophia Antipolis.

Figure 4. Globeye stereo sensor and acquisition system.

We designed an experimental setup to test an autonomous robotic needle insertion method based on visual servoing 7.6.2 . The experimental setup is composed with a gelatin phantom simulating soft tissues, a flexible biopsy needle actuated by an Adept Viper arm and a 3D ultrasound probe held by the second Adept Viper arm (see Fig. 5 .b).

This year, 5 papers enclose experimental results obtained with this platform [49][48][47][33][32].



(a) (b)

Figure 5. a) Lagadic medical robotics platforms. On the right Viper S850 robot arm equipped with a SonixTouch 3D ultrasound probe. On the left Viper S650 equipped with a tool changer that allows to attach a classical camera or biopsy needles. b) Robotic setup for autonomous needle insertion by visual servoing.

6.11. Humanoid robot platform

Participants: Giovanni Claudio, Fabien Spindler [correspondant].

Romeo is a humanoid robot from Aldebaran Robotics which is intended to be a genuine personal assistant and companion. For the moment only the upper part of the body (trunk, arms, neck, head, eyes) is working. This research platform is used to validate our researches in visual servoing and visual tracking. We continue to improve the work initiated last year to grasp a box and deliver it to a human introducing especially joint limits avoidance (see Fig. 6). We started also to work on a visual servoing framework able to control both arms to manipulate an object using only vision.

This year one paper encloses experimental results obtained with this platform [54].

6.12. Unmanned Aerial Vehicles (UAVs) platform

Participants: Thomas Bellavoir, Paolo Robuffo Giordano [correspondant].

From 2014, the team also started some activities involving perception and control for single and multiple quadrotor UAVs, especially thanks to a grant from “Rennes Métropole” (see Section 9.1.5) and the ANR project “SenseFly” (see Section 9.2.4). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (Fig. 7 .a), and one quadrotor from 3DRobotics, USA (Fig. 7 .b). The Mikrokopter quadrotors have been heavily customized by: (i) reprogramming from scratch the low-level attitude controller onboard the microcontroller of the quadrotors, (ii) equipping each quadrotor with an Odroid XU4 board (Fig. 7 .d)

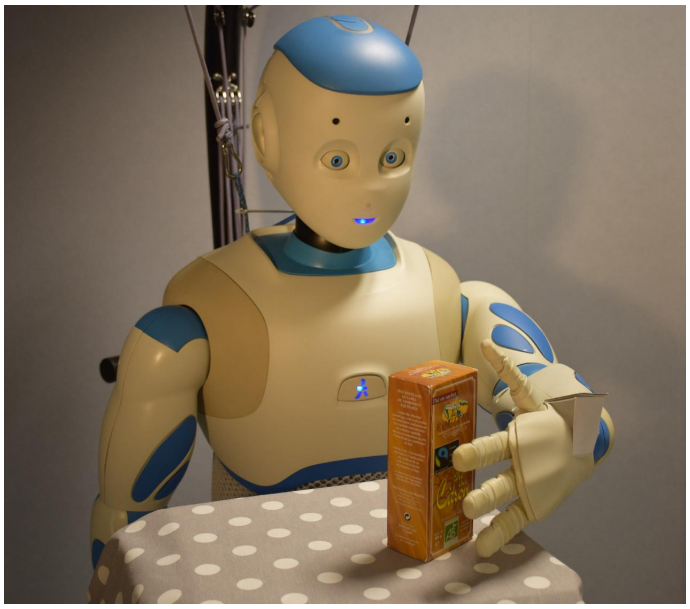


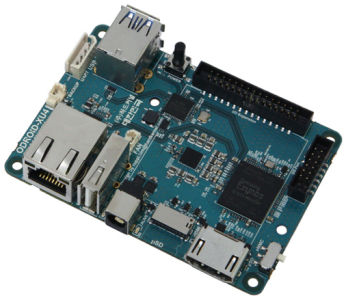
Figure 6. Romeo experimental platform.

running Linux Ubuntu and the TeleKyb software (the middleware used for managing the experiment flows and the communication among the UAVs and the base station), and (iii) purchasing the Flea Color USB3 cameras together with the gimbal needed to mount them on the UAVs (Fig. 7 .c). The quadrotor group will be used as robotic platforms for testing a number of single and multiple flight control schemes with a special attention on the use of onboard vision as main sensory modality.

(a)

(b)

(c)



(d)

Figure 7. a) Quadrotor XL1 from Mikrokopter, b) Quadrotor Iris from 3DRobotics, c) Flea Color USB3 camera, d) Odroid XU4 board

LEMON Team

6. New Software and Platforms

6.1. SW2D

Participants: Carole Delenne, Vincent Guinot.

Urban floods are usually simulated using two-dimensional shallow water models. A correct representation of the urban geometry and hydraulics would require that the average computational cell size be between 0.1 m and 1 m. The meshing and computation costs make the simulation of entire districts/conurbations impracticable in the current state of computer technology.

An alternative approach consists in upscaling the shallow water equations using averaging techniques. This leads to introducing storage and conveyance porosities, as well as additional source terms, in the mass and momentum balance equations. Various versions of porosity-based shallow water models have been proposed in the literature. The Shallow Water 2 Dimensions (SW2D) computational code embeds various finite volume discretizations of these models. Ituses fully unstructured meshes with arbitrary numbers of edges. The key features of the models and numerical techniques embedded in SW2D are

- specific momentum/energy dissipation models that are active only under transient conditions. Such models, that are not present in classical shallow water models, stem from the upscaling of the shallow water equations and prove essential in modeling the features of fast urban flow transients accurately
- modified HLLC solvers for an improved discretization of the momentum source terms stemming from porosity gradients
- higher-order reconstruction techniques that allow for faster and more stable calculations in the presence of wetting/drying fronts.

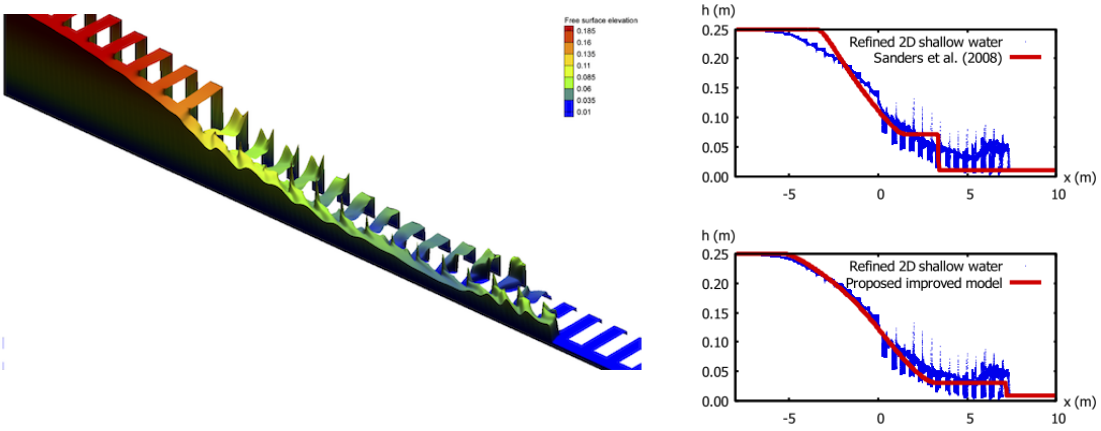


Figure 2. Propagation of a flood wave into a channel with lateral storage. Refined 2D simulation using the SW2D computational code

- Contact: Vincent Guinot
- URL: http://vincentguinot.free.fr

6.2. WindPoS

Participant: Antoine Rousseau.

