RESEARCH CENTER

FIELD
Digital Health, Biology and Earth

Activity Report 2014

Section Software

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ABS Project-Team

4. New Software and Platforms

4.1. Software

Until October 2014, ABS was distributing isolated programs to solve selected tasks in computational structural biology, including:

- `vorpatch` and `compatch`: Modeling and Comparing Protein Binding Patches,
- `intervor`: Modeling Macro-molecular Interfaces,
- `vorlume`: Computing Molecular Surfaces and Volumes with Certificates,
- `ESBTL`: the Easy Structural Biology Template Library.

This software has been completely repackaged within the *Structural Bioinformatics Library*, a C++ library developed in the scope of an Inria supported *ADT*. The SBL will be released early 2015. Below, we briefly review its spirit and contents.

The Structural Bioinformatics Library (SBL): overview. The Structural Bioinformatics Library (`SBL`) is a generic C++/python library providing combinatorial, geometric and topological tools to solve problems in computational structural biology (CSB). Its design is meant to accommodate both the variety of models coding the physical and chemical properties of macro-molecular systems, and the variety of operations undertaken on these models. The models supported either consist of unions of balls (van der Waals models, solvent accessible models), or representations of conformations based on Cartesian or internal coordinates (distances and angles between the atoms). The operations provided revolve around the problem of understanding the relationship between the structure and the function of macro-molecules and their complexes, and deal with complementary aspects, namely geometric, topological, and combinatorial methods are used to foster our understanding of bio-physical and biological properties. Software development in this context is especially challenging due to the interactions between these complex models and operations.

To accommodate this complexity, software components of the `SBL` are organized into four categories:

- `SBL-APPLICATIONS`**:** end-user 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.

The `SBL` for end-users. End users will find in the `SBL` portable applications running on Linux, and MacOS. These applications split into the following categories:

- **Space Filling Models:** applications dealing with molecular models defined by unions of balls. Current statistics are:
  - # classes: 151
  - # lines of C++/python: 65,000
  - # pages of documentation (user + reference manuals): $\sim$ 1000
- **Conformational Analysis:** applications dealing with molecular flexibility. Current statistics are:
  - # classes: 110

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

  - # lines of C++/python: 49,000
  - # pages of documentation (user + reference manuals): $\sim$ 800
- **Data Analysis:** 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.
- **Large assemblies:** applications dealing with macro-molecular assemblies involving from tens to hundreds of macro-molecules.

The `SBL` for developers. Development with the `SBL` may occur at two levels.

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

- CADS : Combinatorial Algorithms and Data Structures.
- GT : Computational geometry and computational topology.
- CSB : Computational Structural Biology.
- IO : Input / Output.

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

Intermediate level developments should be based upon modules, since 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.

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/).

Releases, distribution, and licence. The `SBL` will be released under a proprietary open source licence. In a nutshell, academic users can use and modify the code at their discretion, for private purposes. But distributing these changes, or doing business with the `SBL` is forbidden. However, novel capabilities matching the design choices of the library will be welcome, and may be integrated.

The source code will be distributed from http://structural-bioinformatics-library.org/, as a tarball and also via a git repository. Bugzilla will be used to handle user's feedback and bug tracking.

The releases are scheduled as follows:

- February 2015: applications from the *space filling model* group, and the accompanying low level classes.
- April 2015: applications from *conformational analysis* group, and the accompanying low level classes.
- July 2015: applications from *large assemblies* group, and the accompanying low level classes.

AMIB Project-Team

4. New Software and Platforms

4.1. Cartaj

Participant: Alain Denise [correspondant].

CARTAJ is a software that automatically predicts the topological family of three-way junctions in RNA molecules, from their secondary structure only : :the sequence and the canonical Watson–Crick pairings. The Cartaj software http://cartaj.lri.fr that implements our method can be used online. It is also meant for being part of RNA modelling softwares and platforms. The methodology and the results of CARTAJ are presented in [59]. More than 300 visits since its release in January 2012.

4.2. DiMoVo

Participant: Julie Bernauer [correspondant].

DIMOVO, *DIscriminate between Multimers and MOnomers by VOronoi tessellation* : Knowing the oligomeric state of a protein is necessary to understand its function. his tool, accessible as a webserver and still used and maintained, provides a reliable discrimination function to obtain the most favorable state of proteins.
Availability : released in 2008.

4.3. VorScore

Participant: Julie Bernauer [correspondant].

VORSCORE, *Voronoi Scoring Function Server* : Scoring is a crucial part of a protein-protein procedure and having a quantitave function to evaluate conformations is mandatory. This server provides access to a geometric knowledge-based evaluation function. It is still maintained and widely used. See Bernauer et al., Bioinformatics, 2007 23(5):555-562 for further details.

4.4. ConQuR-Bio

Participants: Bryan Brancotte, Sarah Cohen-Boulakia [correspondant], Alain Denise.

ConQuR-Bio assists scientists when they query public biological databases. Various reformulations of the user query are generated using medical terminologies (MeSH, OMIM, ...). Such alternative reformulations are then used to rank the query results using a new consensus ranking strategy. The originality of our approach thus lies in using consensus ranking techniques within the context of query reformulation. The ConQuR-Bio system is able to query the Entrez-Gene NCBI database. The benefit of using ConQuR-Bio compared to what is currently provided to users has been demonstrated on a set of biomedical queries.
Availability : http://conqur-bio.lri.fr/

4.5. VARNA (Visualization Application for RNA)

Participants: Yann Ponty [correspondant], Alain Denise.

A lightweight Java Applet dedicated to the quick drawing of an RNA secondary structure. VARNA is open-source and distributed under the terms of the GNU GPL license. Automatically scales up and down to make the most out of a limited space. Can draw multiple structures simultaneously. Accepts a wide range of documented and illustrated options, and offers editing interactions. Exports the final diagrams in various file formats (svg,eps,jpeg,png,xfig) [52]...
VARNA currently ships in its 3.9 version, and consists in $\sim$50 000 lines of code in $\sim$250 classes.
Availability : Distributed at http://varna.lri.fr since 2009 under the GPL v3 license.

Impact: Downloaded ∼15k times and cited by ∼250 research manuscripts (source: Google Scholar).

4.6. GenRGenS (GENeration of Random GENomic Sequences)

Participants: Yann Ponty [correspondant], Alain Denise.

A software dedicated to the random generation of sequences. Supports different lasses of models, including weighted context-free grammars, Markov models, PROSITE patterns... [69] GENRGENS currently ships in its 2.0 version, and consists in ∼25 000 lines of code in ∼120 Java classes.
Availability : Distributed at http://www.lri.fr/~genrgens/ since 2006 under the terms of the GPL v3 license.
Impact: Downloaded ∼5k times and cited by ∼60 times (source: Google Scholar).

4.7. GeneValorization

Participants: Bryan Brancotte, Sarah Cohen-Boulakia [correspondant].

High-throughput technologies provide fundamental informations concerning thousands of genes. Most of the current biological research laboratories daily use one or more of these technologies and identify lists of genes. Understanding the results obtained includes accessing to the latest publications concerning individual or multiple genes. Faced to the exponential growth of publications avaliable, this task is becoming particularly difficult to achieve.
Here, we introduce a web-based Java application tool named GeneValorization which aims at making the most of the text-mining effort done downstream to all high throughput technology assays. Regular users come from the Curie Institute, but also the EBI.
Impact : 925 distinct international users have used GeneValorization and about a hundred use it on a regular basis. The tool is on average used once to twice every day.
Availability : it is available at http://bioguide-project.net/gv with Inter Deposit Digital Number (*depot APP*, June 2013).

4.8. HSIM

Participant: Patrick Amar [correspondant].

HSIM (Hyperstructure Simulator) is a simulation tool for studying the dynamics of biochemical processes in a virtual bacteria. The model is given using a language based on probabilistic rewriting rules that mimics the reactions between biochemical species. HSIM is a stochastic automaton that implements an entity-centered model of objects. This kind of modelling approach is an attractive alternative to differential equations for studying the diffusion and interaction of the many different enzymes and metabolites in cells which may be present in either small or large numbers.

The new version of HSIM includes a Stochastic Simulation Algorithm *a la* Gillespie that can be used with the same model in a standalone way or in a mixed way with the entity-centered algorithm. This new version offers also the possibility to export the model in SciLab for a ODE integration. Last, HSIM can export the differential equations system, equivalent to the model, to LaTeX for pretty-printing.

This software is freely available at http://www.lri.fr/~pa/Hsim; A compiled version is available for the Windows, Linux and MacOSX operating systems.

4.9. Pint

Participant: Loïc Paulevé [correspondant].

PINT provides several command-line tools to model, simulate, and analyse the dynamics of automata networks. Its main application domain is systems biology for modelling and analysis of very large interaction networks. Besides a textual language for specifying networks and standard stochastic simulation algorithms, PINT implements static analysis for analysing and controlling the transient reachability. In particular, PINT provides the computation of cut sets for transient reachability, that gives sets of key automata states, whose mutation would prevent the concerned reachability to occur.

PINT has been applied to extremely large biological networks, from 100 to 10,000 interacting components, demonstrating its scalability and potential to handle full databases of interactions.

PINT is distributed under the CeCiLL licence, and is available at http://loicpauleve.name/pint.

BAMBOO Project-Team

5. New Software and Platforms

5.1. AcypiCyc

Participants: Hubert Charles [EPI], Patrice Baa Puyoule [Contact, Patrice.Baa-Puyoulet@lyon.inra.fr], Stefano Colella [Contact, stefano.colella@lyon.inra.fr], Ludovic Cottret, Marie-France Sagot [EPI], Augusto Vellozo [Contact, augusto@cycadsys.org], Amélie Véron.

Database of the metabolic network of *Acyrthosiphon pisum*.
http://acypicyc.cycadsys.org/

5.2. AlViE

Participants: Pierluigi Crescenzi [Contact, pierluigi.crescenzi@unifi.it, ext. member EPI], Giorgio Gambosi, Roberto Grossi, Carlo Nocentini, Tommaso Papini, Walter Verdese.

ALVIE is a post-mortem algorithm visualization Java environment, which is based on the interesting event paradigm. The current distribution of ALVIE includes more than forty visualizations. Almost all visualizations include the representation of the corresponding algorithm C-like pseudo-code. The ALVIE distribution allows a programmer to develop new algorithms with their corresponding visualization: the included Java class library, indeed, makes the creation of a visualization quite an easy task (once the interesting events have been identified).
http://piluc.dsi.unifi.it/alvie/

5.3. Cassis

Participants: Christian Baudet [EPI, Contact, christian.baudet@inria.fr], Christian Gautier [EPI], Claire Lemaitre [Contact, claire.lemaitre@inria.fr], Marie-France Sagot [EPI], Eric Tannier.

Algorithm for precisely detecting genomic rearrangement breakpoints.
http://pbil.univ-lyon1.fr/software/Cassis/

5.4. Coala

Participants: Christian Baudet [EPI, Contact, christian.baudet@inria.fr], Pielrluigi Crescenzi, Bea Donati [EPI, Contact, bea.donati@inria.fr], Christian Gautier [EPI], Catherine Matias, Blerina Sinaimeri [EPI, Contact, blerina.sinaimeri@inria.fr], Marie-France Sagot [EPI, Contact, marie-france.sagot@inria.fr].

COALA stands for "CO-evolution Assessment by a Likelihood-free Approach". It is thus a likelihood-free method for the co-phylogeny reconstruction problem which is based on an Approximative Bayesian Computation (ABC).
http://coala.gforge.inria.fr/

5.5. C3Part & Isofun

Participants: Frédéric Boyer, Yves-Pol Deniélou, Anne Morgat [EPI, ext. member], Marie-France Sagot [EPI], Alain Viari [EPI, Contact, alain.viari@inria.fr].

The C3Part / Isofun package implements a generic approach to the local alignment of two or more graphs representing biological data, such as genomes, metabolic pathways or protein-protein interactions, in order to infer a functional coupling between them. It is based on the notion of "common connected components" between graphs.http://www.inrialpes.fr/helix/people/viari/lxgraph/index.html

5.6. CycADS

Participants: Hubert Charles [EPI], Patrice Baa Puyoule [Contact, Patrice.Baa-Puyoulet@lyon.inra.fr], Stefano Colella [Contact, stefano.colella@lyon.inra.fr], Ludovic Cottret, Marie-France Sagot [EPI], Augusto Vellozo [Contact, augusto@cycadsys.org].

Cyc annotation database system.
http://www.cycadsys.org/

5.7. Eucalypt

Participants: Christian Baudet [EPI, Contact, christian.baudet@inria.fr], Pielrluigi Crescenzi, Bea Donati [Contact, bea.donati@inria.fr], Blerina Sinaimeri, Marie-France Sagot [EPI].

Algorithm for enumerating all optimal (possibly time-unfeasible) mappings of a parasite tree unto a host tree.
http://eucalypt.gforge.inria.fr/

5.8. Gobbolino & Touché

Participants: Vicente Acuña [EPI], Etienne Birmelé, Ludovic Cottret, Pierluigi Crescenzi, Fabien Jourdan, Vincent Lacroix, Alberto Marchetti-Spaccamela [EPI, ext. member], Andrea Marino, Paulo Vieira Milreu [EPI, Contact, pvmilreu@gmail.com], Marie-France Sagot [EPI, Contact, marie-france.sagot@inria.fr], Leen Stougie [EPI, ext. member].

Designed to solve the metabolic stories problem, which consists in finding all maximal directed acyclic subgraphs of a directed graph G whose sources and targets belong to a subset of the nodes of G, called the black nodes. Biologically, stories correspond to alternative metabolic pathways that may explain some stress that affected the metabolites corresponding to the black nodes by changing their concentration (measured by metabolomics experiments).
http://gforge.inria.fr/projects/gobbolino

5.9. KisSNP

Participants: Vincent Lacroix [EPI], Pierre Peterlongo [Contact, pierre.peterlongo@inria.fr], Nadia Pisanti, Marie-France Sagot [EPI], Nicolas Schnel.

Algorithm for identifying SNPs without a reference genome by comparing raw reads. KISSNP has now given birth to DISCOSNP in a work involving V. Lacroix from BAMBOO and the GenScale Inria Team at Rennes (contact: pierre.peterlongo@inria.fr).
http://alcovna.genouest.org/kissnp/, http://colibread.inria.fr/software/discosnp/

5.10. KisSplice & KisSplice2igv7

Participants: Lilia Brinza [EPI], Alice Julien-Laferrière [EPI], Janice Kielbassa, Vincent Lacroix [Contact, EPI], Camille Marchet [EPI], Vincent Miele, Gustavo Sacomoto [EPI], Marie-France Sagot [EPI].

Enables to analyse RNA-seq data with or without a reference genome. It is an exact local transcriptome assembler, which can identify SNPs, indels and alternative splicing events. It can deal with an arbitrary number of biological conditions, and will quantify each variant in each condition. KISSPLICE2IGV is a pipeline that combines the outputs of KISSPLICE to a reference transcriptome (obtained with a full-length transcriptome assembler or a reference database). It provides a visualisation of the events found by KISSPLICE in a longer context using a genome browser (IGV).
http://kissplice.prabi.fr/

5.11. kissDE

Participants: Lilia Brinza [EPI], Janice Kielbassa, Vincent Lacroix [Contact, EPI], Camille Marchet [EPI], Vincent Miele.

KISSDE is an R Package enabling to test if a variant (genomic variant or splice variant) is enriched in a condition. It takes as input a table of read counts obtained from NGS data pre-processing and gives as output a list of condition specific variants. http://kissplice.prabi.fr/tools/kissDE/

5.12. LASAGNE

Participants: Pierluigi Crescenzi [Contact, pierluigi.crescenzi@unifi.it, ext. member EPI], Roberto Grossi, Michel Habib, Claudio Imbrenda, Leonardo Lanzi, Andrea Marino.

LASAGNE is a Java application which allows the user to compute distance measures on graphs by making a clever use either of the breadth-first search or of the Dijkstra algorithm. In particular, the current version of LASAGNE can compute the exact value of the diameter of a graph: the graph can be directed or undirected and it can be weighted or unweighted. Moreover, LASAGNE can compute an approximation of the distance distribution of an undirected unweighted graph. These two features are integrated within a graphical user interface along with other features, such as computing the maximum (strongly) connected component of a graph.
http://piluc.dsi.unifi.it/lasagne/?page_id=142

5.13. MetExplore

Participants: Michael Barrett, Hubert Charles [EPI], Ludovic Cottret [Contact, Ludovic.Cottret@toulouse.inra.fr], Fabien Jourdan, Marie-France Sagot [EPI], Florence Vinson, David Wildridge.

Web server to link metabolomic experiments and genome-scale metabolic networks.
http://metexplore.toulouse.inra.fr/metexplore/

5.14. Migal

Participants: Julien Allali [Contact, julien.allali@labri.fr], Marie-France Sagot [EPI, Contact, marie-france.sagot@inria.fr].

RNA, tree comparison
Algorithm for comparing RNA structures.
http://www-igm.univ-mlv.fr/~allali/logiciels/index.en.php

5.15. Mirinho

Participants: Cyril Fournier [EPI], Susan Higashi [EPI, Contact, susan.higashi@inria.fr], Christian Gautier [EPI], Christine Gaspin, Marie-France Sagot [EPI].

Predicts, at a genome-wide scale, microRNA candidates.
http://mirinho.gforge.inria.fr/

5.16. MotusWEB

Participants: Ludovic Cottret, Fabien Jourdan, Vincent Lacroix [EPI, Contact, vincent.lacroix@univ-lyon1.fr], Odile Rogier, Marie-France Sagot [EPI].

Algorithm for searching and inferring coloured motifs in metabolic networks (web-based version - offers different functionalities from the downloadable version).
http://pbil.univ-lyon1.fr/software/motus_web/

5.17. Motus

Participants: Ludovic Cottret, Fabien Jourdan, Vincent Lacroix [EPI, Contact, vincent.lacroix@univ-lyon1.fr], Odile Rogier, Marie-France Sagot [EPI].

Algorithm for searching and inferring coloured motifs in undirected graphs (downloadable version - offers different functionalities from the web-based version).
http://pbil.univ-lyon1.fr/software/motus/

5.18. PhEVER

Participants: Christian Gautier [EPI], Vincent Lotteau, Leonor Palmeira [Contact, mlpalmeira@ulg.ac.be], Chantal Rabourdin-Combe, Simon Penel.

Database of homologous gene families built from the complete genomes of all available viruses, prokaryotes and eukaryotes and aimed at the detection of virus/virus and virus/host lateral gene transfers.
http://pbil.univ-lyon1.fr/databases/phever/

5.19. PepLine

Participants: Jérôme Garin, Alain Viari [EPI, Contact, alain.viari@inria.fr].

Pipeline for the high-throughput analysis of proteomic data.

5.20. Pitufo and family

Participants: Vicente Acuña [EPI], Ludovic Cottret [Contact, Ludovic.Cottret@toulouse.inra.fr], Alberto Marchetti-Spaccamela [EPI, ext. member], Paulo Vieira Milreu [EPI, Contact, pvmilreu@gmail.com], Marie-France Sagot [EPI], Leen Stougie [EPI, ext. member], Fabio Viduani-Martinez.

Algorithms to enumerate all minimal sets of precursors of target compounds in a metabolic network.
http://sites.google.com/site/pitufosoftware/

5.21. RepSeek

Participants: Guillaume Achaz [Contact, achaz@abi.snv.jussieu.fr], Eric Coissac, Alain Viari [EPI].

Finding approximate repeats in large DNA sequences.
http://wwwabi.snv.jussieu.fr/public/RepSeek/

5.22. Smile

Participants: Laurent Marsan, Marie-France Sagot [EPI, Contact, marie-france.sagot@inria.fr].

Motif inference algorithm taking as input a set of biological sequences.

5.23. UniPathway

Participants: Eric Coissac, Anne Morgat [EPI, Contact, anne.morgat@inria.fr], Alain Viari [EPI].

Database of manually curated pathways developed with the Swiss-Prot group.
http://www.unipathway.org

BEAGLE Project-Team

4. New Software and Platforms

4.1. Aevol (artificial evolution)

Participants: Guillaume Beslon, Jonathan Rouzaud-Cornabas, Carole Knibbe, Priscila Biller, Bérénice Batut.

- Contact: Carole Knibbe (carole.knibbe@inria.fr).
- Aevol is a simulation software dedicated to the study of genome evolution. It allows to carry out *in silico* experimental evolution. Populations of digital organisms reproduce and mutate randomly, with both small mutations and large chromosomic rearrangements, in a steady or varying environment. A curve-fitting task is used to determine the fitness of the organisms and thus their rate of reproduction. The number of genes, their order, their sequences, their intergenic distances are all free to evolve. Thanks to a two-year grant from Inria's Technological Development Department (ADT « aevol »), the development of an improved and parallel version of the software has started in October.
- URL: http://www.aevol.fr

4.2. EvoEvo modelization tool

Participants: Charles Rocabert, Guillaume Beslon, Carole Knibbe.

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

4.3. FluoBacTracker

Participants: Hugues Berry, David P Parsons, Magali Vangkeosay.

- Contact: Hugues Berry (hugues.berry@inria.fr)
- FluoBacTracker is a software for automated quantification of bacterial cells in microscopy movies, developed in collaboration with INSERM U1001 and Paris 5 MAP (Applied Mathematics) Labs. The development (started october 2012) has been supported by a 2-year grant (ADT) funded by Inria's Technological Development Department (Sept 2012- July 2014, project name: "MultiPop"). We hope this software will be useful to all the experimental biology labs that tries to derive single-cell data from bacteria growth microscopy movies. Co-developers include Magali Vangkeosay (BEAGLE), David P Parsons (SED, Inria Grenoble) and Xiaohu Song (INSERM U1001).

4.4. Ancestral Genome Reconstructions

Participant: Eric Tannier.

- Contact: Eric Tannier (eric.tannier@inria.fr).
- We participated in the development of a series of softwares for genome organization analysis:
  - ANGES, for ANcestral GEnomeS maps, is a toolkit for ordering ancestral genomic markers in chromosomes. An application note has been published in *Bioinformatics* in 2012 to advertise its first release. It is hosted at SFU in Vancouver, URL: http://paleogenomics.irmacs.sfu.ca/ANGES/, under a GNU license, 2012.
  - DeCo and DeCoLT, for Detection of Co-evolution (with Lateral gene Transfer), reconstruct neighborhood relationships between genes of ancient genomes, in the presence of gene duplications, transfer and losses. Both are hosted at the PRABI, the bioinformatics platform in Lyon, under a Cecill license, 2012 and 2013. URL: http://pbil.univ-lyon1.fr/software/DeCo/ and http://pbil.univ-lyon1.fr/software/DeCoLT/.
  - DCJ2HP provides bayesian samples of rearrangements scenarios between two genomes. It is hosted at the Renyi Institute in Budapest. URL: http://www.renyi.hu/~miklosi/DCJ2HP/

4.5. DMT4SP mining tool

Participant: Christophe Rigotti.

- Contact: Christophe Rigotti (christophe.rigotti@insa-lyon.fr).
- DMT4SP (Data-Mining Tool For Sequential Patterns) – DMT4SP is command-line tool to extract episodes and episode rules over a single sequence or several sequences of events. It allows to specify constraints on the episodes or on the rules. Three kinds of patterns can be extracted: (1) serial episodes, (2) serial episode rules having a single event type in the consequent, and (3) quantitative episodes (aka grouping of "homogeneous" occurrences of serial episodes with respect to the time gap between events). DMT4SP is a prototype that is freely distributed (http://liris.cnrs.fr/~crigotti/dmt4sp.html).

BIGS Project-Team

4. New Software and Platforms

4.1. Online data analysis

Participants: J.-M. Monnez

An R package performing most of the methods of factorial analysis in an online way has been developed by R. Bar and J.-M. Monnez. Starting from a simulated data flow, the main goal of the program is to perform online factorial analyses (Principal Component Analyses, Canonical Correlation Analysis, Canonical Discriminant Analysis, Correspondence Analysis). Data are supposed to be independent and identically distributed observations of a random vector (whose distribution is a priori unknown). Defining stochastic approximation processes, the procedure is adaptative in the sense that the results of the analyses are updated recursively each time that a new piece of data is taken into account.

From a theoretical point of view, the i.i.d case has been recently extended to the case of an expectation and/or covariance matrix of the random vector varying with time. We plan to include these improvements into our software.

4.2. Socio-economic index

Participants: J.-M. Monnez

A R package called SesIndexCreatoR has been written by B. Lalloué and J.-M. Monnez in order to implement our socio-economic index for health inequalities. The version 1.0 of this package is currently freely available on the website of the Equit'Area project: http://www.equitarea.org/documents/packages_1.0-0/. It contains the functions needed to run the procedure (either integrally or partially) and obtain the corresponding SES index. The user may also create categories of this index with different methods (hierarchical clustering with or without k-nearest neighbors, quantiles, or intervals) and generate automatic reports of the results. Visualization and plotting functions are provided in the package.

4.3. Angio-Analytics

Participants: T. Bastogne

A software *Angio-Analytics* has been developed by J.-B. Tylcz, E. Djermoune and T. Bastogne. This tool allows the pharmacodynamic characterization of anti-vascular effects in anti-cancer treatments. It uses time series of *in vivo* images provided by intra-vital microscopy. Such *in vivo* images are obtained owing to skinfold chambers placed on mice skin, as illustrated in Fig. 1 . The automatized analysis is split up into two steps that were completely performed separately and manually before. The first steps corresponds to image processing to identify characteristics of the vascular network, as illustrated in Fig. 2 . The last step is the system identification of the pharmacodynamic response and the statistical analysis of the model parameters as shown in Fig. 3 and Fig. 4 . An article has been submitted to a journal (Biomedical Signal Processing and Control) and is currently in revision process. Moreover, the current version of the software has been registered to the *Agence de Protection des Programmes*.

