informatics *mathematics*

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RESEARCH CENTER

FIELD
Digital Health, Biology and Earth

Activity Report 2013

Section Software

Edition: 2014-03-20

MODELING AND CONTROL FOR LIFE SCIENCES

ABS Project-Team

5. Software and Platforms

5.1. Software

This section briefly comments on all the software distributed by ABS . On the one hand, the software released in 2013 is briefly described as the context is presented in the sections dedicated to new results. On the other hand, the software made available before 2013 is briefly specified in terms of applications targeted.

In any case, the website advertising a given software also makes related publications available.

5.1.1. *addict: Stoichiometry Determination from Mass Spectrometry Data*

Participants: Deepesh Agarwal, Frédéric Cazals, Noël Malod-Dognin.

Context. Given the individual masses of the proteins present in a complex, together with the mass of that complex, *stoichiometry determination* (SD) consists of computing how many copies of each protein are needed to account for the overall mass of the complex. Our work on the stoichiometry determination (SD) problem for noisy data in structural proteomics is described in [17]. The `addict` software suite not only implements our algorithms `DP++` and `DIOPHANTINE` , but also important algorithms to determine the so-called Frobenius number of a vector of protein masses, and also to estimate the number of solutions of a SD problem, from an unbounded knapsack problem.

Distribution. Binaries for the `addict` software suite are made available from http://team.inria.fr/abs/software/addict/.

5.1.2. *vorpatch and compatch: Modeling and Comparing Protein Binding Patches*

Participants: Frédéric Cazals, Noël Malod-Dognin.

Context. Modeling protein binding patches, i.e. the sets of atoms responsible of an interaction, is a central problem to foster our understanding of the stability and of the specificity of macro-molecular interactions. We developed a binding patch model which encodes morphological properties, allows an atomic-level comparison of binding patches at the geometric and topological levels, and allows estimating binding affinities—with state-of-the-art results on the protein complexes of the binding affinity benchmark. Given a binary protein complex, `vorpatch` identifies the binding patches, and computes a topological encoding of each patch, defined as an *atom shelling tree* generalizing the core-rim model. The program `compatch` allows comparing two patches via the comparison of their atom shelling trees, by favoring either a geometric or a topological comparison.

Distribution. Binaries for `VORPATCH` and `COMPATCH` are available from http://team.inria.fr/abs/software/vorpatch-compatch.

5.1.3. *voratom: Modeling Protein Assemblies with Toleranced Models*

Participants: Frédéric Cazals, Tom Dreyfus.

Context. Large protein assemblies such as the Nuclear Pore Complex (NPC), chaperonin cavities, the proteasome or ATP synthases, to name a few, are key to numerous biological functions. Modeling such assemblies is especially challenging due to their plasticity (the proteins involved may change along the cell cycle), their size, and also the flexibility of the sub-units. To cope with these difficulties, a reconstruction strategy known as Reconstruction by Data Integration (RDI), aims at integrating diverse experimental data. But the uncertainties on the input data yield equally uncertain reconstructed models, calling for quantitative assessment strategies.

To leverage these reconstruction results, we introduced TOleranced Model (TOM) framework, which inherently accommodates uncertainties on the shape and position of proteins represented as density maps — maps from cryo electron-microscopy or maps stemming from reconstruction by data integration. In a TOM, a fuzzy molecule is sandwiched between two union of concentric balls, the size of the region between these two unions conveying information on the uncertainties.

The corresponding software package, VORATOM , includes programs to (i) perform the segmentation of (probability) density maps, (ii) construct toleranced models, (iii) explore toleranced models (geometrically and topologically), (iv) compute Maximal Common Induced Sub-graphs (MCIS) and Maximal Common Edge Sub-graphs (MCES) to assess the pairwise contacts encoded in a TOM.

Distribution. Binaries for the software package VORATOM are made available from http://team.inria.fr/abs/software/voratom/.

5.1.4. *intervor: Modeling Macro-molecular Interfaces*
Participant: Frédéric Cazals.

In collaboration with S. Loriot (The GEOMETRY FACTORY*)*

Context. Modeling the interfaces of macro-molecular complexes is key to improve our understanding of the stability and specificity of such interactions. We proposed a simple parameter-free model for macro-molecular interfaces, which enables a multi-scale investigation —from the atomic scale to the whole interface scale. Our interface model improves the state-of-the-art to (i) identify interface atoms, (ii) define interface patches, (iii) assess the interface curvature, (iv) investigate correlations between the interface geometry and water dynamics / conservation patterns / polarity of residues.

Distribution. The following website http://team.inria.fr/abs/software/intervor serves two purposes: on the one hand, calculations can be run from the website; on the other hand, binaries are made available. To the best of our knowledge, this software is the only publicly available one for analyzing Voronoi interfaces in macro-molecular complexes.

5.1.5. *vorlume: Computing Molecular Surfaces and Volumes with Certificates*
Participant: Frédéric Cazals.

In collaboration with S. Loriot (The GEOMETRY FACTORY*, France)*

Context. Molecular surfaces and volumes are paramount to molecular modeling, with applications to electrostatic and energy calculations, interface modeling, scoring and model evaluation, pocket and cavity detection, etc. However, for molecular models represented by collections of balls (Van der Waals and solvent accessible models), such calculations are challenging in particular regarding numerics. Because all available programs are overlooking numerical issues, which in particular prevents them from qualifying the accuracy of the results returned, we developed the first certified algorithm, called vorlume. This program is based on so-called certified predicates to guarantee the branching operations of the program, as well as interval arithmetic to return an interval certified to contain the exact value of each statistic of interest—in particular the exact surface area and the exact volume of the molecular model processed.

Distribution. Binaries for Vorlume is available from http://team.inria.fr/abs/software/vorlume.

5.1.6. *ESBTL: the Easy Structural Biology Template Library*
Participant: Frédéric Cazals.

In collaboration with S. Loriot (The GEOMETRY FACTORY*, France) and J. Bernauer (Inria AMIB, France).*

Context. The ESBTL (Easy Structural Biology Template Library) is a lightweight C++ library that allows the handling of PDB data and provides a data structure suitable for geometric constructions and analyses, such as those proposed by INTERVOR, VORPATCH and COMPATCH.

Distribution. The C++ source code is available from http://esbtl.sourceforge.net/http://esbtl.sourceforge.net/.

AMIB Project-Team

4. Software and Platforms

4.1. VARNA

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) [55]...
VARNA currently ships in its 3.9 version, and consists in ∼50 000 lines of code in ∼250 classes.
Impact: Downloaded ∼10 000 times and is cited by more than ∼170 research manuscripts (source: Google Scholar).
Availability: Distributed under the terms of the GPL v3 licence since 2009 on simple demand to the author(s) at http://varna.lri.fr.

4.2. 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 [63]. More than 300 visits since its release in January 2012.

4.3. Rna3Dmotif

Participant: Alain Denise [correspondant].

Rna3Dmotif is a free bundle of three easy-to-install programs aimed to be used in combination to automatically extract recurrent RNA local tertiary motifs. The approach used is based on a graph representation of the RNA tertiary structure using LW nomenclature. It was applied to several widely studied ribosomal RNA structures and the motifs thus found were deposited in a dedicated repository.
Impact: Cited in 17 research manuscripts (source: Google Scholar).
Availability: Distributed under the terms of the licence since 24/03/2009 on simple demand to the author(s) at http://rna3dmotif.lri.fr.

4.4. GenRGenS

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... [72] GENRGENS currently ships in its 2.0 version, and consists in ∼25 000 lines of code in ∼120 Java classes.
Impact: Downloaded ∼5 000 times and is cited by more than ∼50 research manuscripts (source: Google Scholar).
Availability: Distributed under the terms of the GPL v3 licence since 2006 on simple demand to the author(s) at https://www.lri.fr/ genrgens/.

4.5. 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.

4.6. 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.

4.7. 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. SPFlow

Participant: Sarah Cohen-Boulakia [correspondant].

Scientific workflow systems are numerous and equipped of provenance modules able to collect data produced and consumed during workflow runs to enhance reproducibility. An increasing number of approaches have been developed to help managing provenance information. Some of them are able to process data in a polynomial time but they require workflows to have series-parallel (SP) structures. Rewriting any workflow into an SP workflow is thus particularly important.
SPFLOW answers this need and takes in a workflow (from the Taverna system) and provide a runnable and provenance equivalent (Taverna) workflow."
Impact: The tool is currently used by Taverna's users from the University of Manchester and more generally by myExperiment users.
Availability: Distributed under the terms of the licence since 04/02/2013 on simple demand to the author(s) at http://www.lri.fr/ chenj/SPFlow/.

4.9. SPChecker

Participant: Sarah Cohen-Boulakia [correspondant].

Scientific workflow systems are numerous and equipped of provenance modules able to collect data produced and consumed during workflow runs to enhance reproducibility. An increasing number of approaches have been developed to help managing provenance information. Some of them are able to process data in a polynomial time but they require workflows to have series-parallel (SP) structures.

SPChecker is able to detect whether or not any Taverna workflow has a series-parallel structure.

Impact: The tool is currently used by Taverna's users from the University of Manchester and more generally by myExperiment users (a collaboration with Manchester has started and should significantly augment the number of potential users).

Availability: Distributed under the terms of the licence since 01/02/2013 on simple demand to the author(s) at http://www.lri.fr/ chenj/SPChecker/.

4.10. BioGuide

Participants: Sarah Cohen-Boulakia [correspondant], Christine Froidevaux.

BioGuide/BioGuideSRS : this software helps the scientists choose suitable sources and tools, find complementary information in sources, and deal with divergent data.

Reference : Sarah Cohen-Boulakia, Olivier Biton, Susan Davidson, Christine Froidevaux, BioGuideSRS: Querying Multiple Sources with a user-centric perspective, Bioinformatics, March, 23(10), 1301-1303, 2007.

Impact: The paper related to the tool has been cited by ∼26 research manuscripts (source: Google Scholar) so far. Since 2007 and up to now, BioGuide has 8,030 distinct users including regular users from the EBI (European Bioinformatics Institute), the Institut Curie and the Children's Hospital of Philadelphia.

Availability: Distributed under the terms of the licence since 01/09/2006 on simple demand to the author(s) at http://bioguide-project.net/.

4.11. 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.

BAMBOO Project-Team

5. 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@univ-lyon1.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@univ-lyon1.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@univ-lyon1.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.
http://alcovna.genouest.org/kissnp/

5.10. kisSplice & KisSplice2igv

Participants: Lilia Brinza [EPI], Rayan Chikhi, Alice Julien-Lafferière [EPI], Janice Kielbassa, Vincent Lacroix [Contact, EPI], Camille Marchet [EPI], Claire Lemaitre, Pierre Peterlongo, Gustavo Sacomoto [EPI], Marie-France Sagot [EPI], Raluca Uricaru.

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. 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://amici.dsi.unifi.it/lasagne/?page_id=324

5.12. 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/

5.13. 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

5.14. 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/

5.15. 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/

5.16. 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/

5.17. 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/

5.18. PepLine

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

Pipeline for the high-throughput analysis of proteomic data.

5.19. 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/

5.20. 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/

5.21. 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.

5.22. Tuiuiu

Participants: Alair Pereira Do Lago, Pierre Peterlongo [Contact, pierre.peterlongo@inria.fr], Nadia Pisanti, Gustavo Sacomoto [EPI], Marie-France Sagot [EPI].

Multiple repeat search filter with edit distance.
http://mobyle.genouest.org/cgi-bin/Mobyle/portal.py?form=tuiuiu

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

5. Software and Platforms

5.1. aevol (artificial evolution)

Participants: Guillaume Beslon, Stephan Fischer, Carole Knibbe, David P Parsons, 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.
- URL: http://www.aevol.fr

5.2. 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) is supported by is 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).

5.3. 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/

5.4. 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).

<p style="text-align:center; color:red;">**BIGS Project-Team**</p>

5. Software and Platforms

5.1. Light diffusion into tissues

We are currently considering the possibility to implement our Matlab algorithms concerning light diffusion into tissues into the Matlab toolbox *Contsid*, developed by the System Identification team of the CRAN (http://www.iris.cran.uhp-nancy.fr/contsid/).

5.2. Online data analysis

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 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.

5.3. Socio-economic index

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.

<h2 style="text-align:center; color:red">BONSAI Project-Team</h2>

5. Software and Platforms

5.1. YASS – Local homology search

Actively maintained.

Software self-assessment following the mechanisms provided by Inria Evaluation Committee for software evaluation: **A-4**, **SO-3**, **SM-2**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://bioinfo.lifl.fr/yass/

Licence: GPL

YASS is a software devoted to the classical problem of genomic pairwise alignment, and use most of our knowledge to design and implement efficient seeding techniques these last years. It is frequently used, it always receives more than 300 web queries per month (excluding local queries), and is also frequently downloaded and cited.