The computation of the wind at small scale and the estimation of its uncertainties is of particular importance for applications such as wind energy resource estimation. To this aim, starting in 2005, we have developed a new method based on the combination of an existing Numerical Weather Prediction model providing a coarse prediction, and a Lagrangian Stochastic Model for turbulent flows. This Stochastic Downscaling Method (SDM) requires a specific modeling of the turbulence closure, and involves various simulation techniques whose combination is totally original (such as Poisson solvers, optimal transportation mass algorithm, original Euler scheme for confined Langevin stochastic processes, and stochastic particle methods).

In 2013, WindPoS became the kernel of the wind farm modeling of the Fundacion Inria Chile. In France, its development is going on through the collaborative Modéol project on the evaluation of wind potential.

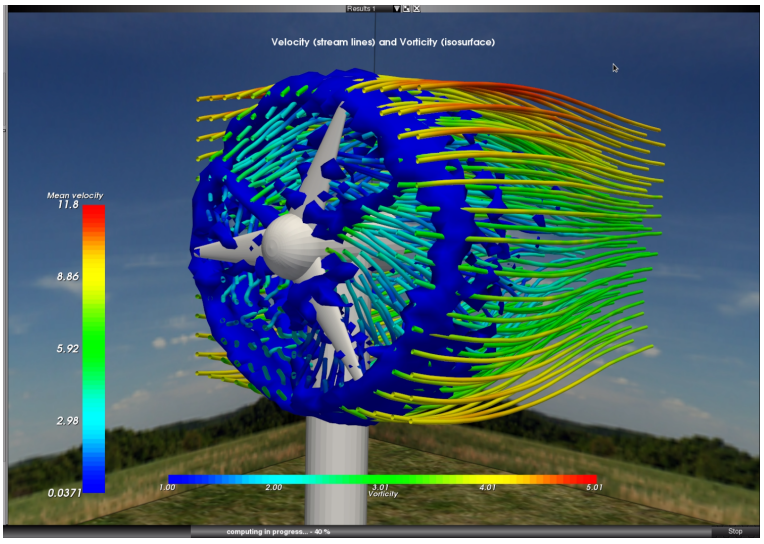


Figure 3. Velocity streamlines and vorticity around a wind mill (artistic view). WINDPOS Project.

This is a joint work with Mireille Bossy from the team TOSCA.

- Contact: Antoine ROUSSEAU
- URL: http://windpos.inria.fr

MAESTRO Project-Team

6. New Software and Platforms

6.1. marmoteCore

Markov Modeling Tools and Environments - the Core
KEYWORDS: Modeling - Stochastic models - Markov model
FUNCTIONAL DESCRIPTION

marmoteCore is a C++ environment for modeling with Markov chains. It consists in a reduced set of high-level abstractions for constructing state spaces, transition structures and Markov chains (discrete-time and continuous-time). It provides the ability of constructing hierarchies of Markov models, from the most general to the particular, and equip each level with specifically optimized solution methods.

This software is developed within the ANR MARMOTE project: ANR-12-MONU-00019.

- Participants: Alain Jean-Marie, Issam Rabhi
- Partner: UVSQ
- Contact: Alain Jean-Marie
- URL: http://marmotecore.gforge.inria.fr/

6.2. ns-3

KEYWORDS: Simulation - Communication networks
FUNCTIONAL DESCRIPTION

ns-3 is a discrete-event network simulator for Internet systems, targeted primarily for research and educational use.

In the framework of the research project with ALSTOM Transport (see §8.1.3), we have extensively validated several modules of ns-3, related to the PHY and the MAC layers. We have implemented a directional antenna using 3-dimensional data for the radiation diagram. Modules related to the Automatic Train Protection function used in train systems have been implemented and validated. Last, we have developped objects that allow to generate easily simulation scenarios.

- Participants: Sara Alouf, Abdulhalim Dandoush, Giovanni Neglia and Alina Tuholukova

MARELLE Project-Team

5. New Software and Platforms

5.1. Coq

KEYWORDS: Proof - Certification - Formalisation
FUNCTIONAL DESCRIPTION

Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

- Participants: Benjamin Grégoire, Enrico Tassi, Bruno Barras, Yves Bertot, Pierre Boutillier, Xavier Clerc, Pierre Courtieu, Maxime Denes, Stéphane Glondu, Vincent Gross, Hugo Herbelin, Pierre Letouzey, Assia Mahboubi, Julien Narboux, Jean-Marc Notin, Christine Paulin-Mohring, Pierre-Marie Pédrot, Loïc Pottier, Matthias Puech, Yann Régis-Gianas, François Ripault, Matthieu Sozeau, Arnaud Spiwack, Pierre-Yves Strub, Benjamin Werner, Guillaume Melquiond and Jean-Christophe Filliâtre
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Hugo Herbelin
- URL: http://coq.inria.fr/

Enrico Tassi and Maxime Dénès brought notable contributions to the Coq system in 2015. In particular, Enrico worked on the new user-interface that makes it possible to have several logical engines working on proofs simultaneously and Maxime Dénès supervised the release process for Coq 8.5, to be released in the early days of January.

In 2015, the Coq system is the object of intense activity within the Marelle project-team. Yves Bertot and Maxime Dénès are working at creating a consortium around this system, so that academic and industrial users find a suitable structure to voice there wishes for the evolution of the system, fund improvements, and coordinate developments for further improvement. This work is done in close collaboration with the $\pi.r^2$ project-team.

A first outcome of this animation work is the organization of regular events for developers to meet (coding sprints), the first of which happened in Sophia Antipolis in June 2015. Subsequently, Maxime Dénès was hired in Sophia Antipolis (in the Marelle project-team), and Matej Kosik was hired in Paris (in the $\pi.r^2$) team. A close collaboration was also set up with the Massachusetts Institute of Technology (MIT), with a software engineer to be hired at MIT to work on Coq in early 2016.

5.2. Easycrypt

FUNCTIONAL DESCRIPTION

EasyCrypt is a toolset for reasoning about relational properties of probabilistic computations with adversarial code. Its main application is the construction and verification of game-based cryptographic proofs. EasyCrypt can also be used for reasoning about differential privacy.

- Participants: Gilles Barthe, Benjamin Grégoire and Pierre-Yves Strub
- Contact: Gilles Barthe
- URL: https://www.easycrypt.info/trac/

5.3. Math-Components

Mathematical Components library
FUNCTIONAL DESCRIPTION

The Mathematical Components library is a set of Coq libraries that cover the mechanization of the proof of the Odd Order Theorem.

- Participants: Andrea Asperti, Jeremy Avigad, Yves Bertot, Cyril Cohen, François Garillot, Georges Gonthier, Stéphane Le Roux, Assia Mahboubi, Sidi Ould Biha, Ioana Pasca, Laurence Rideau, Alexey Solovyev, Enrico Tassi and Russell O'connor
- Contact: Assia Mahboubi
- URL: http://www.msr-inria.fr/projects/mathematical-components-2/

5.4. Ssreflect

FUNCTIONAL DESCRIPTION

Ssreflect is a tactic language extension to the Coq system, developed by the Mathematical Components team.

- Participants: Cyril Cohen, Yves Bertot, Laurence Rideau, Enrico Tassi and Laurent Théry
- Contact: Yves Bertot
- URL: http://ssr.msr-inria.inria.fr/

5.5. Zoocrypt

FUNCTIONAL DESCRIPTION

ZooCrypt is an automated tool for analyzing the security of padding-based public-key encryption schemes (i.e. schemes built from trapdoor permutations and hash functions). This years we extended the tool to be able to deal with schemes based on cyclic groups and bilinear maps.

- Participants: Benjamin Grégoire, Gilles Barthe and Pierre-Yves Strub
- Contact: Gilles Barthe
- URL: https://www.easycrypt.info/zoocrypt/

MCTAO Project-Team

5. New Software and Platforms

5.1. Hampath

KEYWORDS: Geometric control - Second order conditions - Differential homotopy - Ordinary differential equations
FUNCTIONAL DESCRIPTION

Hampath is a software developped to solve optimal control problems but also to study Hamiltonian flow.