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

Participants: T. Bastogne

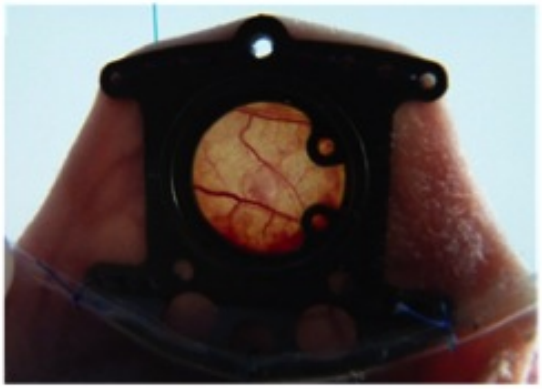


Figure 1. Example of a skinfold chamber placed on a mouse skin

More than eight million people die from cancer worldwide each year. Current treatment such as chemotherapy and radiotherapy are still limited in terms of benefit/risk ratio. Nevertheless, engineered nanoparticles have opened new interesting perspectives in cancerology, as emphasized by Brigger et al. since 2002. One of these promising solutions is based on the development of nanoparticles able to enhance the cytotoxic effect of radiotherapy. Nevertheless, the preclinical development in nano-medicine is slow, risky and expensive. Recently, Etheridge et al. (2013) highlighted the fact that many of the revolutionary nano-medicine technologies anticipated in the literature may be 20 or more years from clinical use. To speed up the preclinical development of medical engineered nanomaterials, we have designed an integrated computing platform dedicated to the virtual screening of nanostructured materials activated by X-ray making it possible to select nano-objects presenting interesting medical properties faster. That innovation gathers stochastic simulations and statistical modeling to estimate the impact of each design parameter describing the nano-object. That allows us to optimize composition factors in order to suggest one or few promising architectures regarding the medical purpose. The main advantage of this *in silico* design approach is to virtually screen a lot of possible formulations and to rapidly select the most promising ones. The platform can currently handle the accelerated design of radiation therapy enhancing nanoparticles and medical imaging nano-sized contrast agents as well as the comparison between nano-objects and the optimization of existing materials. Other applications related to nano-medicines will be subject to further developments (e.g., photodynamic therapy). That contribution has received the best innovation award from the Institut Mines-Telecom in 2014 and application results will be presented at the 36th PAMM-EORTC Winter Meeting in January 2015.

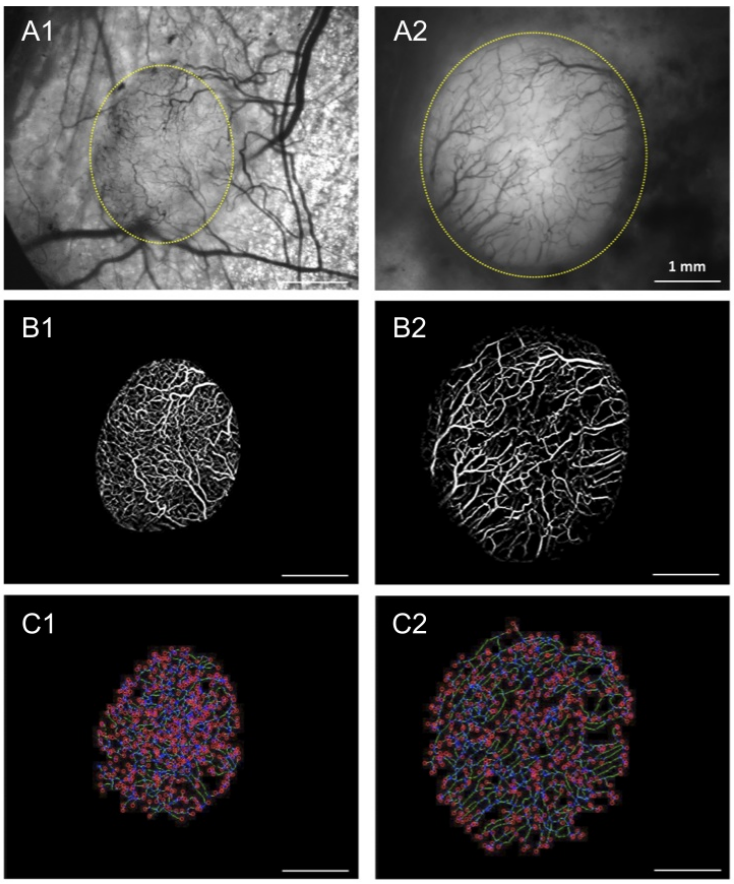


Figure 2. Example of segmentation process on a control (left) and treated tumor (right) at day -7: manual segmentation (ROI) of cancerous tissues is done in yellow on step A, vessel segmentation is performed on step B (vessels are in white), step C presents the quantification (blue and red circles) on the skeletonized vascular network (green lines)

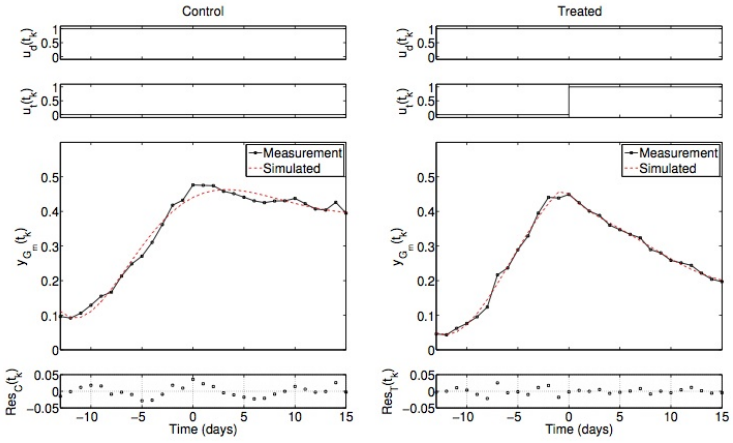


Figure 3. Measurements and estimated outputs for control and treated batches. Input signals and residuals are respectively plotted above and below

Batch	Param.	Estimate	c_v (%)
Control	b_{d_0}	0.023	12
	f_{d_1}	0.23	13
	f_{d_2}	0.057	10
	b_{t_0}	0	-
	b_{t_1}	0	-
	f_{t_1}	0	-
Treated	b_{d_0}	0.021	18
	f_{d_1}	0.16	35
	f_{d_2}	0.051	19
	b_{t_0}	-0.032	45
	b_{t_1}	-0.068	22
	f_{t_1}	0.35	50

Figure 4. Parameter estimates and coefficients of variation c_v for control and treated batches

BONSAI Project-Team

5. New Software and Platforms

5.1. SortMeRNA – Metatranscriptome classification

Software web site: http://bioinfo.lille.inria.fr/RNA/sortmerna

Licence: GPL

Objective: *SortMeRNA* is a tool designed to rapidly filter ribosomal RNA fragments from metatranscriptomic data produced by next-generation sequencers. It is available for download from our website, or through the open web-based platform Galaxy. The development version is also available on GitHub. *SortMeRNA* was first released in October 2012. It is now used in production by Genoscope (French National Center for Sequencing) to process all metatranscriptomic data of the Tara Ocean Expedition, and has been integrated in several other computational pipelines (Qiime developed at University of Colorado at Boulder, MetaMetadb developed at University of Tokyo, Leimena pipeline developed at Wageningen University,...).

SortMeRNA is still under development through a partnership with the Knight lab (University of Colorado at Boulder). Version 2.0 has been released in November 2014, and has extended functionalities. It can now perform sequence alignments to any ribosomal RNA database, which allows the user to study the taxonomic content of a microbial sample. This new version has been presented at the international workshops [12], [11].

5.2. Vidjil – Quantifying lymphocyte rearrangements in high-throughput sequencing data

Software web site: http://bioinfo.lille.inria.fr/vidjil/

Objective: **Vidjil** is a platform for high-throughput V(D)J recombinations analysis. containing three components. The Vidjil *algorithm* process high-througput sequencing data to extract V(D)J junctions and gather them into clones. Vidjil starts from a set of reads and detects "windows" overlapping the actual CDR3. This is based on an fast and reliable seed-based heuristic and allows to output all sequenced clones. The analysis is extremely fast because, in the first phase, no alignment is performed with database germline sequences [5]. The Vidjil dynamic *browser* is made for the visualization and analysis of clones and their tracking along the time in a "minimal residual disease" setup or in a immunological study. The browser visualize data processed by the Vidjil algorithm or by other V(D)J analysis pipeline and enables to explore further cluterings. Finally, a *patient database* with a server links the browser and the algorithmic part. The goal is that the clinicians will be able to upload, manage and process their runs on a server hosted in their hospital.

In 2014, the development of Vidjil was supported by the SIRIC OncoLille (Marc Duez). We developed the new patient database and added features both on the browser and on the algorithm (multi-system analysis). Several hospital labs in France and in Europe are testing Vidjil. The Lille hospital plans to use Vidjil in 2015 in a pre-production pipeline.

5.3. Norine – A resource for nonribosomal peptides

Software web site: http://bioinfo.lille.inria.fr/norine/

Objective: **Norine** is a public computational resource that contains a database of NRPs with a web interface and dedicated tools, such as a 2D graph viewer and editor for peptides or comparison of NRPs. Norine was created and is maintained by members of BONSAI team, in tight collaboration with members of the ProBioGEM lab, a microbial laboratory of Lille1 University. Since its creation in 2006, Norine has gained an international recognition as the unique database dedicated to non-ribosomal peptides because of its high quality and manually curated annotations, and has been selected by wwPDB as a reference database. It is queried from all around the world by biologists or biochemists. It receives more than 3000 queries per month.

To enhance the Norine resource, we have recently developed a new module, named MyNorine, which is an open interface for biologists and biochemists dedicated to the submission of new non-ribosomal peptides in Norine database. Up to now, peptides were manually inputted and verified before being added in the database, which could potentially lead to human errors. The goal of MyNorine is to help users during the submission of peptides and monomers, by guiding them during all steps. For that, users, all over the world, can create an account on MyNorine. Thus, they contribute to the Norine resource and become curators (author of a peptide entry is mentioned in the corresponding page of Norine). Submitted peptides/monomers are validated, through a workflow process, by Norine team members, to ensure correct and consistent entries.

5.4. miRkwood –microRNAs in plant genomes

Software web site: http://bioinfo.lille.inria.fr/mirkwood/

Objective: **miRkwood** is a web server for the identification of hairpin precursors of both conserved and non-conserved miRNAs in plant genomes. It is able to face the diversity of plant pre-miRNAs and is optimised to take advantage of their distinctive properties: Sequence length, secondary structure, free energy, miRNA conservation, stability of the miRNA/miRNA* duplex, ... Moreover, it offers an intuitive and comprehensive user interface to navigate in the data, as well as many export options to allow the user to conduct further analyses on a local computer. Ongoing work is concerned with integrating small RNA-seq data.

5.5. ProCARs

Software web site: http://bioinfo.lille.inria.fr/procars

Objective: **ProCARs** is a program used to reconstruct ancestral gene orders as CARs (Contiguous Ancestral Regions) with a progressive homology-based method. The method runs from a phylogeny tree, without branch lengths needed, with a marked ancestor and a block file. The method output CARs as sets of ordered contiguous blocks in the targeted ancestor. ProCARs has been developped with Python 2.7.5.

DYLISS Project-Team

5. New Software and Platforms

5.1. Platforms and toolboxes

Among others, a goal of the team is to facilitate interplays between tools for biological data analysis and integration. Our tools are based on formal systems. They aim at guiding the user to progressively reduce the space of models (families of sequences of genes or proteins, families of keys actors involved in a system response, dynamical models) which are compatible with both knowledge and experimental observations.

Most of our tools are available both as stand-alone software and through portals such as Mobyle or Galaxy interfaces. Tools are developed in collaboration with the GenOuest resource and data center hosted in the IRISA laboratory, including their computer facilities [more info].

We present here three toolboxes which each contain complementary tools with respect to their targeted sub-domain of bioinformatics.

5.1.1. Integrative Biology: (constraint-based) toolbox for network filtering

The goal is to offer a toolbox for the reconstruction of networks from genome, literature and large-scale observation data (expression data, metabolomics...) in order to elucidate the main regulators of an observed phenotype. Most of the optimization issues are addressed with Answer Set Programming.

MeMap and MeMerge. We develop a workflow for the **Au**tomatic **Re**construction of **Me**tabolic networks (AuReMe). In this workflow, we use heterogeneous sources of data with identifiers from different namespaces. MeMap (**Me**tabolic network **Map**ping) consists in mapping identifiers from different namespaces to a unified namespace. Then, MeMerge (**Me**tabolic network **Merge**) merges two metabolic networks previously mapped on the same namespace. [web server].

meneco [*input*: draft metabolic network & metabolic profiles. *output*: metabolic network]. It is a qualitative approach to elaborate the biosynthetic capacities of metabolic networks. In fact, large-scale metabolic networks as well as measured datasets suffer from substantial incompleteness. Moreover, traditional formal approaches to biosynthesis require kinetic information, which is rarely available. Our approach builds upon formal systems for analyzing large-scale metabolic networks. Mapping its principles into Answer Set Programming allows us to address various biologically relevant problems [57] [50] [python package][web server].

shogen [*input*: genome & metabolic network. *output* : functional regulatory modules]. This software is able to identify genome portions which contain a large density of genes coding for enzymes that regulate successive reactions of metabolic pathways [48] [python package].

lombarde [*input*: genome, modules & several gene-expression datasets. *output*: oriented regulation network]. This tool is useful to enhance key causalities within a regulatory transcriptional network when it is challenged by several environmental perturbations [26] [web server].

bioquali [*input*: signed regulation network & one gene-expression dataset. *output*: consistency-checking and gene-expression prediction]. It is a plugin of the Cytoscape environment. BioQuali analyses regulatory networks and expression datasets by checking a global consistency between the regulatory model and the expression data. It diagnoses a regulatory network searching for the regulations that are not consistent with the expression data, and it outputs a set of genes which predicted expression is decided in order to explain the expression inputed data. It also provides the visualization of this analysis with a friendly environment to encourage users of different disciplines to analyze their regulatory networks [5] [web server][cytoscape plugin] .

ingranalyze [*input*: signed regulation network & one gene-expression dataset. *output*: network repair gene-expression prediction] This tool is an extension to the bioquali tool. It proposes a range of different operations for altering experimental data and/or a biological network in order to re-establish their mutual consistency, an indispensable prerequisite for automated prediction. For accomplishing repair and prediction, we take advantage of the distinguished modeling and reasoning capacities of Answer Set Programming [4] [Python package][web server].

Unifier. [*input*: sbml file with Palsson's metabolites identifiers *output*: sbml file with standard identifiers for metabolites]. This software is a Decision Support Tool to help biologists to normalize a file, containing Palsson's identifiers to refer to reactions and metabolites, using well known identifiers. Submit a list of Palsson identifiers to retrieve the corresponding database entries. Typically it maps with Metacyc identifiers but it would be used with Kegg or other databases later. A Unifier web service will be soon available.

NetWikiMaker. This tool generates (half) automatically a wiki on our reconstruction workflow. It contains information and data about the network reconstruction process such as different versions of draft metabolic networks files, parameters of tools, log files. It also displays the reactions, genes and metabolites that the workflow has found to be involved in the metabolic network, and provides a powerful search tool.

5.1.2. Dynamics and invariant-based prediction

We develop tools predicting some characteristics of a biological system behavior from incomplete sets of parameters or observations.

cadbiom. Based on Guarded transition semantic, this software provides a formal framework to help the modeling of biological systems such as cell signaling network. It allows investigating synchronization events in biological networks. [software][web server].

caspo: Cell ASP Optimizer This soft provides an easy to use software for learning Boolean logic models describing the immediate-early response of protein signaling networks. Given a network describing causal interactions, and a phospho-proteomics dataset, caspo is able to searches for optimal Boolean logic models explaining the dataset. Optimality includes both the size of the boolean network and the distance of predictions to real-data observations. It is useful to boolean networks inference, cancer research, drug discovery, and experimental design. It is used in the CellNOpt environment [0]. [python package][web server].

nutritionAnalyzer. This tool is dedicated to the computation of allocation for an extremal flux distribution. It allows quantifying the precursor composition of each system output (AIO) and to discuss the biological relevance of a set of flux in a given metabolic network by computing the extremal values of AIO coefficients. This approach enables to discriminate diets without making any assumption on the internal behaviour of the system [14][webserver][software and doc].

POGG. The POGG software allows scoring the importance and sensibility of regulatory interactions with a biological system with respect to the observation of a time-series quantitative phenotype. This is done by solving nonlinear problems to infer and explore the family of weighted Markov chains having a relevant asymptotic behavior at the population scale. Its possible application fields are systems biology, sensitive interactions, maximal entropy models, natural language processing. It results from our collaboration with the LINA-Nantes [1][matlab package].

5.1.3. Sequence annotation

We develop tools for discovery and search of complex pattern signatures within biological sequences, with a focus on protein sequences.

Logol Logol is a swiss-army-knife for pattern matching on DNA/RNA/Protein sequences, using a high-level grammar to permit a large expressivity. Allowed patterns can consist in a combination of motifs, structures (stem-loops, repeats), indels etc. It allows pseudo-knot identification, context sensitive grammatical formalism and full genome analysis. Possible fields of application are the detection of mutated binding sites or stem-loop identification (e.g. in CRISPR [0] [9]) [software]

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

Protomata learner This tool is a grammatical inference framework suitable for learning the specific signature of a functional protein family from unaligned sequences by partial and local multiple alignment and automata modeling. It performs a syntactic characterization of proteins by identification of conservation blocks on sequence subsets and modelling of their succession. Possible fields of application are new members discovery or study (for instance, for site-directed mutagenesis) of, possibly non-homologous, functional families and subfamilies such as enzymatic, signaling or transporting proteins [49][3] [web server]

5.1.4. Integration of toolboxes and platforms in webservices

Most of our software were designed as "bricks" that can combined through workflow application such as Mobyle. It worths considering them into larger dedicated environments to benefit from the expertise of other research groups.

Web servers In collaboration with the GenOuest ressource center, most our tools are made available through several web portals.

- The **mobyle@GenOuest portal** is the generic web server of our ressource center. It hosts the ingranalysis, meneco, caspo, lombarde and shogun tools [website].
- The **Mobyle@Biotempo server** is a mobyle portal for system biology with formal approaches. It hosts the memap, memerge, meneco, ingranalysis, cadbiom and pogg tools [website].
- The **GenOuest galaxy portal** now provides access to most tools for integrative biology and sequence annotation (access on demand).

Dr Motif This resource aims at the integration of different software commonly used in pattern discovery and matching. This resource also integrates Dyliss pattern search and discovery software [website].

ASP4biology and BioASP It is a meta-package to create a powerful environment of biological data integration and analysis in system biology, based on knowledge representation and combinatorial optimization technologies (ASP). It provides a collection of python applications which encapsulates ASP tools and several encodings making them easy to use by non-expert users out-of-the-box. [Python package][website].

ASP encodings repository This suite comprises projects related to applications of Answer Set Programming using Potassco systems (the Potsdam Answer Set Solving Collection, bundles tools for Answer Set Programming developed at the University of Potsdam). These are usually a set of encodings possibly including auxiliary software and scripts [respository].

5.2. New tools for integrative biology

Participants: Anne Siegel [contact], Jeanne Cambefort [contact], Guillaume Collet, Damien Eveillard, Sylvain Prigent, Marie Chevallier.

The tools MeMap and MeMerge were complemented with new tools in order to analyze reference networks from litterature database and to vizualize the product of reconstructed metabolic networks.

Unifier. [*input*: SBML file with Palsson's metabolites identifiers *output*: sbml file with standard identifiers for metabolites]. This software is a Decision Support Tool to help biologists to normalize a file, containing Palsson's identifiers to refer to reactions and metabolites, using well known identifiers. Submit a list of Palsson identifiers to retrieve the corresponding database entries. Typically it maps with Metacyc identifiers but it would be used with Kegg or other databases later. A Unifier web service will be soon available.

NetWikiMaker. This tool generates (half) automatically a wiki on our reconstruction workflow. It contains information and data about the network reconstruction process such as different versions of draft metabolic networks files, parameters of tools, log files. It also displays the reactions, genes and metabolites that the workflow has found to be involved in the metabolic network, and provides a powerful search tool.

[0] http://crispi.genouest.org/

5.3. New tools for dynamics

Participants: Jérémie Bourdon [contact], Jeanne Cambefort [contact], Damien Eveillard, Anne Siegel, Nathalie Théret, Santiago Videla [contact].

In 2014, the tool caspo was extended to new functionnalities.

caspo: Cell ASP Optimizer In the new version of caspo, *automated inference* of logical networks from experimental data allows for identifying admissible large-scale logic models saving a lot of efforts and without any a priori bias. Next, once a family a logical networks has been identified, one can suggest or *design new experiments* in order to reduce the uncertainty provided by this family. Finally, one can look for *intervention strategies* (i.e. inclusion minimal sets of knock-ins and knock-outs) that force a set of target species or compounds into a desired steady state. Altogether, this constitutes a pipeline for automated reasoning on logical signaling networks. Hence, the aim of caspo is to implement such a pipeline providing a powerful and easy-to-use software tool for systems biologists. [doc and download as a python package][web server].

GENSCALE Project-Team

5. New Software and Platforms

5.1. Next Generation Sequencing

Participants: Alexan Andrieux, Gaëtan Benoit, Charles Deltel, Erwan Drezen, Dominique Lavenier, Claire Lemaitre, Antoine Limasset, Pierre Peterlongo, Chloé Riou, Guillaume Rizk.

GATB: Genome Analysis Tool Box
The GATB software toolbox aims to lighten the design of NGS algorithms. It offers a panel of high-level optimized building blocks to speed-up the development of NGS tools related to genome assembly and/or genome analysis. The underlying data structure is the de Bruijn graph, and the general parallelism model is multithreading. The GATB library targets standard computing resources such as current multicore processor (laptop computer, small server) with a few GB of memory. From high-level API, NGS programming designers can rapidly elaborate their own software based on domain state-of-the-art algorithms and data structures. The GATB library is written in C++ and is available under the GNU Affero GPL License. [contact: D. Lavenier] https://gatb.inria.fr

Mapsembler: targetted assembly
The Mapsembler tool enables the micro assembly of one or several area(s) of interest. It takes as input one or more read set(s) and a one or more sequences fragments used as "starters" of each micro-assembly. This task provides a way to check the existence/absence of an area for which the user has an *a priori* interest. Moreover, for each extended "starter", the output is either a flat fasta sequence or a portion of the assembly graph. In this latter case, Mapsembler offers a visualization interface on which each graph (including the read coverage per read set) can be visualized, annotated, and manipulated. [contact: P. Peterlongo] http://colibread.inria.fr/mapsembler2/

Leon: NGS data compressor
Leon is a lossless compression software that achieves compression of DNA sequences of high throughput sequencing data, without the need of a reference genome. Techniques are derived from assembly principles that better exploit NGS data redundancy. A reference is built de novo from the set of reads as a probabilistic de-Bruijn graph stored in a Bloom filter. Each read is encoded as a path in this graph, storing only an anchoring kmer and a list of bifurcations indicating which path to follow in the graph. This new method will allow to have compressed read files containing its underlying de-Bruijn Graph, thus directly re-usable by many tools relying on this structure. Leon achieved encoding of a *C. elegans* reads set with 0.7 bits/base, outperforming state of the art reference-free methods. Leon is available under the GNU Affero GPL License. [contact: C. Lemaitre] https://gatb.inria.fr/software/leon/

Bloocoo: read corrector
Bloocoo is a k-mer spectrum-based read error corrector, designed to correct large datasets with a very low memory footprint. It uses the disk streaming k-mer counting algorithm contained in the GATB library, and inserts solid k-mers in a bloom-filter. The correction procedure is similar to state-of-the-art approaches. Bloocoo yields similar results while requiring far less memory: as an example, it can correct whole human genome re-sequencing reads at 70 x coverage with less than 4GB of memory [32]. [contact: C. Lemaitre] https://gatb.inria.fr/bloocoo-read-corrector/

MindTheGap: insertion variant detection

MindTheGap is a software that performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It takes as input a set of reads and a reference genome. It outputs two sets of FASTA sequences: one is the set of breakpoints of detected insertion sites, the other is the set of assembled insertions for each breakpoint. For each breakpoint, MindTheGap either returns a single insertion sequence (when there is no assembly ambiguity), or a set of candidate insertion sequences (due to ambiguities) or nothing at all (when the insertion is too complex to be assembled). MindTheGap performs de novo assembly using the de Bruijn Graph implementation of GATB. Hence, the computational resources required to run MindTheGap are significantly lower than that of other assemblers. [contact: C. Lemaitre] http://mindthegap.genouest.org/

TakeABreak: de novo inversion variant discovery
TakeABreak is a tool that can detect inversion breakpoints directly from raw NGS reads, without the need of any reference genome and without de novo assembling the genomes. Its implementation is based on the Genome Assembly Tool Box (GATB) library, and has a very limited memory impact allowing its usage on common desktop computers and acceptable runtime (Illumina reads simulated at 80x coverage from human chromosome 22 can be treated in less than two hours, with less than 1GB of memory). TakeABreak is available under the GNU Affero GPL License. [contact: C. Lemaitre] http://colibread.inria.fr/software/takeabreak/

discoSnp: de novo SNP discovery
The discoSnp tool detects isolated SNPs given one, two or more raw read set(s) without using any reference genome. discoSnp ranks predictions and outputs quality and coverage per allele. Compared to finding isolated SNPs using a state-of-the-art assembly and mapping approach, discoSnp requires significantly less computational resources, shows similar precision and recall values, and highly ranked predictions are less likely to be false positives. [contact: P. Peterlongo] http://colibread.inria.fr/discosnp/

5.2. High throughput sequence comparisons

Participants: Sébastien Brillet, Erwan Drezen, Dominique Lavenier, Pierre Peterlongo, Ivaylo Petrov.

KLAST: bank-to-bank alignment search tool
KLAST is a fast, accurate and NGS scalable bank-to-bank sequence similarity search tool providing significant accelerations of seeds-based heuristic comparison methods, such as the Blast suite. KLAST is a new optimized implementation of the PLAST algorithm to which several improvements have been made in 2014. KLAST is fully designed to compare query and subject comprised of large sets of DNA, RNA and protein sequences. It is significantly faster than original PLAST, while providing comparable sensitivity to BLAST and SSearch algorithms. KLAST contains a fully integrated data-filtering engine capable of selecting relevant hits with user-defined criteria (E-Value, identity, coverage, alignment length, etc.). Klast is developed with the Korilog Company and an academic version is now freely available for the scientific community [contact: D. Lavenier]. [34] https://koriscale.inria.fr/klast/

COMMET: de novo comparison of metagenomic datasets
Commet is an extension of the Comparead tool that proposes to compute similarity between set of raw non assembled (and usually non-assemblable with current state of the art assemblers) reads. Commet enables to factorize computations when n read sets have to be compared all together. Moreover, Commet proposes a new representation of sub-read sets that has the main advantages to save huge disk space and to enable efficient logical operations between sub-read sets. [contact: P. Peterlongo] https://colibread.inria.fr/software/commet/

5.3. 3D Protein structures

Participants: Douglas Goncalves, Antonio Mucherino.

MD-jeep version 0.2
MD-jeep is the result of a strong collaboration among Antonio Mucherino, Leo Liberti, Carlile Lavor and Nelson Maculan. Over the years, PhD and postdoc students under our supervision have also been contributing to this research topic. The new method for the computation of atomic coordinates in MD-jeep v.0.2 was developed in collaboration with Douglas Soares Gonçalves [13], who was a postdoc student in Rennes for one year [contact: A. Mucherino]. http://www.antoniomucherino.it/en/mdjeep.php

IBIS Project-Team

4. New Software and Platforms

4.1. Genetic Network Analyzer (GNA)

Participants: Hidde de Jong [Correspondent], Michel Page, François Rechenmann.