5.2. RNA tools – RNA structure prediction and comparison

http://bioinfo.lifl.fr/rna/

Actively maintained/Actively developed

Inria Evaluation Committee Criteria for Software Self-Assessment: A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4

The RNA tools provide a suite of programs to help analysing RNA secondary structures, together with visualisation tools for RNA 2D structures and RNA multiple alignments. Our first tool was *carnac* for RNA structure prediction by comparative analysis. *carnac* was issued in 2004 [1], independently benchmarked [2], and re-designed in 2009. It is still cited and used. Over the years, we have add new programs: *regliss* for locally optimal secondary structures, *gardenia* for structure comparison, *CG-seq* for gene prediction by comparative analysis, ...

5.3. TFM-Explorer – Identification and analysis of transcription factor binding sites

Actively maintained.

Software self-assessment: **A-4**, **SO-3**, **SM-2**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://bioinfo.lifl.fr/TFM/

Licence: GPL

The TFM suite is a set of tools for analysis of transcription factor binding sites modeled by Position Weight Matrices. In this suite, the TFM-EXPLORER tool is designed to analyze regulatory regions of eukaryotic genomes using comparative genomics and local over-representation.

5.4. RNAspace – A platform for noncoding RNA annotation

Actively developped.

Software self-assessment: **A-5**, **SO-3**, **SM-3-up4**, **EM-2-up3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://www.rnaspace.org/

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[1]CARNAC: folding families of related RNAs. H. Touzet *et al.*, Nucleic Acids Research, 2004

[2]A comprehensive comparison of comparative RNA structure prediction approaches. P. Gardner *et al.*, BMC Bioinformatics, 2004

Licence: GPL

RNAspace is a national collaborative initiative conducted with Genopole Midi-Pyrénées and originally supported by IBISA [3]. The goal is to develop an open source platform for structural and functional noncoding RNA annotation in genomes (see Section 6.2): http://www.rnaspace.org. The project will be pursued within France Génomique (see Section 7.2.1).

5.5. CGseq – A toolbox for comparative analysis

Actively maintained.
Software self-assessment: **A-4**, **SO-3**, **SM-2**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://bioinfo.lifl.fr/CGseq/

Licence: GPL

CG-seq is a toolbox for identifying functional regions in a genomic sequence by comparative analysis using multispecies comparison.

5.6. SortMeRNA – Metatranscriptome classification

Actively developed.
Software self-assessment: **A-4**, **SO-3**, **SM-2**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site: http://bioinfo.lifl.fr/RNA/sortmerna

Licence: GPL

+   *SortMeRNA*: Metatranscriptome classification

http://bioinfo.lifl.fr/RNA/sortmerna/

Actively developed

Inria Evaluation Committee Criteria for Software Self-Assessment: A-4, SO-3, SM-3, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4

SortMeRNA is a tool designed to rapidly filter ribosomal RNA fragments from metatranscriptomic data produced by next-generation sequencers. The distribution includes curated ribosomal RNA databases. It is available for download from our website, or through the open web-based platform Galaxy. *SortMeRNA* was released in October 2012, and is used in production by Genoscope (French National Center for Sequencing) to process metatranscriptomic data. Moreover, it has already been integrated in two published computational pipelines [4],[5] and have identified users in multiple research laboratories worldwide [6].

5.7. Vidjil – Quantifying lymphocytes rearrangements in high-throughput sequencing data

Actively developed
Software self-assessment: **A-3-up4**, **SO-3**, **SM-2-up3**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://bioinfo.lifl.fr/vidjil

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[3]IBISA is a French consortium for evaluating and funding national technological platforms in life sciences.

[4]A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. M. Leimena et al., *BMC genomics*, 2013

[5]Metagenome survey of a multispecies and algae-associated biofilm reveals key elements of bacterial-algae interactions in photobioreactors. I. Krohn-Molt et al. Applied and environmental microbiology, 2013

[6]Umeå University (Sweden), Leibniz Institute DSMZ (Germany), NGS department of Campus Science Support Facilities GmbH (Austria), Oxford Centre for Integrative Systems Biology (Great Britain), Laboratoire d'Ecologie Alpine (Grenoble), PRABI (Lyon), Wageningen University (Netherlands), ...

Vidjil implements a two-stage strategy for fast clustering and quantification of clones coming from immunological rearrangements in genomic sequences. It is currently used in "minimal residual disease" following, but could have other uses in immunology research. *Vidjil* is currently under test at the Lille hospital, and is planned to be tested in another hematological lab. In 2013, the development of Vidjil was supported by the regional project ABILES: an engineer (Marc Duez) developed for 5 months a graphical interface for using *Vidjil*. We plan to release a first production version to the hospital during 2014.

5.8. Biomanycores.org – A community for bioinformatics on manycore processors

Actively developped.
Software self-assessment: **A-3**, **SO-2**, **SM-3**, **EM-3down2**, **SDL-4up5**, OC-4 (DA-4, CD-4, MS-4, TPM-4)

Software web site : http://biomanycores.org/

Manycore architectures are an emerging field of research full of promises for parallel bioinformatics. However the usage of GPUs is not so widespread in the end-user bioinformatics community. The goal of the `biomanycores.org` project is to gather open-source CUDA and OpenCL parallel codes and to provide easy installation, benchmarking, and interoperability. The last point includes interfaces to popular frameworks such as Biopython, BioPerl and BioJava.

The development of Biomanycores was supported by a national ADT [7] from October 2010 to October 2012.

5.9. Norine – A resource for nonribosomal peptides

Actively maintained.
Software self-assessment: **A-5**, **SO-3**, **SM-3-up4**, **EM-2-up3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-4

Software web site : http://bioinfo.lifl.fr/norine/ 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 nonribosomal 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. Norine main users come for 13% from the United States of America, for 12% from the United Kingdom, for 5% from China or for 4% from Germany where renowned biology laboratories work on nonribosomal peptides (NRPs) or on their synthetases.

5.10. Crac – RNA-seq read analysis

Actively maintained.
Software self-assessment: **A-4**, **SO-3**, **SM-3**, **EM-3**, **SDL-4**, DA-4, CD-4, MS-4, TPM-3

Software web site: http://crac.gforge.inria.fr/

Objective: CRAC aims at identifying biological variations in RNAs by comparing short reads to a reference genome. It detects point mutations, short indels, splice events, and fusion genes or transcripts.

This library is the result of a collaboration with N. Philippe and T. Commes (IGH laboratory, Montpellier) and É. Rivals (LIRMM laboratory, Montpellier).

5.11. GkArrays – Indexing high throughput sequencer reads

Actively maintained.
Software self-assessment: **A-3**, **SO-3**, **SM-3**, **EM-2**, **SDL-4**, DA-4, CD-4, MS-4, TPM-3

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[7]ADT (Action for Technological Development) is an Inria internal call

Software web site : http://crac.gforge.inria.fr/gkarrays/

Objective : Gk-Arrays is a C++ library specifically dedicated to indexing reads produced by high-throughput sequencers. This index allows to answer queries centred on reads. It also takes benefits from the input specificity to lower space consumption.

This library is the result of a collaboration with N. Philippe and T. Commes (IGH laboratory, Montpellier), M. Léonard and T. Lecroq (LITIS laboratory, Rouen) and É. Rivals (LIRMM laboratory, Montpellier).

DYLISS Project-Team

5. Software and Platforms

5.1. Platform

Our tools are based on formal systems. They aim at guiding the user to progressively reduce the space of models (gene or protein families, set of main 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]. .

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

Participants: Anne Siegel [contact], Andres Aravena, Jeanne Cambefort [contact], Guillaume Collet, Damien Eveillard, Sylvain Prigent, Sven Thiele [contact].

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 [44] [27] [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 [26] [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 [13] [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 [6] [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 [5] [Python package][web server].

5.3. Dynamics: invariant-based prediction

Participants: Oumarou Abdou-Arbi, Geoffroy Andrieux, Jérémie Bourdon [contact], Jeanne Cambefort [contact], Damien Eveillard, Michel Le Borgne, Anne Siegel, Sven Thiele, Santiago Videla [contact].

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 [1]. [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 [15][webserver][software and doc].

POGG. The POGG software allows scoring the importance and sensibility of regulatory interactions with a biological system with respect to the observation of a time-series quantitative phenotype. This is done by solving nonlinear problems to infer and explore the family of weighted Markov chains having a relevant asymptotic behavior at the population scale. Its possible application fields are systems biology, sensitive interactions, maximal entropy models, natural language processing. It results from our collaboration with the LINA-Nantes [2][matlab package].

5.4. Sequence annotation

Participants: François Coste [contact], Aymeric Antoine-Lorquin, Catherine Belleannée [contact], Gaëlle Garet, Olivier Quenez, Jacques Nicolas.

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 [2] [10]) [software]

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[1]http://www.cellnopt.org/
[2]http://crispi.genouest.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 [38][4] [web server]

5.5. Integration of our tools in larger software environments

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].

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].

GENSCALE Project-Team

5. Software and Platforms

5.1. Next Generation Sequencing

Participants: Alexan Andrieux, Dominique Lavenier, Claire Lemaitre, Nicolas Maillet, Pierre Peterlongo, Guillaume Rizk, Erwan Drezen, Charles Deltel.

- **Genome assembly** [contact: P. Peterlongo]
    - **Minia : ultra low memory footprint assembly** Minia is a short-read assembler based on a de Bruijn graph, capable of assembling a human genome on a desktop computer in a day. The output of Minia is a set of contigs. Minia produces results of similar contiguity and accuracy to other de Bruijn assemblers (e.g. Velvet). http://minia.genouest.org/
    - **Mapsembler: targeted assembly software.** Mapsembler is a targeted assembly software. From sets of NGS raw reads and a set of input sequences (starters), it determines if each starter could be constructed from the reads. Then for each "read-coherent" starter, Mapsembler outputs its sequence neighborhood as a linear sequence or as a graph, depending on the user choice. http://colibread.inria.fr/mapsembler2/
    - **Bloocoo: memory-efficient read correction** Bloocoo is a software to identify sequencing errors in short-read datasets and correct them. It is based on an efficient data structure that enables to keep a very low memory footprint. http://gatb.inria.fr
- **Variant detection** [contact: C. Lemaitre]
    - **discoSnp and kisSplice : variant identification without the use of a reference genome**. discoSnp is a tool to find single nucleotide polymorphisms (SNP) by comparing two sets of raw NGS reads. http://colibread.inria.fr/discosnp/ KisSplice finds alternative splicings but also short insertions, deletions and duplications, SNPs and sequencing errors in one or two RNA-seq sets, without assembly nor mapping on a reference genome. http://colibread.inria.fr/software/kissplice/
    - **Kissreads: quantification of variants** Kissreads considers sets of NGS raw reads and a set of input sequences (starters). Mapping reads to each starter, it provides quantitative (coverage depth) and qualitative (mapped read quality) information about each starter.
    - **MindTheGap : detection of large insertions** MindTheGap is a tool to detect large insertion events in re-sequencing data with respect to a reference genome. http://gatb.inria.fr
- **Read mapping** [contact: D. Lavenier]
    - **GASSST: short reads mapper** The GASSST software (Global Alignment Short Sequence Search Tool) is a general purpose mapper. GASSST finds global alignments of short DNA sequences against large DNA banks. One main characteristic of GASSST is its ability to perform fast gapped alignments and to process long reads compared to other current similar tools. http://www.irisa.fr/symbiose/projects/gassst/

5.2. High throughput sequence analysis

Participants: Erwan Drezen, Dominique Lavenier, Claire Lemaitre, Nicolas Maillet, Pierre Peterlongo.

- **PLAST : efficient bank-to-bank alignments** PLAST (Parallel Local Alignment Search Tool) is a parallel alignment search tool for comparing large protein banks. PLAST runs 3 to 5 times faster than the NCBI-BLAST software. An improved version is commercialized by the Korilog Company, including the DNA bank-to-bank option. [contact: D. Lavenier] http://www.irisa.fr/symbiose/projects/plast/
- **Compareads : efficient comparison of large metagenomics NGS datasets** This software extracts similar DNA sequences (reads) between two metagenomic datasets. It requires a small and fixed amount of memory and can thus be used on huge datasets. [contact: P. Peterlongo] http://alcovna.genouest.org/compareads/

5.3. 3D Protein structures

Participants: Rumen Andonov, Guillaume Chapuis, Mathilde Le Boudic-Jamin, Antonio Mucherino.