- Participants: Jean-Baptiste Caillau, Olivier Cots and Joseph Gergaud
- Contact: Jean-Baptiste Caillau
- URL: http://cots.perso.enseeiht.fr/hampath/index.html

MODEMIC Project-Team

6. New Software and Platforms

6.1. Landfill Recirculation Management Simulator

FUNCTIONAL DESCRIPTION

Following the first works on modeling and control of landfills performed in the framework of the associated team DYMECOS with Chile, that have proposed an optimal feedback strategy for the leachate recirculation under the assumption of a perfectly mixed medium [40], a first mock-up software has been conceived in view of studying the effects of inhomogeneity along with identification procedures of spatial network structures on data (interconnection of bioreactors as in VITELBIO project). The development of the software is in progress.

- Participants: Andres Donoso-Bravo (PUCV, Chile), J.R. de Dreuzy (GéoSciences Rennes), Alain Rapaport, Hector Ramirez, Alejandro Rojas Palma
- Contact: Alain Rapaport
- URL: https://sites.google.com/site/eadymecos/resultats

6.2. Action Dépollution

FUNCTIONAL DESCRIPTION

Action Dépollution is a serious game made for learning how to purify fast and well a water reservoir, such as lakes. In the scope of the international initiative Mathematics of Planet Earth, this game shows an application of mathematics related to environmental education and sustainable development. The player can act as a researcher, that compares different strategies and looks for the best solution.

- Participants: Alain Rapaport, Antoine Rousseau (EPI LEMON)
- Contact: Antoine Rousseau
- URL: https://depollution.inria.fr/

6.3. VITELBIO (VIrtual TELluric BIOreactors)

FUNCTIONAL DESCRIPTION

Vitelbio is a simulator of the microbial activity in soils, for which the spatialization is represented as a network of interconnected reservoirs. The software allows to draw an interconnections graph, that respects the constraint of the maximum flow, and to choose the biological characteristics of various bacterial species in competition for a single nutrient. The simulator computes the time evaluations of the different populations in each compartment, and compares the overall yielding of the ecosystem in terms of bio-conversion of the substrate. This software has been developed in the framework of the INRA/Inria project VITELBIO (VIrtual TELluric BIOreactors), with the help of the company ITK. It is today mainly used for educational purposes (in MSC and PhD lectures).

- Participants: Jérôme Harmand, Alain Rapaport
- Contact: Alain Rapaport
- URL: http://vitelbio.itkweb.fr/vitelbio/

MORPHEME Project-Team

5. New Software and Platforms

5.1. BioLib

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION

Library of image analysis for biology: object detection, tracking. This year some new developments for embedding attractive interactions in the Multiple Births and Cut algorithm have been included.

- Participants: Sylvain Prigent, Xavier Descombes, Grégoire Malandain, Étienne Delclaux, Emmanuel Soubies and Sen Wang.
- Contact: Xavier Descombes

5.2. PIB

Biological imaging platform
FUNCTIONAL DESCRIPTION

This platform, based on the DTK meta-platform, aims at gathering the team software development, and at providing a visual development tool.

- Participants: Étienne Delclaux, Grégoire Malandain and Xavier Descombes
- Contact: Xavier Descombes

5.3. Stracking

KEYWORDS: Bioinformatics - Biology - Biomedical imaging
SCIENTIFIC DESCRIPTION

Head Tracking and Flagellum Tracing for Sperm Motility Analysis : Sperm quality assessment plays an essential role in human fertility and animal breeding. Manual analysis is time-consuming and subject to intra- and inter-observer variability. To automate the analysis process, as well as to offer a means of statistical analysis that may not be achieved by visual inspection, we present a computational framework that tracks the heads and traces the tails for analyzing sperm motility, one of the most important attributes in semen quality evaluation. Our framework consists of 3 modules: head detection, head tracking, and flagellum tracing. The head detection module detects the sperm heads from the image data, and the detected heads are the inputs to the head tracking module for obtaining the head trajectories. Finally, a flagellum tracing algorithm is proposed to obtain the flagellar beat patterns.
FUNCTIONAL DESCRIPTION

This software is developed within the ANR project MOTIMO. It allows to segment and track spermatozoons from confocal microscopy image sequences.

- Participants: Huei Fang Yang, Xavier Descombes, Sylvain Prigent and Grégoire Malandain
- Contact: Xavier Descombes

NACHOS Project-Team

5. New Software and Platforms

5.1. MAXW-DGTD

- Participants: Alexandra Christophe-Argenvillier, Loula Fezoui, Stéphane Lanteri, Raphaël Léger, Jonathan Viquerat
- Contact: Stéphane Lanteri
- Keywords: Computational electromagnetics, Maxwell equations, discontinuous Galerkin, tetrahedral mesh.
- OS/Middelware: Linux
- Required library or software: MPI (Message Passing Interface), CUDA
- Programming language: Fortran 77/95

MAXW-DGTD is a software suite for the simulation of time domain electromagnetic wave propagation. It implements a solution method for the Maxwell equations in the time-domain. MAXW-DGTD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes [13]. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. This discontinuous Galerkin method combines a centered scheme for the evaluation of numerical fluxes at a face shared by two neighboring elements, with an explicit Leap-Frog time scheme. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with message passing programming using the MPI standard. Besides, a peripheral version of the software has been recently developed which is able to exploit the processing capabilities of a hybrid parallel computing system comprising muticore CPU and GPU nodes.

5.2. MAXW-DGFD

- Participants: Thomas Frachon, Stéphane Lanteri, Ludovic Moya
- Contact: Stéphane Lanteri
- Keywords: Computational electromagnetics, Maxwell equations, discontinuous Galerkin, tetrahedral mesh.
- OS/Middelware: Linux
- Required library or software: MPI (Message Passing Interface)
- Programming language: Fortran 77/95

MAXW-DGFD is a software suite for the simulation of time-harmonic electromagnetic wave propagation. It implements a solution method for the Maxwell equations in the frequency domain. MAXW-DGFD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. The resolution of the sparse, complex coefficients, linear systems resulting from the discontinuous Galerkin formulation is performed by a hybrid iterative/direct solver whose design is based on domain decomposition principles. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with a message passing programming using the MPI standard. Some recent achievements have been the implementation of non-uniform order DG method in the 2d case and of a new hybridizable discontinuous Galerkin (HDG) formulation also in the 2d and 3d cases.

5.3. SISMO-DGTD

- Participants: Nathalie Glinsky, Stéphane Lanteri
- Contact: Stéphane Lanteri

SISMO-DGTD is a software for the simulation of time-domain seismic wave propagation. It implements a solution method for the velocity-stress equations in the time-domain. SISMO-DGTD is based on a discontinuous Galerkin method formulated on unstructured triangular (2d case) or tetrahedral (3d case) meshes [2]. Within each element of the mesh, the components of the electromagnetic field are approximated by an arbitrary high order nodal polynomial interpolation method. This discontinuous Galerkin method combines a centered scheme for the evaluation of numerical fluxes at a face shared by two neighboring elements, with an explicit Leap-Frog time scheme. The software and the underlying algorithms are adapted to distributed memory parallel computing platforms thanks to a parallelization strategy that combines a partitioning of the computational domain with a message passing programming using the MPI standard.