Keywords. Gene regulatory networks, qualitative simulation, model checking

GENETIC NETWORK ANALYZER (GNA) is the implementation of methods for the qualitative modeling and simulation of gene regulatory networks developed in the IBIS project. The input of GNA consists of a model of the regulatory network in the form of a system of piecewise-linear differential equations (PLDEs), supplemented by inequality constraints on the parameters and initial conditions. From this information, GNA generates a state transition graph summarizing the qualitative dynamics of the system. In order to analyze large graphs, GNA allows the user to specify properties of the qualitative dynamics of a network in temporal logic, using high-level query templates, and to verify these properties on the state transition graph by means of standard model-checking tools, either locally installed or accessible through a remote web server. GNA is currently distributed by the company Genostar, but remains freely available for academic research purposes. The current version is GNA 8.7. In comparison with the previously distributed versions, GNA 8.7 has the following additional functionalities: (1) it supports the editing and visualization of regulatory networks, in an SBGN-compatible format, (2) it semi-automatically generates a prototype model from the network structure, thus accelerating the modeling process, and (3) it allows models to be exported in the SBML Qual standard. For more information, see http://www-helix.inrialpes.fr/gna.

4.2. WellReader, WellFARE, and WellInverter

Participants: Johannes Geiselmann, Hidde de Jong [Correspondent], Michel Page, Delphine Ropers, Valentin Zulkower.

Keywords. Gene expression, reporter gene data

WELLREADER is a program for the analysis of gene expression data obtained by means of fluorescent and luminescent reporter genes. WELLREADER reads data files in an XML format or in a format produced by microplate readers, and allows the user to detect outliers, perform background corrections and spline fits, compute promoter activities and protein concentrations, and compare expression profiles across different conditions. WELLREADER has been written in MATLAB and is available under an LGPL licence, both as source code (M files) and compiled code (platform-specific binary files). For more information, see: http://ibis.inrialpes.fr/article957.html.

In the past year, we developed novel approaches towards the analysis of reporter gene data, based on regularized linear inversion (Section 5.3). The linear inversion methods were implemented in the Python package WELLFARE, relying on the scientific Python libraries NumPy and SciPy. In addition, the package provides utilities for parsing data files and removing possible outliers from the absorbance and fluorescence signals. The WELLFARE package is available under an LGPL license, but has also been integrated into a web application called WELLINVERTER, which provides a graphical user interface allowing access to the linear inversion methods through a web browser (Figure 5). The user can upload data files by means of WELLINVERTER, remove outliers and subtract background, and launch the procedures for computing growth rates, promoter activities, and protein concentrations. For more information, see: http://ibis.inrialpes.fr/article1080.html?menu=menu4.

LIFEWARE Team

5. New Software and Platforms

5.1. The Biochemical Abstract Machine

Participants: François Fages, François-Marie Floch, Thierry Martinez, Sylvain Soliman, Pauline Traynard.

5.1.1. BIOCHAM V3.6

The Biochemical Abstract Machine (BIOCHAM) is a software environment for modeling and analyzing biochemical reaction systems, making simulations, performing static analyses, specifying behaviors in temporal logic. It is distributed under the GPL license since 2002.

The new features of version v3.6 released in October 2014 include:

- Hybrid boolean-stochastic-continuous models and simulations
- Quantitative temporal logic patterns with dedicated solvers (based on [20])
- Trace simplifications (based on [19])
- `export_sbml3` added
- `curate_model` and `curate_sbml` added (based on [8])
- Refinements of the types for command arguments (no effect on Biocham models)
- Bug fixes

5.1.2. BIOCHAM-web

BIOCHAM-WEB is a web service which makes it possible to try BIOCHAM on line without any installation, through a spreadsheet. A new version BIOCHAM-web was released in March 2014 and is kept evolving since.

That web service will evolve to a complete graphical user interface, named BIOCHAM-gui, and will replace the current graphical user interface.

5.1.3. BIOCHAM-parallel

A (non-distributed) parallel version of BIOCHAM is also maintained for our own use on a cluster of 10000 cores at GENCI CINES. This version speeds-up (linearly in the number of processors) the search of parameter values by parallelizing the evaluation of the fitness function (computed by numerical integration) for both the different parameter sets and the different conditions (perturbations, gene knock down or stress).

5.2. ClpZinc

Participants: François Fages, Thierry Martinez, Philippe Morignot, Sylvain Soliman.

CLP2ZINC is a rule-based modeling language for constraint programming. It extends the MiniZinc modeling language with Horn clauses which can be used to express search strategies as constraints in the model. This system is developed in the framework of the ANR Net-WMS-2 project and is a follow-up of the RULES2CP modeling language.

5.3. CellStar: Long-term tracking of single cells from brightfield microscopy images

Participants: Grégory Batt, Pascal Hersen, Artémis Llamosi, Szymon Stoma.

In close collaboration with Kirill Batmanov, Cédric Lhoussaine and Cristian Versari from the LIFL (CNRS/Lille Univ), we developed CELLSTAR, a tool-chain for image processing and analysis dedicated to segmentation and tracking of yeast cells in brightfield time-lapse microscopy movies. To estimate algorithm quality we developed a benchmark made of manually-verified images illustrating various situations. On this benchmark, CELLSTAR outperformed 5 other state-of-the-art methods. The tool-chain is implemented in MATLAB and is provided together with the Python YEAST IMAGE TOOLKIT benchmark tool.

5.4. Other software

The team also develops several software primarily for internal use. Some of them are specific to particular hardware and are not distributed. Some others are general purpose and currently on the web page for free downloading.

MAGNOME Project-Team

5. New Software and Platforms

5.1. Magus: Genome exploration and analysis

Participants: David James Sherman [correspondant], Pascal Durrens, Florian Lajus, Xavier Calcas.

The MAGUS genome annotation system integrates genome sequences and sequences features, *in silico* analyses, and views of external data resources into a familiar user interface requiring only a Web navigator. MAGUS implements annotation workflows and enforces curation standards to guarantee consistency and integrity. As a novel feature the system provides a workflow for simultaneous annotation of related genomes through the use of protein families identified by *in silico* analyses; this results in an n-fold increase in curation speed, compared to curation of individual genes. This allows us to maintain standards of high-quality manual annotation while efficiently using the time of volunteer curators. MAGUS can be used on small installations with a web server and a relational database on a single machine, or scaled out in clusters or elastic clouds using Apache Cassandra for NoSQL data storage and Apache Hadoop for Map-Reduce (figure 1). For more information see the MAGUS Gforge web site. [0] MAGUS 2.0 was developed in an Inria Technology Development Action (ADT) and is distributed with an open-source license.

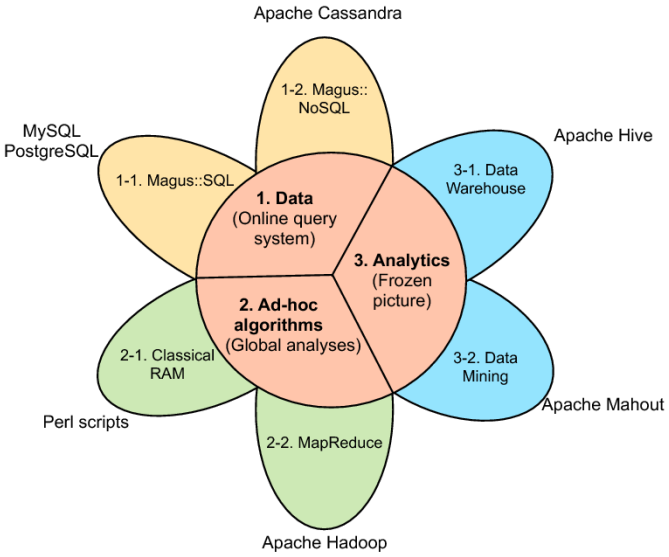


Figure 1. General architecture of the Tsvetok system implemented in MAGUS, showing the role of the NoSQL (Apache Cassandra) and Map-Reduce (Apache Hadoop) paradigms

5.2. Pantograph: Inference of metabolic networks

Participants: David James Sherman [correspondant], Pascal Durrens, Anna Zhukova.

[0] http://magus.gforge.inria.fr

Pantograph is a software tool developed by Nicolás Loira for his thesis, that infers whole-genome metabolic models for eukaryote cell factories from reference models and genome comparison. A novel feature of Pantograph is that it uses expert knowledge implicitly encoded in the scaffold's gene associations, and explicitly transfers this knowledge to the new model. Pantograph is available under an open-source license. For more information see the Pantograph Gforge web site. [0].

5.3. Mimoza: Generalizing and Visualizing Metabolic Models

Participants: David James Sherman [correspondant], Anna Zhukova.

Mimoza uses metabolic model generalization and cartographic paradigms to allow human experts to explore a metabolic model in a hierarchical manner. The software creates an zoomable representation of a model submitted by the user in SBML [0] format. The most general view represents the compartments of the model; the next view shows the visualization of generalized versions of reactions and metabolites in each compartment (see section 6.3); and the most detailed view visualizes the initial model with the generalization-based layout (where similar metabolites and reactions are placed next to each other). The zoomable representation is implemented using the Leaflet [0] JavaScript library for mobile-friendly interactive maps. Users can click on reactions and compounds to see the information about their annotations. The resulting map can be explored on-line, or downloaded in a COMBINE archive. The software and examples are available at http://mimoza.bordeaux.inria.fr.

5.4. Génolevures On Line: Comparative Genomics of Yeasts

Participants: Pascal Durrens [correspondant], David James Sherman.

The Génolevures online database provides archival data for exploring the annotated genome sequences of more than 20 genomes, determined and manually annotated by the Génolevures Consortium to facilitate comparative genomic studies of hemiascomycetous yeasts. Data are presented with a focus on relations between genes and genomes: conservation of genes and gene families, speciation, chromosomal reorganization and synteny. Génolevures online uses our open-source MAGUS system for genome navigation, with project-specific extensions developed by MAGNOME. For more information see the Génolevures web site. [0]

[0] http://pathtastic.gforge.inria.fr
[0] http://sbml.org
[0] http://leafletjs.com
[0] http://www.genolevures.org/

MORPHEME Project-Team

4. New Software and Platforms

4.1. New Software

4.1.1. Stracking

This software is developed within the ANR project MOTIMO. It allows to segment and track spermatozoons from confocal microscopy image sequences [12]. It has been transferred to IFMT, one of our partner of MOTIMO.

4.2. Platforms

4.2.1. Biological Image Platform (PIB)

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

SERPICO Project-Team

5. New Software and Platforms

5.1. Software for live cell imaging

Participants: Charles Kervrann [(contact)], Patrick Bouthemy, Thierry Pécot.

Motion2d: Parametric motion model estimation

The MOTION2D software written in C++ (APP deposit number: FR.001.520021.001.S.A.1998.000.21000 / release 1.3.11, January 2005) and JAVA (plug-in IMAGEJ (http://rsbweb.nih.gov/ij/) is a multi-platform object-oriented library to estimate 2D parametric motion models in an image sequence. It can handle several types of motion models, namely, constant (translation), affine, and quadratic models. Moreover, it includes the possibility of accounting for a global variation of illumination and more recently for temporal image intensity decay (e.g. due to photo-bleaching decay in fluorescence microscopy). The use of such motion models has been proved adequate and efficient for solving problems such as optic flow computation, motion segmentation, detection of independent moving objects, object tracking, or camera motion estimation, and in numerous application domains (video surveillance, visual servoing for robots, video coding, video indexing), including biological imaging (image stack registration, motion compensation in videomicroscopy). Motion2D is an extended and optimized implementation of the robust, multi-resolution and incremental estimation method (exploiting only the spatio-temporal derivatives of the image intensity function) [48]. Real-time processing is achievable for motion models involving up to six parameters. Motion2D can be applied to the entire image or to any pre-defined window or region in the image.

Free academic software distribution: Motion2D Free Edition is the version of Motion2D available for development of Free and Open Source software only. More information on Motion2D can be found at http://www.irisa.fr/vista/Motion2D and the software can be downloaded at the same Web address (about 1650 downloads registered).
On-line demo: Mobyle@SERPICO http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Motion2D.

Collaborator: Fabien Spindler (Inria Lagadic team).

ND-Safir and Fast2D-SAFIR: Image denoising software

The ND-SAFIR software (APP deposit number: IDDN.FR.001.190033.002.S.A.2007.000.21000 / new release 3.0 in 2013) written in C++, JAVA and MATLAB, removes additive Gaussian and non-Gaussian noise in still 2D or 3D images or in 2D or 3D image sequences (without any motion computation) [4]. The method is unsupervised and is based on a pointwise selection of small image patches of fixed size (a data-driven adapted way) in spatial or space-time neighbourhood of each pixel (or voxel). The main idea is to modify each pixel (or voxel) using the weighted sum of intensities within an adaptive 2D or 3D (or 2D or 3D + time) neighbourhood and to use image patches to take into account complex spatial interactions. The neighbourhood size is selected at each spatial or space-time position according to a bias-variance criterion. The algorithm requires no tuning of control parameters (already calibrated with statistical arguments) and no library of image patches. The method has been applied to real noisy images (old photographs, JPEG-coded images, videos, ...) and is exploited in different biomedical application domains (time-lapse fluorescence microscopy, video-microscopy, MRI imagery, X-ray imagery, ultrasound imagery, ...).

The FAST-2D-SAFIR software (APP deposit number: IDDN.FR.001.190033.001.S.A.2007.000.21000) written in C++ removes mixed Gaussian-Poisson noise in large 2D images, typically $10^3 \times 10^3$ pixels, in a few seconds. The method is unsupervised and is a simplified version of the method related to the SAFIR-nD software. The software dedicated to microarrays image denoising, was licensed to the INNOPSYS company which develops scanners for disease diagnosis and multiple applications (gene expression, genotyping, aCGH, ChIP-chip, microRNA, ...).
On-line demo: Mobyle@SERPICO http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::NDSafir.
Free download binaries: Binaries of the software ND-SAFIR are freely and electronically distributed. Developed in standard C/C++ under Linux using the CImg library, it has been tested over several platforms such as Linux/Unix, Windows XP and Mac OS.
Academic licence agreements: Institut Curie, CNRS, ENS Ulm, Oxford University, Weizmann Institute, UCSF San-Francisco, Harvard University, Berkeley University, Stanford University, Princeton University, Georgia-Tech, Kyoto UNiversity, IMCB Singapore ...
Commercial licence agreements: Innopsys, Roper Scientfic, Photmetrics, Nikon (2015).
Collaborators: Jérôme Boulanger and Jean Salamero (UMR 144 CNRS-Institut Curie, STED team), Peter Elbau (RICAM Linz, Austria) and Jean-Baptiste Sibarita (UMR 5091, University of Bordeaux 2).

HullkGround: Background subtraction by convex hull estimation

The HULLKGROUND software (APP deposit number: IDDN.FR.001.400005.000.S.P.2009.000.21000) written in JAVA (plug-in IMAGEJ) decomposes a fluorescence microscopy image sequence into two dynamic components: i) an image sequence showing mobile objects; ii) an image sequence showing the slightly moving background. Each temporal signal of the sequence is processed individually and analyzed with computational geometry tools. The convex hull is estimated automatically for each pixel and subtracted to the original signal. The method is unsupervised, requires no parameter tuning and is a simplified version of the α shapes-based scale-space method [35].

On-line demo: Mobyle@SERPICO http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Hullkground.
Collaborators: Anatole Chessel and Jean Salamero (UMR 144 CNRS-Institut Curie, STED team).

5.2. Software for cryo-electron tomography

Participant: Charles Kervrann [(contact)].

TubuleJ: Straightening of microtubule cryo-EM projection views

The TUBULEJ software (APP deposit number: IDDN.FR.001.240023.000.S.P.2011.000.21000) written in JAVA (plug-in IMAGEJ) is devoted to the analysis of microtubules and helical structures in 2D cryo-electron microscope images. The software straightens curved microtubule images by estimating automatically points locations on the microtubule axis. The estimation of microtubule principal axis relies on microtubule cylindrical shape analyzed in the Fourier domain. A user-friendly interface enables to filter straight fiber images by selecting manually the layer lines of interest in the Fourier domain. This software can be used to generate a set of 2D projection views from a single microtubule projection view and a few parameters of this microtubule structure. These projection views are then back projected, by using the IMOD plug-in (http://rsbweb.nih.gov/ij/), to reconstruct 3D microtubules.

On-line demo: see http://equipes.igdr.univ-rennes1.fr/en/tips/Software/TubuleJ/.

Collaborators: Sophie Blestel and Denis Chrétien (UMR 6290, CNRS, University of Rennes 1).

Cryo-Seg: Segmentation of tomograms in cryo-electron microscopy

The CRYO-SEG software written in C++ and JAVA (plug-in MAGEJ) has been developed to detect microtubule structures and helical structures in 2D cryo-electron microscope images. Cryo-electron tomography allows 3D observation of biological specimens in their hydrated state. Segmentation is formulated as Maximum A Posteriori estimation problem and exploits image patches to take into account spatial contexts (Markov Random Fields). Because of the contrast anisotropy in the specimen thickness direction, the whole tomogram is segmented section by section, with an automatic update of reference patches. This algorithm has been evaluated on synthetic data and on cryo-electron tomograms of in vitro microtubules [19]. On real data, this segmentation method extracts the most contrasted regions of microtubules, and 3D visualization is improved.

Collaborators: Sophie Blestel and Denis Chrétien (UMR 6290, CNRS-University of Rennes 1).

5.3. Image Processing software distribution and Mobyle plateform

Participants: Tinaherinantenaina Rakotoarivelo, Thierry Pécot [(contact)], Charles Kervrann.

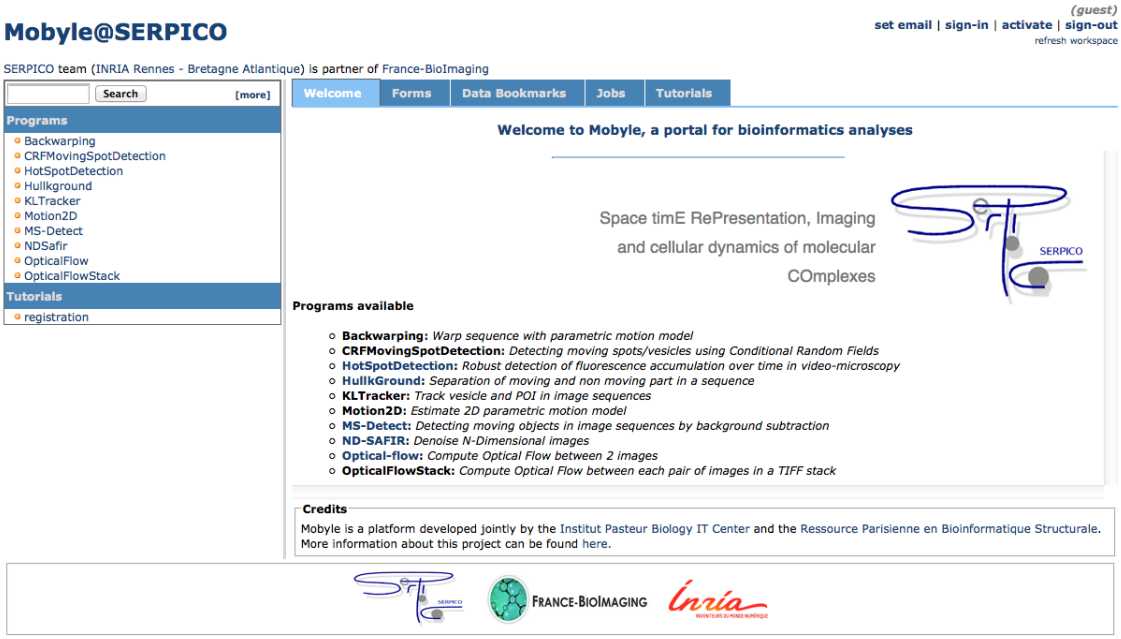


Figure 2. Mobyle@SERPICO web portal.

The objective is to disseminate the distribution of SERPICO image processing software for biologist users:

- *Free binaries:* software packages have been compiled for the main operating systems (Linux, MacOS, Windows) using CMake (see http://www.cmake.org/). They are freely available on the team website under a proprietary license (e.g. ND-SAFIR and HULLKGROUND are distributed this way at http://serpico.rennes.inria.fr/doku.php?id=software:index).
- *Mobyle@SERPICO web portal*: An on-line version of the image processing algorithms has been developped using the Mobyle framework (Institut Pasteur, see http://mobyle.pasteur.fr/). The main role of this web portal (see Fig. 2) is to demonstrate the performance of the programs developed by the team: C-CRAFT[13], ATLAS[23], HOTSPOTDETECTION[51], HULLKGROUND[35], KL-TRACKER[50], MOTION2D[49], MS-DETECT[37], ND-SAFIR[4] and OPTICALFLOW. The web interface makes our image processing methods available for biologist users at Mobyle@SERPICO

(http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#welcome) without any installation or configuration on their own. The size of submitted images is limited to 200 MegaBytes per user and all the results are kept 15 days. The web portal and calculations run on a server with 2 CPU x 8 cores, 64 GigaBytes of RAM.

- IMAGEJ *plug-ins*: IMAGEJ (see http://rsb.info.nih.gov/ij/) is a widely used image visualization and analysis software for biologist users. We have developed IMAGEJ plug-in JAVA versions of the following software: ND-SAFIR [4], HULLKGROUND [35], MOTION2D [49], HOTSPOTDETECTION [51]. The C-CRAFT algorithm [13] has been developped for the image processing ICY platform (http://icy.bioimageanalysis.org/).
- *Institut Curie CID iManage database*: The microscopy facility of Institut Curie has co-developped a commercial database system (CID iManage/Strand Avadis company). The database can be searched via meta-data and includes menu selections that enable to run remote processing from a cluster. We have integrated ND-SAFIR and HULLKGROUND in the interface environment to allow the database users to process their images easily, and store associated results and parameters used.

Collaborators: Charles Deltel (Inria Rennes SED) and Perrine Paul-Gilloteaux (UMR 144 CNRS-Institut Curie, STED team and PICT-IBiSA).

VIRTUAL PLANTS Project-Team

4. New Software and Platforms

4.1. OpenAlea

4.1.1. OpenAlea 2.0

Participants: Julien Coste, Guillaume Baty, Christophe Pradal, Christophe Godin, Frédéric Boudon, Christian Fournier.

Plant models are usually developed at different scales using various modeling paradigms: (i) imperative using a script or a compiled language, (ii) declarative to define a set of rewriting rules like in L-systems, (iii) interactive using a sketch-based interface for creating 3D models of plants, or (iv) visual programming to combine existing components.

However, all these computational paradigms have been developed in different software platforms in the plant modeling community, and, as of today, none of them provides all the modeling paradigms in an integrated software environment. However, the need to develop more complex and integrated models, often assembling many sub-models, led us to consider a modeling framework capable of supporting multiple design paradigms and models, and make them interoperable.

To address this problem we developed the OpenAlea platform. The Version 1.0 of the platform consisted of a middleware implementing a modular and component-based software architecture for assembling models written in different computer languages. *OpenAlea 2.0* adds to OpenAlea 1.0 a high-level formalism dedicated to the modeling of morphogenesis that makes it possible to use several modeling paradigms (Blackboard, L-systems, Agents, Branching processes, Cellular Automata) expressed with different languages (Python, L-Py, R, Visual Porgramming, ...) to analyse and simulate shapes and their development.

It offers an integrated modeling software environment *OpenAleaLab* that provides users with flexible and interactive tools to combine different modeling paradigms to support the computational investigation.

4.1.2. OpenAleaLab

Participants: Julien Coste, Guillaume Baty, Christophe Pradal, Christophe Godin, Frédéric Boudon, Christian Fournier.

This research theme is supported by the Inria ADT OpenAlea.

OpenAleaLab is a new integrated modeling environment (IME) for OpenAlea. This IME provides an IPython shell, a text editor, a project manager, a toolbox installer, a world data structure containing the objects and state variables shared by the different models and a 3D viewer window that makes it possible to observe the objects of the world. Different modelling paradigms, languages and tools for plant modelling are available as plug-ins, such as a visual programming environment, a L-system language, or a R editor and interpreter. OpenAleaLab is based on IPython architecture and is built using PyQt.

The core of the system is made up of a central data structure (the blackboard) called the world. This data structure may contain various computational objects that altogether define the state of the modeling system, and can be accessed (in read and write) by all the models. The investigation process can be seen as executing the system's models in turn to explore or change dynamically the world objects.

Models are knowledge sources that can modify the world when executed. A model can call for the execution of another model as a function. In this case the model passes an input value to the called model, that inturn returns an output value. In addition it may be possible that the called model changed the world as a side effect. The user launches the execution of a first model (then referred to as the master model), which then entails recursively the hierarchical execution of all the other models downstream of it. One can see that in this framework, the execution controller is then itself considered as a model (the master model).

4.1.3. Similarity and Provenance in OpenAlea workflows

Participants: Sarah Cohen-Boulakia, Christophe Pradal, Moussa Yattara [IBC], Patrick Valduriez [Inria].

This research theme is supported by IBC and Inria.

The number of available scientific workflows, designed in OpenAlea or in other worflow systems such as Galaxy or Taverna, is increasing over time. Methods to compare the scientific workflows become a necessity, to allow duplicate detection or similarity search. Scientific workflows are complex objects, and their comparison entails a number of distinct steps from comparing atomic elements to comparison of the workflows as a whole. Various studies have implemented methods for scientific workflow comparison and came up with often contradicting conclusions upon which algorithms work best. Comparing these results is cumbersome, as the original studies mixed different approaches for different steps and used different evaluation data and metrics.

We first contribute to the field [27] by (i) comparing in isolation different approaches taken at each step of scientific workflow comparison, reporting on an number of unexpected findings, (ii) investigating how these can best be combined into aggregated measures, and (iii) making available a gold standard of over 2000 similarity ratings contributed by 15 workflow experts on a corpus of 1500 workflows and re-implementations of all methods we evaluated.

Then, we introduced a novel and intuitive workflow similarity measure that is based on layer decomposition [39]. Layer decomposition accounts for the directed dataflow underlying scientific workflows, a property which has not been adequately considered in previous methods. We comparatively evaluate our algorithm using our gold standard and show that it a) delivers the best results for similarity search, b) has a much lower runtime than other, often highly complex competitors in structure-aware workflow comparison, and c) can be stacked easily with even faster, structure-agnostic approaches to further reduce runtime while retaining result quality.