- **CSA and DALIX** CSA (Comparative Structural Alignment) is a webserver for computing and comparing protein structure alignments. CSA is able to compute score-optimal alignments with respect to various inter-residue distance-based scoring schemes. [contact: R. Andonov] http://csa.project.cwi.nl/

- **A_purva** A_purva is a Contact Map Overlap maximization (CMO) solver. Given two protein structures represented by two contact maps, A_purva computes the amino-acid alignment which maximize the number of common contacts. [contact: R. Andonov] http://mobyle.genouest.org/cgi-bin/Mobyle/portal.py?forms::A_Purva

- **MD-Jeep** MD-jeep is a software tool for solving distance geometry problems. It is able to solve a subclass of instances of the problem for which a discrete reformulation can be supplied. We refer to this subclass of instances as the Discretizable Molecular Distance Geometry Problem (DMDGP). We employ a Branch & Prune (BP) algorithm for the solution of DMDGPs. [contact: A. Mucherino] http://www.antoniomucherino.it/en/mdjeep.php

5.4. HPC and Parallelism

Participants: Guillaume Chapuis, Dominique Lavenier, François Moreews, Charles Deltel.

- **QTLmap** QTLMap is a tool dedicated to the detection of Quantitative Trait Loci (QTL) from experimental designs in outbred population. QTLMap was recently ported to GPU and offers reduced run times. [contact: D. Lavenier] http://www.inra.fr/qtlmap/

- **SLICEE** (Service Layer for Intensive Computation Execution Environment) is part of the BioWIC project. This software proposes (1) to abstract the calls to the cluster scheduler by handling command submission; (2) to take care of exploiting the data parallelism with data specific methods; (3) to manage data using a cache references mecanism and route data between tasks. [contact: F. Moreews] http://vapor.gforge.inria.fr/

IBIS Project-Team

4. Software and Platforms

4.1. Genetic Network Analyzer (GNA)

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

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 8.5. In comparison with the previously distributed versions, GNA 8.5 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 [6]. For more information, see http://www-helix.inrialpes.fr/gna.

4.2. WellReader

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

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.

<p style="text-align:center; color:red;">**MAGNOME Project-Team**</p>

5. Software and Platforms

5.1. Magus: Genome exploration and analysis

Participants: David James Sherman [correspondant], Pascal Durrens, Natalia Golenetskaya, 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. For more information see the MAGUS Gforge web site. [1] MAGUS $1.x$ is mature software used since 2006 by our collaboration partners. MAGUS 2.0 is developed in an Inria Technology Development Action (ADT) with an open-source license and is being deposited with the APP.

5.2. Pantograph: Inference of metabolic networks

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

Pantograph is a software tool for inferring whole-genome metabolic models for eukaryote cell factories. It is based on metabolic scaffolds, abstract descriptions of reactions and pathways on which inferred reactions are hung are are eventually connected by an interative mapping and specialization process. Scaffold fragments can be repeatedly used to build specialized subnetworks of the complete model. 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. [2].

5.3. MetaModGen: Generalizing Metabolic Models

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

The metabolic model generalization and navigation software allows a human expert to explore a metabolic model in a layered manner. The software creates an on-line semantically zoomable representation of a model submitted by the user in SBML [3] 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). Zoomable representation is implemented using the Leaflet[4] JavaScript library for mobile-friendly interactive maps. Users can click on reactions and compounds to see the information about their annotations. An example of a zoomable representation of the peroxisome compartment of *Y. lipolytica* is available at http://metamogen.gforge.inria.fr/map.html.

5.4. BioRica: Multi-scale Stochastic Modeling

Participants: David James Sherman [correspondant], Rodrigo Assar Cuevas, Joaquin Fernandez.

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[1] http://magus.gforge.inria.fr
[2] http://pathtastic.gforge.inria.fr
[3] http://sbml.org
[4] http://leafletjs.com

BioRica is a high-level modeling framework integrating discrete and continuous multi-scale dynamics within the same semantics field. A model in BioRica node is hierarchically composed of nodes, which may be existing models. Individual nodes can be of two types:

- Discrete nodes are composed of states and transitions described by guarded events. Behavior can be stochastic (defined by the likelihood that an event fires when activated) and timed (defined by the delay between an event's activation and the moment that its transition occurs).

- Continuous nodes are described by ODE systems, potentially a hybrid system whose internal state flows continuously while having discrete jumps.

The system has been implemented as a distributable software package. The BioRica compiler reads a specification for hierarchical model and compiles it into an executable simulator. The modeling language is a stochastic extension to the AltaRica [5] Dataflow language, inspired by work of Antoine Rauzy. Input parsers for SBML 2 version 4 are curently being validated. The compiled code uses the Python runtime environment and can be run stand-alone on most systems. For more information see the BioRica Gforge web site. [6] BioRica was developed as an Inria Technology Development Action (ADT) with an open-source license and is deposited with the APP.

5.5. Génolevures On Line: Comparative Genomics of Yeasts

Participants: Pascal Durrens [correspondant], Natalia Golenetskaya, Tiphaine Martin, David James Sherman.

The Génolevures online database provides tools and 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. The Génolevures site includes a private collaboration area for specific studies by members of its international community. The contents of the knowledge base are expanded and maintained by the CNRS through GDR 2354 Génolevures, and full data may be downloaded from the site. Génolevures online uses our open-source MAGUS system for genome navigation, with project-specific extensions developed by David Sherman, Pascal Durrens, and Tiphaine Martin; these extensions are not made available due to incertainty about intellectual property rights. For more information see the Génolevures web site. [7]

5.6. Inria Bioscience Resources

Participants: Olivier Collin [correspondant], Frédéric Cazals, Mireille Régnier, Marie-France Sagot, Hélène Touzet, Hidde De jong, David James Sherman, Marie-Dominique Devignes, Dominique Lavenier.

Inria Bioscience Resources is a portal designed to improve the visibility of bioinformatics tools and resources developed by Inria teams. This portal will help the community of biologists and bioinformatians understand the variety of bioinformatics projects in Inria, test the different applications, and contact project-teams. Eight project-teams participate in the development of this portal. Inria Bioscience Resources is developed in an Inria Technology Development Action (ADT).

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[5] http://altarica.labri.fr
[6] http://biorica.gforge.inria.fr
[7] http://www.genolevures.org/

MORPHEME Project-Team (section vide)

<p style="text-align:center; color:red;">**SERPICO Project-Team**</p>

5. Software and Platforms

5.1. Software for live cell imaging

Participants: Charles Kervrann [(contact)], Patrick Bouthemy, Tristan Lecorgne, 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) [47]. 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.

Partner: 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) (see Figure 3) [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 ...
Partners: J. Boulanger, J. Salamero (UMR 144, CNRS-Institut Curie), P. Elbau (RICAM Linz, Austria), J.B. Sibarita (UMR 5091, University of Bordeaux 2).

../../../../projets/serpico/IMG/DN-Rab6AGFP-WF.png

Figure 3. ND-SAFIR *software: denoising of a 3D image sequence in wide-field microscopy (GFP-Rab6A (Hela cell), UMR 144, CNRS-Institut Curie).*

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, see Fig. 4) 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 [32].

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

../../../../projets/serpico/IMG/hullkground_imagej.png

Figure 4. HULLKGROUND *software: plug-in* IMAGEJ.

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/

Partners: S. Blestel and D. 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. On real data, this segmentation method extracts the most contrasted regions of microtubules, and 3D visualization is improved.

Partners: S. Blestel and D. Chrétien (UMR 6290, CNRS-University of Rennes 1)

5.3. Image Processing software distribution

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

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. 5) is to demonstrate the performance of the programs developed by the team: CRFMOVINGSPOTDETECTION (under review), HOTSPOTDETECTION [50], HULLK-GROUND [32], KLTRACKER [48], MOTION2D[19], MS-DETECT [35], ND-SAFIR[4] and OPTI-CALFLOW. 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 [32] (see Fig. 4), MOTION2D[19], HOTSPOTDETECTION [50].

- *Institut Curie CID iManage database*: Institut Curie is currently acquiring a commercial database system (CID iManage / Strand Avadis company) to store mass of data. The database can be searched via meta-data and includes menu selections that enable to run remote processing. We have integrated ND-SAFIR in the interface environment to allow the database users to denoise images easily.

Partners: C. Deltel (Inria Rennes SED) and Perrine Paul-Gilloteaux (UMR 144, PICT IBiSA, CNRS-Institut Curie)

../../../../projets/serpico/IMG/MobyleatSERPICO.png

Figure 5. Mobyle@SERPICO web portal.

<p style="text-align:center; color:red;">**VIRTUAL PLANTS Project-Team**</p>

4. Software and Platforms

4.1. V-Plants

Participants: Frédéric Boudon, Christophe Godin [coordinator], Yann Guédon, Christophe Pradal [software architect], Jean-Baptiste Durand, Pascal Ferraro, Julien Coste, Guillaume Baty.

Computer algorithms and tools developed by the Virtual Plants team are integrated in a common software suite *V-Plants*, dedicated to the modeling and analysis of plant development at different scales (e.g. cellular tissue, whole plant, stand). The VPlants packages are integrated in OpenAlea as Python components. Several components are distributed and usable through the visual programming environment (see figure 1):

- Multi-scale geometric modeling and visualization. VPlants.PlantGL is a geometric library which provides a set of graphical tools and algorithms for 3D plant modeling at different scales [7]. It is used by many other components to represent the geometry of biological shapes from 3D meristems, plant architectures to plant populations. VPlants.PlantGL is built around a scene-graph data structure and provides efficient algorithms and original geometrical shapes (parametric surfaces, dedicated envelops), that are useful for plant modeling.

- Statistical sequence and tree analysis. Different statistical packages (i.e. VPlants.StatTool, VPlants.SequenceAnalysis, VPlants.TreeMatching and VPlants.TreeAnalysis) are now available in OpenAlea. They provide different models and algorithms for plant architecture analysis and simulation.

- Meristem functioning and development. A first set of components has been created in the last 4-years period to model meristem development in OpenAlea. These tools are currently being integrated thoroughly in the platform so that modelers and biologists can use them, and reuse components easily (for meristem 3D reconstruction, cell tracking, statistical analysis of tissues, creating and manipulating atlases, creating or loading models of growth that can further be run on digitized structures, etc).

- Standard data structure for plants. A new implementation of the MTG formalism for representing and manipulating multiscale plant architecture has been developed. It provides a central data-structure to represent plants in a generic way in OpenAlea. This implementation is available through the packages OpenAlea.MTG. These components make it possible to share plant representations between users and fosters the interoperability of new models.

- Simulation system. The study of plant development requires increasingly powerful modeling tools to help understand and simulate the growth and functioning of plants. In the last decade, the formalism of L-systems has emerged as a major paradigm for modeling plant development. Previous implementations of this formalism were made based on static languages, i.e. languages that require explicit definition of variable types before using them. These languages are often efficient but involve quite a lot of syntactic overhead, thus restricting the flexibility of use for modelers. We developed L-Py [2] an adaptation of L-systems to the Python language (basis of OpenAlea). Thanks to its dynamic typing property, syntax is simple, code execution is made easy and introspection property of the language makes it possible to parameterize and manipulate simply complex models. Independent L-systems can be composed to build-up more complex modular models. MTG structures (that are a common way to represent plants at several scales) can be translated back and forth into L-system data-structure and thus make it easy to reuse in L-systems tools for the analysis of plant architecture based on MTGs. Extensions to integrate multiscale dynamic models are currently being developed in collaboration with P. Prusinkiewicz and his team from the University of Calgary.

../../../../projets/virtual_plants/IMG/alea.png

Figure 1. V-Plants components of the OpenAlea platform: simulating plant processes at different scales. Top Left: Reconstruction of a virtual meristem, analysis and simulation of the auxin fluxes inside the meristem. Top Right: Reconstruction of a virtual apple tree from digitized data. Bottom: Simulation of an ecosystem (A beech "Fagus Sylvatica L." trees forest) with a multi level approaches. On the left, explicit representation of the crown volumes that serves as input to generate the detailed representation, on the right.

4.2. OpenAlea

Participants: Frédéric Boudon, Christophe Godin, Yann Guédon, Christophe Pradal [coordinator], Christian Fournier, Julien Coste.

This research theme is supported by the Inria ADT Grant OpenAlea 2.0 and by an Agropolis RTRA Grant named OpenAlea.

OpenAlea[8] is an open source and collaborative software project primarily dedicated to the plant research community. It is designed as a component framework to dynamically glue together models from different plant research labs, and to enhance re-usability of existing models in the plant research community.