NEUROMATHCOMP Project-Team

5. New Software and Platforms

5.1. ENAS

Event Neural Assembly Simulation
KEYWORDS: Neurosciences - Health - Physiology
FUNCTIONAL DESCRIPTION Enas is a software for the analysis of spike trains either coming from neural simulators or from biological experiments. Spike trains statistical analysis is based on the estimation of a Gibbs distribution with a spatio-temporal potential optimaly characterizing the statistics of empirical spike trains by minimisation of the Kullback-Leibler divergence between the empirical measure and the Gibbs measure. From this, classical statistical indicators such as firing rate, correlations, higher order moments statistical entropy, effective connectivity graph, confidence plots and so on are obtained. Also, the form of the Gibbs potential provides essential informations on the underlying neural network and its structure. This method does not only allows us to estimate the spikes statistics but also to compare different models, thus answering such questions about the neural code as, e.g., are correlations (or time synchrony or a given set of spike patterns, etc.) significant with respect to rate coding? The software includes classical Maximum Entropy Models such as Ising model, but also more general forms of potentials with spatio-temporal interactions. It also has a functionality attempting to guess the shape of the potential from data and a procedure fitting an Integrate and Fire Neural Network reproducing the empirical rasters statistics. Finally, it allows to generate artificial rasters having a given distribution (e.g. corresponding to biological spike trains).

- Participants: Bruno Cessac, Sélim Kraria, Hassan Nasser, Thierry Viéville, Rodrigo Cofre Torres, Audric Drogoul, Geoffrey Portelli, Pierre Kornprobst, Theodora Karvouniari and Daniela Pamplona
- Contact: Bruno Cessac
- URL: https://enas.inria.fr

5.2. Virtual Retina

KEYWORDS: Neurosciences - Simulation - Biology
FUNCTIONAL DESCRIPTION Virtual Retina [14] allows large-scale simulations of biologically-plausible retinas, with customizable parameters. Virtual Retina has been shown to reproduce a wide range of experimental data from salamander, cat and primate retinas [14], and has been used in several theoretical studies [79], [82], [83], [56]. It has recently been shown to predict spikes in a mouse retina more accurately than linear-nonlinear (LN) models [93]. The underlying model includes a non-separable spatio-temporal linear model of filtering in the Outer Plexiform Layer, a shunting feedback at the level of bipolar cells, and a spike generation process using noisy leaky integrate-and-fire neurons to model retinal ganglion cells (RGCs). All parameters for the different stages of the model are customizable so that the visual field can be paved with different RGC types.

- Participants: Bruno Cessac, Maria-Jose Escobar, Pierre Kornprobst, Adrien Wohrer and Thierry Viéville
- Contact: Pierre Kornprobst
- URL: http://www-sop.inria.fr/neuromathcomp/public/software/virtualretina/

SCALE Team

6. New Software and Platforms

6.1. BigGrph

- Participants: Eric Madelaine, Fabrice Huet
- Contact: Luc Hogie
- The objective of "biggrph" is to provide a distributed platform for very large graphs processing. A typical data set for testing purpose is a sample of the Twitter graph : 240GB on disk, 398M vertices, 23G edges, average degree of 58 and max degree of 24,635,412.

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

  The development of the "biggrph" platform is now at the stage where we focus on the quality and the improvement of the code.

  In particular we have designed strong test suites and some non trivial bugs have been fixed. We have also solved problems of scalability, in particular concerning the communication layer with billions of messages exchanged between BSP steps. Moreover, we have implemented specific data structures for BSP and support for distributed debugging. This comes along with the implementation of algorithms such as BFS or strongly connected components that are run on the NEF cluster (a facility maintained at Inria Sophia Antipolis).
- This project is a joint work of the three EPs Coati, Diana and Scale and is supported by an ADT grant.
- URL : http://www.i3s.unice.fr/~hogie/software/?name=biggrph

6.2. BtrPlace

FUNCTIONAL DESCRIPTION

BtrPlace dynamically adapts the VM placement depending on pluggable expectations using a network and memory-aware migration scheduler. It currently addresses affinity constraints, resource booking, node state manipulation and hosting restrictions. BtrPlace is a complete rewrite of the reconfiguration algorithm that was inside OW2 project Entropy with a clear focus on extensibility. It embeds the constraint programming library Choco to compute solutions.

BtrPlace has been released 5 times this year. The current code amounts for 44000 lines of Java (production and test code, comments) and the online documentation amounts for around 1500 lines. BtrPlace is available from the Maven central repository. In 2015, it has been downloaded around 480 times from unique IPs and 2400 unique visitors accessed the Website.

- Contact: Fabien Hermenier
- Participants: Fabien Hermenier, Vincent Kherbache
- URL: http://www.btrplace.org/
- APP registration code: IDDN.FR.001.330025.000.S.C.2014.000.31235

6.3. EventCloud

SCIENTIFIC DESCRIPTION

The EventCloud architecture is based on a structured P2P overlay network targetting high-performance elastic data processing. Consequently it aims to be deployed on infrastructures like grids, clouds, i.e. whose nodes acquisition and relinquishment can be dynamic and subject to a pay-per-use mode. Each node participating in the overlay networks constituting EventCloud instances, is responsible for managing the storage of subsets of the events, and helps in matching potential looked up events and disseminating them in a collaborative manner. As such, each node is also potentially an event broker responsible for managing subscriptions and routing notifications. The EventCloud provides a high level publish-subscribe API where users can register their interests using SPARQL. When matching RDF data are added, subscribers are automatically notified. Recent work around the EventCloud has focused on efficient algorithms for managing subscription and notification.
FUNCTIONAL DESCRIPTION

The EventCloud is an open source middleware that aims to act as a distributed datastore for data fulfiling the W3C RDF specification (http://www.w3.org/RDF/). It allows to store and retrieve quadruples (RDF triples with context) through SPARQL but also to manage events represented as quadruples.

- Participants: Laurent Pellegrino, Fabrice Huet, Françoise Baude, Maeva Antoine and Iyad Alshabani
- Partner: CNRS
- Contact: Françoise Baude

6.4. OSA

Open Simulation Architecture
FUNCTIONAL DESCRIPTION

OSA on of new or existing contributions at every level of its architecture. The platform core supports discrete-event simulation engine(s) built on top of the ObjectWeb Consortium?s Fractal component model. In OSA, the systems to be simulated are modeled and instrumented using Fractal components. In OSA, the event handling is mostly hidden in the controller part of the components, which alleviates noticeably the modeling process, but also eases the replacement of any part of the simulation engine. Apart the simulation engine, OSA aims at integrating useful tools for modeling, developing, experimenting, and analysing simulations. OSA is also a platform for experimenting new techniques and approaches in simulation, such as aspect oriented programming, separation of concerns, innovative component architectures, and so on.

- Participant: Olivier Dalle
- Contact: Olivier Dalle
- URL: http://osa.inria.fr/

6.5. Vercors Component Editor (VCE)

VERification of models for distributed communicating COmponants, with safety and Security
FUNCTIONAL DESCRIPTION

The Vercors tools include front-ends for specifying the architecture and behaviour of components in the form of UML diagrams. We translate these high-level specifications, into behavioural models in various formats, and we also transform these models using abstractions. In a final step, abstract models are translated into the input format for various verification toolsets. Currently we mainly use the various analysis modules of the CADP toolset.

- Participants: Eric Madelaine, Antonio Cansado, Ludovic Henrio, Marcela Rivera, Oleksandra Kulankhina, Bartlomiej Szejna, Nassim Jibai and Siqi Li
- Contact: Eric Madelaine
- URL: http://team.inria.fr/scale/software/vercors/

STARS Project-Team

6. New Software and Platforms

6.1. CLEM

FUNCTIONAL DESCRIPTION

The Clem Toolkit is a set of tools devoted to design, simulate, verify and generate code for LE programs. LE is a synchronous language supporting a modular compilation. It also supports automata possibly designed with a dedicated graphical editor and implicit Mealy machine definition.