Ongoing work includes considering *provenance* traces of executions in the similarity metrics and augmenting the number of workflows to be shared between scientists by working on the *provenance-equivalence* aspects between workflows and (Python) scripts. This work will be done in the context of the IBC Young researcher grant we obtained (co-leaded by S. Cohen-Boulakia and Ch. Pradal) in collaboration with members of Zenith and the INRA phenome platform.

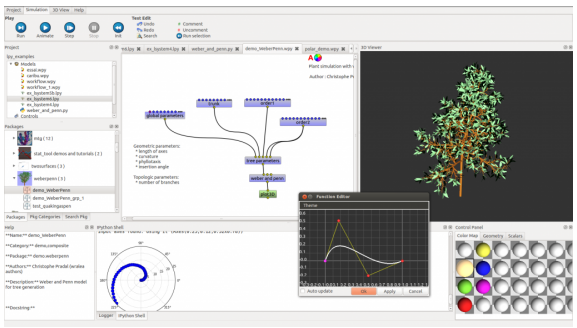


Figure 1. OpenAleaLab - A highly modular environment for modeling morphogenesis.

ARAMIS Project-Team

5. New Software and Platforms

5.1. SACHA

Participants: Marie Chupin [Correspondant], Ludovic Fillon.

SACHA ("Segmentation Automatisée Compétitive de l'Hippocampe et de l'Amygdale") is a software for the fully automatic segmentation of the hippocampus and the amygdala from MRI 3D T1 brain scans. It has been validated in various populations including healthy controls and patients with Alzheimer's disease, epilepsy and depression. It has been successfully applied to over 3,000 subjects, both controls, from adolescents to elderly subjects, and patients with different types of pathologies. The current stable version is fully automatic and focused on cross-sectional segmentation. The software can be used both as a command-line program or through a graphical user interface (GUI). The core of the program is coded in C++. It has a dependency to the AIMS library (http://www.brainvisa.info) and preprocessing steps rely on processes in Matlab from SPM (http://www.fil.ion.ucl.ac.uk/spm/). The GUI is coded in Python and is based on BrainVISA (http://www.brainvisa.info). The software has been registered at the APP (French agency for software protection).

5.2. WHASA

Participants: Marie Chupin [Correspondant], Ludovic Fillon, Thomas Samaille.

WHASA ("White matter Hyperintensity Automatic Segmentation Algorithm") is a software for the fully automatic segmentation of age-related white matter hyperintensities from MRI FLAIR and 3D T1 brain scans. It has been validated on a population showing a wide range of lesion load, and is being further evaluated on elderly subjects with few clinical abnormalisties and with different acquisition characteristics. The current stable version is fully automatic and focused on cross-sectional segmentation. The software can be used both as a Matlab command-line or through a graphical user interface (GUI). The core of the program is coded in Matlab. It has a dependency to the SPM environment (http://www.fil.ion.ucl.ac.uk/spm/). The GUI is coded in Python and is based on BrainVISA (http://www.brainvisa.info). The software has been registered at the APP (French agency for software protection).

5.3. Deformetrica

Participants: Stanley Durrleman [Correspondant], Alexandre Routier, Pietro Gori, Marcel Prastawa, Ana Fouquier, Joan Glaunès, Benjamin Charlier, Cedric Doucet.

Deformetrica is a software which estimates diffeomorphic deformations between sets of geometric objects in 2D and 3D. Those deformations are estimated either for the registration of two of such objects sets or for the construction of an atlas from several of such sets (a template model set and deformations mapping the template model to each set). Geometric objects could be grey-level images, surface meshes, polygonal lines or unstructured point sets. The method relies on the metric on currents for the comparison of point sets and the sum of squared differences for the comparison of images.

The software is written in C++ and relies on the ITK and VTK libraries. Core functions are coded with CUDA for their parallelization on GPU. It is a command-line software.

The version 2.1 of the software has been released on December 19, 2014. It is freely accessible to the scientific community at www.deformetrica.org.

5.4. qualiCATI

Participants: Marie Chupin [Correspondant], Hugo Dary, Urielle Thoprakarn, Amadou Tall, David Gay, Nicolas Vibet, Aude Costard, Cyril Poupon, Vincent Perlbarg, Mélanie Pélégrini-Issac, Alexandre Vignaud.

qualiCATI is a software designed for comprehensive quality control of multimodal MRI data acquisition in large multicentre clinical studies. The software is built as a platform receiving several modules, developped by several CATI engineers. The first module is dedicated to acquisition requirement checking and conversion to nifti format. The second module aims at making 3DT1 acquisition quality check more systematic, and relies both on visual inspection and quantitative indices. The third module allows a simultaneous evaluation of the clinical part of the CATI acquisition protocol. The fourth module embeds automatic indices to evaluate resting state fMRI acquisition. The fifth module is dedicated to first preprocessings and quality indices for dMRI. The sixth module is dedicated to qMRI, with visual and automated quality control together with preprocessings. The last module is dedicated to data and project management. QualiCATI requires training for the visual parts, and is closely linked with a team of clinical research assistants. It has been used to analyse about 5000 subjects from about 15 multi centre research projects initiated before or after the CATI started. Other modules will be added in the future to embed new aspects of the MRI protocol proposed by the CATI. The Aramis team is in charge of the second and third modules and jointly in charge of the first module. The software is centered on a graphical user interface (GUI). The whole program is coded in Python within the pyPTK environment developped by Cyril Poupon (Neurospin). It has dependencies to SPM (http://www.fil.ion.ucl.ac.uk/spm/) and brainVISA environments as well as specific tools for DICOM management.

5.5. Brain Networks Toolbox

Participants: Mario Chavez, Fabrizio de Vico Fallani [Correspondant].

Brain Networks Toolbox is a collection of Matlab routines developed to quantify topological metrics of complex brain networks. These routines are associated with published publications with application to real data and freely distributed via the FreeBorn (French Brain Networks) consortium https://sites.google.com/site/fr2eborn/download

ASCLEPIOS Project-Team

4. New Software and Platforms

4.1. SOFA

Participants: Hervé Delingette [correspondent], Federico Spadoni, Stéphanie Marchesseau, Hugo Talbot, Sophie Giffard-Roisin, Roch-Philippe Mollero.

SOFA is an Open Source framework primarily targeted at real-time simulation, with an emphasis on medical simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows : the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA; the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file; the building of complex models from simpler ones using a scene-graph description; the efficient simulation of the dynamics of interacting objects using abstract equation solvers; the reuse and easy comparison of a variety of available methods. It was developed mainly by the Inria team projects Shacra, Evasion and Asclepios.
See also the web page http://www.sofa-framework.org/.

- ACM: J.2 Physics, J.3 LIFE AND MEDICAL SCIENCES
- Software benefit:- Simulation of the human body
- License: LGPL
- Type of human computer interaction: console, opengl, qt
- OS/Middelware: linux, windows, mac
- Required library or software: Qt - GPL - GLEW - BSD/MIT - Tinyxml - zlib
- Programming language: C/C++
- Documentation: - each function of the core API and each class in the SOFA modules - doxygen
- ACM: J.3
- Programming language: C/C++

4.2. MedInria

Participants: Maxime Sermesant [correspondent], Florian Vichot, Hakim Fadil, Loïc Cadour, Michael Buckingham.

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, 2.2.1, was made in September 2014. See also the web page https://med.inria.fr.

- Version: 2.2.1
- License: BSD
- Keywords: Medical Image Processing
- Dependencies: Qt, DTK, VTK, ITK, TTK, MIPS
- Programming language: C++
- Supported OSes: Windows (XP/Vista/7/8), Linux (Fedora/Ubutu), Mac OS X (10.6-10.9)

4.3. MUSIC

Participants: Maxime Sermesant [correspondent], Florian Vichot, Hakim Fadil, Loïc Cadour, Florent Collot, Mathilde Merle [Software Engineer IHU LIRYC].

MUSIC is a software developed by the Asclepios research project in close collaboration with the IHU LIRYC in order to propose functionalities dedicated to cardiac interventional planning and guidance. This includes specific tools (algorithms of segmentation 1 , registration, etc.) as well as pipelines. The software is based on the MedInria platform.

For more information, see the web page https://team.inria.fr/asclepios/software/music/. See also: http://videotheque.inria.fr/videotheque/media/28294 for a video on the MUSIC software application.

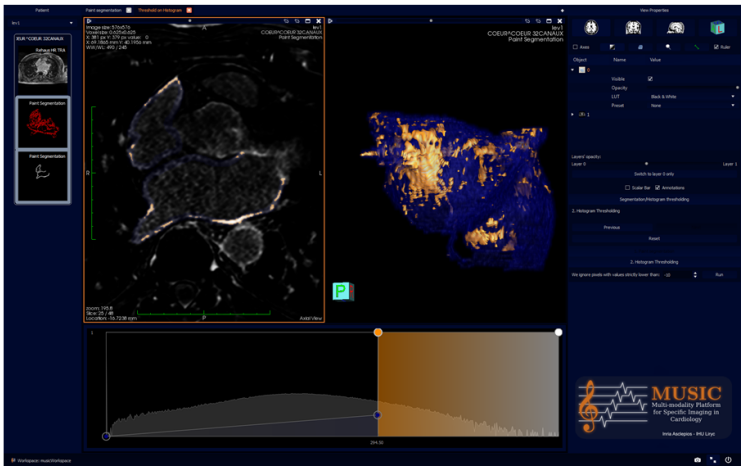


Figure 1. Segmentation of atrial fibrosis using adaptive histogram thresholding based on the MUSIC Software.

- Version: 1.0
- License: Proprietary
- Dependencies: MedInria, Qt, DTK, VTK, ITK, TTK, MIPS
- Programming language: C++
- Supported OSes: Windows (XP/Vista/7/8), Linux (Fedora/Ubuntu), Mac OS X (10.6-10.10)

4.4. VP2HF platform

Participants: Maxime Sermesant [correspondent], Hakim Fadil, Loïc Cadour.

The VP2HF software is developed by the Asclepios team and brings together all the research produced by the VP2HF's partners. It contains MedInria plugins implemented by teams such as UPF Barcelona, KCL, and specific tools provided by Philips (algorithms of segmentation 2 , scar segmentation, ...). It aims at integrating in a single clinical workflow, tools to improve the therapy selection and treatment optimisation for patients suffering from heart failure.

- Version: 1.0
- License: Proprietary
- Keywords: Medical Image Processing
- Dependencies: MedInria, Qt, DTK, VTK, ITK, TTK, MIPS
- Programming language: C++
- Supported OSes: Windows (XP/Vista/7/8), Linux (Fedora/Ubuntu), Mac OS X (10.6-10.10)

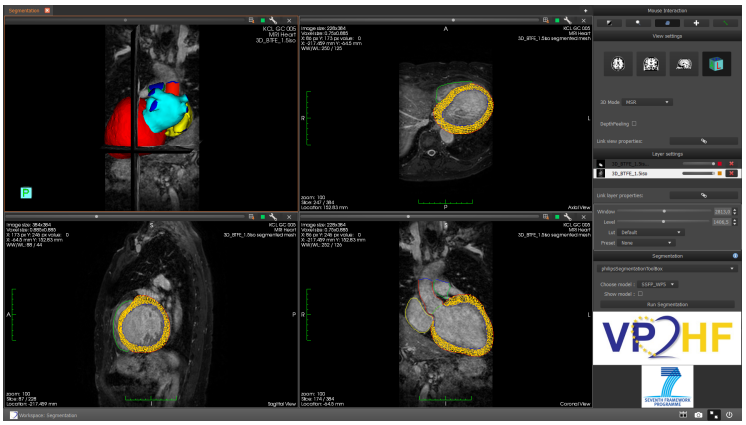


Figure 2. Philips segmentation tool within the VP2HF platform

ATHENA Project-Team

5. New Software and Platforms

5.1. OpenMEEG

Participants: Théodore Papadopoulo, Maureen Clerc, Kai Dang, Alexandre Gramfort [Telecom ParisTech].

OpenMEEG provides state-of-the art tools for low-frequency bio-electromagnetism, notably solving forward problems related to EEG and MEG [60], [61]. It implements the symmetric BEM which provides excellent accuracy and versatility. OpenMEEG is a free open software written in C++. It can be accessed either through a command line interface or through Python/Matlab interfaces. The first release has been directly downloaded about 600 times since October 2008. Our last release (in September 2011) has been downloaded more than 2000 times to this date. OpenMEEG has been integrated in the neuro-debian distribution (http://neuro.debian.net/) and matlab suites (such as BrainStorm, FieldTrip or SPM) which may represent many more indirect downloads. Work is under progress to integrate it into the BESA commercial software, and discussions with other software companies are also ongoing.

See also the web page http://openmeeg.gforge.inria.fr.

- Version: 2.2
- License: French opensource license CeCILL-B
- Multiplatform: Windows - Linux - MacOSX
- Programming language: C++
- 17 000 lines of code.
- 1800 downloads in 2012-2013.
- Web: http://openmeeg.gforge.inria.fr

5.2. High Performance Diffusion MRI

Participants: Aurobrata Ghosh, Théodore Papadopoulo, Rachid Deriche.

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.

So far, ODF estimation from the ATHENA-dMRI C++ library has been successfully included in medInria 1.9, and in the process to be re-adapted for medInria 2.1. Otherwise, the ATHENA-dMRI C++ library has been mostly used internally for research purposes. However, this is now changing with a fresh restructuring of the entire library so that it can be successfully ported and used externally – primarily to be included in parts with the cutting-edge software developed by OLEA MEDICAL.

- License: French opensource license CeCILL-B - To change when it is to be sourced to OLEA MEDICAL.
- Platform: Linux and (medInria platforms)
- Programming language: C++

5.3. Contributions to the open source dMRI platform DIPY

Participants: Demian Wassermann, Rutger Fick.

DIPY (Diffusion Imaging in Python) is a fast growing open source platform for dMRI image processing. It aims to be a reference implementation platform for most dMRI processing technologies and it has several contributors around the world including Stanford Universtiy, USA; Berkeley University, USA; Sherbrooke University, Canada; and University of Cambridge, UK. This aims to provide a dMRI library easy to use in research-intensive cases where developments of new technologies are simpler than in high performance C++ libraries.

In 2014 D. Wassermann and R. Fick got involved in this open source platform. Their work spans from minor public extensions to private developments within this framework. They developed an improved implementation of the 3D-SHORE [72] basis, which is designed to reconstruct the three-dimensional diffusion propagator from three-dimensional q-space measurements. Moreover, they optimized the computation of the basis coefficients and introduced the analytical Laplacian regularization [19]. They also implemented the MAP-MRI basis [73], which is an extension of the 3D-SHORE basis to better deal with highly anisotropic data. Finally, they extended this work by again introducing the analytical Laplacian regularization. Also, we implemented a novel generalized basis that fits diffusion MRI data over both three-dimensional q-space and diffusion times (3D+t). The theoretical developments related to these two last contributions have been submitted to ISBI 2015 and IPMI 2015 respectively.

- License: Revised BSD license.
- Platform: Multiplatform
- Programming language: Python & C

5.4. medInria

Participants: Jaime Garcia Guevara, Théodore Papadopoulo.

The ATHENA team is heavily involved in the development of medInria 2.0 along with the ASCLEPIOS, PARIETAL and VISAGES research teams. medInria is a free software platform dedicated to medical data visualization and processing. medInria 2.0, it is a complete re-write of the first version of medInria in order to be modular and allow a distributed development. It aims at providing an integrative platform for medical image processing and to be a framework for disseminating various research tools not only to other researchers but also to clinicians. New algorithms or data formats can be added as plugins.

It aims at providing to clinicians and researchers state-of-the-art algorithms developed at Inria and elsewhere (for the future), through an intuitive user interface. medInria offers from standard to cutting-edge processing functionalities for medical images such as 2D/3D/4D image visualization, image registration, diffusion MR processing and tractography.

ATHENA's contributions so far consist in various improvements on the infrastructure, the core application as well as several plugins which are already available with version 2.1 (ODF vizualization) or in future ones: advanced dMRI processing, M/EEG signal visualisation (by integrating code from the software AnyWave developed by Bruno Colombet and J.-M. Badier INSERM U1106 and Aix-Marseille University).

In 2013, the source code of the core of medInria was made public. Regular releases and bug fixes are provided on a large number of Linux, Windows and Mac versions, thanks to the Continuous Integration platform proposed at Inria.

After 4 years of important development, medInria is now rather mature and can be used as a basis for collaborations and projects. We now receive regular feedback through the forum and the mailing list, from both academic and clinical users.

- Version: 2.1
- Keywords: Medical Image Processing and Visualization
- License: BSD 4

- Multiplatform: Windows - Linux - MacOSX
- Programming language: C++
- 250 000 lines of code.
- 5000 downloads on 2012-2013.
- Web: http://med.inria.fr.

5.5. FindSources3D

Participants: Maureen Clerc, Juliette Leblond [APICS project-team], Jean-Paul Marmorat [APICS project-team], Théodore Papadopoulo.

FindSources3D is a Matlab software program dedicated to solving inverse source localization problems in electroencephalography (EEG), and in the future, magnetoencephalography (MEG). FindSources3D implements a new formalism for source localization, based on rational approximations in the complex plane. It is able to estimate, with high precision, and with no a priori on the number of sources, pointwise dipolar current sources within the brain. The head model used is a spherical model with concentric layers of homogenous conductivity.

Contributors: APICS and ATHENA Project Teams, Inria Sophia-Antipolis Méditerranée, Centre de Mathématiques Appliquées (CMA), Ecole des Mines de Paris.

- Version: 1.0
- Keywords: Medical Image Processing and Visualization
- License: CeCILL
- Multiplatform: Windows - Linux - MacOSX
- Programming language: Matlab
- Web: http://www-sop.inria.fr/apics/FindSources3D/fr/index.html

5.6. CoAdapt P300 Stimulator

Participants: Maureen Clerc, Théodore Papadopoulo, Loïc Mahé, Nathanaël Foy, Jérémie Mattout [Centre de Recherche en Neurosciences de Lyon, INSERM], Emmanuel Maby [Centre de Recherche en Neurosciences de Lyon, INSERM].

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. This software was developped in the context of the ANR project CoAdapt. It runs with OpenViBE as an external plugin.

- Version: 1.0
- Keywords: Brain Computer Interfaces
- Multiplatform: Windows - Linux - MacOSX
- Programming language: C++
- APP IDDN FR.001.020003.000.S.P.2015.000.31235

DEMAR Project-Team

4. New Software and Platforms

4.1. New Software and Platforms

4.1.1. RdP to VHDL tool

Participants: David Andreu, Thierry Gil, Robin Passama, Baptiste Colombani, Thibaut Possompes.

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, 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 interconnected 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)) is regulary updated.

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 (H. Leroux PhD thesis).

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).

4.1.2. SENISManager

Participants: Robin Passama, David Andreu.

We developed a specific software environment called SENISManager 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.

SENISManager (registered at the french Agence de Protection des Programmes (APP) with the industrial partner) has been transferred to the industrial partner that develops a new version according to an Eclipse-based design.

4.1.3. Synergy Neurostimulation Software

Participants: David Andreu, Amandine Pantel, Arthur Hiairrassary.

We are developing a specific software environment called Synergy Neurostimulation Software 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 will be soon registered at the french Agence de Protection des Programmes (APP).

4.1.4. MOS2SENS: Model Optimization and Simulation To Selective Electrical Neural Stimulation

Participants: Melissa Dali, Olivier Rossel, David Guiraud.

Multipolar electric stimulation of the nerve is a main issue, to access selective activation of organ or muscles. Knowing that electrodes configurations have to be specific to the type of nerve and to the organic or muscular targeted, we work on an accurate and flexible nerve modeling (work extension of Jérémy Laforêt PhD thesis, 2009), and we have developed new software MOS2SENS (from Model Optimization and Simulation To Selective Electrical Neural Stimulation) (fig.1). 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.

There are two programs that perform the following functions:

- Generation of 3D geometric model
- Mathematical description of the link between stimulation currents and extracellular voltage present inside the nerve
- Nerve fiber activation prediction based on the current stimulation
- Optimization of the current injected according to the chosen target

The software has been implemented in Matlab with graphical user interface and use OpenMEEG open source software to compute electric fields from the electrode to the fibers.

MOS2SENS is filed in the Agency for the Protection of Programs (APP) under the identifier

IDDN.FR.001.490036.000.S.P.2014.000.31230

4.1.5. SENSBIOTK

As low cost and highly portable sensors, inertial measurements units (IMU) have become increasingly used in different topics, such as gait analysis, embodying an efficient alternative to motion capture systems. Meanwhile, being able to compute reliably accurate spatial parameters using few sensors remains a relatively complex problematic. The use of inertial data calls on various algorithms able to compute from raw sensors (accelerometer, magnetometer and gyrometer) different features (position, angle, etc...). SensbioTK (for Tool Kit) has been implemented using a Python programming environment. This opensource library provides to any IMU user a set of tools enabling the following functions :

- Conversion from inertial raw data to .csv file
- Computation of optimized scale and offset parameters for inertial sensors calibration (Gauss newton optimization)
- AHRS sensor fusion algorithms (Kalmann filter and gradient descent based) : Madgwick, Mahony and Martin-Salaun implementation
- Stride length calculation from one shank located IMU
- 3D transformations and quaternion library

Many "ready to use" examples with relative data and scripts : goniometer, compass, pedometer, motion capture validation...
https://github.com/sensbio/sensbiotk

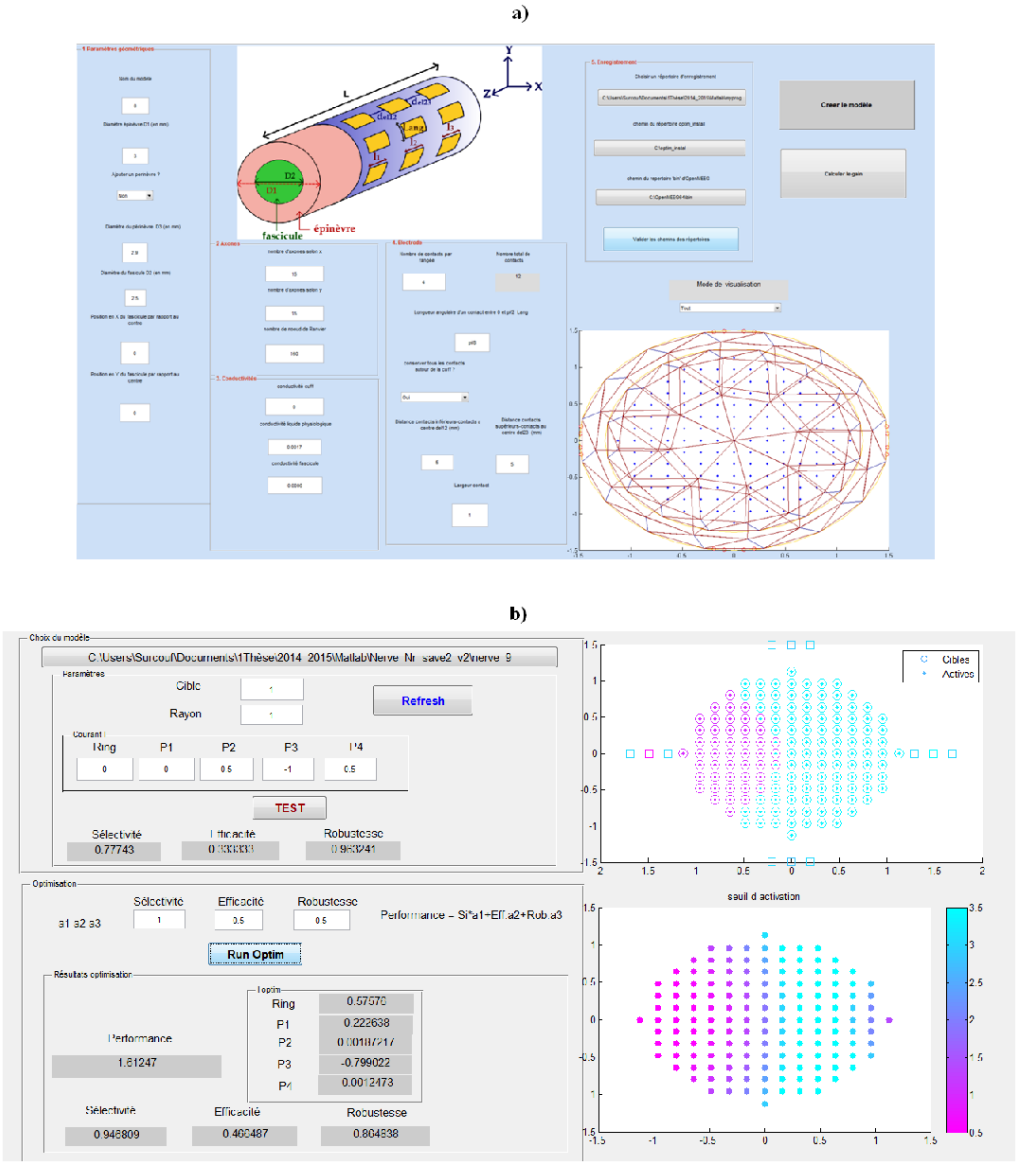


Figure 1. MOS2SENS interface. a) interface for the calculation of the electric field induced by electrical stimulation, b) interface for the configuration optimization

GALEN Project-Team

5. New Software and Platforms

5.1. Deformable Registration Software

Participant: Nikos Paragios [Correspondant].

deformable image and volume registration, is a deformable registration platform in C++ for the medical imaging community (publicly available at http://www.mrf-registration.net) developed mainly at Ecole Centrale, Technical University of Munich and University of Crete. This is the first publicly available platform which contains most of the existing metrics to perform registration under the same concept. The platform is used for clinical research from approximately 3,000 users worldwide.

5.2. Dense image and surface descriptors

Participant: Iasonas Kokkinos [Correspondant].

Scale-Invariant Descriptor, Scale-Invariant Heat Kernel Signatures DISD (publicly available at http://vision.mas.ecp.fr/Personnel/iasonas/descriptors.html) implements the SID, SI-HKS and ISC descriptors. SID (Scale-Invariant Descriptor) is a densely computable, scale- and rotation- invariant descriptor. We use a log-polar grid around every point to turn rotation/scalings into translation, and then use the Fourier Transform Modulus (FTM) to achieve invariance. SI-HKS (Scale-Invariant Heat Kernel Signatures) extract scale-invariant shape signatures by exploiting the fact that surface scaling amounts to multiplication and scaling of a properly sampled HKS descriptor. We apply the FTM trick on HKS to achieve invariance to scale changes. ISC (Intrinsic Shape Context) constructs a net-like grid around every surface point by shooting outwards and tracking geodesics. This allows us to build a meta-descriptor on top of HKS/SI-HKS that takes neighborhood into account, while being invariant to surface isometries.