The architecture of OpenAlea is based on a component architecture. It provides a set of standard components (OpenAlea.Stdlib), a package manager to dynamically add and retrieve new components, and a port graph data-structure to compose models by interconnecting components into a data-flow.

Visualea provides a visual programming environment, used by scientists to build new model interactively by connecting available components together through an easy-to-use graphical user interface.

In 2013, the following progresses were accomplished:
1. Development and extension of OpenAlea and Visualea:
    – The standard library of components has been extended with useful scientific packages such as a flexible data plotting package (Openalea.Pylab), 2D and 3D image manipulation (Openalea.Image) and linear algebra operations (Openalea.Numpy).
    – Several models of computation have been implemented on the data-flow data-structure to enable discrete event simulation and control flow inside OpenAlea.
2. Animation and diffusion
    – A scientific board has been defined to manage the development and diffusion of OpenAlea. It is composed by 12 scientists.
    – StandAlone binary installers have been released on Windows and Mac to ease the installation of a large number of packages without relying on a web server. A Ubuntu repository has been set up on Launchpad.
    – The OpenAlea project is hosted at the Inria gforge (link http://openalea.gforge.inria.fr). The web site is visited by more than 370 unique visitor each month; 650000 web pages have been visited and the different available components of OpenAlea have been downloaded more than 540,000 times during the last two years. OpenAlea is the first project at Inria Gforge in term of number of downloads and of page views.

4.3. Alinea

Participants: Christian Fournier, Christophe Pradal, Frédéric Boudon.

Other participants : Bruno Andrieu, Michael Chelle, Gaëtan Louarn, Benoit de Solan, Mariem Abichou, Liqi Han, Elmer Ccopa-Rivera, Frédéric Baret, Rafaële Casa, Guillaume Garin, Corinne Robert, Sébastien Saint-Jean, Didier Combes, Camille Chambon, Romain Barillot, Jean-Christophe Soulie, Delphine Luquet.

The Alinea software suite is distributed as a meta-package of the OpenAlea Platform. It is produced by a consortium of modelers from INRA , and consists of various ecophysiological and biophysical models of simulation (radiative transfer, interaction between plant and pest, circulation of hydric fluxes, and dispersion). The project is suported by 5 INRA teams and the Inria Virtual Plants project. This project has been homologated as strategic ressource for INRA, and is integrated in the CATI IUMA (Centre Automatisé de Traitement de l'Information, : Informatisation et Utilisation des Modèles dédiés aux Agro-Ecosystemes). The five following components are distributed with the OpenAlea platform:

- Alinea.Adel is a module to simulate the 3D architectural development of gramineous crops. In 2013, a new parameterisation procedure was developed for wheat, that allows to use the model for the simulation of agronomic experiments with a minimal set of measurements [28].

- Alinea.Alep is a generic model developed in 2013 to simulate pathosystems from the scale of leaf to the scale of the canopy

- Alinea.Caribu is a modeling suite for lighting 3D virtual scenes, especially designed for the illumination of virtual plant canopies such as virtual crop fields. It uses a special algorithm, the nested radiosity, that allows for a precise estimation of light absorption at the level of small canopy elements.

- Alinea.pyRATP allows to simulate the light interception, photosynthesis and transpiration of a plant canopy.

- Alinea.TopVine is a component to reconstruct grapevine canopy structure. Other components are in developmental state and will be released after publication by their autors.

CORTEX Team

5. Software and Platforms

5.1. Spiking neural networks simulation

Participants: Dominique Martinez, Yann Boniface.

A spiking neuron is usually modeled as a differential equation describing the evolution over time of its membrane potential. Each time the voltage reaches a given threshold, a spike is sent to other neurons depending on the connectivity. A spiking neural network is then described as a system of coupled differential equations. For the simulation of such a network we have written two simulation engines: (i) Mvaspike based on an event-driven approach and (ii) sirene based on a time-driven approach.

- Mvaspike: The event-driven simulation engine was developed in C++ and is available on http://mvaspike.gforge.inria.fr. Mvaspike is a general event-driven purpose tool aimed at modeling and simulating large, complex networks of biological neural networks. It allows to achieve good performance in the simulation phase while maintaining a high level of flexibility and programmability in the modeling phase. A large class of spiking neurons can be used ranging from standard leaky integrate-and-fire neurons to more abstract neurons, e.g. defined as complex finite state machines.

- Sirene: The time-driven simulator engine was written in C and is available on http://sirene.gforge.inria.fr. It has been developed for the simulation of biologically detailed models of neurons —such as conductance-based neurons— and synapses. Its high flexibility allows the user to implement easily any type of neuronal or synaptic model and use the appropriate numerical integration routine (e.g. Runge-Kutta at given order).

5.2. CLONES: Closed-Loop Neural Simulations

Participant: Thomas Voegtlin.

The goal of this work is to provide an easy-to-use framework for closed-loop simulations, where interactions between the brain and body of an agent are simulated.

We developed an interface between the Sofa physics engine, (http://www.sofa-framework.org) and the Brian neural simulator (http://www.briansimulator.org). The interface consists in a Sofa plugin and a Python module for Brian. Sofa and Brian use different system processes, and communicate via shared memory. Synchronization between processes is achieved through semaphores.

As a demonstration of this interface, a physical model of undulatory locomotion in the nematode *c. elegans* was implemented, based on the PhD work of Jordan H. Boyle.

ARAMIS Team

5. 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.

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. It is a command-line software.

The release of the software to the scientific community is planned for 2014.

5.4. qualiCATI

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

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, developed 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 last module, up to now, is dedicated to first preprocessings and quality indices for dMRI. qualiCATI requires training for the visual parts, and is closely linked with a team of clinical research assistants. It has been used to analyse over 3000 subjects from over 10 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.

ASCLEPIOS Project-Team

4. Software and Platforms

4.1. SOFA

Participants: Hervé Delingette [correspondant], Brina Goyette, Federico Spadoni, Stéphanie Marchesseau, Hugo Talbot.

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 Shaman, 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: GPL
- 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 [Correspondant], Florian Vichot, Moulay Fadil, Loïc Cadour.

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, 2.1.2, was made in September 2013. See also the web page http://med.inria.fr.

- Version: 2.1.2
- 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)

ATHENA Project-Team

5. Software and Platforms

5.1. OpenMEEG

Participants: Théodore Papadopoulo, Maureen Clerc, 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 [57], [58]. 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 several more indirect downloads. Work is under progress to integrate it in a commercial package (BESA).

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. 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. 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.

5.4. 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

5.5. ImplicitFEM

Participants: Théodore Papadopoulo, Sylvain Vallaghé.

ImplicitFEM is a software to simulate the forward EEG/MEG problem. It uses a volumic finite element approach (FEM) that allows the modeling of anisotropic conductivities (which OpenMEEG cannot). Its main originality is to avoid the need of meshes that can be very complicated to build for the head. Instead, it uses directly representations of tissue interfaces as levelsets (that can be provided directly by some segmentation program based on levelsets or can be generated from other representations). It also uses non-differentiable elements so as to properly model continuity of both potential and normal current across the tissues interfaces (which correspond to conductivity discontinuities). This tool is currently used only internally by students and researchers.

- Version: 0.5
- Programming language: C++

5.6. External Stimulator for OpenViBE

Participants: Maureen Clerc, Loïc Mahé, Dieter Devlaminck.

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.

- Version: 1.0
- Keywords: Brain Computer Interfaces
- Multiplatform: Windows - Linux - MacOSX
- Programming language: C++

DEMAR Project-Team

5. Software and Platforms

5.1. Software and Platforms

5.1.1. RdP to VHDL tool

Participants: Gregory Angles, David Andreu, Thierry Gil, Robin Passama.

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 unit's 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 inter-connected as well as signals it exports or imports. The interconnection of those components, from a behavioral point out view, consists in the interconnection of places and/or transitions according to well-defined mechanisms: interconnection by means of oriented arcs or by means of the "merging" operator (existing for both places and transitions).

GALS (Globally Asynchronous Locally Synchronous) systems can be specified, connecting different clocks to HILECOP components, and interconnecting them by means of asynchronous signals.

Undergoing work includes the modification of the formalism in order to allow behavior agregation as well as exception handling, both for analysis and implementation sides.

The Eclipse-based version of HILECOP is regulary updated. The last version of HILECOP (registered at the french Agence de Protection des Programmes (APP)) is accessible to the academic community (http://www.lirmm.fr/~gil/Temp/).

5.1.2. 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 has been transferred to the industrial partner and a new version is under development according to an Eclipse-based design. This new version should be available by the end of 2014.

<div align="center">

GALEN Project-Team

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5. 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. Dissimilarity Coefficient learning

Participant: Pawan Kumar [Correspondant].

weakly supervised learning, dissimilarity coefficient, structured prediction DISC (publicly available at http://cvn.ecp.fr/personnel/pawan/code/DISCAPI.zip) software provides a convenient API for dissimilarity coefficient (DISC) based learning. DISC allows the use of weakly supervised datasets (with missing information) by jointly learning a structured prediction classifier and a conditional probability distribution of the missing information. The parameters of the classifier and the distribution are learned by minimizing a user-specified dissimilarity coefficient between them.

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.

5.9. Sparse Prediction

Participant: Andreas Argyriou [Correspondant].

Sparse prediction, K-support norm, SPARSE_K is a sparse prediction code (publicly available at http://cvn.ecp.fr/personnel/andreas/code/sparse_k/sparse_k.tar) using regularization with the k-support norm, which we have introduced [39]. The algorithm uses an accelerated first-order method similar to Nesterov's method.

MNEMOSYNE Team

5. Software and Platforms

5.1. Positioning

Our previous works in the domain of well-defined distributed asynchronous adaptive computations [48], [45], [50] have already made us define a library (DANA [44]), 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". In 2013, we have also integrated in this C/C++ middleware early-vision perception routines developed within the scope of the KEOpS project.

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 subneural or neural models [34], 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 [44] 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. ENAS: Event Neural Assembly Simulation

Participants: Frédéric Alexandre, Nicolas Rougier, Thierry Viéville.

EnaS (that stands for "Event Neural Assembly Simulation") is a middleware implementing our last numerical and theoretical developments, allowing to simulate and analyze so called "event neural assemblies". The recent achievements include (in collaboration with the Neuromathcomp EPI): spike trains statistical analysis via Gibbs distributions, spiking network programing for exact event's sequence restitution, discrete neural field parameters algorithmic adjustments and time-constrained event-based network simulation reconciling clock and event based simulation methods. On the mnemosyne side, this middleware includes since 2013 functional simulations of the non-standard perceptive behavior of the retina (detection of visual events) based on intensity and local spatial intensity cues, while in 2014 we are going to extend these new developments to motion cues. We have also made a strong effort in terms of interoperability on our side, since main functions are now usable from other languages (especially the python wrapper, actually in use), while we still maintain the interoperability with . This development is a complement of what has been developed on the Neruomathcomp side where colleagues have invested in a GUI for their routines.

5.4. 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 are going to 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 will consist of a platform associated to a scenario that would be the closest possible to a survival situation (foraging, predator-prey relationship, partner approach to reproduction) and in which it would be 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 will be slowed down enough to be able to run non trivial brainy-bot implementations. This platform has already being used by two students of the team and is now a new deliverable of the KEOpS project.

NEUROMATHCOMP Project-Team

4. 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 developed by Adrien Wohrer during his PhD [73], [72] 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 [72] 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., [64]).

- 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], Gaia Lombardi, Hassan Nasser, Wahiba Tahouali.

Enas is a library providing numerical tools for the simulation of neural networks and the analysis of spike trains either coming from neural simulators or from biological experiments. The goal is to provide statistical methods allowing to estimate a spatio-temporal statistical model of spike train statistics (including thus pairwise spatio-temporal correlations, but also higher order correlations) from experimental rasters. More precisely, the algorithms are based on our theoretical results on spike trains statistical analysis via Gibbs distributions. We estimate a parametric Gibbs potential optimally characterizing the statistics of empirical spike trains (by minimisation of the Kullback-Leibler divergence between the empirical measure and the Gibbs measure). From this, classical statistical indicators such as firing rate, correlations, higher order moments and statistical entropy are obtained. Also, the form of the Gibbs potential provides essential informations on the underlying neural network and its structure. This method does not only allows us to estimate the spikes statistics but also to compare different models, thus answering such questions about the neural code as: are correlations (or time synchrony or a given set of spike patterns,...) significant with respect to rate coding?

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. The C/C++ code has been organized as "bean java" to ease its use by programmers non specialized in advanced object programming. As a consequence the code is distributed in the form of an include source for the lightest and the most universal integration into users codes.

Event neural assembly simulation is developed under CeCILL C licence
APP logiciel Enas: IDDN.FR.OO1.360008.000.S.P.2009.000.10600.