- Participants: Daniel Gaffé and Annie Ressouche
- Contact: Annie Ressouche
- URL: http://www-sop.inria.fr/teams/pulsar/projects/Clem/

6.2. EGMM-BGS

FUNCTIONAL DESCRIPTION

This software implements a generic background subtraction algorithm for video and RGB-D cameras, which can take feedback from people detection and tracking processes. Embedded in a people detection framework, it does not classify foreground / background at pixel level but provides useful information for the framework to remove noise. Noise is only removed when the framework has all the information from background subtraction, classification and object tracking. In our experiment, our background subtraction algorithm outperforms GMM, a popular background subtraction algorithm, in detecting people and removing noise.

- Participants: Anh Tuan Nghiem, François Brémond and Vasanth Bathrinarayanan
- Contact: François Brémond

6.3. MTS

FUNCTIONAL DESCRIPTION

This software consists of a retrieval tool for a human operator to select a person of interest in a network of cameras. The multi-camera system can re-identify the person of interest, wherever and whenever (s)he has been observed in the camera network. This task is particularly hard due to camera variations, different lighting conditions, different color responses and different camera viewpoints. Moreover, we focus on non-rigid objects (i.e. humans) that change their pose and orientation contributing to the complexity of the problem. In this work we design two methods for appearance matching across non-overlapping cameras. One particular aspect is the choice of the image descriptor. A good descriptor should capture the most distinguishing characteristics of an appearance, while being invariant to camera changes. We chose to describe the object appearance by using the covariance descriptor as its performance is found to be superior to other methods. By averaging descriptors on a Riemannian manifold, we incorporate information from multiple images. This produces mean Riemannian covariance that yields a compact and robust representation. This new software has made digital video surveillance systems a product highly asked by security operators, especially the ones monitoring large critical infrastructures, such as public transportation (subways, airports, and harbours), industrials (gas plants), and supermarkets.

- Participants: Slawomir Bak and François Brémond
- Contact: François Brémond

6.4. Person Manual Tracking in a Static Camera Network (PMT-SCN)

FUNCTIONAL DESCRIPTION

This software allows tracking a person in a heterogeneous camera network. The tracking is done manually. The advantage of this software is to give the opportunity to operators in video-surveillance to focus on tracking the activity of a person without knowing the positions of the cameras in a considered area. When the tracked person leaves the field-of–view (FOV) of a first camera, and enters the FOV of a second one, the second camera is automatically showed to the operator. This software was developed conjointly by Inria and Neosensys.

- Participants: Bernard Boulay, Anaïs Ducoffe, Sofia Zaidenberg, Anais Ducoffe, Annunziato Polimeni and Julien Gueytat
- Partner: Neosensys
- Contact: Anaïs Ducoffe

6.5. PrintFoot Tracker

FUNCTIONAL DESCRIPTION

This software implements a new algorithm for tracking multiple persons in a single camera. This algorithm computes many different appearance-based descriptors to characterize the visual appearance of an object and to track it over time. Object tracking quality usually depends on video scene conditions (e.g. illumination, density of objects, object occlusion level). In order to overcome this limitation, this algorithm presents a new control approach to adapt the object tracking process to the scene condition variations. More precisely, this approach learns how to tune the tracker parameters to cope with the tracking context variations. The tracking context, or video context, of a video sequence is defined as a set of six features: density of mobile objects, their occlusion level, their contrast with regard to the surrounding background, their contrast variance, their 2D area and their 2D area variance. The software has been experimented with three different tracking algorithms and on long, complex video datasets.

- Participants: Duc Phu Chau, François Brémond and Monique Thonnat
- Contact: François Brémond

6.6. Proof of Concept Néosensys (Poc-NS)

FUNCTIONAL DESCRIPTION

This is a demonstration software which gathers different technologies from Inria and Neosensys: PMT-SCN, re-identification and auto-side switch. This software is used to approach potential clients of Neosensys.

- Participants: Bernard Boulay, Sofia Zaidenberg, Julien Gueytat, Slawomir Bak, François Brémond, Annunziato Polimeni and Yves Pichon
- Partner: Neosensys
- Contact: François Brémond

6.7. SUP

Scene Understanding Platform
KEYWORDS: Activity recognition - 3D - Dynamic scene
FUNCTIONAL DESCRIPTION

SUP is a software platform for perceiving, analyzing and interpreting a 3D dynamic scene observed through a network of sensors. It encompasses algorithms allowing for the modeling of interesting activities for users to enable their recognition in real-world applications requiring high-throughput.

- Participants: François Brémond, Carlos Fernando Crispim Junior and Etienne Corvée
- Partners: CEA - CHU Nice - USC Californie - Université de Hamburg - I2R
- Contact: François Brémond
- URL: https://team.inria.fr/stars/software

6.8. VISEVAL

FUNCTIONAL DESCRIPTION

ViSEval is a software dedicated to the evaluation and visualization of video processing algorithm outputs. The evaluation of video processing algorithm results is an important step in video analysis research. In video processing, we identify 4 different tasks to evaluate: detection, classification and tracking of physical objects of interest and event recognition.

- Participants: Bernard Boulay and François Brémond
- Contact: François Brémond
- URL: http://www-sop.inria.fr/teams/pulsar/EvaluationTool/ViSEvAl_Description.html

6.9. py_ad

py action detection
FUNCTIONAL DESCRIPTION

Action Detection framework which allows user to detect action in video stream. It uses model trained in py_ar.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.10. py_ar

py action recognition
FUNCTIONAL DESCRIPTION

Action Recognition training/evaluation framework. It allows user do define action recognition experiment (on clipped videos). Train, test model, save the results and print the statistics.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.11. py_sup_reader

FUNCTIONAL DESCRIPTION

This is a library which allows to read video saved in SUP format in Python.

- Participant: Michal Koperski
- Contact: Michal Koperski

6.12. py_tra3d

py trajectories 3d
SCIENTIFIC DESCRIPTION

New video descriptor which fuse trajectory information with 3D information from depth sensor.
FUNCTIONAL DESCRIPTION

3D Trajectories descriptor Compute 3D trajectories descriptor proposed in (http://hal.inria.fr/docs/01/05/49/49/PDF/koperski-icip.pdf)

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

6.13. sup_ad

sup action detection

SCIENTIFIC DESCRIPTION

This software introduces the framework for online/real-time action recognition using state-of-the-art features and sliding window technique.

FUNCTIONAL DESCRIPTION

SUP Action Detection Plugin is a plugin for SUP platform which performs action detection using sliding window and Bag of Words. It uses an input data model trained in py_ar project.

- Participants: Michal Koperski and François Brémond
- Contact: Michal Koperski

TITANE Project-Team

6. New Software and Platforms

6.1. CGAL Barycentric coordinates 2D

SCIENTIFIC DESCRIPTION

The package 2D Generalized Barycentric Coordinates offers an efficient and robust implementation of two-dimensional closed-form generalized barycentric coordinates defined for simple two-dimensional polygons. If coordinates with respect to multivariate scattered points instead of a polygon are required, please refer to natural neighbour coordinates from the package 2D and Surface Function Interpolation. The package includes an implementation of Wachspress, mean value, and discrete harmonic coordinates and provides some extra functions to compute barycentric coordinates with respect to segments (segment coordinates) and triangles (triangle coordinates).

- Participants: Pierre Alliez and Dmitry Anisimov
- Contact: Pierre Alliez

6.2. Module CGAL: Point Set Processing

SCIENTIFIC DESCRIPTION

This component implements methods to analyze and process unorganized point sets. The input is an unorganized point set, possibly with normal attributes (unoriented or oriented). The point set can be analyzed to measure its average spacing, and processed through functions devoted to the simplification, outlier removal, smoothing, normal estimation, normal orientation and feature edges estimation.