5.3. Ranking with High-Order Information

Participant: Puneet Dokania [Correspondant].

Average precision optimization, high-order information, ranking The software (publicly available at http://cvn.ecp.fr/projects/ranking-highorder/) provides a convenient API for learning to rank with high-order information. The samples are ranked according to a scorethat is proportional to the difference of max-marginals of the positive and the negative class. The parameters of the score function are computed by minimizing an upper bound on the average precision loss. The software also provides an instantiation of the API for ranking samples according to their relevance to an action, using the poselet features.

5.4. Efficient bounding-based object detection

Participant: Iasonas Kokkinos [Correspondant].

branch-and-bound, parts detection, segmentation, DPMS implements branch-and-bound object detection, cutting down the complexity of detection from linear in the number of pixels to logarithmic (publicly available at http://vision.mas.ecp.fr/Personnel/iasonas/dpms.html). The results delivered are identical to those of the standard deformable part model detector, but are available in 5 to 20 times less time. This website has been visited 1500 times in 10 months.

5.5. Fast Primal Dual Strategies for Optimization of Markov Random Fields

Participant: Nikos Komodakis [Correspondant].

discrete optimization, Markov random field, duality, graph cuts, FASTPD is an optimization platform in C++ for the computer vision and medical imaging community (publicly available at http://www.csd.uoc.gr/~komod/FastPD/) developed mainly at Ecole Centrale and University of Crete. This is the most efficient publicly available platform in terms of a compromise of computational efficiency and ability to converge to a good minimum for the optimization of generic MRFs. The platform is used from approximately 1,500 users worldwide.

5.6. imaGe-based Procedural Modeling Using Shape Grammars

Participant: Iasonas Kokkinos [Correspondant].

procedural modeling, image-based building reconstruction, shape grammars GRAPES is a generic image parsing library based on re-inforcement learning (publicly available at http://vision.mas.ecp.fr/Personnel/teboul/grapesPage/index.php). It can handle grammars (binary-split, four-color, Hausmannian) and image-based rewards (Gaussian mixtures, Randomized Forests) of varying complexity while being modular and computationally efficient both in terms of grammar and image rewards. The platform is used from approximately 500 users worldwide.

5.7. Learning-based symmetry detection

Participant: Stavros Tsogkas [Correspondant].

Scale-Invariant Descriptor, Scale-Invariant Heat Kernel Signatures LBSD (publicly available at http://cvn.ecp.fr/personnel/tsogkas/code.html implements the learning-based approach to symmetry detection. It includes the code for running a detector, alongside with the ground-truth symmetry annotations that we have introduced for the Berkeley Segmentation Dataset (BSD) benchmark.

5.8. Texture Analysis Using Modulation Features and Generative Models

Participant: Iasonas Kokkinos [Correspondant].

Texture, modulation, generative models, segmentation, TEXMEG is a front-end for texture analysis and edge detection platform in Matlab that relies on Gabor filtering and image demodulation (publicly available at http://cvsp.cs.ntua.gr/software/texture/). Includes frequency- and time- based definition of Gabor- and other Quadrature-pair filterbanks, demodulation with the Regularized Energy Separation Algorithm and Texture/Edge/Smooth classification based on MDL criterion. The platform is used from approximately 250 users worldwide.

MNEMOSYNE Project-Team

5. New Software and Platforms

5.1. Positioning

Our previous works in the domain of well-defined distributed asynchronous adaptive computations [43], [40], [45] have already made us define a library (DANA [39]), closely related to both the notion of artificial neural networks and cellular automata. From a conceptual point of view, the computational paradigm supporting the library is grounded on the notion of a unit that is essentially a (vector of) potential that can vary along time under the influence of other units and learning. Those units can be organized into layers, maps and networks.

We also gather in the middleware EnaS (that stands for *Event Neural Assembly Simulation*; cf. http://gforge.inria.fr/projects/enas) our numerical and theoretical developments, allowing to simulate and analyze so called "event neural assemblies".

We will also have to interact with the High Performance Computing (HPC) community, since having large scale simulations at that mesoscopic level is an important challenge in our systemic view of computational neuroscience. Our approach implies to emulate the dynamics of thousands, or even millions, of integrated computational units, each of them playing the role of a whole elementary neural circuit (e.g. the microcolumn for the cortex). Mesoscopic models are considered in such an integrative approach, in order to exhibit global dynamical effect that would be hardly reachable by compartment models involving membrane equations or even spiking neuron networks.

The vast majority of high performance computing softwares for computational neuroscience addresses sub-neural or neural models [30], but coarser grained population models are also demanding for large scale simulations, with fully distributed computations, without global memory or time reference, as it is specified in (*cf.* § 3.2).

5.2. Dana

Participant: Nicolas Rougier.

DANA [39] is a python framework (http://dana.loria.fr) whose computational paradigm is grounded on the notion of a unit that is essentially a set of time dependent values varying under the influence of other units via adaptive weighted connections. The evolutions of a unit's value are defined by a set of differential equations expressed in standard mathematical notation which greatly ease their definition. The units are organized into groups that form a model. Each unit can be connected to any other unit (including itself) using a weighted connection. The DANA framework offers a set of core objects needed to design and run such models. The modeler only has to define the equations of a unit as well as the equations governing the training of the connections. The simulation is completely transparent to the modeler and is handled by DANA. This allows DANA to be used for a wide range of numerical and distributed models as long as they fit the proposed framework (e.g. cellular automata, reaction-diffusion system, decentralized neural networks, recurrent neural networks, kernel-based image processing, etc.).

5.3. Virtual Enaction

Participants: Frédéric Alexandre, André Garenne, Nicolas Rougier, Thierry Viéville.

The computational models studied in this project have applications that extend far beyond what is possible to experiment yet in human or non-human primate subjects. Real robotics experimentations are also impaired by rather heavy technological constraints; for instance, it is not easy to dismantle a given embedded system in the course of emerging ideas. The only versatile environment in which such complex behaviors can be studied both globally and at the level of details of the available modeling is a virtual environment, as in video games, Such a system can be implemented as “brainy-bot” (a programmed player based on our knowledge of the brain architecture) which goal is to survive in a complete manipulable environment.

In order to attain this rather ambitious objective we both (i) deploy an existing open-source video game middleware in order to be able to shape the survival situation to be studied and (ii) revisit the existing models in order to be able to integrate them as an effective brainy-bot. It consists of a platform associated to a scenario that is the closest possible to a survival situation (foraging, predator-prey relationship, partner approach to reproduction) and in which it is easy to integrate an artificial agent with sensory inputs (visual, touch and smell), emotional and somatosensory cues (hunger, thirst, fear, ..) and motor outputs (movement, gesture, ..) connected to a "brain" whose architecture will correspond to the major anatomical regions involved in the issues of learning and action selection (cortex areas detailed here, basal ganglia, hippocampus, and areas dedicated to sensorimotor processes). The internal game clock can be slowed down enough to be able to run non trivial brainy-bot implementations. This platform [13] has already being used by two students of the team and is now a new deliverable of the KEOpS project.

NEUROMATHCOMP Project-Team

4. New Software and Platforms

4.1. Virtual Retina: A Large-Scale Simulator of Biological Retina

Participants: Bruno Cessac, Maria-Jose Escobar [Universidad Técnica Federico Santa María, Valparaiso, Chile], Christobal Nettle [Universidad Técnica Federico Santa María, Valparaiso, Chile], Pierre Kornprobst, Adrien Wohrer [Group for Neural Theory - ENS, Paris, France].

Virtual Retina is a simulation software developped by Adrien Wohrer during his PhD [85], [84] that allows large-scale simulations of biologically-plausible retinas.

Virtual Retina has a variety of biological features implemented such as (i) spatio-temporal linear filter implementing the basic center/surround organization of retinal filtering, (ii) non-linear contrast gain control mechanism providing instantaneous adaptation to the local level of contrast; (iii) spike generation by one or several layers of ganglion cells paving the visual field.

Virtual Retina is under Inria CeCill C open-source licence, so that one can download it, install it and run it on one's own image sequences. Virtual Retina also offers a web service (v 2.1), so that users may test directly the main software on their own data, without any installation. This webservice was developed in collaboration with Nicolas Debeissat (engineer, 2002).

We are now interested in the analysis of the collective behavior of ganglion cells responses. To take this collective behavior into account, Virtual Retina needs to be extended since in its current version, ganglion cells are independent. The goal is to produce better retinal models from experimental recordings obtained with our collaborators at the Institut de la Vision (Olivier Marre and Serge Picaud), Evelyne Sernagor (New Castle University) and Luca Berdondini (IIT) using e.g. multi-electrode arrays. This will allow us to better understand the correlations between retina spikes trains and to improve the Virtual Retina model [84] in such a way that it could reproduce the retinal response at the population level. Another application is to the electric stimulation of a retina with implanted multi-electrode arrays in collaboration with the Institut de la Vision and the INT (Frédéric Chavane). Other evolutions of Virtual Retina are also investigated by external partners like the role/implementation of starbust amacrine cells involved in direction selectivity (collaboration with Universidad Técnica Federico Santa María, Valparaiso, Chile, and Centro de Neurociencia de Valaparaiso) (see also e.g., [74]).

- IDDN number: IDDN.FR.001.210034.000.S.P.2007.000.31235
- Version: v 2.2.2 (September 2011)
- Link: http://www-sop.inria.fr/neuromathcomp/public/software/virtualretina

4.2. Event Neural Assembly Simulation

Participants: Bruno Cessac, Sélim Kraria [Inria DREAM], Theodora Karvouniari, Hassan Nasser, Daniela Pamplona, Thierry Viéville [Inria Mnemosyne Bordeaux].

With the advent of new Multi-Electrod Arrays (MEA) techniques, the simultaneously recording of the activity of groups of neurons (up to several hundreds) over a dense configuration, supplies today a critical database to unravel the role of specific neural assemblies. Thus, the analysis of spike trains obtained from in vivo or in vitro experimental data, requires suitable statistical models. The Enas software offers new computational methods taking into account time constraints in neural networks (such as memory effects). It also offers several statistical model choices, some of these models already used in this community, and some others developed by us, and allows a quantitative comparison between these models. It also offers a control of finite-size sampling effects inherent to empirical statistics.

Compared to existing software (Pandora; Sigtool; Spyke Viewer; Orbital Spikes) Enas offers new computational methods taking into account time constraints in neural networks (such as memory effects), based on theoretical methods rooted in statistical physics and applied mathematics. The algorithms used are based on linear programming, nonlinear parameter estimations, statistical methods.

EnaS allows interfaces with existing toolboxes used by this community such as Matlab.

EnaS is developed joinly by the Neuromathcomp, CORTEX/Mnemosyne, and DREAM Inria teams, under CeCILL-C licence, APP logiciel Enas : IDDN.FR.OO1.190004.000.S.P.2014.000.31235. It can be freely downloaded.

It has benefited from the support of an ADT Inria from 2011 to 2013.

The software is freely downloadable at https://enas.inria.fr/#download.

Website: `https://enas.inria.fr/`

NEUROSYS Team

5. New Software and Platforms

5.1. Software

5.1.1. Visualization

- The NeuralFieldSimulator [0] computes numerically activity in two-dimensional neural fields by solving integral-differential equations involving transmission delays and visualizes the spatio-temporal activity. The tool includes a GUI that allows the user to choose field parameters. It is written in Python, open-source and is aimed to be promoted to become a major graphical visualization tool in the domain of neural field theory. We aim to establish this simulation software as the first open-source standard simulator for the neural field research community.
- *A*naesthesiaSimulator [0] simulates the activity of networks of spiking neurons subject to specific receptor dynamics. The tool is a platform to test effects of anaesthetics on neural activity and is still in its first stage of development. The neural activity is planned to be visualized in a 2D and 3D-plot evolving in time. It is written in Python, open-source and involves heavily the simulation package BRIAN [0].

5.2. Platforms

5.2.1. OpenViBE

This platform [0] is a C++ open-source software devoted to the design, test and use of Brain-Computer Interfaces. The OpenViBE platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. Key features of the platform are its modularity, high-performance, portability, its multiple-users facilities and its connection with high-end/Virtual Reality displays. The designer tool of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge [0] under the terms of the LGPL-V2 license. The development of OpenVibe is done in association with other Inria research teams (Hybrid, Athena, Potioc) for the national Inria project: ADT OpenViBE-NT. Neurosys is in charge of machine learning techniques and the interoperability with other tools such as Matlab, BCI2000, or TOBI.

[0] https://gforge.inria.fr/projects/nfsimulator/
[0] https://gforge.inria.fr/projects/anasim/
[0] http://briansimulator.org/
[0] http://openvibe.inria.fr/
[0] https://gforge.inria.fr/projects/openvibe/

PARIETAL Project-Team

5. New Software and Platforms

5.1. Scikit learn

Participants: Olivier Grisel [correspondant], Gaël Varoquaux, Bertrand Thirion, Michael Eickenberg, Loïc Estève, Alexandre Gramfort, Fabian Pedregosa Izquierdo.

Scikit-learn is an open-source machine learning toolkit written in Python/C that provides generic tools to learn information for the classification of various kinds of data, such as images or texts. It is tightly associated to the scientific Python software suite (Numpy/Scipy) for which it aims at providing a complementary toolkit for machine learning (classification, clustering, dimension reduction, regression). There is an important focus on code quality (API consistency, code readability, tests, documentation and examples), and on efficiency, as the scikit-learn compares favorably to state-of-the-art modules developed in R in terms of computation time or memory requirements. Scikit-learn is currently developed by more than 60 contributors, but the core developer team has been with the Parietal Inria team at Saclay-Île-de-France since January 2010. The scikit-learn has recently become the reference machine learning library in Python.

- Version: 0.15.2
- Programming language: Python, C/Cython

5.2. Nilearn

Participants: Gaël Varoquaux [correspondant], Bertrand Thirion, Loïc Estève, Alexandre Abraham, Michael Eickenberg, Alexandre Gramfort, Fabian Pedregosa Izquierdo, Elvis Dohmatob, Virgile Fritsch.

NiLearn is the neuroimaging library that adapts the concepts and tools of scikit-learn to neuroimaging problems. As a pure Python library, it depends on scikit-learn and nibabel, the main Python library for neuroimaging I/O. It is an open-source project, available under BSD license. The two key components of NiLearn are *i)* the analysis of functional connectivity (spatial decompositions and covariance learning) and *ii)* the most common tools for multivariate pattern analysis. A great deal of efforts has been put on the efficiency of the procedures both in terms of memory cost and computation time. NiLearn is maintained both through the help of Inria: a developer funded by Saclay CRI in 2012-2013, a 2013-2014 ADT and through the NiConnect project.

- Version: 0.1
- Programming language: Python

5.3. Mayavi

Participant: Gaël Varoquaux [Correspondant].

Mayavi is the most used scientific 3D visualization Python software (http://mayavi.sourceforge.net/). It has been developed by Prabhu Ramachandran (IIT Bombay) and Gaël Varoquaux (PARIETAL, Inria Saclay). Mayavi can be used as a visualization tool, through interactive command line or as a library. It is distributed under Linux through Ubuntu, Debian, Fedora and Mandriva, as well as in PythonXY and EPD Python scientific distributions. Mayavi is used by several software platforms, such as PDE solvers (fipy, sfepy), molecule visualization tools (http://pyrx.scripps.edu) and brain connectivity analysis tools (connectomeViewer).

See also the web page http://mayavi.sourceforge.net/ and the following paper http://hal.inria.fr/inria-00528985/en.

- Version: 3.4.0

5.4. Nipy

Participants: Bertrand Thirion [correspondant], Elvis Dohmatob, Gaël Varoquaux.

Nipy is an open-source Python library for neuroimaging data analysis, developed mainly at Berkeley, Stanford, MIT and Neurospin. It is open to any contributors and aims at developing code and tools sharing. Some parts of the library are completely developed by Parietal. It is devoted to algorithmic solutions for various issues in neuroimaging data analysis. The Nipy project is available, under BSD license, and within NeuroDebian.

See also the web page http://nipy.org.

- Version: 0.3

5.5. PyHRF

Participants: Philippe Ciuciu [correspondant], Aina Frau Pascual, Salma Torkhani.

PyHRF is a set of tools for within-subject fMRI data analysis, focused on the characterization of the hemodynamics. Within the chain of fMRI data processing, these tools provide alternatives to the classical within-subject GLM estimation step. The inputs are preprocessed within-subject data and the outputs are statistical maps and/or fitted HRFs. The package is mainly written in Python and provides the implementation of the two following methods:

- The joint-detection estimation (JDE) approach, that divides the brain into functionally homogeneous regions and provides one HRF estimate per region as well as response levels specific to each voxel and each experimental condition. This method embeds a temporal regularization on the estimated HRFs and an adaptive spatial regularization on the response levels.
- The Regularized Finite Impulse Response (RFIR) approach, that provides HRF estimates for each voxel and experimental conditions. This method embeds a temporal regularization on the HRF shapes, but proceeds independently across voxels (no spatial model).

The development of PyHRF is now funded by an Inria ADT, in collaboration with MISTIS.

- Version: 0.1
- Keywords: Hemodynamic response function; estimation; detection; fMRI
- License: BSD 4
- Multiplatform: Windows - Linux - MacOSX
- Programming language: Python

POPIX Team

5. New Software and Platforms

5.1. Monolix

Participants: Marc Lavielle, Célia Barthélémy.

MONOLIX is an easy, fast and powerful tool for parameter estimation in nonlinear mixed-effect models, model diagnosis and assessment, and advanced graphical representation. It is a platform of reference for model-based drug development. Pharmacometricians and biostatisticians can rely on MONOLIX for population analysis and to model PK/PD and other complex biochemical and physiological processes.

MONOLIX was developed by Inria until June 2011. The start-up Lixoft now develops and supports MONOLIX. POPIX collaborates closely with Lixoft to convert research results into new user features available in MONOLIX.

5.2. MLXtran

Participant: Marc Lavielle.

MONOLIX is associated with MLXtran, a powerful and immediately readable declarative language for describing complex pharmacometric and statistical models. MLXtran can be used and interfaced with various environments, e.g., R, Matlab, etc.

POPIX collaborates closely with Lixoft on the definition of the specifications and the syntax of MLXtran. Implementation is then ensured by Lixoft.

5.3. Clinical trial simulator

Participants: Marc Lavielle, Fazia Bellal, Célia Barthélémy.

A clinical trial simulator (CTS) enables effective implementation of the learn-and-confirm paradigm in drug development. Through simulations the anticipated success rate of a future trial can be estimated. For various reasons industry has not embraced currently available software for trial simulation. A new tool is essential for Model Based Drug Development (MBDD).

POPIX is responsible for developing a new CTS within the DDMoRe project (see below). A new version of the CTS is available as a R package since December 2014. The capabilities of this new version comprise:

- Flexible study designs used in Phase 2 of clinical drug development: parallel group studies, crossover studies, complex treatments defined as a combination of different treatments
- Simulation of patients sampled from a joint distribution or using an external data file
- Simulation of exposure to the investigated drug and several types of drug effects related to drug exposure (continuous, categorical, count, time-to-event)
- Inter individual and intra individual variability models
- Graphics and statistical tests

5.4. MLXplore

Participant: Marc Lavielle.

MLXplore is a graphical and interactive software for the exploration and visualization of complex pharmacometric models. MLXplore also includes the ability to study the statistical variability of the models, and to model and study complex administration designs.

MLXplore does not require MONOLIX, although they make for a powerful combination, enabling to use the same, human-readable model description, to finely explore the properties of the model on the one hand, and on the other hand use the same model for advanced parameter estimation in the context of population analysis and mixed effect statistics.

MLXplore is an ideal tool to learn about pharmacometric models and population analysis, and is used extensively in the online wiki WikiPopix created by POPIX, found at: https://wiki.inria.fr/popix. MLXplore is developed by Lixoft but POPIX collaborates closely with Lixoft on on the definition of the specifications of MLXplore.

SHACRA Project-Team

4. New Software and Platforms

4.1. SOFA

4.1.1. Description of the SOFA framework

SOFA [0] is an open-source software framework targeted at real-time multi-physics simulation, with an emphasis on medical simulation. The idea of SOFA was initiated by members of the SHACRA team, strongly supported by Inria and still actively developed within the SHACRA team. Based on C++, the SOFA engine provides many algorithms, physiological models and anatomical data, made available within a plugin architecture. With its high level of modularity, SOFA appears to be an efficient tools to benchmark and develop new medical technologies using existing algorithms.

The SOFA framework relies on a multi-model representation which allows to have several representations (e.g. mechanical, thermal and visual) of the same object. Those different representations are connected together through a mechanism called mapping. With this features, it is also possible to have models of very different nature interacting together, for instance rigid bodies, deformable objects, and fluids. CPU and GPU implementations can be transparently combined to exploit the computational power of modern hardware architectures.

SOFA is at the heart of a number of research projects, including cardiac electro-physiology modeling, interventional radiology planning and guidance, planning for cryosurgery and deep brain stimulation, robotics, percutaneous procedures, laparoscopic surgery, non-rigid registration, etc. As proof of its success, SOFA has been downloaded nearly 150,000 times, and is used today by many research groups around the world, as well as a number of companies. The mailing list used to exchange with the community includes several hundreds of researchers, from about 50 different institutions. SOFA is currently used by a number of companies (Siemens Corporate Research, Digital Trainers, Epona Medical, Moog, SenseGraphics, etc.) and also provides the key technology on which our newly created start-up (InSimo) is relying. We strongly believe that today SOFA has become a reference for academic research, and is increasingly gaining recognition for product prototyping and development. The best illustration of this worldwide positioning is the role of SOFA in the challenge set by the HelpMeSee foundation to win the contract for the development of a very ambitious and high-risk project on cataract surgery simulation.

4.1.2. Consortium

At the end of the year 2014, the creation of a consortium SOFA has been enacted. The purpose of this consortium is to define the suitable orientation in terms of development, lead to its achievement while creating a propitious ecosystem for research, industry and for the creation of numerous startups. Beside lead the development of SOFA, this consortium has to maintain the existing code, and last but not least, manage the SOFA community and help it to grow.

4.1.3. SOFA Day after ISBMS'14

On the occasion of the 6^{th} ISBMS conference, we organized a "SOFA Day" giving us a unique opportunity to meet SOFA users from various research institutes or companies, and exchange about the future improvements and development of the engine. We use these occasions to share and discuss with SOFA users, to refine the roadmap and stay tuned with our audience.

4.1.4. A new website

Finally, a new website has been developed during the last month of the year. The final version of the website will be released in spring 2015. The website is a very important tool for the community (especially new users). The SOFA consortium will be in charge of this assignment.

[0] More information about SOFA at http://www.sofa-framework.org

SISTM Team

5. New Software and Platforms

5.1. New Software

5.1.1. TcGSA

An *R* package for the gene set analysis of longitudinal gene expression data sets. Under development, and soon to be available on the CRAN website, this package implements a Time-course Gene Set Analysis method and provides useful plotting functions facilitating the interpretation of the results.

5.2. Upgraded Software

5.2.1. NIMROD

We have written a specific program called NIMROD for estimating parameter of ODE based population models. It has been regularly updated. For instance, we have adapted the program for parallel computing, in collaboration with the MCIA (Mésocentre de calcul intensif Aquitain) facility, which makes available a large computer with more than 3000 cores. This program is described in [43]. Although the program is available on the ISPED website [0], it is not user-friendly and needs further improvement to be more widely used. By now, the users are the current or previous (Jérémie Guedj, Julia Drylewicz, Mélanie Prague) members of the team and close collaborators (Andrew Yates). Furthermore, as a validation step, it would need a head-to-head comparison with other available softwares. We bet that our program can be very competitive for parameter identification in ODE models with more than two compartments.

5.2.2. marqLevAlg

An *R* package for function optimization. Available on CRAN, this package performs a minimization of function based on the Marquardt-Levenberg algorithm. This package is really useful when the surface to optimize is non-strictly convex or far from a quadratic function. A new convergence criterion, the relative distance to maximum (RDM), allows the user to have a better confidence in the stopping points, other than basic algorithm stabilization.

5.2.3. VSURF

An *R* package for Variable Selection Using Random Forests. Available on CRAN, this package performs an automatic (meaning completely data-driven) variable selection procedure. Originally designed to deal with high dimensional data, it can also be applied to standard datasets.

5.2.4. R2GUESS

R2GUESS package is a wrapper of the GUESS (Graphical processing Unit Evolutionary Stochastic Search) program. GUESS is a computationally optimised C++ implementation of a fully Bayesian variable selection approach that can analyse, in a genome-wide context, single and multiple responses in an integrated way. The program uses packages from the GNU Scientific Library (GSL) and offers the possibility to re-route computationally intensive linear algebra operations towards the Graphical Processing Unit (GPU) through the use of proprietary CULA-dense library.

[0] http://etudes.isped.u-bordeaux2.fr/BIOSTATISTIQUE/NIMROD/documentation/html/index.html.

VISAGES Project-Team

5. New Software and Platforms

5.1. Shanoir

Participants: Justine Guillaumont, Michael Kain, Yao Yao, Christian Barillot.

Shanoir (Sharing NeurOImaging Resources) is an open source neuroinformatics platform designed to archive, structure, manage, visualize and share neuroimaging data with an emphasis on multi-centric collaborative research projects (Figure 2). It provides a user-friendly interface, a secure web access and offers an intuitive workflow to facilitate the collecting and retrieving of neuroimaging data from multiple sources and a wizard to make the completion of metadata easy. Shanoir comes along many features of neuroimaging data management systems along with research-oriented data imaging organization and enhanced data accessibility, support multi-centers clinical studies on subjects or group of subjects and other functionalities such as anonymization of data. For a better distribution/replication of stored data on a Shanoir server an export and import function on base of XML has been developed for the usage of server administrators.

Shanoir APP registration number is: IDDN.FR.001.520021.003.S.A.2008.000.31230

See also the web page http://www.shanoir.org

- Keywords: neuroimaging, ontology, sharing neuroimages
- Version: 0.5
- Software benefit: full featured neuroimaging management system with additionnal web services
- APP: IDDN.FR.001.520021.000.S.P.2008.000.31230
- License: Licence QPL
- Type of human computer interaction: Online web application, web service (SOAP messages based)
- OS/Middleware: Windows, Mac et Linux.
- Required library or software: Java 1.6, JBoss server, JBoss Seam, JSF, JPA Hibernate, EJB, Richfaces, Faceless, Ajax4JSF, Dcmtk, Dcm4chee.
- Programming language: Java / J2EE
- Documentation: see the website

5.2. ShanoirUploader

Participants: Justine Guillaumont, Michael Kain, Christian Barillot.