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

The software is freely downloadable at http://enas.gforge.inria.fr/v3/download.html.

Website: http://enas.gforge.inria.fr/

<p style="text-align:center">NEUROSYS Team</p>

5. Software and Platforms

5.1. Software and Platform

5.1.1. Visualization

- The NeuralFieldSimulator [1] 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.

- *A*naesthesiaSimulator [2] 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 [3].

5.1.2. Platforms

OpenViBE [4] 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 [5] 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.

5.1.3. Others

The package DEvariants [6] includes Matlab routines which implements new variants of the Differential Evolution (an evolutionary algorithm) strategies. The novelty lies in the selection process where we proposed to use a multinomial law to recombine the individuals/vectors. Compared to the standard strategies, our variants allow a faster convergence and a better avoidance of local minima. The different variants are provided with a test sample of functions, the DeJong benchmark. The audience is any scientific user familiar with evolutionary optimization.

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[1] https://gforge.inria.fr/projects/nfsimulator/
[2] https://gforge.inria.fr/projects/anasim/
[3] http://briansimulator.org/
[4] http://openvibe.inria.fr/
[5] https://gforge.inria.fr/projects/openvibe/
[6] https://sites.google.com/site/laurebuhry/publications/optimization-algorithms

<p style="text-align:center">**PARIETAL Project-Team**</p>

5. Software and Platforms

5.1. Scikit learn

Participants: Bertrand Thirion, Gaël Varoquaux, Olivier Grisel [correspondant], Jaques Grobler, Alexandre Gramfort, Fabian Pedregosa, Virgile Fritsch.

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: 0.14
- Programming language: Python, C/Cython

5.2. Nilearn

Participants: Bertrand Thirion, Gaël Varoquaux [correspondant], Philippe Gervais, Jaques Grobler, Alexandre Gramfort, Fabian Pedregosa, Alexandre Abraham, Michael Eickenberg.

NiLearn is the neuroimaging library that adapts the concepts and tools of the 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 (P. Gervais).

- 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], Virgile Fritsch, 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 and LNAO (CEA, DSV, Neurospin). It is devoted to algorithmic solutions for various issues in neuroimaging data analysis. All the nipy project is freely available, under BSD license. It is available in NeuroDebian.

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

- Version: 0.3

5.5. MedInria

Participants: Pierre Fillard [correspondant], Sergio Medina, Viviana Siless.

MedInria is a free collection of softwares developed within the ASCLEPIOS, ATHENA and VISAGES research projects. It aims at providing to clinicians 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. MedInria is available for Microsoft windows XP/Vista, Linux Fedora Core, MacOSX, and is fully multi-threaded.
See also the web page http://med.inria.fr/.

- Version: 2.0

5.6. PyHRF

Participants: Philippe Ciuciu [correspondant], Solveig Badillo, Aina Frau Pascual.

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. Software and Platforms

5.1. Monolix

Participants: Marc Lavielle, Hector Mesa, 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 MONO-LIX. 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, Elodie Maillot, Laura Brocco, 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). Version 3 of the CTS is available since June 2013. 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)
- Graphics and statistical tests
- Automatic reporting

5.4. MLXplore

Participants: Marc Lavielle, Laura Brocco.

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. POPIX collaborates closely with Lixoft on on the definition of the specifications of MLXplore.

<p style="text-align:center"><strong style="color:red">SHACRA Project-Team</p>

5. Software and Platforms

5.1. SOFA

SOFA http://www.sofa-framework.org is an open-source software framework targeted at interactive computational (medical) simulation. The idea of SOFA was initiated by members of the SHACRA team, and strongly supported by Inria through a development program that we lead. SOFA facilitates collaborations between specialists from various domains, by decomposing complex simulators into components designed independently. Each component encapsulates one of the key aspects of a simulation, such as the degrees of freedom, the forces and constraints, the differential equations, the linear solvers, the collision detection algorithms or the interaction devices. The simulated objects can be represented using several models, each of them optimized for a different task such as the computation of internal forces, collision detection, haptics or visual display. These models are synchronized during the simulation using a mapping mechanism. CPU and GPU implementations can be transparently combined to exploit the computational power of modern hardware architectures. Thanks to this flexible yet efficient architecture, SOFA can be used as a test-bed to compare models and algorithms, or as a basis for the development of complex, high-performance simulators. 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 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. SOFA is the only software developed by our team, but practically speaking it is a collection of plugins (each one aimed at a specific application) organized around a common core that provides a large number of functionalities. As mentioned previously, 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.

We also gave a 4 hours workshop on SOFA at MMVR/NextMed conference in february 2013 in San Diego. This workshop was done in collaboration with the swedish company SenseGraphics. The topic was to demonstrate the setup of a dental surgery simulation in Sofa, and use SenseGraphics visual tools for the rendering. The attendees feedback was beyond our expectations, with an unexpected interest in new SOFA features like the SofaPython plugin. Still about SOFA, like last year we gave in october a 3 days training session in Montpellier for about twenty SOFA beginners (mostly engineers). These are new engineers of the three teams involved in SOFA development, and employees of companies using SOFA in their business. Last, a "SOFA Day" in november in prelude of the Vriphys conference gave 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.

VISAGES Project-Team

5. Software and Platforms

5.1. CLARCS: C++ Library for Automated Registration and Comparison of Surfaces

Participants: Juan Francisco Garamendi Bragado, Sylvain Prima.

In collaboration with Benoit Combès (Géosciences Rennes, UMR 6118) and Alexandre Abadie (Inria Saclay Île-de-France), within the 3D-MORPHINE ARC project (http://3dmorphine.inria.fr), we conceived and implemented a C++ library (named CLARCS) for the automated analysis and comparison of surfaces. One of the primary goal of this library is to allow the assessment and quantification of morphological differences of free-form surfaces from medical or paleoanthropological data.

- APP: IDDN.FR.001.130002.000.S.P.2011.000.21000
- Programming language: CC++

CLARCS was presented at the MeshMed MICCAI workshop (http://www2.imm.dtu.dk/projects/MeshMed/2011/index.html) [57] and is to be distributed through a dedicated website (http://clarcs.inria.fr).

We also developed a surface viewer (named 'Surface').

- APP: IDDN.FR.001.110019.000.S.P.2011.000.21000
- Programming language: C++, Python

5.2. Shanoir

Participants: Justine Guillaumont, Michael Kain, Christian Barillot.

Shanoir (Sharing NeurOImaging Resources) is an open source neuroinformatics platform designed to share, archive, search and visualize neuroimaging data. It provides a user-friendly secure web access and offers an intuitive workflow to facilitate the collecting and retrieving of neuroimaging data from multiple sources and a wizzard to make the completion of metadata easy. Shanoir comes along many features such as anonymization of data, support for multi-centres clinical studies on subjects or group of subjects. 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 (Figure 2).

Shanoir APP registration number is: IDDN.FR.001.520021.000.S.P.2008.000.31230

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

- Keywords: neuroimaging, ontology, sharing neuroimage
- 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/Middelware: 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
- Documentation: see the website

../../../../projets/visages/IMG/shanoir1.png ../../../projets/visages/IMG/shanoir2.png
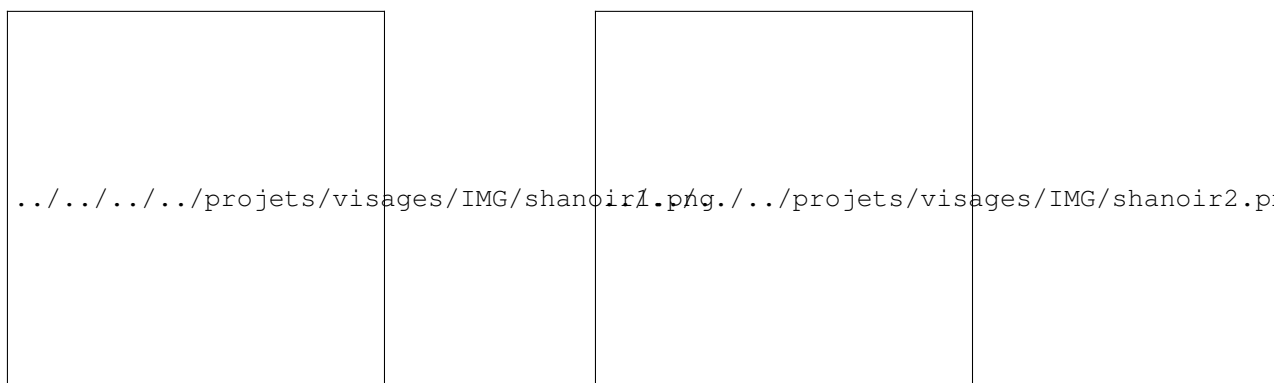
Figure 2. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

5.3. ShanoirUploader

Participants: Justine Guillaumont, Michael Kain.

The ShanoirUploader is a desktop application on base of JavaWebStart (JWS). The app can be downloaded and installed using an internet browser. The app 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 app 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://www.shanoir.org as the ShanoirUploader documentation is integrated on this page.

- Keywords: neuroimaging, ontology, sharing neuroimage
- 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 licence for the moment
- Type of human computer interaction: desktop application on base of JavaWebStart (JWS), web service (SOAP messages based)
- OS/Middelware: Linux, Windows and Mac
- Required library or software : Java SDK, installed on client machine
- Programming language: Java
- Documentation : see the website

5.4. AutoMRI

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

AutoMRI Based on MATLAB and the SPM8 toolbox, autoMRI provides complete pipelines to pre-process and analyze various types of images (anatomical, funcional, 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 normalisation 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 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 3).

- 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/
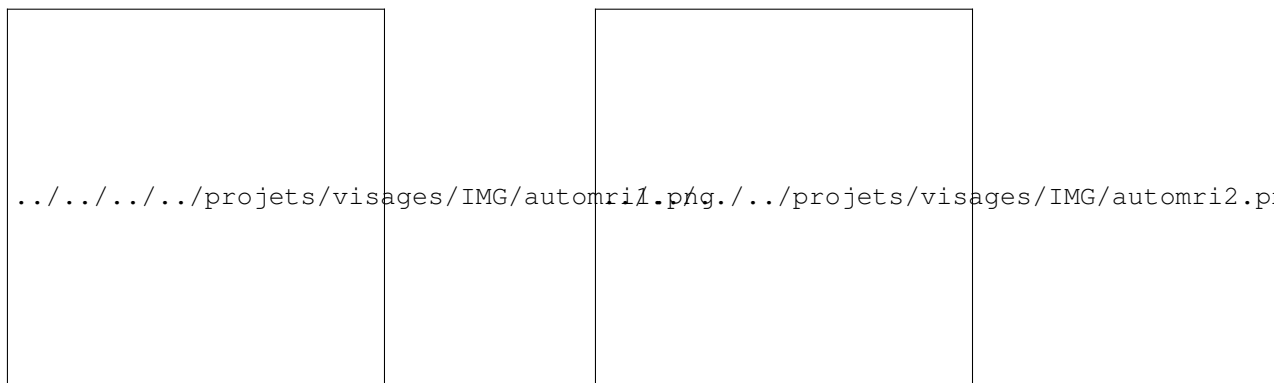

Figure 3. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (right), Detection of relaxometry defect in an MS patient (left).

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 for two years 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 2.1.2 has been released in September 2013 for the main distribution platforms. medInria core API source code has also been released under a BSD license.

See also Figure 4 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/Middelware: Windows, Mac et Linux.
- Required library or software : Qt, DTK, ITK, VTK.
- Programming language: C++

```
../../../../projets/visages/IMG/fibers.png  ../../../projets/visages/IMG/registratio
```

Figure 4. The medInria software platform : Side by side registration using fast algorithms Optimus (right), Tractography overlapped with 3D image (left)

5.6. Anima

Participants: René-Paul Debroize, Guillaume Pasquier, Aymeric Stamm, Fang Cao, Olivier Commowick.

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 simpler 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++

<p style="text-align:center">**ANGE Team**</p>

5. 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.

The development of robust and efficient numerical tools has been a strong point of the activities within the BANG project-team. ANGE aims at pursuing this effort as most publications of the team members contain both modelling and simulation/validation aspects. For the simulation of the free surface Navier-Stokes equations, numerical tools have been developed namely FRESHKISS2D[1] 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.

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[1]FRESHKISS: FREe Surface Hydrodynamics using KInetic SchemeS

<p style="text-align:center">**BANG Project-Team**</p>

5. Software and Platforms

5.1. Software and Platforms

5.1.1. *Continuation of M3N*

A large part of the software currently in use in the project-team was initiated and developed within former projects (Menusin, M3N).