- Participants: Pierre Alliez, Laurent Saboret and Clément Jamin
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Point_set_processing_3/index.html

6.3. Module CGAL: Scale-space surface reconstruction

KEYWORD: Geometric algorithms
SCIENTIFIC DESCRIPTION

This package implements a surface reconstruction method which takes as input an unordered point set and computes a triangulated surface mesh interpolating the point set. We assume that the input points were sampled from the surface of an object. The method can also process point sets sampled from the interior of the object, although we cannot provide guarantees on the output. This method can handle a decent amount of noise and outliers. The point set may greatly undersample the object in occluded regions, although no surface will be reconstructed to fill these regions.

See http://doc.cgal.org/latest/Scale_space_reconstruction_3/index.html
FUNCTIONAL DESCRIPTION

This method reconstructs a surface that interpolates a set of 3D points. This method provides an efficient alternative to the Poisson surface reconstruction method. The main difference in output is that this method reconstructs a surface that interpolates the point set, as opposed to approximating the point set. How the surface connects the points depends on a scale variable, which can be estimated semi-automatically.

- Participants: Pierre Alliez and Thijs Van Lankveld
- Contact: Pierre Alliez
- URL: http://doc.cgal.org/latest/Scale_space_reconstruction_3/index.html

6.4. Skeleton-Blockers

Skeleton-Blockers data-structure
KEYWORDS: C++ - Mesh - Triangulation - Topology - 3D
FUNCTIONAL DESCRIPTION

Skeleton-Blockers is a compact, efficient and generic data-structure that can represent any simplicial complex. The implementation is in C++11.

- Participant: David Salinas
- Contact: David Salinas
- URL: https://project.inria.fr/gudhi/software/

6.5. Structure-preserving Decimation

KEYWORDS: Mesh - 3D - Multi-View reconstruction
FUNCTIONAL DESCRIPTION

Structure-preserving decimation is a software that can simplify 3D meshes while preserving some of their structure. Simplification is performed through either a command line or a graphical user interface that can combine several operations including several simplification methods.

- Participants: David Salinas, Pierre Alliez and Florent Lafarge
- Contact: David Salinas

TOSCA Project-Team

6. New Software and Platforms

6.1. ExitBM

FUNCTIONAL DESCRIPTION

The ExitBM library provides methods to simulate random variables related to the first exit time and position of the Brownian motion from simple domains, namely intervals, squares and rectangles. This is a new software of 2015.

- Participants: Madalina Deaconu and Antoine Lejay
- Contact: Antoine Lejay
- URL: http://exitbm.gforge.inria.fr/

6.2. SDM

Stochastic Downscaling Method
FUNCTIONAL DESCRIPTION

The computation of the wind at small scale and the estimation of its uncertainties is of particular importance for applications such as wind energy resource estimation. To this aim, we have developed a computer code belonging to the family of codes of atmospheric flow calculation, in the atmospheric boundary layer. SDM especially concerns the simulation of wind at small space scales (meaning that the horizontal resolution is one kilometer or less), based on the combination of an existing Numerical Weather Prediction model providing a coarse prediction, and a Lagrangian Stochastic Model for turbulent flows.

This year we added to SDM a software tool for Configuration Interface and Visualization (CIV) of the SDM simulations. This dedicated GUI restitutes the 3D simulation view of all SDM outputs (including the rendering of interactions with mills). It is also a key environment tool to visualize a coarse resolution input, to extract time boundary condition of any chosen subdomain simulation for a NetCDF (Network Common DataForm) input file, to prepare the compilation procedure of any simulation case of SDM, to execute codes.

- Participants: Mireille Bossy, Sélim Kraria
- Contact: Mireille Bossy
- URL: http://windpos.inria.fr

6.3. Triton

KEYWORDS: Image analysis - Oceanography
FUNCTIONAL DESCRIPTION

The Triton software aims at providing a toolbox to analyze nearshore waves images recorded by a camera on the beach. More precisely, it aims at estimating the height, length and speed of waves, to find speed and direction of currents, and to reconstruct the bathymetry from these images. This is a new software of 2015.

- Participants: Stanislas Larnier, Rafael Almar and Antoine Lejay
- Contact: Antoine Lejay

VIRTUAL PLANTS Project-Team

5. New Software and Platforms

5.1. OpenAleaLab

KEYWORDS: Bioinformatics - Biology - Workflow - Modelling Environment
FUNCTIONAL DESCRIPTION

OpenAleaLab is an integrated modelling environment (IME) designed for scientists based on IPython and on OpenAlea components. This open source environment is extensible via plug-ins and allows user to work with a set of diverse modelling paradigms like imperative languages (Python, R), scientific workflows (visual programming) or rule-based language (L-System). This IME, built using PyQt, provides an IPython shell, a text editor, a project manager, a graphical package installer and a world, containing the objects and state variables shared by the different paradigms. The world can be graphically interpreted in 3D or 2D. Different paradigms and tools for plant modelling are available as plug-ins, such as a visual programming environment, a L-system language, a 3D viewer, and an R editor and interpreter. The plug-in system is based on setuptools entry-points and provide both functional and GUI components. This environment is designed to be easily extensible in order to include new plant modelling paradigms in the future or to be customized for other scientific domains. Several dedicated extensions (TissueLab, PlantLab) have been developed or are in development.

- Participants: Christophe Pradal, Guillaume Baty, Julien Coste, Christophe Godin.
- Contact: Christophe Pradal, Christophe Godin
- URL: http://virtualplants.github.io/

5.2. TissueLab

KEYWORDS: Bioinformatics - Biology - Modelling Environment
FUNCTIONAL DESCRIPTION

TissueLab is an OpenAleaLab extension dedicated to studies plant morphogenesis at the scale of tissues. This extension was built on the basis of several key concepts of OpenAleaLab (project, world, interactive panels, etc.) and using its plugin mechanism (dynamically discovered, modular, extensible, etc.). TissueLab enables the visualization, interaction, reconstruction, analysis and simulation of tissue development based on image sequences. It contains for instance the PyThor module, dedicated to 3D real-time interaction and modification of segmented images for the creation of ground truth segmentations.

- Participants: Sophie Ribes, Guillaume Baty, Guillaume Cerutti, Alizon Konig, Gregoire Malandain, Christophe Pradal, Christophe Godin.
- Contact: Christophe Godin
- URL: https://gforge.inria.fr/projects/oalab

5.3. TissueMeca

KEYWORDS: Bioinformatics - Biology - Mechanics - Morphogenesis
FUNCTIONAL DESCRIPTION

A mechanical model of growing tissue has been implemented using the open source software SOFA and OpenAlea. Using OpenAlea, a generic tissue representation can be defined with attributes giving structural, geometrical and physical parameters of the simulation. Then, based on SOFA and its modular approach, it is possible to combine different element types (triangle and edge elements), forces (elastic forces and turgor) and positional constraints within the same model to find the static elastic equilibrium, given a current configuration. The use of an implicit integration scheme makes it possible to achieve close-to interactive simulation of growth. The module implements also growth equations for the different cell walls after each elastic equilibrium step. Algorithms to simulate division and refinement of each element of the modelled tissue are also available.

- Participants: Frédéric Boudon, Olivier Ali, Jean-Philippe Bernard, Benjamin Gilles, Christophe Godin.
- Contact: Frédéric Boudon
- https://gforge.inria.fr/projects/tissuemeca/

5.4. PlantScan3D

KEYWORDS: Bioinformatics - Biology - Laser scanners - 3D Reconstruction
FUNCTIONAL DESCRIPTION

This software aims at semi-automatically reconstructing the 3D structures of plants from laser scans. For this, it encapsulates automatic reconstruction method developed by the Virtual Plants team (Preuksakarn et al., 2010) or by the literature (Vernoust and Lazarus, 2000). Once reconstructed the structure can be graphically edited by adding, deleting, repositioning or reorganizing segments in the structure. The original pointset can be processed with contraction operators to shift the points toward the center of the shape. Some post processing procedures are available to retrieve automatically botanical features such as divergence angle sequences.