The ShanoirUploader (Fig. 3) is a desktop application on base of JavaWebStart (JWS). The application can be downloaded and installed using an internet browser. It interacts with a PACS to query and retrieve the data stored on any PACS. After this the ShanoirUploader sends the data to a Shanoir server instance to import these data into a Shanoir server instance. This application bypasses the situation, that in most of the clinical network infrastructures a server to server connection is complicated to set up between the PACS and a Shanoir server instance.

An APP registration is in progress. See also the web page http://shanoir.gforge.inria.fr as the ShanoirUploader documentation is integrated on this page.

- Keywords: neuroimaging, ontology, sharing neuroimages
- Version: 0.1
- Software benefit: offers a great solution to query a PACS server, download the data and send the data to a Shanoir server
- License: no defined license for the moment
- Type of human computer interaction: desktop application on base of JavaWebStart (JWS), web service (SOAP messages based)
- OS/Middleware: Linux, Windows and Mac
- Required library or software : Java SDK, installed on client machine
- Programming language: Java
- Documentation : see the website

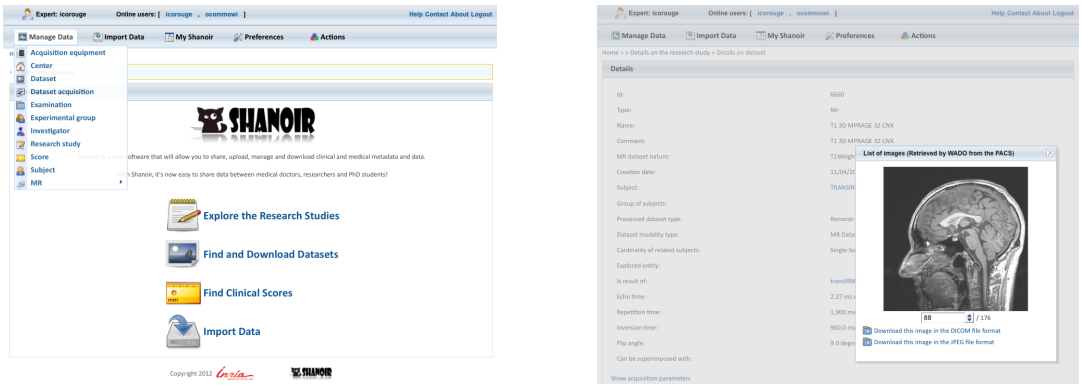


Figure 2. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

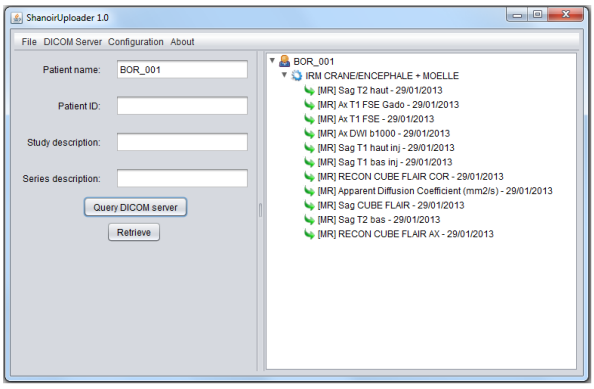


Figure 3. The ShanoirUploader software is a desktop application designed to interact with a PACS to query and retrieve the data stored on any PACS.

5.3. iShanoir

Participants: Michael Kain, Christian Barillot.

iShanoir (Fig. 4) is an iOS application, designed for iPhone and iPad. On base of this application a Shanoir server can be accessed. For this the Shanoir SOAP web-services are called. iShanoir can be used to access and navigate in the data tree structure, stored on a Shanoir server. iShanoir displays as well additional meta data corresponding to the data entities in the tree structure. On base of these informations image files (NIfTI and DICOM) can be selected and downloaded on a local iPhone/iPad in a temporary cache. From this cache the files can be opened and displayed with a corresponding viewer, the user already has to have installed on his device. This project is the result of the internship of Hélène Gérome in the team. An APP registration is in progress.

See also the web page http://shanoir.gforge.inria.fr as the iShanoir documentation is integrated on this page.

- Keywords: neuroimaging, ontology, sharing neuroimages
- Version: 0.1
- Software benefit: offers access to data stored on a Shanoir server from native iOS devices, like iPhones and iPads
- License: no defined license for the moment
- Type of human computer interaction: mobile iOS Cocoa Touch application with web service connection
- OS/Middleware: iOS
- Required library or software: none
- Programming language: Objective-C
- Documentation : see the website

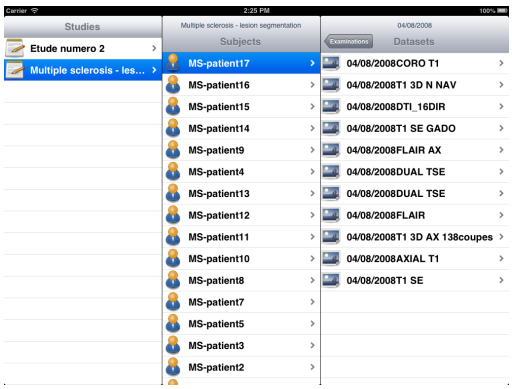


Figure 4. The iShanoir software is a desktop application designed to...

5.4. AutoMRI

Participants: Fang Cao, Isabelle Corouge, Pierre Maurel, Elise Bannier.

AutoMRI Based on MATLAB and the SPM8 toolbox, autoMRI provides complete pipelines to pre-process and analyze various types of images (anatomical, functional, perfusion, metabolic, relaxometry, vascular). This software is highly configurable in order to fit to a wide range of needs. Pre-processing includes segmentation of anatomical data, as well as co-registration, spatial normalization and atlas building of all data types. The analysis pipelines perform either within-group analysis or between-group or one subject-versus-group comparison and produce statistical maps of regions with significant differences. These pipelines can be applied to structural data to exhibit patterns of atrophy or lesions, to ASL (both pulsed or pseudo-continuous sequences) or PET data to detect perfusion or metabolic abnormalities, to relaxometry data to detect deviations from a template, to functional data - either BOLD or ASL - to outline brain activations related to block or event-related paradigms. In addition to the standard General Linear Model approach, the ASL pipelines implement an a contrario approach and, for patient-specific perfusion study, an heteroscedastic variance model. Besides, the vascular pipeline processes 4D MRA data and enables accurate assessment of hemodynamic patterns (Figure 5).

- Keywords: fMRI, MRI, ASL, fASL, SPM, automation
- Software benefit: Automatic MRI data analysis based on SPM. Once the parameters are set, the analysis is performed without human interaction.
- APP: Part in IDDN.FR.001.130017.000.S.A.2012.000.31230
- License: Part under CeCILL
- Type of human computer interaction: Matlab function (script, no GUI)
- OS/Middleware: Windows, OS X, Linux
- Required library or software: Matlab, SPM, SPM toolboxes : Marsbar, LI-toolbox, NS
- Programming language: Matlab
- Documentation: available at https://gforge.inria.fr/projects/autofmri/ and https://gforge.inria.fr/projects/asl/

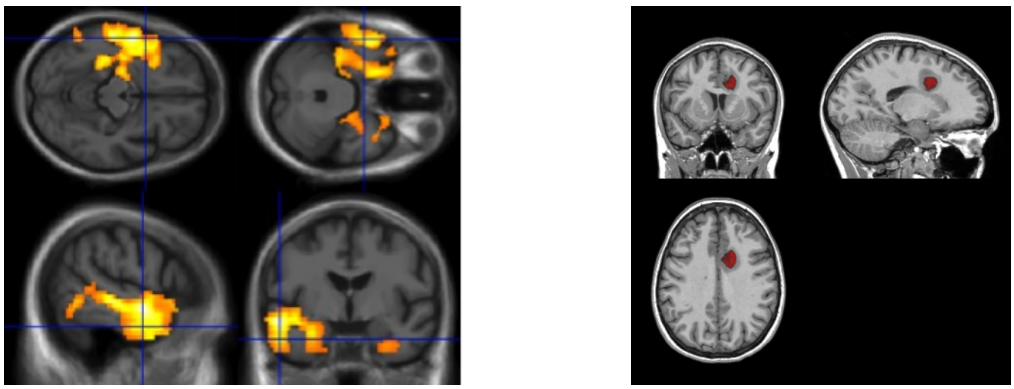


Figure 5. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (right), Detection of relaxometry defect in an MS patient (left).

5.5. medInria

Participants: René-Paul Debroize, Guillaume Pasquier, Laurence Catanese, Olivier Commowick.

medInria is a national Inria project shared between 4 Inria teams (Asclepios, Athena, Parietal and Visages). 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. medInria 2.2.1 has been released in September 2014 for the main distribution platforms. medInria core API source code is also released under a BSD license.

See also Figure 6 and the web page http://med.inria.fr

- Keywords: medical imaging, diffusion imaging, registration, filtering, user-friendly interface
- Software benefit: user-friendly interface to cutting-edge research tools for research clinicians. Straightforward to add functionalities through plugins.
- License: core: BSD, plugins: choice of each team.
- Type of human computer interaction: Qt-based GUI
- OS/Middleware: Windows, Mac et Linux.
- Required library or software : Qt, DTK, ITK, VTK.
- Programming language: C++

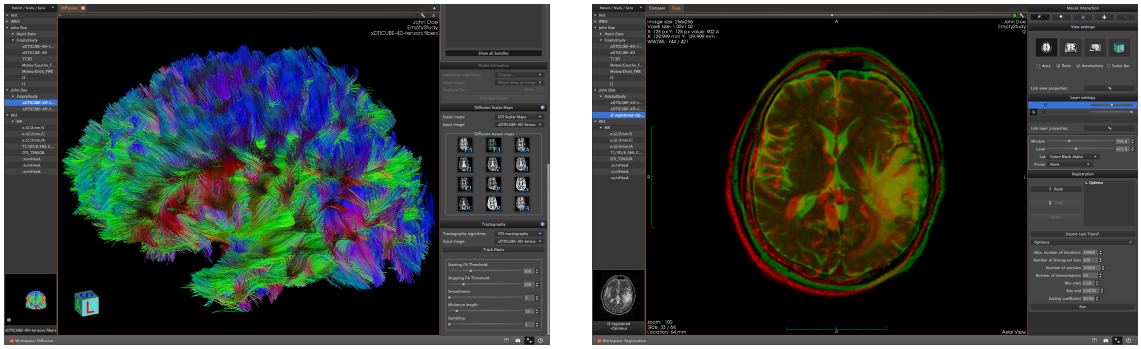


Figure 6. The medInria software platform: Fused view of registered images (right), Tractography overlapped with 3D image (left)

5.6. Anima

Participants: Fang Cao, Laurence Catanese, Olivier Commowick, René-Paul Debroize, Florent Leray, Renaud Hédouin, Guillaume Pasquier.

Anima is a set of libraries and tools developed by the team as a common repository of research algorithms. As of now, it contains tools for image registration, statistical analysis (group comparison, patient to group comparison), diffusion imaging (model estimation, tractography, etc.), quantitative MRI processing (quantitative relaxation times estimation, MR simulation), image denoising and filtering, and segmentation tools. All of these tools are based on stable libraries (ITK, VTK), making it simple to maintain.

- Keywords: medical imaging, diffusion imaging, registration, filtering, relaxometry
- Software benefit: New methodological image processing, common place for team code
- Type of human computer interaction: C++ API
- OS/Middleware: Windows, Mac and Linux.
- Required library or software : ITK, VTK.
- Programming language: C++

5.7. Integration of EEG and fMRI

Participants: Marsel Mano, Lorraine Perronnet.

Related to the project Hemisfer there have been development of new functions, scripts and demos for the acquisition and processing of the EEG and fMRI data in Real-time. These include:

- Functions for fMRI header info reader, volume reader, motion correction, slice time correction nifty output conversion, real time fMRI initialization, real time fMRI processing, z-score calculation, volume smoother, alignment, etc., functions for real time EEG data acquisition, filtering, power calculation and display.
- Scripts for various protocols used in offline fMRI experiments, real time processing loop for EEG and fMRI.
- Demo for real time acquisition of the EEG and fMRI data, demo for real time processing efficiency of the fMRI data, demo for the real time processing of EEG data, real time z-Score for fMRI data.
- Several small aux functions for I/O interfaces (e.g. com, serial)

In the current stage the prototype also relies on various other free toolboxes (e.g. SPM, pnet)

- Keywords: medical imaging, EEG, fMRI
- Software benefit: integration of EEG and fMRI processing
- Type of human computer interaction: C++ API, shell scripts
- OS/Middleware: Windows, Mac and Linux.
- Required library or software : SPM, pnet.
- Programming language: C++, shell scripts

5.8. Platforms

5.8.1. The Neurinfo Platform

VISAGES is the founding actor of a new experimental research platform which was installed in August 2009 at the University Hospital of Rennes. The University of Rennes 1, Inria, Inserm for the academic side, and the University Hospital of Rennes and the Cancer Institute “Eugene Marquis“ for the clinical side, are partners of this neuroinformatics platform called NeurINFO (http://www.neurinfo.org). This platform has been supported under the “Contrat de Projets Etat-Région” (C. Barillot is the PI) and has received a total amount of 5.1 Meuros for the period 2007–2013. European (FEDER), National (through Ministry of research, Inria, Inserm and ANR) and local councils (Brittany Region, Ille et Vilaine, and Rennes Metropolis) have joined their effort to support this operation for a total amount of 5070 keuros (600keuros for the infrastructures, 3670keuros for the equipments and 800keuros for the functioning). This application was set up through the Regional PIMATGI initiative coordinated by INSERM in Brittany (C. Roux). The overall PIMATGI initiative served for the financing of three distinct, but complementary, platforms: NeurINFO, TheraFONC as a technical platform dedicated to therapy guided by functional imaging especially in the oncology domain (Inserm U 650 - LaTIM, Dir. Ch. Roux, Brest), and TherA-Image as a platform dedicated to image guided mini-invasive surgery and therapy especially in the domain of cardio-vascular diseases (U 642 -LTSI, Dir. L. Senhadji, Rennes).

Concerning the NeurINFO Platform, the activity domain is a continuum between methodological and technological research built around specific clinical research projects. The ambition is to do innovation in science, technology and medical technology transfer for the implementation on the clinical field. On the medical field, the translational research domain mainly concerns medical imaging and more specifically the clinical neurosciences. Among them are multiple sclerosis, epilepsy, neurodegenerative, neurodevelopmental and psychiatric diseases, surgical procedures of brain lesions, neuro-oncology and radiotherapy planning. Beyond these CNS applications, the platform is also open to alternative applications. Neurinfo ambitions to support the emergence of research projects based on their level of innovation, their pluri-disciplinarity and their ability to foster collaborations between different actors (public and private research entities, different medical specialties, different scientific profiles). In this context, a new research 3T MRI system (Siemens Verio system) was

acquired in summer 2009 in order to develop the clinical research in the domain of morphological, functional, structural and cellular in-vivo imaging. In 2014 a new equipment for simultaneous recording of EEG and MRI images has been acquired from Brain Product. Visages and its partners in the Neurinfo project are committed to use this new research platform for developing new regional, national and international collaborations around fundamental and applied clinical research projects dealing with in-vivo medical imaging. In 2014, the two engineers running the platform (Elise Bannier and Isabelle Corouge), members of the Visages team, moved from temporary employment contracts to open-ended research engineers contracts.

ANGE Project-Team

5. New Software and Platforms

5.1. FRESHKISS

Although the Saint-Venant system is the cornerstone of flow modelling in geosciences, this does not mean that the transfer of the efficient dedicated simulation tools is achieved in the geoscience community.

ANGE collaborates with scientists, laboratories and companies that are interested in scientific advances which makes the valuation and the transfer of results easier.

ANGE aims at developing robust and efficient numerical tools. For the simulation of the free surface Navier-Stokes equations, numerical tools have been developed namely FRESHKISS2D[0] and FRESHKISS3D. These tools are used by several scientists typically in the BIOCORE Inria project-team, at EDF and in public research laboratories.

FRESHKISS3D is a numerical code solving the 3D hydrostatic and incompressible Navier-Stokes equations with variable density. This code was initially dedicated to research activities within the team but we now aim at turning it into a numerical tool being used by non-mathematicians. Indeed, there is a demand in research laboratories and companies to use this tool. A young engineer (R. Hamouda) has been hired (ADT In@lgae funded by Inria) and its assignment is to improve/enrich the code and to make it user-friendly. Notice that FRESHKISS3D is used for teaching (master students in geosciences) at university Denis Diderot Paris 7 and IPGP.

5.2. TSUNAMATHS

TSUNAMATHS is an educational platform aiming at simulating historical tsunamis. Real data and mathematical explanations are provided to enable people to better understand the overall process of tsunamis. It is available on the Internet:

http://ange.raoufhamouda.com/tsunami/en_animation.htm

It was presented in the framework of the 2013 UNESCO year of "Mathematics of Planet Earth" and then exhibited at the ICM 2014 session (see § 9.3).

[0] FRESHKISS: FREe Surface Hydrodynamics using KInetic SchemeS

CASTOR Project-Team

5. New Software and Platforms

5.1. Free boundary equilibrium codes

5.1.1. CEDRES++

Participants: Jacques Blum, Cédric Boulbe, Blaise Faugeras, Holger Heumann, Sylvain Bremond [CEA], Eric Nardon [CEA].

In Tokamaks, at the slow resistive diffusion time scale, the magnetic configuration in the plasma can be described by the MHD equilibirum 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 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). The aim of the inverse problem is to find currents in the PF coils in order to best fit a given plasma shape. An evolutive version of the code has also been recently developed. This version takes into account the circuit equations in the PF coils. These equations give a time dependent relation between the voltages, the total current in the coils and the time derivative of the magnetic flux. Induced currents in passive structures like the vacuum vessel are also considered in this dynamic equilibrium problem. This new version of the code is an important tool for plasma scenario development and Tokamak design studies. A version of CEDRES++ is avalaible in the environment of the european projet Eurofusion WPCD.

5.1.2. FEEQS.M

Participant: Holger Heumann.

FEEQS.M (Finite Element Equilibrium Solver in Matlab) is a MATLAB implementation of the numerical methods in [15] 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.

5.2. Equinox

Participants: Jacques Blum, Cédric Boulbe, Blaise Faugeras.

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.

5.3. VacTH

Participants: Jacques Blum, Cédric Boulbe, Blaise Faugeras.

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 (see [45]). 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 [13] 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 (see [46]).

5.4. FBGKI

Participants: Sébastian Minjeaud, Richard Pasquetti.

The Full Braginskii solver considers the equations proposed by Braginskii (1965), in order to describe the plasma turbulent transport in the edge part of tokamaks. These equations rely on a two fluid (ion - electron) description of the plasma and on the electroneutrality and electrostatic assumptions. One has then a set of 10 coupled non-linear and strongly anisotropic PDEs. FBGKI makes use in space of high order methods: Fourier in the toroidal periodic direction and spectral elements in the poloidal plane. The integration in time is based on a Strang splitting and Runge-Kutta schemes, with implicit treatment of the Lorentz terms (DIRK scheme). The spectral vanishing viscosity (SVV) technique is implemented for stabilization. Static condensation is used to reduce the computational cost. In its sequential version, a matrix free solver is used to compute the potential. The parallel version of the code is under development.

5.5. Platforms

5.5.1. FluidBox

Participants: Boniface Nkonga [contact], Hervé Guillard.

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. The linear solver PaStiX is integrated in FluidBox. A partitioning tool exists in the package and uses Scotch.

5.5.2. Plato

Participants: Hervé Guillard [contact], Boniface Nkonga, Giorgio Giorgiani, Afeintou Sangam, Elise Estibals.

PlaTo (A platform for Tokamak simulation) is a suite of data and softwares 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. The use of this platform for large scale simulation has been validated up to $\mathcal{O}(1000)$ CPU [14] [10]

The numerical schemes used in the platform are of finite element or finite volume type. To deal with the geometry of tokamaks, Plato uses curved prisms made of a tensor product of unstructured triangular meshes in the poloidal plane by 1D meshes in the toroidal direction. The numerical strategy uses 3D finite volume schemes for the first-order terms and P1 finite element for second-order terms. Several models (anisotropic diffusion, Grad-Shafranov equilibrium, reduced MHD model) have been validated and are presently available. In addition, a stabilized finite element method using a tensor product of C^1 (Powell-Sabin) triangular element by 1D cubic splines in the toroidal direction has been recently developed and is presently in a validation phase.

5.5.3. Jorek-Inria

Participants: Hervé Guillard, Boniface Nkonga, Emmanuel Franck [Tonus, Inria Nancy - Grand Est], Ahmed Ratnani [IPP Garching].

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

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

The new formulation of the Jorek-Inria code extends this approximation strategy by introducing more flexibility and a variety of finite elements used in the poloidal plane and in the toroidal direction. It also proposes a sparse matrix interface SPM (Sparse Matrix Manager) that allows to develop clean code without a hard dependency on any linear solver library (i.e. PetSc, Pastix, Mumps, ...). It is expected that the two developments PlaTo and Jorek-Inria will merge in the next years.

CLIME Project-Team

5. New Software and Platforms

5.1. Data assimilation library: Verdandi

Participants: Nicolas Claude, Vivien Mallet, Dominique Chapelle [M3DISIM], Philippe Moireau [M3DISIM].

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

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

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

In 2014, version 1.6 was released with a lot of new unit tests, within the Google Test framework. The extended Kalman filter now supports model error. For users of C++11, a native random perturbation manager has been added and allows to circumvent the use of Newran. The overall compatibility with Clang has been reinforced. The documentation was significantly improved, especially about the installation under Windows and Linux.

5.2. Image processing library: Heimdali

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

The initial aim of the image processing library Heimdali was to replace an internal Inria library (named Inrimage) by a library based on standard and open source tools, and mostly dedicated to satellite acquisitions.

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

- making easier the sharing and development of image assimilation softwares. For that purpose, the installation is easily achieved with the package manager Conda.
- developing generic tools for image processing and assimilation based on ITK (Insight Segmentation and Registration Toolkit http://www.itk.org). In reverse providing tools to ITK and contribute to the ITK community. Our software corresponds to issues related to satellite acquisitions but could be of interest for processing medical image sequences.

The main components of Heimdali concern:

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

In 2014, prototypes of the two first items have been defined. The development of the whole library should be available in 2015.

5.3. Polyphemus

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

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

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

Fig. 1 depicts a typical result produced by Polyphemus.

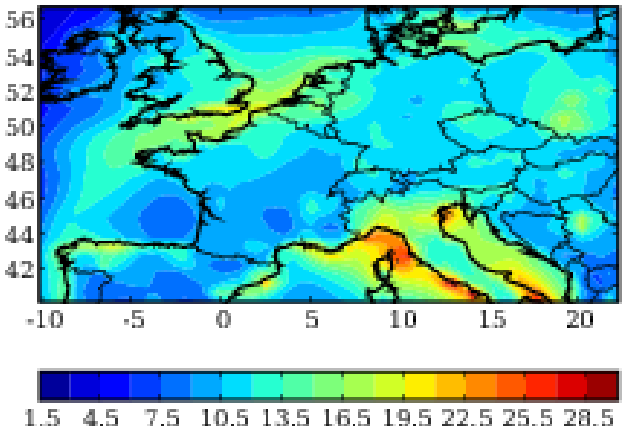


Figure 1. Map of the relative standard deviation (or spread, %) of an ensemble built with Polyphemus (ozone simulations, $\mu g\ m^{-3}$). The standard deviations are averaged over the summer of 2001. They provide an estimation of the simulation uncertainties.

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

In 2014, Polyphemus was developed to better handle in-cloud and below-cloud scavenging. The interface of its Eulerian model, Polair3D, was extended to allow for detailed sensitivity analysis.

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.

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.

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.

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.

FLUMINANCE Project-Team

5. New Software and Platforms

5.1. DenseMotion software - Estimation of 2D dense motion fields

Participant: Etienne Mémin.

This code allows the computation from two consecutive images of a dense motion field. The estimator is expressed as a global energy function minimization. The code enables the choice of different data models and different regularization functionals depending on the targeted application. Generic motion estimators for video sequences or fluid flows dedicated estimators can be set up. This software allows in addition the users to specify additional correlation based matching measurements. It enables also the inclusion of a temporal smoothing prior relying on a velocity vorticity formulation of the Navier-Stoke equation for Fluid motion analysis applications. The different variants of this code correspond to research studies that have been published in IEEE transaction on Pattern Analysis and machine Intelligence, Experiments in Fluids, IEEE transaction on Image Processing, IEEE transaction on Geo-Science end Remote Sensing. The binary of this code can be freely downloaded on the FLUID web site http://fluid.irisa.fr.

5.2. 2DLayeredMotion software - Estimation of 2D independent mesoscale layered atmospheric motion fields

Participant: Etienne Mémin.

This software enables to estimate a stack of 2D horizontal wind fields corresponding to a mesoscale dynamics of atmospheric pressure layers. This estimator is formulated as the minimization of a global energy function. It relies on a vertical decomposition of the atmosphere into pressure layers. This estimator uses pressure data and classification clouds maps and top of clouds pressure maps (or infra-red images). All these images are routinely supplied by the EUMETSAT consortium which handles the Meteosat and MSG satellite data distribution. The energy function relies on a data model built from the integration of the mass conservation on each layer. The estimator also includes a simplified and filtered shallow water dynamical model as temporal smoother and second-order div-curl spatial regularizer. The estimator may also incorporate correlation-based vector fields as additional observations. These correlation vectors are also routinely provided by the Eumetsat consortium. This code corresponds to research studies published in IEEE transaction on Geo-Science and Remote Sensing. It can be freely downloaded on the FLUID web site http://fluid.irisa.fr.

5.3. 3DLayeredMotion software - Estimation of 3D interconnected layered atmospheric motion fields

Participant: Etienne Mémin.

This software extends the previous 2D version. It allows (for the first time to our knowledge) the recovery of 3D wind fields from satellite image sequences. As with the previous techniques, the atmosphere is decomposed into a stack of pressure layers. The estimation relies also on pressure data and classification clouds maps and top of clouds pressure maps. In order to recover the 3D missing velocity information, physical knowledge on 3D mass exchanges between layers has been introduced in the data model. The corresponding data model appears to be a generalization of the previous data model constructed from a vertical integration of the continuity equation. This research study has been published in IEEE trans. on Geo-Science and Remote Sensing. The binary of this code can be freely downloaded on the FLUID web site http://fluid.irisa.fr.

5.4. Low-Order-Motion - Estimation of low order representation of fluid motion

Participants: Anne Cuzol, Etienne Mémin.