5.1.2. *CellSys*

Participants: Géraldine Cellière [PhD student], Dirk Drasdo [correspondent], Stefan Höhme, Adrian Friebel [PhD student, University of Leipzig], Tim Johann [Software Engineer, University of Leipzig], Johannes Neitsch [PhD student], Paul Van Liedekerke [Research Engineer].

Based on an earlier submitted software (Hoehme and Drasdo, Bioinformatics, 2010) a modular computer simulation software for image analysis of tissue samples at histological scales, as well as for individual cell (agent)-based modeling of tumour and tissue growth, and tissue regeneration has been developed. Cell movement is solved either by systems of coupled equations of motion for each individual cell or by Kinetic Monte Carlo methods. The software uses a git framework to facilitate coordinated contributions of multiple developers. The image analysis part allows analysis of structures down to sub-cellular scale such as liver micro-capillaries and bile cannaliculi structures. So far, blood flow as well as growth and regeneration processes, fluxes of chemicals by diffusion and flow etc can be modelled, finite element solvers, ITK and VTK have been integrated.

The software CellSys is calibrated to allow use by external and internal researchers. The idea is to perspectively go open-source and offer consultancy for potential users.

Moreover in 2013 the image processing and analysis chain was refined to capture high resolution laser scanning micrographs. The algorithms were integrated into CELLSYS (see: software) and our experimental partner labs within the projects VLN and NOTOX were provided with the software to allow image analysis directly in their lab and with their people. Along the same line an experimental partner lab at the German Cancer center was provide with a small image analysis tool permitting them to efficiently analyze their bright field images on growing and invasive cancer cell populations in vitro (LUNGSYS).

CASTOR Team

5. Software and Platforms

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.

5.2. PlaTo

Participant: Hervé Guillard [contact].

PlaTo (Platform for Tokamak simulation) is a specialized set of softwares dedicated to the geometry of Tokamaks whose main objective is to provide the researchers of the CASTOR team a common development tools. The platform integrates Fortran90 modules using the MPI communication library for parallel computations and some python and C codes. The PlaTo platform has been developed thanks to a 2010 ADT of Inria and the ANR ESPOIR. The construction of this platform integrates the following developments :

- The set-up of a (small) database corresponding to axisymmetric solutions of the equilibrium plasma equations for realistic geometrical and magnetic configurations (JET, ITER and the Tore-Supra upgrade WEST).The construction of meshes is always an important and time consuming task. PlaTo provides meshes and solutions corresponding to equilibrium solutions that will be used as initial data for more complex computations.
- A set of interfaces (PlaTo ToolBox) allowing easy transfer between different solution and mesh formats.
- Numerical templates allowing the use of 3D discretization schemes using finite element/volume methods. At present, several applications (reduced MHD, Euler equations, two fluid Euler model) are available in PlaTo .

5.3. PaMPA

Participants: Cécile Dobrzynski [Bacchus], Hervé Guillard, Laurent Hascoët [Ecuador], Cédric Lachat, François Pellegrini [Bacchus].

PaMPA ("Parallel Mesh Partitioning and Adaptation") is a middleware library dedicated to the management of distributed meshes. Its purpose is to relieve solver writers from the tedious and error prone task of writing again and again service routines for mesh handling, data communication and exchange, remeshing, and data redistribution. An API of the future platform has been devised, and the coding of the mesh handling and redistribution routines is in progress. PaMPA will be used as a base module for the PLATO solvers, to balance dynamically, refine and coarsen its distributed mesh.

5.4. Cedres++

Participants: Jacques Blum, Cédric Boulbe, Blaise Faugeras, 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 vaccuum 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.

5.5. 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.

<p style="text-align:center;color:red;font-weight:bold;">CLIME Project-Team</p>

5. Software and Platforms

5.1. Polyphemus

Participants: Sylvain Doré, Vivien Mallet, Florian Couvidat [CEREA], Yiguo Wang [CEREA], Nora Duhanyan [CEREA], Yelva Roustan [CEREA].

Polyphemus (see the web site http://cerea.enpc.fr/polyphemus/) is a modeling system for air quality. As such, it is designed to yield up-to-date simulations in a reliable framework: data assimilation, ensemble 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 postprocessing abilities (AtmoPy);
- programs for physical preprocessing 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.

Figure 1 depicts a typical result produced by Polyphemus.

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 2013, Polyphemus has received numerous improvements on aerosol modeling, including better dynamics for organic aerosol formation and interactions between organic and inorganic aerosols. The data assimilation part of Polyphemus can now perform 3D data assimilation, taking advantage of Lidar data. Further integration of the data assimilation library Verdandi was also carried out.

## 5.2. Data assimilation library: Verdandi

Participants: Vivien Mallet, Dominique Chapelle [M3DISIM], Philippe Moireau [M3DISIM], Anne Tilloy, Paul Baudin, Tristan Perotin.

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 2013, version 1.5 was released with better consistency between the methods. Verdandi received improvements in its test cases. Increased flexibility was introduced in error descriptions, especially for uncertainty quantification.

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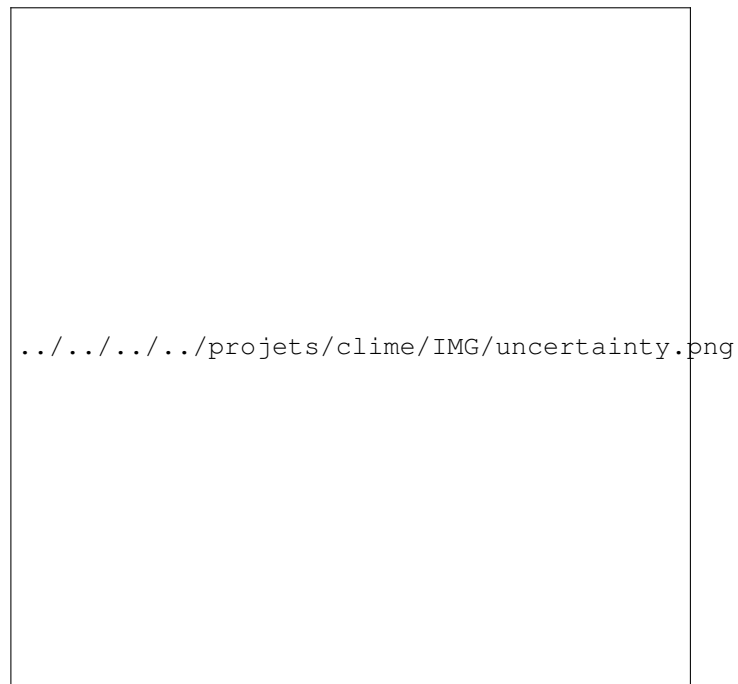
Figure 1. Map of the relative standard deviation (or spread, %) of an ensemble built with Polyphemus (ozone simulations, $\mu g \; m^{-3}$). The standard deviations are averaged over the summer of 2001. They provide an estimation of the simulation uncertainties.

A C++ interface to the Nucleus for European Modelling of the Ocean (see the web site NEMO http://www.nemo-ocean.eu/) has been developed so that it can be plugged to Verdandi. The interface currently enables the application of Monte Carlo simulations and the ensemble Kalman filter.

5.3. Urban air quality analysis

Participants: Anne Tilloy, Vivien Mallet, Raphaël Périllat.

"Urban Air Quality Analysis" carries out data assimilation at urban scale. It merges the outputs of a numerical model (maps of pollutant concentrations) with observations from an air quality monitoring network, in order to produce the so-called analyses, that is, corrected concentration maps. The data assimilation computes the Best Linear Unbiased Estimator (BLUE), with a call to the data assimilation library Verdandi. The error covariance matrices are parameterized for both model simulations and observations. For the model state error covariances, the parameterization primarily relies on the road network. The software handles ADMS Urban output files, for a posteriori analyses or in an operational context.

In 2013, the software introduced new models for error covariances. It may now take into account tunnels. New options were added to filter out certain observations. The software was extended to handle new file formats.

<p align="center" style="color:red">COFFEE Project-Team</p>

5. Software and Platforms

5.1. NS2DDV

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

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.

<p style="text-align: center; color: red;">**FLUMINANCE Project-Team**</p>

5. Software and Platforms

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

Participants: Thomas Corpetti, Patrick Héas, 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

Participants: Patrick Héas, 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

Participants: Patrick Héas, 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.

<div style="text-align: center; color: red;">**MAGIQUE-3D Project-Team**</div>

5. Software and Platforms

5.1. Hou10ni

Participant: Julien Diaz [correspondant].

5.1.1. *Hou10ni-Time-Domain*

This software, written in FORTRAN 90, simulates the propagation of acoustic waves in heterogeneous 2D and 3D media. It is based on an Interior Penalty Discontinuous Galerkin Method (IPDGM). The 2D version of the code has been implemented in the Reverse Time Migration (RTM) software of TOTAL in the framework of the Ph.D thesis of Caroline Baldassari. The 2D code allows for the use of meshes composed of cells of various order (p-adaptivity in space). For the time discretization, we used the local time stepping strategy described at section 3.2 , item **High-Order Schemes in Space and Time** which permits not only the use of different time-step, but also to adapt the order of the time-discretization to the order of each cells (hp-adaptivity in time).

The main competitors of Hou10ni are codes based on Finite Differences, Spectral Element Method or other Discontinuous Galerkin Methods (such as the ADER schemes). During her Ph.D thesis, Caroline Baldassari compared the solution obtained by Hou10ni to the solution obtained by a Finite Difference Method and by a Spectral Element Method (SPECFEM). To evaluate the accuracy of the solutions, we have compared them to analytical solutions provided by the codes Gar6more (see below). The results of these comparisons are: a) that Hou10ni outperforms the Finite Difference Methods both in terms of accuracy and of computational burden and b) that its performances are similar to Spectral Element Methods. Since Hou10ni allows for the use of meshes based on tetrahedrons, which are more appropriate to mesh complex topographies, and for the p-adaptivity, we decided to implement it in the RTM code of TOTAL. Of course, we also used these comparisons to validate the code.

5.1.2. *Hou10ni-Frequency-Domain*

Recently, we have extended the 2D version of Hou10ni for computing the solution of the harmonic wave equation (Helmholtz), in the framework of the PhD thesis of Élodie Estécahandy. This new version is able to deal with both acoustic and elastodynamic media, but also to model elastoacoustic problems. The surfaces between the different media can be approximated by curved elements. We can use up to P^{15} elements when dealing with curved elements and element of arbitrary order (with of course a limitation depending on the machine precision) when dealing with non-curved elements. The construction of the global matrix is perform using OpenMP and the extension to hybrid MPI/OpenMP parallelism is on development. This code has been also implemented in a solver which determine the shape of an elastic obstacle from the knowledge of its scattered field.

The 3D version of Hou10ni-Frequency-Domain is under development. The code is now able to solve acoustic problems up to P^3 elements. It has been parallelized using MPI and is able to deal with partitioned meshes. Preliminary tests have been performed up to 16.000.000 unknowns. We are now considering the following features : hybrid MPI/OpenMP parallelism; extension to arbitrary polynomial degrees; extension to elastodynamic.

5.2. Gar6more2D and Gar6more3D

Participant: Julien Diaz [correspondant].

This codes compute the analytical solution of problems of waves propagation in two layered 3D media such as- acoustic/acoustic- acoustic/elastodynamic- acoustic/porous- porous/porous, based on the Cagniard-de Hoop method.

See also the web page http://web.univ-pau.fr/~jdiaz1/software.html.

The main objective of these codes is to provide reference solutions in order to validate numerical codes. They have been already used by J. Tromp and C. Morency to validate their code of poroelastic wave propagation [96]. They are freely distributed under a CECILL license and can be downloaded on the website http://web.univ-pau.fr/~jdiaz1/software.html. As far as we know, the main competitor of this code is EX2DELDEL (available on http://www.spice-rtn.org), but this code only deals with 2D acoustic or elastic media. Our codes seem to be the only ones able to deal with bilayered poroelastic media and to handle the three dimensional cases.

- ACM: J.2
- AMS: 34B27 35L05 35L15 74F10 74J05
- Programming language: Fortran 90

5.3. 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 2013, an implementation of non-linear 1-D Maxwell's equations (non-linear Kerr effect) has been added as well as various 1-D non-linear Schrödinger-like equations. Thin layer models are also available for Maxwell's equations and elastodynamics.

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

<p style="text-align:center; color:red">MOISE Project-Team</p>

5. Software and Platforms

5.1. Adaptive Grid Refinement

Participants: Laurent Debreu, Marc Honnorat.

AGRIF (Adaptive Grid Refinement In Fortran, [85], [84]) 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).