- Participants: Frédéric Boudon, Chakkrit Preuksakarn, Christophe Godin
- Contact: Frédéric Boudon
- URL: http://plantscan3d.gforge.inria.fr/

5.5. ASTEC

KEYWORDS: Segmentation - Tracking - High resolution
FUNCTIONAL DESCRIPTION A new algorithmic pipeline, ASTEC (Adaptative Segmentation and Tracking of Embryonic Cells), has been developed to segment and track cell shapes in 3D from movies with high spatio-temporal resolution of embryos where the membranes have been labeled (using dye or genetic markers for example). To segment the 3D embryo image at a given time-point, ASTEC takes advantage of the high spatial resolution of the movie in order to propagate the segmentation of the previous time points. This, coupled to biological knwoledge on the studied system, allows to constrain the segmentation and to track cells throughout time simulataneously. Moreover, the propagation allows to bound the potential mistakes of segmentation (e.g. a cells cannot disapear) which enables powerfull post-correction based on the study of the resulting tracking.

- Participants: Léo Guignard, Grégoire Malandain, Patrick Lemaire, Christophe Godin
- Contact: Christophe Godin
- URL: https://gforge.inria.fr/projects/marsalt/

5.6. Alep

KEYWORDS: Foliar Fungus, Pathogen, FSPM, Epidemics, Infectious Cycle, Modelling framework
LONG: Architecture & Leaf Pathogens
FUNCTIONAL DESCRIPTION

Alep is a FSPM library implemented in Python that adapts the concepts and tools of OpenAlea to pathosystem modelling. The key components of Alep are two abstract classes that represent Dispersal Units and Lesions of foliar fungi in a generic form. The equations in these classes are specified to model a given species of fungus. Alep also contains several generic functions to manipulate these objects and define their contract: functions of dispersal by rain and by wind, functions managing the growth and competition of several lesions on the same leaf. A particular pathosystem is modeled by assembling a coherent set of components via a plugin system. This strategy allows the composition of existing algorithms as well as the extension or the inclusion of new algorithms. Their assembly and scheduling of execution uses scientific workflows defined in OpenAlea. This way, models can run at different time and spatial scales.

- Participants: Guillaume Garin, Christophe Pradal, Christian Fournier, Vianey Houles, Corinne Robert, Bruno Andrieu
- Contact: Christophe Pradal
- URL: https://gforge.inria.fr/projects/openaleapkg

5.7. AutoWIG

KEYWORDS: Syntaxic Analysis
FUNCTIONAL DESCRIPTION

The goal of AutoWIG (Automatic Wrapper and Interface Generator) is to provide an automatic approach for the process of Python interfacing of C++ libraries. This Python library relies on two main principles: i) automatic C++ code parsing using LLVM/clang, and ii) Python wrapper generation with C++ code introspection.

- Participants: Pierre Fernique, Christophe Pradal
- Contact: Pierre Fernique
- URL: https://github.com/VirtualPlants/AutoWIG

5.8. Phenomenal

KEYWORDS: Image Analysis
FUNCTIONAL DESCRIPTION

Phenomenal is a Python library that provides a set of algorithms to process images produce by Image-based phenotyping platforms. The library contains algorithms for i) plant image segmentation, ii) 3D reconstruction of plant organs and plant canopies, iii) calculation of intercepted light and radiation use efficiency. All these algorithms are integrated in the OpenAlea platform.

- Participants: Simon Artzet, Jérôme Chopard, Michael Mielewczik, Nicolas Brichet, Christian Fournier, Christophe Pradal
- Contact: Christophe Pradal
- URL: https://gforge.inria.fr/projects/phenomenal/

5.9. Platforms

5.9.1. Platform OpenAlea

OpenAlea is an open-software platform for interdisciplinary research in plant modeling and simulation. This scientific workflow platform is used for the integration and comparison of different models and tools provided by the research community. It is based on the Python (http://www.python.org) language that aims at being both a *glue* language for the different modules and an efficient modeling language for developing new models and tools. *OpenAlea* currently includes modules for plant simulation, analysis and modeling at different scales (*V-Plants* modules), for modeling ecophysiological processes (*Alinea* modules) such as radiative transfer, transpiration and photosynthesis (*RATP*, *Caribu*, *Adel*, *TopVine*, *Ecomeristem*) and for 3D visualization of plant architecture at different scales (*PlantGL*).

OpenAlea is the result of a collaborative effort associating 20 french research teams in plant modeling from Inria, CIRAD, INRA and ENS Lyon. The Virtual Plants team coordinates both development and modeling consortia, and is more particularly in charge of the development of the kernel and of some of the main data structures such as multi-scale tree graphs and statistical sequences.

OpenAlea is a fundamental tool to share models and methods in interdisciplinary research (comprising botany, ecophysiology, forestry, agronomy, applied mathematics and computer science approaches). Embedded in Python and its scientific libraries, the platform may be used as a flexible and useful toolbox by biologists and modelers for various purposes (research, teaching, rapid model prototyping, communication, etc.).

5.9.2. Platform Sofa

Our team is increasingly using the platform SOFA developed at Inria by other teams, in conjunction with OpenAlea, to model biomechanics of plant tissues. SOFA (https://www.sofa-framework.org) is an Open Source framework primarily targeted at real-time simulation, with an emphasis on biological simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods. It has been extensively used by our team in the recent years to conduct virtual mechanical experiments on plant tissues (see section 6.2.3).

WIMMICS Project-Team

6. New Software and Platforms

6.1. CORESE

KEYWORDS: Semantic Web - Web of Data - RDF - SPARQL
FUNCTIONAL DESCRIPTION

Corese is a Semantic Web Factory, it implements W3C recommandations such as RDF, RDFS, SPARQL 1.1 Query and Update. It provides an Inference Rule language, a Transformation Language for RDF graphs and a function language on top of SPARQL. Furthermore, Corese integrates original features such as approximate search and extended Property Path. It also provides distributed federated query processing (cooperation with Johan Montagnat, I3S).

- Participants: Olivier Corby, Erwan Demairy, Fuqi Song.
- Partners: I3S, Mnemotix
- Contact: Olivier Corby
- URL: http://wimmics.inria.fr/corese

6.2. DBpedia

KEYWORDS: French chapter of DBpedia
FUNCTIONAL DESCRIPTION

DBpedia is an international crowd-sourced community effort to extract structured information from Wikipedia and make this information available on the semantic Web as linked open data. The DBpedia triple stores then allow anyone to solve sophisticated queries against Wikipedia extracted data, and to link the different data sets on these data. The French chapter of DBpedia was created and deployed by Wimmics and is now an online running platform providing data to several projects such as: QAKIS, Izipedia, zone47, Sépage, HdA Lab., JocondeLab, etc.

- Participants: Raphaël Boyer and Fabien Gandon
- Contact: Fabien Gandon
- URL: http://fr.dbpedia.org

6.3. Discovery Hub

KEYWORD: Search Engine
FUNCTIONAL DESCRIPTION

Discovery Hub is an Exploratory Search Engine on top of DBpedia.

- Participants: Nicolas Marie, Fabien Gandon, Emilie Palagi and Alain Giboin
- Partner: Alcatel-Lucent
- Contact: Fabien Gandon
- URL: http://discoveryhub.co

6.4. QAKiS

KEYWORD: Natural Language Question Answering
FUNCTIONAL DESCRIPTION Question-Answening wiki framework based system

The QAKiS system implements question answering over DBpedia. QAKiS allows end users to submit a query to an RDF triple store in English and obtain the answer in the same language, hiding the complexity of the non-intuitive formal query languages involved in the resolution process. At the same time, the expressiveness of these standards is exploited to scale to the huge amounts of available semantic data. Its major novelty is to implement a relation-based match for question interpretation, to convert the user question into a query language (e.g. SPARQL). English, French and German DBpedia chapters are the RDF data sets to be queried using a natural language interface.