This code enables the estimation of a low order representation of a fluid motion field from two consecutive images.The fluid motion representation is obtained using a discretization of the vorticity and divergence maps through regularized Dirac measure. The irrotational and solenoidal components of the motion fields are expressed as linear combinations of basis functions obtained through the Biot-Savart law. The coefficient values and the basis function parameters are formalized as the minimizer of a functional relying on an intensity variation model obtained from an integrated version of the mass conservation principle of fluid mechanics. Different versions of this estimation are available. The code which includes a Matlab user interface can be downloaded on the FLUID web site http://fluid.irisa.fr. This program corresponds to a research study that has been published in the International Journal on computer Vision.

KALIFFE Project-Team

5. New Software and Platforms

5.1. New Softwares

5.1.1. Hope : High Order Program for Energy

This software is focused on the numerical simulation of 2D transport equation using fully deterministic methods (high order finite difference solvers, semi-Lagrangian methods).

Numerical simulation of guiding center model [9]

We consider the diocotron instability for an annular electron layer. This plasma instability is created by two sheets of charge slipping past each other and is the analog of the Kelvin-Helmholtz instability in fluid mechanics. We propose a comparison of two different numerical methods : the mixed method (top): this method uses alternatively a semi-Lagrangian and finite difference method with fifth order Hermite WENO reconstruction. The choice is made automatically according to a good preservation of mass (the finite difference method is conservative). the semi-Lagrangian (bottom): this method is based on a cubic spline interpolation for the reconstruction of the distribution function.

Numerical simulation in a D shape [9]

This simulation illustrates an instability development of the solution to the guiding-center model in a D-shaped domain. We present the difference between the perturbed density and the steady state density. An instability develops and generates small filaments. It correspond to the motion of the density in the transverse plane of the tokamak.

Figure 2 illustrates the evolution of density governed by the guiding-center model. We present the difference between the perturbed density and the steady state density, *i.e.*$\delta\rho(t) = \overline{\rho}(t) - \overline{\rho}_0$. We observe that the difference of density $\delta\rho$ revolves, and small filaments appear at time $t = 200$. Until the time $t = 300$, we can clearly identify the filaments.

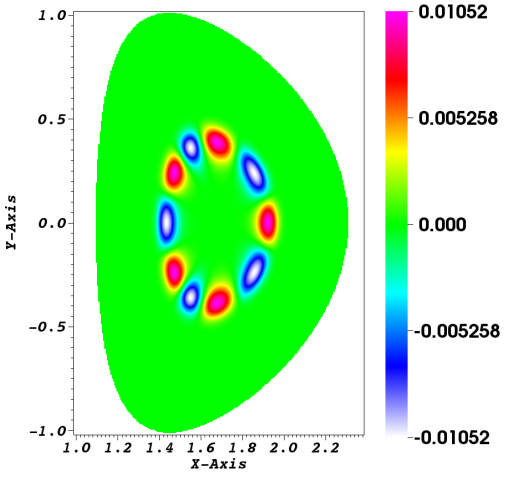
5.1.2. Towards 4D numerical simulations

The discretization of the Drift-Kinetic model can be developed very similarly as the one for the guiding-center model. Here, we present some principle discretization steps.

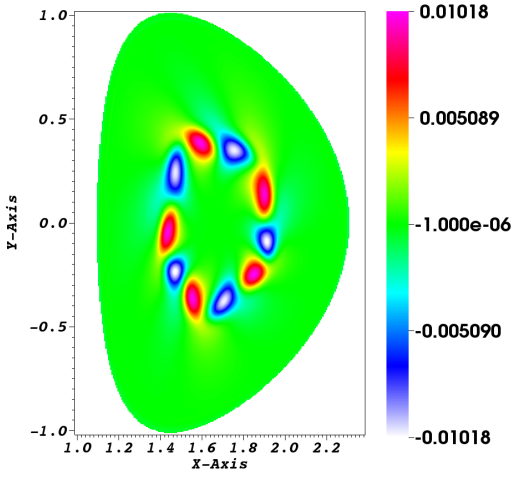
The Vlasov equation of system can be split into three equations :

$$\begin{cases} \dfrac{\partial f}{\partial t} + \mathbf{U} \cdot \nabla_{\mathbf{x}_\perp} f = 0, \\ \dfrac{\partial f}{\partial t} + v_\parallel \partial_z f = 0, \\ \dfrac{\partial f}{\partial t} + E_\parallel \partial_{v_\parallel} f = 0. \end{cases}$$

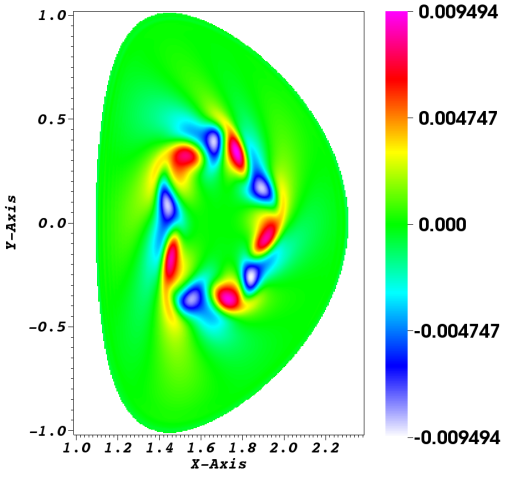
This test represents a snapshot of the charge density when an instability occurs (ion turbulence simulation). This simulation has been realized by different methods but in cylindrical coordinates, here we perform numerical simulation in Cartesian coordinates on a uniform grid. The discretization of the Drift-Kinetic model can be developed very similarly as the one for the guiding-center model.



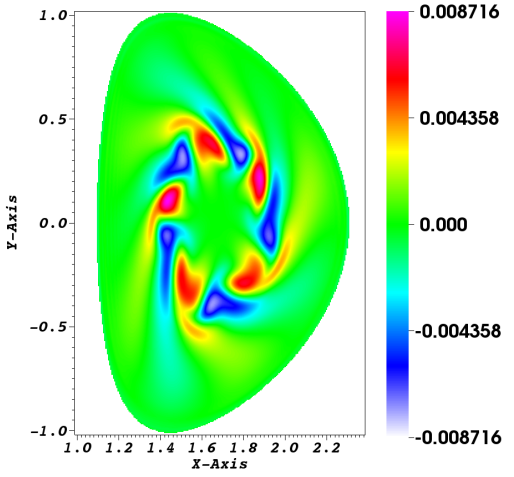
(a) $t = 0$



(b) $t = 100$

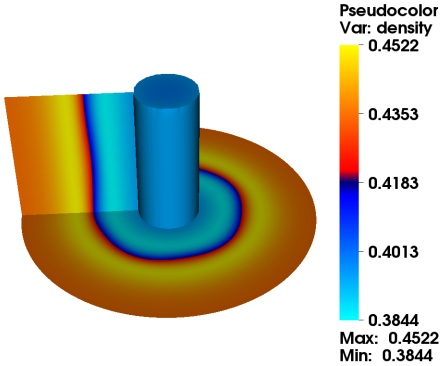


(c) $t = 200$

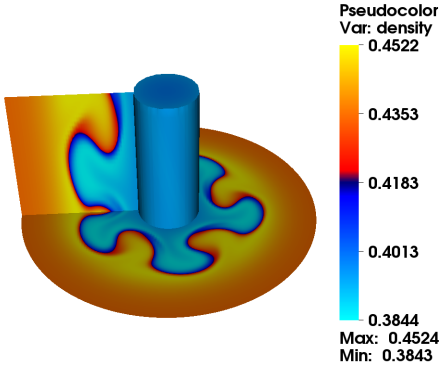


(d) $t = 300$

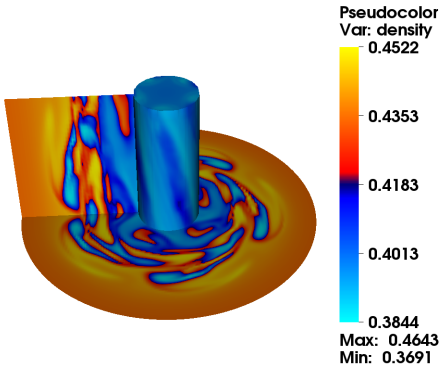
Figure 2. Instability simulation for guiding-center model in D-shaped domain. The difference between the perturbed density and the steady state density is presented, i.e.$\delta\rho(t) = \overline{\rho}(t) - \overline{\rho}_0$.



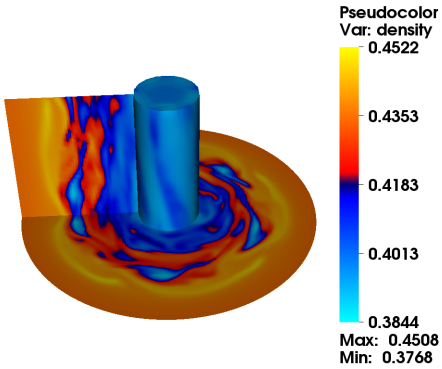
(a) $t = 2000$



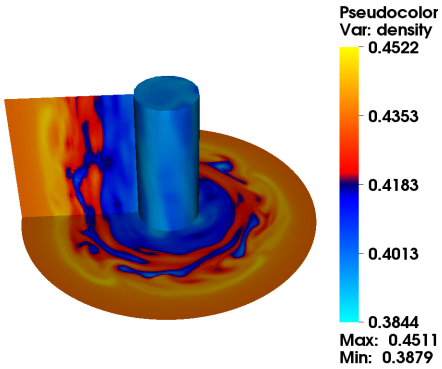
(b) $t = 3000$



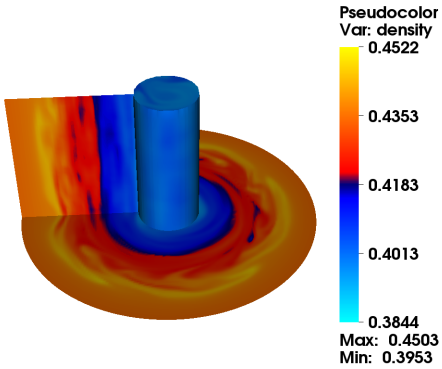
(c) $t = 4000$



(d) $t = 5000$



(e) $t = 6000$



(f) $t = 8000$

Figure 3. Evolution of ion turbulence. The distribution function is shown for the velocity $v_{||} = 0$. The mesh size is $n_x = n_y = 128, n_z = 32, n_v = 65$. Mixed Semi-Lagrangian/finite difference method is used.

LEMON Team

5. New Software and Platforms

5.1. SW2D

Participant: 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.

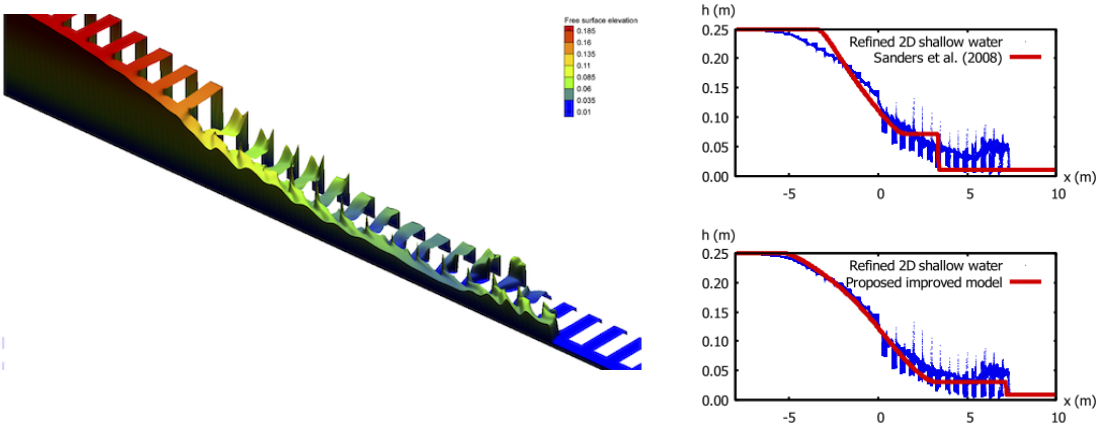


Figure 2. Propagation of a flood wave into a channel with lateral storage. Refined 2D simulation using the SW2D computational code

5.2. Stochastic Downscaling Method

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

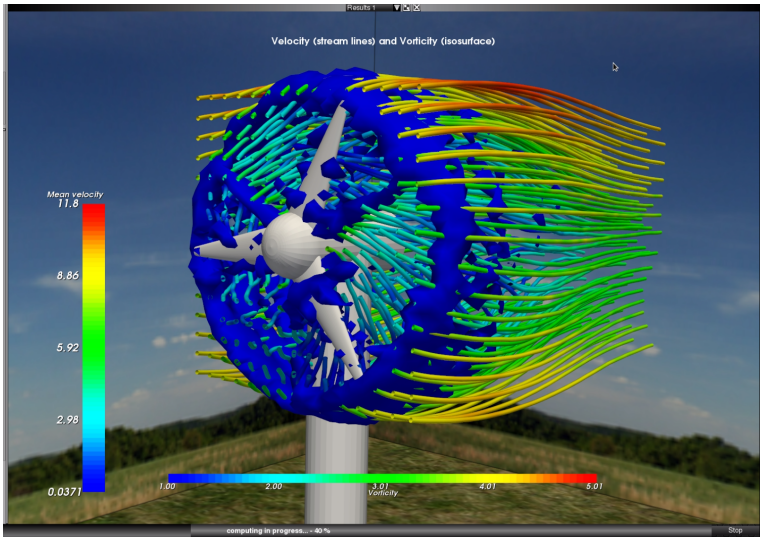


Figure 3. Velocity streamlines and vorticity around a wind mill (artistic view). WINDPOS Project.

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

5.3. Action Dépollution

Participants: Antoine Rousseau, Alexis Pacholik.

Action Dépollution (see website in french) 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. The conception has been achieved in collaboration with the Inria project-team MODEMIC, and the realization with the help of the start-up Funkadelichik, sponsored by the french consortium Cap'Maths and Inria (Direction de la Communication).
This work is in connection with the INRA/Inria patent [19].

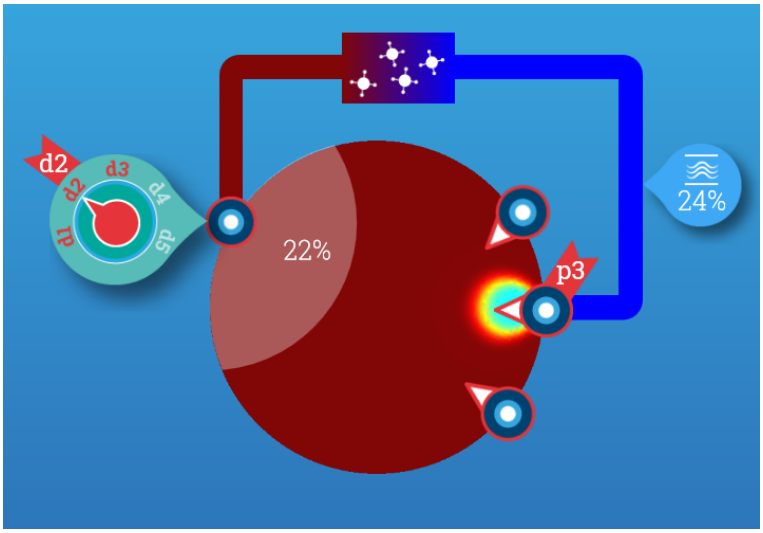


Figure 4. Player interface. Serious game Action Dépollution.

MAGIQUE-3D Project-Team

5. New Software and Platforms

5.1. Hou10ni

Participant: Julien Diaz [correspondant].

This software, written in FORTRAN 90, simulates the propagation of waves in heterogeneous 2D and 3D media in time-domain and in frequency domain. It is based on an Interior Penalty Discontinuous Galerkin Method (IPDGM) and allows for the use of meshes composed of cells of various order (p-adaptivity in space).

This year, we have implemented the 3D version for the simulation of elastodynamic waves. This version handles polynomials of arbitrary order while the previous one was only able to deal with polynomials of degree up to three.

We have also improved the parallelism by coupling the code to a mesh partitioner and we have totally rewritten the code to handle MPI parallelism both for the construction of the matrices and for the time scheme.

5.2. Montjoie

Participant: Marc Duruflé [correspondant].

`Montjoie` is a code developed by Marc Duruflé with contributions of students, including Juliette Chabassier during her PhD. It provides a C++ framework for solving partial differential equations on unstructured meshes with finite element-like methods (continuous finite element, discontinuous Galerkin formulation, edge elements and facet elements). The handling of mixed elements (tetrahedra, prisms, pyramids and hexahedra) has been implemented for these different types of finite elements methods in the context of Morgane Bergot's PhD. Several applications are currently available : wave equation, elastodynamics, aeroacoustics, Maxwell's equations. In 2014, the implementation of linearized Euler equations and Galbrun's equation has been improved and extended to the axisymmetric case. Raman effect has been implemented in the 1-D non-linear Schrödinger equation.

See also the web page http://montjoie.gforge.inria.fr.

5.3. Elasticus

Participant: Simon Ettouati.

Within the framework of the strategic action DIP, Magique-3D collaborates with Total to develop a computing platform, DIVA, meant to produce accurate images of the subsurface. To achieve this, approximate solutions of the first-order wave problem are computed thanks to a Discontinuous Galerkin (DG) Method. It is increasingly difficult to include new numerical schemes developped in the team in the industrial and highly parallel environment of Total.

Elasticus is a sequential library, independent of DIVA and developped in Fortran, to simulate wave propagation in geophysical environment, based on a DG method. It is meant to help PhD students and post-doctoral fellows to easily implement their algorithms in the library. Thus, readability of the code is privileged to optimization of its performances. Developped features should be easily transferred in the computing platform of Total. Contrary to DIVA which only computes approximate solutions with P1, P2 and P3 elements, Elasticus manages arbitrary orders for the spatial discretization with DG method. Matrices on the reference element for arbitrary orders are computed thanks to a library developped by J. Diaz.

5.4. DIVA-DG

Participants: Lionel Boillot, Marie Bonnasse-Gahot, Théophile Chaumont-Frelet, Jérôme Luquel.

DIVA-DG is the simulation code that we develop in collaboration with our partner Total. This year we have implemented

- 2D/3D anisotropic elastic Absorbing Boundary Conditions for time-domain.
- 2D elastic imaging conditions.
- 2D multiscale strategy to take into account fine scale heterogeneities on coarse meshes in frequency domain.
- Hybrydized Discontinuous Galekin method for 2D elastodynamic in frequency domain.

MOISE Project-Team

5. New Software and Platforms

5.1. Adaptive Grid Refinement

Participants: Laurent Debreu, Marc Honnorat.

AGRIF (Adaptive Grid Refinement In Fortran, [85], [83]) is a Fortran 90 package for the integration of full adaptive mesh refinement (AMR) features within a multidimensional finite difference model written in Fortran. Its main objective is to simplify the integration of AMR potentialities within an existing model with minimal changes. Capabilities of this package include the management of an arbitrary number of grids, horizontal and/or vertical refinements, dynamic regridding, parallelization of the grids interactions on distributed memory computers. AGRIF requires the model to be discretized on a structured grid, like it is typically done in ocean or atmosphere modelling. As an example, AGRIF is currently used in the following ocean models: MARS (a coastal model developed at IFREMER-France), ROMS (a regional model developed jointly at Rutgers and UCLA universities), NEMO ocean modelling system (a general circulation model used by the French and European scientific community) and HYCOM (a regional model developed jointly by University of Miami and the French Navy).
Recent applications produced by the NEMO-AGRIF system are described in [12],[19]. AGRIF is licensed under a GNU (GPL) license and can be downloaded at its web site (http://ljk.imag.fr/MOISE/AGRIF/index.html).

5.2. NEMOVAR

Participant: Arthur Vidard.

NEMOVAR is a state-of-the-art multi-incremental variational data assimilation system dedicated to the European ocean modelling platform NEMO for research and operational applications. It is co-developed by MOISE, CERFACS (FR), ECMWF (EU) and MetOffice (UK) under the CeCILL license, written in Fortran and Python. It is now in use in both ECMWF and MetOffice for their operational oceanic forecasting systems. It has also been used for specific studies in collaboration with Mercator-Ocean, LPO, LOCEAN and LEGI in France and University of Namur in Belgium. It has been adopted as the ocean analysis component in the FP7 project ERA-Clim2 (01/2014-12/2016).

Previously part of NEMOVAR, NEMO-TAM (Tangent and adjoint models for NEMO) that have been developed by the MOISE team will be now distributed directly by the NEMO consortium. The first official tagged release including NEMO-TAM has been published early 2013.

5.3. R Packages for Uncertainty Quantification

Participants: Laurent Gilquin, Céline Helbert.

Laurent Gilquin is one of the authors of the R package sensitivity (see http://cran.r-project.org/web/packages/sensitivity/index.html). This package is useful for conducting sensitivity analysis of complex computer codes.

Céline Helbert is now the maintainer of the packages DiceDesign (see http://cran.r-project.org/web/packages/DiceDesign/index.html) and DiceEval (see http://cran.r-project.org/web/packages/DiceEval/index.html). These packages are useful for conducting design and analysis of computer experiments.

POMDAPI Project-Team

4. New Software and Platforms

4.1. FreeFem++

Participants: Martin Vohralík, Martin Čermák, Zuqi Tang.

The scientific calculation code FreeFem++ is an example of a complex software numerical simulation tool. It in particular encompasses all specifications of the problem, the choice and implementation of the numerical method, the choice and implementation of the linearization method (nonlinear solver), and the choice and implementation of the method of solution of the associated linear systems (linear solver). In the post-doc stays of M. Čermák and Z. Tang, we integrated there the most recent advances of the theory of a posteriori error estimation and of adaptive algorithms. In particular, adaptive stopping criteria for the linear and nonlinear solvers were implemented.

Version 3.33

Programming language: C++

http://www.freefem.org/ff++/

4.2. Oqla, Qpalm

Participants: Jean Charles Gilbert, Émilie Joannopoulos.

OQLA and QPALM aim at minimizing a large scale convex quadratic function on a polyhedron by an augmented Lagrangian method. The original features of the approach are its capacity to solve the problem without factorization, which makes them adapted to large scale problems, and to deal with unbounded and infeasible problems. In case the problem is infeasible, the codes solve the *closest feasible problem* with a global linear rate of convergence [3]. In case the problem is unbounded, the solvers build a feasible direction of unboundedness for the closest feasible problem. The solvers OQLA and QPALM only differ by their programming language; they are documented in [16], [14], [15].

Versions: 0.6 (OQLA), 0.5 (QPALM)

Programming languages: `C++` (OQLA), `Matlab` (QPALM)

4.3. Ref-image

Participants: Hend Ben Ameur, François Clément, Pierre Weis.

Ref-image is an image segmentation program using optimal control techniques. Slogan is “no gestalt inside”. Ref-image implements the refinement indicator algorithm, specialized to the case of the inversion of the identity map. It is a first step towards the implementation of a generic inversion platform using the refinement indicator algorithm.

Version: 1.1+pl0 (2014/02/28)

Programming language: OCaml

http://refinement.inria.fr/ref-image/

4.4. Ref-indic

Participants: Hend Ben Ameur, François Clément, Pierre Weis.

Ref-indic is an adaptive parameterization platform using refinement indicators. Slogan is “details only where they are worth it”. Ref-indic implements a generic version of the refinement indicator algorithm that can dock specific programs provided they conform to the generic algorithm API.

Version: 1.4+pl0 (2014/07/01)

Programming language: OCaml

http://refinement.inria.fr/ref-indic/

4.5. Sklml

Participants: François Clément, Pierre Weis.

Sklml is a functional parallel skeleton compiler and programming system for OCaml programs. Slogan is “easy coarse grain parallelization”.

Version: 1.1+pl0 (2014/01/21)

Programming language: OCaml

http://sklml.inria.fr/

SAGE Project-Team

5. New Software and Platforms

5.1. Platforms

5.1.1. Platform H2OLab

Participants: Jean-Raynald de Dreuzy, Jocelyne Erhel [correspondant], Grégoire Lecourt, Géraldine Pichot.

The software platform H2OLab is devoted to stochastic simulations of groundwater flow and contaminant transport in highly heterogeneous porous and fractured geological media. It contains a database which is interfaced through the web portal H2OWeb. It contains also software modules which can be used through the interface H2OGuilde. The platform H2OLab is an essential tool for the dissemination of scientific results. Currently, software and database are shared by the partners of the h2mno4 project (see 7.2.1). Software integrated in the platform and registered at APP are GW-UTIL, GW-NUM, PARADIS, MP-FRAC.

See also the web page http://h2olab.inria.fr.

5.2. Hydrogeology

5.2.1. GRT3D

Participants: Édouard Canot, Jocelyne Erhel [correspondant].

- Version: version 2.0, April 2014
- APP: registered
- Programming language: C
- Abstract: Reactive transport modeling has become an essential tool for understanding complex environmental problems. It is an important issue for MoMaS and C2S@EXA partners (see sections 7.2.5 , 7.2.3), in particular Andra. We have developed a method coupling transport and chemistry, based on a method of lines such that spatial discretization leads to a semi-discrete system of algebraic differential equations (DAE system). The main advantage is to use a complex DAE solver, which controls simultaneously the timestep and the convergence of Newton algorithm. The approach SIA uses a fixed-point method to solve the nonlinear system at each timestep, whereas the approach SNIA uses an explicit scheme.

  The software suite GRT3D has four executable modules:
  - SIA1D: Sequential Iterative Approach for 1D domains;
  - GDAE1D: Global DAE approach for 1D domains;
  - SNIA3D: Sequential Non Iterative Approach for 1D, 2D or 3D domains.
  - GDAE3D: Global DAE approach for 1D, 2D or 3D domains. This module has three variants: the original one with logarithms, an optimized one still with logarithms, an optimized one which does not use logarithms.
- Current work: extension of the chemistry module and parallelization.

5.2.2. SBM

Participant: Géraldine Pichot [correspondant].

- Version: version 1.0, November 2013
- Programming language: C
- Abstract: SBM (Skew Brownian Motion) is a code developed with A. Lejay (Inria, Nancy). This code allows exact or approximated simulations of the Skew Brownian Motion. This code is used for the simulation, with a Monte-Carlo approach, of a 1D diffusion process with a discontinuous diffusion coefficient. Several benchmark tests are also implemented.
- Current work: paper about benchmarking results 5.2.2 .

5.2.3. GENFIELD

Participants: Jean-Raynald de Dreuzy, Jocelyne Erhel, Grégoire Lecourt, Géraldine Pichot [correspondant].

- Version: version 1.0, December 2014
- Programming language: C++
- Abstract: GENFIELD allows the generation of log-normal correlated fields. It is based on a spectral method and uses the FFTW library. Parallelism is implemented using MPI communications. GENFIELD is used in hydrogeology to model natural fields, like hydraulic conductivity or porosity fields.
- Current work: paper about algorithms 6.4.7 .