In 2013, a new contract has been signed with IFREMER to add online degradation capabilities. The software will be used operationally to attain a resolution of 500meters along the French coasts. (http://www.previmer. org) 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

Participants: Arthur Vidard, Pierre-Antoine Bouttier, Bénédicte Lemieux-Dudon.

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 is also a likely candidate for becoming the future Black-Sea forecasting system of the Marine Hydrographical Institute of Ukraine with whom we collaborate actively. 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. DatIce

Participant: Bénédicte Lemieux-Dudon.

Antarctic and Greenland ice cores provide a mean to study the phase relationships of climate changes in both hemispheres. They also enable to study the timing between climate and greenhouse gases or orbital forcings. One key step for such studies is to improve the absolute and relative precisions of ice core age scales (for ice and trapped gas), and beyond that, to try to reach the best consistency between chronologies of paleo-records of any kind.

The DatIce tool is designed to increase the consistency between pre-existing core chronologies (also called background). It formulates a variational inverse problem which aims at correcting three key quantities that uniquely define the core age scales: the accumulation rate, the total thinning function, and the close-off depth. For that purpose, it integrates paleo-data constraints of many types among which age markers (with for instance documented volcanoes eruptions), and stratigraphic links (with for instance abrupt changes in methane concentration). A cost function is built that enables to calculate new chronologies by making a trade-off between all the constraints (background chronologies and paleo-data).

DatIce enables to circumvent the limits encountered with other dating approaches, in particular because it controls the model errors, which are still large despite efforts to better describe the firn densification, the ice flow and the forcing fields (ice sheet elevation, temperature and accumulation rate histories). Controlling the model error makes it possible to assimilate large set of observations, to constrain both the gas and ice age scales, and to apply the process on several cores at the same time by including stratigraphic links between cores. This approach greatly improves the consistency of ice cores age scales.

The method presented in [93], [94] has already been applied simultaneously to EPICA EDML and EDC, Vostok and NGRIP drillings. The code has also been applied in two publications [78] and [106] which aimed at the construction of a unified chronology for Antarctic ice cores. LGGE, LSCE and MOISE are partners to extend the code to marine and terrestrial cores. On going development efforts are made to ensure the robustness of the dating solution (diagnostics on the assimilation system, calibration of the background error covariance matrices).

5.4. SDM toolbox

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, we develop a new method based on the combination of an existing numerical weather prediction model providing a coarse prediction, and a Lagrangian Stochastic Model adapted from a pdf method introduced by S.B. Pope for turbulent flows. This Stochastic Downscaling Method (SDM http://sdm.gforge.inria.fr/) is thus aimed to be used as a refinement toolbox of large-scale numerical models. SDM requires a specific modelling of the turbulence closure, and involves various simulation techniques whose combination is totally new (such as Poisson solvers, optimal transportation mass algorithm, original Euler scheme for confined Langevin stochastic processes, and stochastic particle methods). Since 2011, we work on the comparison of the SDM model (endowed with a physical geostrophic forcing and a wall log law) with simulations obtained with a LES method (Méso-NH code) for the atmospheric boundary layer (from 0 to 750 meters in the vertical direction), in the neutral case.

5.5. CompModSA package

Participants: Clémentine Prieur, Alexandre Janon, Céline Helbert.

Alexandre Janon is a contributor of the packages CompModSA - Sensitivity Analysis for Complex Computer Models (see http://cran.open-source-solution.org/web/packages/CompModSA/index.html), and sensitivity (see http://cran.r-project.org/web/packages/sensitivity/index.html). These packages are useful for conducting sensitivity analysis of complex computer codes.

Celine 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. Software and Platforms

4.1. LifeV

Participant: Michel Kern.

LifeV is a finite element (FE) library providing implementations of state of the art mathematical and numerical methods. It serves both as a research and production library. It has been used already in medical and industrial context to simulate fluid structure interaction and mass transport. LifeV is the joint collaboration between four institutions: École Polytechnique Fédérale de Lausanne (CMCS) in Switzerland, Politecnico di Milano (MOX) in Italy, Inria (Pomdapi) in France and Emory University (Sc. Comp) in the U.S.A.

Version 3.1.1

Programming language: C++

http://www.lifev.org/

4.2. M1cg1

Participant: Jean Charles Gilbert.

M1cg1 solves convex quadratic optimization problems and builds preconditioning matrices.

Version: 1.2

Programming language: Fortran 77

14 downloads in 2013

https://who.rocq.inria.fr/Jean-Charles.Gilbert/modulopt/optimization-routines/m1cg1/m1cg1.html

4.3. M1qn3

Participant: Jean Charles Gilbert.

M1qn3 solves very large scale differentiable optimization problems.

Version: 3.3

Programming language: Fortran 77

36 downloads in 2013

https://who.rocq.inria.fr/Jean-Charles.Gilbert/modulopt/optimization-routines/m1qn3/m1qn3.html

In collaboration with Claude Lemaréchal (project-team Bipop)

4.4. Oqla, Qpalm

Participants: Jean Charles Gilbert, Émilie Joannopoulos.

Oqla and Qpalm aim at solving large scale convex quadratic functions on a polyhedron by an augmented Lagrangian method.

Versions (in development): 0.1 (Oqla), 0.2 (Qpalm)

Programming languages: `C++` (Oqla), `Matlab` (Qpalm)

4.5. 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: 1.0+pl0

> Programming language: OCaml

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

4.6. SQPlab

Participant: Jean Charles Gilbert.

SQPlab solves constrained differentiable optimization problems.

> Version: 0.4.5

> Programming language: Matlab

> 200 downloads in 2013

> https://who.rocq.inria.fr/Jean-Charles.Gilbert/modulopt/optimization-routines/sqplab/sqplab.html

4.7. 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

> Programming language: OCaml

> http://sklml.inria.fr/

4.8. FreeFem++

Participants: Martin Vohralík, Martin Čermák, Zuqi Tang.

The scientific calculation code FreeFem++ is an excellent example of a complex software numerical simulation tool. It in particular encompasses all specification of the problem, the choice and implementation of the numerical method, the choice and implementation of the linearization method (nonlinear solver), and the choice and implementation of the method of solution of the associated linear systems (linear solver). In the post-doc stays of M. Čermák and Z. Tang, we integrate 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 are being implemented.

> Version 3.26-2

> Programming language: C++

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

SAGE Project-Team

5. Software and Platforms

5.1. Hydrogeology

5.1.1. H2OLab

Participants: Thomas Dufaud, Jocelyne Erhel [correspondant], Grégoire Lecourt, Aurélien Le Gentil, 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 8.2.1). 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.

5.1.2. GW-UTIL

Participants: Jocelyne Erhel, Grégoire Lecourt, Aurélien Le Gentil, Géraldine Pichot [correspondant].

- Version: version 1.0, May 2008
- APP: registered
- Programming language: C++
- See also: http://h2olab.inria.fr.
- Abstract: The software GW-UTIL allows to discretize PDE for flow and transport in aquifers and to deal with stochastic models. It contains a set of utilitary modules for geometry, input, output, random numbers, visualization, parallel computing, numerical algorithms, etc. A package is devoted to launch applications.
- Current work: refactoring.

5.1.3. GW-NUM

Participants: Thomas Dufaud, Jocelyne Erhel, Grégoire Lecourt, Aurélien Le Gentil, Géraldine Pichot [correspondant].

- Version: version 1.0, May 2008
- APP: registered
- Programming language: C++
- See also: http://h2olab.inria.fr.
- Abstract: The software GW-NUM is a set of generic modules to discretize PDE of flow and transport in 2D computational domains in order to deal with stochastic models. Methods for flow simulations are either Finite Volume on structured meshes or Mixed Finite Element with unstructured meshes. Method for transport simulations is a particle tracker for advection and a random walker for diffusion. Uncertainty Quantification method is Monte-Carlo. For flow computations, the involved linear system is solved by external software devoted to sparse matrices.
- Current work: refactoring.

5.1.4. MP-FRAC
Participants: Thomas Dufaud, Jocelyne Erhel, Aurélien Le Gentil, Géraldine Pichot [correspondant].

- Version: version 1.0, May 2008
- APP: registered
- Programming language: C++
- See also: http://h2olab.inria.fr.
- Abstract: The software MP-FRAC aims at modelling and simulating numerically flow in a fractured aquifer. The physical domain is a network of fractures, either deterministic or stochastic, with a permeability field either deterministic or stochastic. The software computes the velocity field in the aquifer, by assuming that the medium is saturated and that flow is steady-state. Physical equations are stochastic PDEs, handled by a Monte-Carlo method. This non intrusive approach generates a set of random samples, which are used for simulations. Then, the software analyzes statistically the flow in the stochastic case. The objective is to characterize hydraulic properties in Discrete Fracture Networks. The software MP-FRAC handles a simulation corresponding to one sample, whereas Monte-Carlo method is implemented in a generic way by the software GW-NUM. The software is specific of the physical model (Discrete Fracture Network) and of the application (steady-state flow). Generic numerical methods to discretize PDE are implemented in the software GW-NUM.
- Current work: refactoring and design of libraries.

5.1.5. PARADIS
Participants: Jocelyne Erhel, Grégoire Lecourt, Aurélien Le Gentil, Géraldine Pichot [correspondant].

- Version: version 1.0, May 2008
- APP: registered
- Programming language: C++
- See also: http://h2olab.inria.fr/.
- Abstract: The software PARADIS aims at modelling and simulating numerically flow in a porous aquifer and transport by convection-diffusion of an inert solute. The porous medium is heterogeneous, with a stochastic or deterministic permeability field. A first step computes the velocity filed in the aquifer, by assuming that the medium is saturated and that flow is steady-state. A second step computes the distribution of solute concentration, by assuming a transport by convection and by molecular diffusion. Physical equations are stochastic PDEs, handled by a Monte-Carlo method and discretized by numerical methods. This non intrusive approach generates a set of random samples, which are used for simulations. Then, the software analyzes statistically the flow in the stochastic case. The objectives are to determine asymptotic laws of transport, to characterize pre-asymptotic behavior and to define global laws.

  The software PARADIS handles a simulation corresponding to one sample, whereas Monte-Carlo method is implemented in a generic way by the software GW-NUM. The software is specific of the physical model (heterogeneous porous medium) and of the application (steady-state flow then transport with macro-dispersion). Generic numerical methods to discretize PDE are implemented in the software GW-NUM.
- Current work: refactoring and design of libraries.

5.1.6. GRT3D
Participants: Édouard Canot, Jocelyne Erhel [correspondant], Souhila Sabit.

- Version: version 1.0, April 2011
- 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 partners (see section 8.2.7), in particular Andra (see section 7.1). 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.

5.1.7. 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. High Performance Scientific Computing

5.2.1. 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.

5.2.2. *GPREMS*

Participants: Édouard Canot, Jocelyne Erhel [correspondant].

- Version: version 1.0, May 2008
- APP: registered
- Programming language: C++
- See also: http://www.irisa.fr/sage/.
- Abstract: GPREMS implements a robust hybrid solver for large sparse linear systems that combines a Krylov subspace method as accelerator with a Schwarz-based preconditioner. This preconditioner uses an explicit formulation associated to one iteration of the multiplicative Schwarz method. The Newton-basis GMRES, which aims at expressing a good data parallelism between subdomains is used as accelerator.

5.2.3. *DGMRES*

Participant: Jocelyne Erhel [correspondant].

- Version: version 1.0, June 2011
- APP: distributed with the free software PETSC
- Programming language: C
- See also: http://www.irisa.fr/sage/.
- Abstract: DGMRES implements a preconditioner based on adaptive deflation, which can be used with any preconditioner for the GMRES algorithm.

5.2.4. *AGMRES*

Participant: Jocelyne Erhel [correspondant].

- Version: version 1.0, November 2011
- APP: distributed with the free software PETSC
- Programming language: C
- See also: http://www.irisa.fr/sage/.
- Abstract: AGMRES implements an augmented subspace approach, based on adaptive deflation, which can be used with any preconditioner for the GMRES algorithm. It also implements a Newton basis for enhancing parallelism.

5.2.5. *PPAT*

Participants: Édouard Canot [corresponding author], Bernard Philippe.

PPAT (Parallel PATh following software) is a parallel code, developed by D. Mezher, W. Najem (University of Saint-Joseph, Beirut, Lebanon) and B. Philippe. This tool can follow the contours of a functional from $\mathbb{C}$ to $\mathbb{R}^+$. The present version is adapted for determining the level curves of the function $f(z) = \sigma_{\min}(A - zI)$ which gives the pseudospectrum of matrix A.

The algorithm is reliable: it does not assume that the curve has a derivative everywhere. The process is proved to terminate even when taking into account roundoff errors. The structure of the code spawns many independent tasks which provide a good efficiency in the parallel runs.