- Participants: Elena Cabrio, Amine Hallili (SynchroNext), Alessio Palmero Aprosio (FBK Italy), Fabien Gandon and Serena Villata
- Contact: Elena Cabrio
- URL: http://www.qakis.org/

ZENITH Project-Team

6. New Software and Platforms

6.1. Hadoop_g5k

Participants: Reza Akbarinia, Miguel Liroz-Gistau, Patrick Valduriez.

URL: https://www.grid5000.fr/mediawiki/index.php/Hadoop_On_Execo

Apache Hadoop provides an open-source framework for reliable, scalable, parallel computing. It can be deployed and used in large-scale platforms such as Grid 5000. However, its configuration and management is very difficult, specially under the dynamic nature of clusters. Therefore, we built Hadoop_g5k (Hadoop easy deployment in clusters), a tool that makes it easier to manage Hadoop clusters and prepare reproducible experiments. Hadoop_g5k offers a set of scripts to be used in command-line interfaces and a Python interface. It is actually used by Grid5000 users, and helps them saving much time when doing their experiments with MapReduce.

6.2. LogMagnet

Participants: Julien Diener, Florent Masseglia.

URL: https://team.inria.fr/zenith/software/LogMagnet

LogMagnet is a software for analyzing streaming data, and in particular log data. Log data usually arrive in the form of lines containing activities of human or machines. In the case of human activities, it may be the behavior on a Web site or the usage of an application. In the case of machines, such log may contain the activities of software and hardware components (say, for each node of a computing cluster, the calls to system functions or some hardware alerts). Analyzing such data is often difficult and crucial in the meanwhile. LogMagnet allows to summarize this data, and to provide a first analysis as a clustering. This summary may also be exploited as easily as the original data.

6.3. MultiSite-Rec

Participants: Mohamed Reda Bouadjenek, Florent Masseglia, Esther Pacitti.

Recommender systems are used as a mean to supply users with content that may be of interest to them. They have become a popular research topic, where many aspects and dimensions have been studied to make them more accurate and effective. In practice, recommender systems suffer from cold-start problems. However, users use many online services, which can provide information about their interest and the content of items (e.g. Google search engine, Facebook, Twitter, etc). These services may be valuable data sources, which supply information to help a recommender system in modeling users and items' preferences, and thus, make the recommender system more precise. Moreover, these data sources are distributed, and geographically distant from each other, which raise many research problems and challenges to design a distributed recommendation algorithm. MultiSite-Rec is a distributed collaborative filtering algorithm, which exploits and combine these multiple and heterogeneous data sources to improve the recommendation quality.

6.4. ThePlantGame: crowdsourced plants identification

Participants: Maximilien Servajean [contact], Alexis Joly, Julien Champ.

URL: http://theplantgame.com/

The Plant Game is a participatory game whose purpose is the production of large masses of taxonomic data to improve our knowledge of biodiversity. The interest of the game is twofold: (i) train and progress in botany while having fun, and (ii) participate to a large citizen sciences project in biodiversity. The game relies on consistent scientific contributions compared to classical crowdsourcing models and algorithms that are not scalable to classification problems with thousands of complex classes such as plant species. The most remarkable one is the active training of the users based on innovative sub-task creation and assignment processes that are adaptive to the increasing skills of the user. The first public version of the game was released in July 2015. Nowadays, about 1000 players are registered and produce on average about 35 new validated plant observations per day. The accuracy of the produced taxonnomic tags is about 94%, which is quite impressive considering the fact that a majority of users are beginners when they start playing.

6.5. Pl@ntNet

Participants: Julien Champ, Hervé Goëau, Alexis Joly.

URL: http://goo.gl/CpSrr3

Pl@ntNet is an image sharing and retrieval application for the identification of plants. It is developed in the context of the Floris'tic project that involves four French research organisations (Inria, Cirad, INRA, IRD) and Tela Botanica social network. The key feature of the iOS and Android front ends is to help identifying plant species from photographs, through a server-side visual search engine based on several results of ZENITH team on content-based information retrieval. Since its first release in March 2013 on the apple store, the application was downloaded by around 1M users in more than 170 countries (between 2,500 and 10,000 active users daily with peaks occurring during the week-ends). The collaborative training set that allows the content-based identification is continuously enriched by the users of the application and the members of Tela Botanica social network. At the time of writing, it includes about 200K images covering more than 5000 French plant species about 4/5 of the whole French flora (this is actually the widest identification tool built anytime).

6.6. Snoop & SnoopIm

Participants: Alexis Joly, Julien Champ, Jean-Christophe Lombardo.

URL: http://otmedia.lirmm.fr/

Snoop is a generalist C++ library dedicated to high-dimensional data management and efficient similarity search. Its main features are dimension reduction, high-dimensional feature vectors hashing, approximate k-nearest neighbors search and Hamming embedding. Snoop is a refactoring of a previous library called PMH developed jointly with the French National Institute of Audiovisual. It is based on the joined research work of Alexis Joly and Olivier Buisson. SnoopIm is a content-based image search engine built on top of Snoop and allowing to retrieve small visual patterns or objects in large collections of pictures. The software is being experimented/used in several contexts including a logo retrieval application set up in collaboration with INA (DigInPix: http://diginpix.ina.fr), a whale's individuals matching application set up in collaboration with CetaMada NGO (IdentyWhale, to be publicly released soon), a hieroglyphs recognition application currently under development in collaboration with the Egyptology department of Montpellier University Paul-Valéry.

6.7. SciFloware

Participants: Dimitri Dupuis, Didier Parigot.

URL: http://www-sop.inria.fr/members/Didier.Parigot/pmwiki/Scifloware

SciFloware is an action of technology development (ADT Inria) with the goal of developing a middleware for the execution of scientific workflows in a distributed and parallel way. It capitalizes on our experience with SON and an innovative algebraic approach to the management of scientific workflows. SciFloware provides a development environment and a runtime environment for scientific workflows, interoperable with existing systems. We validate SciFloware with workflows for analyzing biological data provided by our partners CIRAD, INRA and IRD.

6.8. CloudMdsQL Compiler

Participants: Carlyna Bondiombouy, Boyan Kolev, Oleksandra Levchenko, Patrick Valduriez.

URL: http://cloudmdsql.gforge.inria.fr

The CloudMdsQL (Cloud Multi-datastore Query Language) compiler transforms queries expressed in a common SQL-like query language into an optimized query execution plan to be executed over multiple cloud data stores (SQL, NoSQL, HDFS, etc.) through a query engine. The compiler/optimizer is implemented in C++ and uses the Boost.Spirit framework for parsing context-free grammars. CloudMdsQL is being validated on relational, document and graph data stores in the context of the CoherentPaaS European project.

6.9. Chiaroscuro

Participants: Tristan Allard, Florent Masseglia, Esther Pacitti.

URL: http://people.irisa.fr/Tristan.Allard/chiaroscuro/

Chiaroscuro is a software developped in the context of a research contract with EDF. It aims at clustering time series with privacy preserving guarantees. It is a distributed system, working in a P2P environment. It is used by the team for experiments and by EDF as a proof-of-concept. Chiaroscuro is the first software for that purpose. It is written in Java. The distributed algorithm implemented in Chiaroscuro has been filed by EDF in a patent (with Inria and University of Montpellier)

6.10. FP-Hadoop

Participants: Reza Akbarinia, Miguel Liroz, Patrick Valduriez.

https://gforge.inria.fr/plugins/mediawiki/wiki/fp-hadoop

FP-Hadoop is an extension of Hadoop that efficiently deals with the problem of data skew in MapReduce jobs. In FP-Hadoop, there is a new phase, called intermediate reduce (IR), in which blocks of intermediate values, constructed dynamically, are processed by intermediate reduce workers in parallel, by using a scheduling strategy.