5.3. High Performance Scientific Computing

5.3.1. PALMTREE

Participants: Lionel Lenôtre [correspondant], Géraldine Pichot.

- Version: version 1.0, November 2013
- Programming language: C++
- Abstract: We present an easy-to-use package for the parallelization of Lagrangian methods for partial differential equations. In addition to the reduction of computation time, the code aims at satisfying three properties:
  - simplicity: the user just has to add the algorithm governing the behaviour of the particles.
  - portability: the possibility to use the package with any compiler and OS.
  - action-replay: the ability of the package to replay a selected batch of particles.

  The last property allows the user to replay and capture the whole sample path for selected particles of a batch. This feature is very useful for debugging and catching some relevant information.
- Current work: paper about performance results.

5.3.2. MUESLI

Participant: Édouard Canot [corresponding author].

Muesli is a library designed to help in coding scientific problems in Fortran using a vector-oriented syntax like Matlab. One of its aims is therefore to speed-up the development process. It contains all the necessary materials to work numerically with a dynamic array (dynamic in size, shape, type, and storage structure), called mfArray. Muesli includes all or some parts of the following numerical libraries: Blas and Lapack, Arpack, Minpack, Slatec, Sparskit, SuiteSparse, Metis, Triangle, RngStreams, and other routines based on ACM algorithms.

The key points of Muesli is to efficiently solve large ODE/DAE systems (which come from, e.g., PDE problems after using the method of lines) or large non-linear minimization problems (where Jacobian matrices can be provided in a sparse format). The user can easily monitor the whole integration process and have access to tools to fix the singularity of the system of equations.

The lastest version of Muesli is 2.9.5 (2014-10-03). More information can be found at: http://people.irisa.fr/Edouard.Canot/muesli.

5.3.3. Zohour

Participant: Édouard Canot [correspondant].

Zohour is a node-based adaptive 2D mesh algorithm, written in Fortran 2003. A basic rectangular, regular set of nodes is recursively refined. Then the cells come from the Voronoi tessellation. While the domain is currently limited to a rectangular shape, its strength is three-fold:

- first, computing the flux via a Finite Element or Finite Volume method is both simple and accurate because each cell-side of cells is the bisection of two nodes;
- second, the transition between zones of different levels of refinement is more progressive than other methods, leading to a smaller number of nodes for the whole mesh;
- third, during successive refinements when dealing with a transient problem, interpolation is needed only by the new nodes, limiting the numerical errors.

It is planned for use in the HeMaTiS code (5.4.1) in order to get a refined mesh zone around the phase change surface.

See also the web page http://people.irisa.fr/Edouard.Canot/zohour.

5.4. Heat diffusion in soils

5.4.1. HeMaTiS

Participants: Édouard Canot [correspondant], Salwa Mansour.

HeMaTiS (**He**at and **Ma**ss **T**ransfer **i**n **S**oils) is a set of Finite Volume programs (variants concern different geometrical configurations: 1D, 1D-radial, 2D, 3D-axisymmetric) for computing the transient heat diffusion in soils when there is a phase change of water. Currently, the soil is modelled by a heterogeneous porous medium having constant thermo-physical properties, and the porous medium is saturated with water. The phase change is treated by means of the Apparent Heat Capacity method. In the near future, we plan to use an unsaturated model (but limited to small water content), and an effective thermal conductivity which depends on the local humidity (this latter law may reveal hysteresis behaviour). The software is written in Fortran 95 and is based on the Muesli library (5.3.2). A Computer Algebra System (Maple or Maxima) is used to compute the Jacobian matrix.

5.4.2. TPIP

Participants: Édouard Canot [correspondant], Salwa Mansour.

TPIP (**T**hermal **P**roperties by **I**nverse **P**roblem) is a program which aims at estimating the thermo-physical of a saturated porous medium after a strong heating which leads to the phase change of the water contained in the pores, knowing the experimental heating curves history at few selected points. The least-square criterion is used, in which sensitivity coefficients are the solution of a huge, complex PDE system in order to take into account the phase change of water. These equations for the sensitivity coefficients are therefore obtained via a Computer Algebra System (Maple or Maxima). In many aspects, the forward problem is similar to the HeMaTiS code (5.4.1), and like it, is based on Muesli (5.3.2). Two different minimization algorithms may be used, Damped Gauss-Newton or Levenberg-Marquardt. A special procedure has been applied in order to obtain a robust convergence, by changing some parameters of the forward problem during the iterations.

5.4.3. GLiMuH

Participants: Édouard Canot [correspondant], Salwa Mansour.

The GLiMuH code (**G**rains with **Li**quid **M**eniscus **u**nder **H**eating) is devoted to the understanding of how heat diffuses in an assembly of solid grains separated by air and water. In the pendular regime, the quantity of water is very small, leading to liquid bridges between the grains. In the current approximation, the grains are spherical in shape, and the numerical simulation is done in a 3D axisymmetric coordinate system. The shape of the liquid/gas interface is computed by integrating a differential algebraic system of equations, with a given quantity of water per unit volume of the porous medium, and under the constraint of a given contact angle between the liquid/gas interface and the solid boundaries. The numerical results allow us to estimate the effective thermal conductivity of a real wet granular medium, which is required to establish more realistic models for the HeMaTiS code (5.4.1).

STEEP Team

5. New Software and Platforms

5.1. REDEM: REDuction Of GHG EMission software

Participant: Emmanuel Prados.

REDEM software (REDuction of EMissions) is a tool designed for the benchmarking of national GHG emission reduction trajectories. We have developed REDEM in collaboration with EDDEN Laboratory (Patrick Criqui and Constantin Ilasca). The actual version of the software is implemented in Visual Basic under Microsoft Excel in order to facilitate handling and diffusion to climate/energy economists. The work related to this software has been published in [5].

5.2. Wassily

Participants: Julien Alapetite, Jean-Yves Courtonne.

In collaboration with the association "Groupe de Réflexion sur les Empreintes Ecologiques Locales" (eco-data.fr), STEEP contributes to the development of Wassily (in tribute to Wassily Leontief who first designed the relevant concepts), to perform input-output analyses applied to environmental issues (see section 4.2). The purpose of this software is to automatize most of the work of standard input-output analysis and to visualize the results in a user-friendly way in order to efficiently address the related key environmental questions.

The software is structured in three different modules:

- the database module stores all the input-output data coming from Eurostat, OCDE, Insee or other sources.
- the computation module performs the input-output calculations
- the visualization module displays the results in a synthetic manner.

The database module is based on the SQlite format and makes use of SQL to manipulate the various tables involved in the process. The goal of this module is to provide a normalized data interface for the computation module, from various types of input-output data which are often stored as Excel sheet on web sites.
The computation module is based on QT and C++ and deals mostly with matrix manipulation.
The visualization module is based on a JavaScript library called D3 and allows the user to visualize the results in a number of different ways, such as bar charts, pie charts, sankey diagrams to name a few. The integration between the C++ and JavaScript pieces of code is performed with QTScript.

5.3. QGIS_Tranus_Reports

Participants: Patricio Inzaghi, Emmanuel Prados, Peter Sturm.

This software allows to graphically visualise data output by the TRANUS LUTI model (and possibly, of any other data of the same structure). In particular, this concerns any data items defined per zone of a modelled territory (productions, indicators, etc.). The software is designed as a plugin for the geographical information system platform QGIS and can be run interactively as well as by the command line or by a call from within another software. The interactive mode (within QGIS) allows the user to define graphical outputs to be generated from TRANUS output files (type of graphs to be generated – 2D or 3D – color coding to be used, choice of data to be displayed, etc.). Visualisation of data is done in the form of 2D graphs or 3D models defined using java-script. The software is about to be registered with the APP.

TONUS Team

5. New Software and Platforms

5.1. SeLaLib

The objective of the Selalib project (SEmi-LAgrangian LIBrary) is to develop a well-designed, organized and documented library implementing several numerical methods for kinetic models of plasma physics. Its ultimate goal is to produce gyrokinetic simulations.

Another objective of the library is to provide to physicists easy-to-use gyrokinetic solvers, based on the semi-lagrangian techniques developed by Eric Sonnendrücker and his collaborators in the past CALVI project. The new models and schemes from TONUS are also intended to be incorporated into Selalib.

In addition, the CEA of Cadarache is interested by the development of this library, which picks up and extends many methods implemented in GYSELA, a code developed at CEA Cadarache for simulating turbulence in magnetic fusion plasmas, in particular, in view of the ITER project. Eric Sonnendrücker who is now in Munich continues to work on Selalib. A joint development of Selalib between Strasbourg and Munich allows both partners to benefit of each other's work.

Selalib is a library of FORTRAN modules. The CEA Cadarache has advised this language, because it is widespread in the engineering and physics communities. In this way, we hope that it will be spread among researchers interested in plasma simulations.

Selalib is under GPL license and available on the Inria Forge [0].

5.2. CLAC

CLAC is a generic Discontinuous Galerkin solver, written in C/C++, based on the OpenCL and MPI frameworks. CLAC means "Conservation Laws Approximation on many Cores".

It is clear now that future computers will be made of a collection of thousands of interconnected multicore processors. Globally it appears as a classical distributed memory MIMD machine. But at a lower level, each of the multicore processors is itself made of a shared memory MIMD unit (a few classical CPU cores) and a SIMD unit (a GPU). When designing new algorithms, it is important to adapt them to this kind of architecture. Our philosophy will be to program our algorithms in such a way that they can be run efficiently on this kind of computers. Practically, we will use the MPI library for managing the coarse grain parallelism, while the OpenCL library will efficiently operate the fine grain parallelism.

We have invested for several years until now into scientific computing on GPUs, using the open standard OpenCL (Open Computing Language). We were recently awarded a prize in the international AMD OpenCL innovation challenge thanks to an OpenCL two-dimensional Vlasov-Maxwell solver that fully runs on a GPU. OpenCL is a very interesting tool because it is an open standard now available on almost all brands of multicore processors and GPUs. The same parallel program can run on a GPU or a multicore processor without modification.

CLAC is also a joint project with a Strasbourg small company, AxesSim, which develops software for electromagnetic simulations.

[0] http://selalib.gforge.inria.fr/

Because of the envisaged applications of CLAC, which may be either academic or commercial, it is necessary to conceive a modular framework. The heart of the library is made of generic parallel algorithms for solving conservation laws. The parallelism can be both fine-grained (oriented towards GPUs and multicore processors) and coarse-grained (oriented towards GPU clusters). The separate modules allow managing the meshes and some specific applications. In this way, it is possible to isolate parts that should be protected for trade secret reasons. The open source part of CLAC will be made freely available on the web later on. We have made an APP deposit of the first version of CLAC in October 2012. The versioning of CLAC project is also registered in the Inria Forge [0].

[0] http://clac.gforge.inria.fr

BIOCORE Project-Team

5. New Software and Platforms

5.1. Supervision software

5.1.1. ODIN

Participants: Olivier Bernard, Francesco Novellis.

The latest developments of the bioreactor supervision platform ODIN were dedicated to software restructuration (together with Mélaine Gauthier, from Inria Chile) in order to get more fluidity and more flexibility between modules and in order to support an on line simulator. The connection with a local data base has simplified the management of previous data acquisition and it also allows to "replay" data which were previously recorded. The coupling with the software developed by INRA (Silex) was refactored into a software named MEMO.

ODIN has been tested on four different processes especially (with Eric Latrille) to supervise the 66m2 high rate pond at the LBE, INRA Narbonne. It has also been used at Lesaffre facilities by the BioEnTech company. New algorithms have been successfully tested to control a high-rate anaerobic digestion process.

5.1.2. In@lgae

Participants: Etienne Delclaux, Francis Mairet, Quentin Béchet, Olivier Bernard.

The In@lgae platform has been optimised to make it faster. Some of the key models have been rewritten in C++ to allow a faster computation. Models have been improved to include, in the growth rate computation, the composition of the light spectrum. The graphical user interface has been enhanced and several sets of parameters describing different microalgal species have been stored. Post treatments with Matlab have been implemented to account for slope of the land, its nature, and the distance to CO2 and nutrient sources. The platform supported a study for the French Agency for the development and master of energy (ADEME) managed by ENEA consulting. We could simulate the potential of micro -and macro-algal cultivation in France in 2030, after using the NEF cluster with 300 CPUs (it took 10 days of computation).

CARMEN Team

5. New Software and Platforms

5.1. CEPS: a Cardiac ElectroPhysiology Simulator

The Carmen team develops a software code to perform high performance numerical simulations in cardiac electrophysiology using unstructured three-dimensional grids. The software, called CEPS (*Cardiac Electrophysiology Simulation*), is developped as a common tool for researchers in the Carmen team and for our partners and colleagues in scientific computing and biomedical engineering. The goal of CEPS is to easily allow the development of new numerical methods and new physical models. Thanks to the ADT, we are now able to use CEPS for the benchmark named *Second N-version Cardiac Electrophysiology Benchmark Specification actual developments*, see (benchmarck) for more details.

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

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

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

5.2. PROPAG

The workhorse for our applied simulation studies of the whole human heart is PROPAG, a code that has its origins at the Université de Montréal in Canada, and has been further developed by the Institute of Computational Science in Lugano, Switzerland. PROPAG is highly configurable and works with arbitrary model geometries. It runs efficiently on high-performance computing systems with many thousands of cores, including a "difficult" system such as the BlueGene/Q "Turing" at IDRIS. It is particularly useful for whole-heart studies, which typically rely on very large model sizes (in the order of 10^8 elements), several different membrane models and cell types in a single simulation run, and several regionally varying parameters.

PROPAG is presently used in our group to study the relation between the substrate, complexity, and electrocardiographic features of atrial fibrillation and of cardiomyopathy-related ventricular arrhythmia, providing the efficiency and flexibility that is required to handle the complex anatomical structures that are involved.

5.3. YAPI: A new project for the development of a platform for the simulation of the electrophysiology cardiac with CEPS

Many of our projects rely on realistic or even patient-tailored meshes to represent the anatomy of the human heart and torso. The construction of such meshes provides challenges on many levels, from the delineation of the anatomical structures in medical images to the construction of high-quality meshes. The construction of such meshes provides challenges on many levels, from the delineation of the anatomical structures in medical images to the construction of high-quality meshes. We presently use a variety of in-house and public software packages to perform this work and are able to produce meshes of sufficient quality, but we strive for an important streamlining of this work. We have initiated a discussion with several groups inside and outside Inria who have similar needs or can offer solutions. We specifically investigate the possibility to build a common software which combines and complements our present solutions. The new code should make various methods

easily accessible and automate the work as much as possible. Because accuracy and mesh quality are important requirements, the new code should also provide convenient options for human intervention where algorithms fall short. For example, manual segmentation and mesh editing should be as easy and efficient as they are in medical-imaging tools and 3D-editing software, respectively, but well integrated into the workflow.

DRACULA Project-Team

5. New Software and Platforms

5.1. CelDyn

Participants: Laurent Pujo-Menjouet, Alen Tosenberger, Vitaly Volpert [correspondant].

Software "Celdyn" is developed in order to model cell population dynamics for biological applications. Cells are represented either as soft spheres or they can have more complex structure. Cells can divide, move, interact with each other or with the surrounding medium. Different cell types can be introduced. When cells divide, the types of daughter cells are specified. A user interface is developed.

M3DISIM Team

5. New Software and Platforms

5.1. FELISCE

Participants: Dominique Chapelle, Sébastien Gilles [correspondant], Sébastien Imperiale, Philippe Moireau.

FELISCE – standing for "Finite Elements for LIfe SCiences and Engineering" – is a new finite element code which the MACS and REO teams have decided to jointly develop in order to build up on their respective experiences concerning finite element simulations. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex cardiovascular models considered in the two teams – namely involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena. FELISCE is written in C++, and may be later released as an opensource library. See https://gforge.inria.fr/projects/felisce/.

In FELISCE we have prepared a branch called HappyHeart, which aims at providing a user-friendly interface able to deal efficiently with complex cardiovascular simulations. Started in 2013, the code is already quite large (about 55 000 lines of code in almost 700 different files) and its core is about to be complete in early 2015. It includes among others full HPC functionalities, high-order finite elements, physics coupling and topology capabilities. Our purpose will then be to use the library to implement the sophisticated cardiovascular models of the team and couple them with Verdandi (data assimilation library) to provide patient-specific simulations.

- Software benefit: HappyHeart is a multiphysics HPC FEM Library with cardiac simulation concerns
- Type of human computer interaction: Command line and configuration files.
- OS/Middleware: MacOS, Linux.
- Required library or software: OpenMpi (parallelism), Petsc (linear algebra), Seldon (linear algebra), Parmetis (partitioner), Mumps (solver), Ops (input parameter file management), STL and Yuni (generic C++ libraries).
- Programming language: C++ 11/14.
- Documentation: Doxygen and user's manual in English.

5.2. HeartLab

Participants: Matthieu Caruel, Dominique Chapelle, Alessandro Felder, Philippe Moireau [correspondant].

The heartLab software is a library written in (64-bit compatible) Matlab and C (mex functions) designed to perform both simulation and estimation (based on various types of measurements, e.g. images) of the heart mechanical behavior. Started in 2006, it is already quite large (about 60,000 lines), and is used within various collaborations.

The code relies on OpenFEM – to which the team has previously contributed, see http://www.openfem.net – for the finite element computations, and the implementation was performed with a particular concern for modularity, since modeling and estimation use the same finite element operators. This modularity also allows to couple the code with other FEM solvers, such as LifeV and Mistral developed in the Reo team-project. In particular, we are now able to include perfusion and electrical coupling with LifeV using PVM, and fluid-structure interaction using Mistral.

We also included geometric data and tools in the code to define cardiac anatomical models compatible with the simulation requirements in terms of mesh quality, fiber direction data defined within each element, and the referencing necessary for handling boundary conditions and estimation, in particular. These geometries are analytical or come from computerized tomography (CT) or magnetic resonance (MR) image data of humans or animals.

We incorporated numerous non-linear data assimilation observation operators based on medical imaging post-processing to be able to now perform estimation with a large variety of medical imaging modalities. And recently we have worked on generalized micro-macro cardiac law using stochastic formulations.

5.3. Verdandi

Participants: Aurora Armiento [Mamba team], Dominique Chapelle, Annabelle Collin, Vivien Mallet [Clime team], Karine Mauffrey, Philippe Moireau [correspondant].

Verdandi is an opensource (LGPL) software library aiming at providing data assimilation methods and related tools. Mainly targeted at large systems arising from the discretization of PDEs, it is intentionally devised as generic, which allows for applications in a wide range of problems (biology and medicine, environment, image processing...). See also the web page http://verdandi.gforge.inria.fr/, with a complete documentation in English. The first stable version (1.0) was released in June 2012 and contains most of the major data assimilation algorithms of both variational and sequential types. The current version (1.6) contains additional estimation algorithm and parallel capabilities. Note that some specific developments are performed with particular regard to cardiac modeling applications, as Verdandi is partly funded by – and distributed within – the VPH-Share and VP2HF projects and is now referenced in the peer-reviewed article [4].

- ACM: Mathematical software
- AMS: System theory; control
- Software benefit: Verdandi is the only *generic* data assimilation library
- License: LGPL (2.1 or any later version)
- Type of human computer interaction: Command line and configuration files
- OS/Middelware: Linux, MacOS ou Windows
- Required library or software: Seldon (LGPL, http://seldon.sourceforge.net/)
- Programming language: C++, ISO/IEC 14882: I998(E) Python, version 2.6
- Documentation: Doxygen and utilisation manual in English

Moreover a Matlab module called VerdandinMatlab is developed in the team for pedagogical and test purposes.

MAMBA Team

5. New Software and Platforms

5.1. Logiciels

5.1.1. TiQuant

Systems biology and medicine on histological scales require quantification of images from histological image modalities such as confocal laser scanning or bright field microscopy. The latter can be used to calibrate the initial state of a mathematical model, and to evaluate its explanatory value, which hitherto has been little recognized ([7]). We generated a software for image analysis of histological material and demonstrated its use in analysing liver confocal micrografts, called TiQuant (Tissue Quantifier) [10]. The software is part of an analysis chain detailing protocols of imaging, image processing and analysis in liver tissue, permitting 3D reconstructions of liver lobules down to a resolution of less than a micrometer. (This work is a collaboration with the group of JG Hengstler, IfADo, Germany)

5.1.2. TiSim

We advanced the complementary software TiSim (Tissue Simulator) that will soon be provided. TiSim permits agent-based simulations of multicellular systems and can be directly fed by processed image data from TiQuant.

MASAIE Project-Team (section vide)

MODEMIC Project-Team

5. New Software and Platforms

5.1. Action Depollution

Participant: Alain Rapaport.

Action Depollution is a "serious" game 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. The conception has been achieved with the Inria project-team LEMON, and the realization with the help of the start-up Funkadelichik, sponsored by the french consortium Cap'Maths.

This work is in connection with the INRA/Inria patent [47] that has been deposited jointly with LEMON Team.

5.2. VITELBIO (VIrtual TELluric BIOreactors)

Participants: Jérôme Harmand, Alain Rapaport.

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).

5.3. Mass-structured chemostat simulators

Participants: Fabien Campillo, Coralie Fritsch.

We developed in `Python` two pieces of software. The first one aims at simulating a chemostat dynamics with a mass-structured bacterial population: first with an IBM approach, second with a integro-differential equation. The latter approach is using uncentered difference scheme; the former one is stochastic and so needs numerous runs to built empirical representation of the distribution law [27].

The second piece of software is a graphical user interface for the previous one, allowing for runs on remote number cruncher and graphical post-treatment of runs.

The need of reusability of these codes leads us to develop them in an oriented programming framework. This work was done with the help of MISTEA (P. Neveu) and I3M (P. Pudlo).

MYCENAE Project-Team

5. New Software and Platforms

5.1. Platforms

5.1.1. DynPeak

In collaboration with the SED (George Rosca) and Serge Steer (SISYPHE), we have deployed a web resource version of our algorithm for the detection of peaks in pulsatile hormone patterns, DynPeak, that is accessible at the https://dynpeak.inria.fr url.

NUMED Project-Team

4. New Software and Platforms

4.1. SimPHyT

SimPHyt has been developed by Morgan Martinet (junior engineer). SimPHyt is an implementation in Python of the low grad glioma model developped by Benjamin Ribba. The aim is to predict the evolution of the glioma size of patients. It is used by Dr François Ducray in Pierre Wertheimer Hospital in Lyon.

4.2. SETIS

We are currently developing the SETIS software which is a GUI allowing to treat DICOM medical images to extract pathological data. These data can then be exported and used in a SAEM software (including Monolix (Inria & Lixoft)) for the parameters' estimation of models in the context of population approaches. As an example SETIS can be used to segment and compute the tumor size of a patients from MRI scans taken at different times. The software is sufficiently general to be used in various situations by clinicians (already done by our colleagues in Lyon Hospital). It will be freely distributed and is based on open source technology, so that it can easily be adapted to specific needs by other users.

SETIS is filed under APP number IDDN.FR.001.150013.000.S.A.2014.000.21000.

4.3. OptimChemo

Participants: Violaine Louvet [correspondant], Emmanuel Grenier, Paul Vigneaux, Ehouarn Maguet.

OptimChemo is a userfriendly software designed to study numerically the effect of multiple chemotherapies on simple models of tumour growth and to optimize chemotherapy schedules.

4.4. Simstab

Stability prediction of vaccine, property of Sanofi, developper by E. Grenier

4.5. Bingham flows

A 1D and 2D code with a new method for the computation of viscoplatic flows with free-surface. It essentially couples Optimization methods and Well-Balanced Finite-Volumes schemes for viscous shallow-water equations (induced by the viscoplastic nature of the fluid). Currently applied to avalanches of dense snow, it is a private code currently actively developed (in C++). One of the key feature is that its well-balanced property allows to obtained the stationary states which are linked to the stopping of the snow avalanche for this highly non-linear type of fluid.

REO Project-Team

5. New Software and Platforms

5.1. FELiScE

Participants: Grégory Arbia, Cédric Doucet, Miguel Ángel Fernández Varela, Justine Fouchet-Incaux, Benoit Fabrèges, Axel Fourmont, Jean-Frédéric Gerbeau [correspondant], Mikel Landajuela Larma, Damiano Lombardi, Elisa Schenone, Saverio Smaldone, Marina Vidrascu, Irène Vignon-Clementel, Vincent Martin.

FELiScE – standing for "Finite Elements for Life Sciences and Engineering" – is a finite element code which the M3DISYM and REO project-teams have decided to jointly develop in order to build up on their respective experiences concerning finite element simulations. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex respiratory and cardiovascular models considered in the two teams – namely involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena. FELISCE is written in C++, and may be later released as an opensource library.

It was registered in July 2014 at the *Agence pour la Protection des Programmes* under the Inter Deposit Digital Number IDDN.FR.001.350015.000.S.P.2014.000.10000.

Gforge web site: https://gforge.inria.fr/projects/felisce/

5.2. LiFE-V library

Participants: Miguel Ángel Fernández Varela [correspondant], Jean-Frédéric Gerbeau.

LiFE-V [0] is a finite element library providing implementations of state of the art mathematical and numerical methods. It serves both as a research and production library. LiFE-V is the joint collaboration between three institutions: Ecole Polytechnique Fédérale de Lausanne (CMCS) in Switzerland, Politecnico di Milano (MOX) in Italy and Inria (REO) in France. It is a free software under LGPL license.

5.3. SHELDDON

Participant: Marina Vidrascu [correspondant].

SHELDDON (SHELls and structural Dynamics with DOmain decomposition in Nonlinear analysis) is a finite element library based on the Modulef package which contains shell elements, nonlinear procedures and PVM subroutines used in domain decomposition or coupling methods, in particular fluid-structure interaction.

Gforge web site: https://gforge.inria.fr/projects/shelddon

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

SISYPHE Project-Team

4. New Software and Platforms

4.1. The Cardiovascular Waves Analysis toolbox for Scilab

Participants: Lisa Guigue, Claire Médigue, Michel Sorine, Serge Steer.

The work about Heart Failure with preserved Ejection Fraction required the development of a set of tools for ECG signal manipulation and analysis. These tools, developed by Serge Steer, have been included in a Scilab toolbox named Cardiovascular Waves Analysis toolbox that will be available soon as a Scilab module. It extends the former Cardiovascular Toolbox and provides functions for:
- ECG reading multi channel ECG files in various formats (ISHNE, MIT, TMS32),
- Handling huge ECG files obtained through Holter devices,
- ECG pretreatment (filtering, subsampling, power line interference and base line wander removal),
- ECG events detection (P, Q, R, S, T) peaks, onset and end, based on former tools developed by Qinghua Zhang,
- Cardiovascular signals analysis using various approaches like frequency or time-frequency analysis, complex demodulation, non parametric, multilevel and multifractal methods,
- Specialized plotting facilities.