The software can be downloaded under the GPL licence from: http://sourceforge.net/projects/ppat.

5.2.6. *MUESLI*

Participant: Édouard Canot [corresponding author].

Doing linear algebra with sparse and dense matrices is somehow difficult in scientific computing. Specific libraries do exist to deal with this area (*e.g.* BLAS and LAPACK for dense matrices, SPARSKIT for sparse ones) but their use is often awful and tedious, mainly because of the large number of arguments which must be used. Moreover, classical libraries do not provide dynamic allocation. Lastly, the two types of storage (sparse and dense) are so different that the user must know in advance the storage used in order to declare correctly the corresponding numerical arrays.

MUESLI is designed to help in dealing with such structures and it provides the convenience of coding in Fortran with a matrix-oriented syntax; its aim is therefore to speed-up development process and to enhance portability. It is a Fortran 95 library split in two modules: (i) FML (Fortran Muesli Library) contains all necessary material to numerically work with a dynamic array (dynamic in size, type and structure), called `mfArray`; (ii) FGL (Fortran Graphics Library) contains graphical routines (some are interactive) which use the `mfArray` objects.

MUESLI includes some parts of the following numerical libraries: Arpack, Slatec, SuiteSparse, Triangle, BLAS and LAPACK.

Linux is the platform which has been used for developing and testing MUESLI. Whereas the FML part (numerical computations) should work on any platform (*e.g.* Win32, Mac OS X, Unix), the FGL part is intended to be used only with X11 (*i.e.* under all UNIXes).

Last version of MUESLI is 2.6.6 (2012-08-29). More information can be found at: http://people.irisa.fr/Edouard.Canot/muesli

5.2.7. *CANARD*

Participant: Édouard Canot [corresponding author].

When dealing with non-linear free-surface flows, mixed Eulerian-Lagrangian methods have numerous advantages, because we can follow marker particles distributed on the free-surface and then compute with accuracy the surface position without the need of interpolation over a grid. Besides, if the liquid velocity is large enough, Navier-Stokes equations can be reduced to a Laplace equation, which is numerically solved by a Boundary Element Method (BEM); this latter method is very fast and efficient because computing occur only on the fluid boundary. This method has been applied to the spreading of a liquid drop impacting on a solid wall and to the droplet formation at a nozzle; applications take place, among others, in ink-jet printing processes.

The code used (CANARD) has been developped with Jean-Luc Achard (LEGI, Grenoble) for fifteen years and is used today mainly through collaborations with Carmen Georgescu at UPB (University Polytechnica of Bucarest, Romania), and with Alain Glière (CEA-LETI, Grenoble).

5. Software and Platforms

5.1. TEOS: Tranus Exploration and Optimization Software

Participants: Anthony Tschirhard, Mathieu Vadon, Elise Arnaud, Emmanuel Prados.

The TEOS software offers a set of tools to help the calibration of the land use and transport integrated model TRANUS. It uses some exploration and optimization procedures of the relevant parameters.

5.2. 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. We envisage to distribute this software as an open source software.

5.3. Wassily

Participants: Julien Alapetite, Jean-Yves Courtonne, Lara Antonela Colombo, Pablo Virgolini.

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.

<p align="center">**BIOCORE Project-Team**</p>

5. Software and Platforms

5.1. Supervision software

We are developing a software for the supervision of bioreactors: this platform, named ODIN, has been built for the smart management of bioreactors (data acquisition, fault diagnosis, automatic control algorithm,...). This software was developed in C++ and uses a Scilab engine to run the advanced algorithms developed within BIOCORE. It has been implemented and validated with four different applications.

CARMEN Team

5. 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 an ADT, actual developments started at the end of 2012 and still continue.

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 [30]. We use the platform GForge (gforge.inria.fr/projects/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 Université de Pau et des Pays de l'Adour;
- R. Turpault, LMA Université de Nantes;
- L. Gerardo-Giorda, BCAM Bilbao.

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, runs with complex model geometries, and runs efficiently on high-performance computing systems with many thousands of cores. 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. Model construction – A new project

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.

5. 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.

<div align="center">

M3DISIM Team

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5. Software and Platforms

5.1. FELISCE

Participants: Dominique Chapelle, Sébastien Gilles [correspondant], 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/.

5.2. HeartLab

Participants: Matthieu Caruel, Dominique Chapelle, Alexandre Imperiale, Philippe Moireau [correspondant].

The heartLab software is a library written in (64 bits 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 recently 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.

5.3. Verdandi

Participants: Dominique Chapelle, Marc Fragu, Vivien Mallet [Clime team], Philippe Moireau [correspondant].

Verdandi is an opensource (LGPL) software library aiming at providing assimilation data 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 (1.5) 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 project and is now referenced in the peer-reviewed article [16].

- 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

MASAIE Project-Team (section vide)

MODEMIC Project-Team

5. Software and Platforms

5.1. SMC Demos (Sequential Monte Carlo demos)

Participant: Fabien Campillo.

SMC Demos proposes a set of demonstration Matlab procedures for nonlinear filtering approximation via particle filtering (sequential Monte Carlo): bearing-only tracking with obstacles, tracking in digital terrain model, track-before-detect in a sequence of digital picture, mobile phone tracking based on the signal strength to nearby antenna. This software is deposited with the "Agence pour la Protection des Programmes" (APP, 7/7/2009) [2].

5.2. IBM Cellulose

Participant: Fabien Campillo.

In the context of the DISCO/ANR and MnMs/RNSC projects (see Sections 7.2.1 and 7.2.2), in collaboration with Ariane Bize (Irstea), the team has developed an individual-based model for the degradation of one cellulose bead (dozens of micrometers in diameter) by cellulolytic bacteria [3].

5.3. VITELBIO (VIrtual TELluric BIOreactors)

Participants: Jérôme Harmand, Alain Rapaport.

VITELBIO is a simulation tool for studying networks of interconnected chemostat models with the objective of mimicking microbial activities in heterogeneous media, such as the soil. This software, that has been developed with the help of ITK Company, is accessible on a server from any web navigator [4] and makes use of Flex for the user interface and Octave for the numerical integration. It is is no longer maintained but serves as a teaching support.

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[2]http://www-sop.inria.fr/members/Fabien.Campillo/software/smc-demos/
[3]http://www-sop.inria.fr/members/Fabien.Campillo/software/ibm-cellulose/
[4]https://sites.google.com/site/vitelbio/logiciel

<p align="center">**NUMED Project-Team**</p>

4. 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.

4.3. Zebre

Participant: Thierry Dumont [correspondant].

Thierry Dumont is currently developing a toolbox to solve stiff reaction diffusion equations using splitting methods, together with refined numerical schemes for ODEs (RADO 5).

This code was first designed to serve as demonstrator of the theoretical results of Descombes and Massot on the solution of stiff reaction-diffusion systems by alternate directions methods, and as a first step towards complex chemistry simulations. Later it was used and improved to solve the ionic model of strokes, and incorporated stabilized explicit Runge Kutta methods for diffusion steps. Coded in C++, it solves stiff systems with various schemes in dimension 1, 2 and 3, in complex geometries. The code is multithreaded.

4.4. OptimChemo

Participants: Violaine Louvet [correspondant], Emmanuel Grenier.

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.

4.5. Simstab

Stability prediction of vaccine, intellectual property of Sanofi, covered by a US patent demand (Sanofi, Benjamin Ribba, Emmanuel Grenier).

4.6. 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. Software and Platforms

5.1. LiFE-V library

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

LiFE-V [2] 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.

5.2. Mistral library

Participant: Jean-Frédéric Gerbeau [correspondant].

Mistral is a finite element library which implements in particular fluid-structure interaction algorithms (ALE and Fictitious domain formulations), fluid surface flow (ALE) and incompressible magnetohydrodynamics equations. Mistral results from a collaboration between Inria and ENPC (CERMICS).

5.3. FELiScE

Participants: Grégory Arbia, Cesare Corrado, Miguel Ángel Fernández Varela, Justine Fouchet-Incaux, David Froger, Jean-Frédéric Gerbeau [correspondant], Damiano Lombardi, Elisa Schenone, Saverio Smaldone, Marina Vidrascu, Irène Vignon-Clementel.

FELiScE – standing for "Finite Elements for Life Sciences and Engineering" – is a new finite element code which the MACS 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 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. https://gforge.inria.fr/projects/felisce/

5.4. 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. (https://gforge.inria.fr/projects/shelddon)

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

<p align="center" style="color:red">SISYPHE Project-Team</p>

5. Software and Platforms

5.1. SITB: The Matlab System Identification ToolBox

Participant: Qinghua Zhang.

This development is made in collaboration with Lennart Ljung (Linköping University, Sweden), Anatoli Juditsky (Joseph Fourier University, France) and Peter Lindskog (NIRA Dynamics, Sweden).

The System Identification ToolBox (SITB) is one of the main Matlab toolboxes commercialized by The Mathworks. Inria participates in the development of its extension to the identification of nonlinear systems which is released since 2007. It includes algorithms for both black box and grey box identification of nonlinear dynamic systems. Inria is mainly responsible for the development of black box identification, with nonlinear autoregressive (NLARX) models and block-oriented (Hammerstein-Wiener) models.

5.2. ISTL: Inverse Scattering for Transmission Lines

Participants: Michel Sorine, Qinghua Zhang.

ISTL is a software for numerical computation of the inverse scattering transform for electrical transmission lines. In addition to the inverse scattering transform, it includes a numerical simulator generating the reflection coefficients of user-specified transmission lines. With the aid of a graphical interface, the user can interactively define the distributed characteristics of a transmission line. It is registered at Agence pour la Protection des Programmes (APP) under the number IDDN.FR.001.120003.000.S.P.2010.000.30705.

5.3. CGAO: Contrôle Glycémique Assisté par Ordinateur

Participants: Alexandre Guerrini, Michel Sorine.

The software CGAO developed with LK2 and P. Kalfon (Hospital Louis Pasteur, Chartres) provides efficient monitoring and control tools that will help physicians and nursing staff to avoid hyperglycaemia and hypoglycaemia episodes in Intensive Care Units. The controller determines the insulin infusion rate, glucose bolus and scheduling of blood glucose measurement on the basis of the standard available glycaemia measurements. A first version, CGAO_v1, has been used in a large clinical study CGAO-REA (see Section 6.3.1). An improved version, CGAO_v2 registered at APP under the number IDDN.FR.001.360019.002.S.P.2009.000.31230 is now used by the company Fresenius Kabi (see Section 7.1).

5.4. DYNPEAK: a Scilab toolbox and a Web service for the analysis of LH (Luteinizing Hormone) secretion rhythms

Participants: Frédérique Clément, Claire Médigue, Serge Steer, Mouhamadoul Bachir Syll, Alexandre Vidal, Qinghua Zhang.

DYNPEAK is a software dedicated to the analysis of the pulsatile rhythm of secretion of the pituitary hormone LH, that aims at providing the final users (experimentalists and clinicians) with a simple-to-use version of the algorithm developed in [25]. It has been implemented as a Scilab atom toolbox (http://atoms.scilab.org/toolboxes/Dynpeak) and registered in APP under the reference Dyn-Peak V1.0, IDDN.FR.001.360015.000.S.P.2013.000.10000. The web service version of DynPeak (https://dynpeak.inria.fr), still in test, has also been updated and a new release is planned for a next future.

5.5. The Cardiovascular toolbox for Scilab

Participants: Claire Médigue, Michel Sorine, Serge Steer.

This Cardiovascular toolbox is an "atom" of Scilab developed by Serge Steer to distribute the cardiovascular signal processing tools designed and intensively used internally in the team for several years by Claire Médigue, Alessandro Monti and Michel Sorine. It includes baroreflex analysis using a multi channel non stationary signal analysis method ; the cardiovascular signal spectral analysis using time-frequency decomposition and signal demodulations methods, e.g. for respiratory sinus arrhythmia analysis. It replaces LARY_CR, the former software package dedicated to the study of cardiovascular and respiratory rhythms [108].

5.6. K-Assessor: assessment of controllers

Participants: Habib Jreige, Michel Sorine.

This development is made in collaboration with the small business enterprise SciWorks Technologies (Jim Pioche). We have defined a method to assess SISO (Single Input / Single Output) controllers based on square or cubic tables of metadata easily manipulated on a computer and easily interpretable by control experts and field experts (emergency doctors in our case) who can use them to jointly tune a risk estimator. The agreement between experts is obtained using a ROC-analysis approach. The software K-Assessor implements this methodology. It is registered at APP under the number IDDN.FR.001.390011.000.S.P.2013.000.10000.