



RESEARCH CENTER
Grenoble - Rhône-Alpes

FIELD

Activity Report 2018

Section Software

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ARIC Project-Team

6. New Software and Platforms

6.1. FPLLL

KEYWORDS: Euclidean Lattices - Computer algebra system (CAS) - Cryptography

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

FUNCTIONAL DESCRIPTION: `fpLLL` contains implementations of several lattice algorithms. The implementation relies on floating-point orthogonalization, and LLL is central to the code, hence the name.

It includes implementations of floating-point LLL reduction algorithms, offering different speed/guarantees ratios. It contains a 'wrapper' choosing the estimated best sequence of variants in order to provide a guaranteed output as fast as possible. In the case of the wrapper, the succession of variants is oblivious to the user.

It includes an implementation of the BKZ reduction algorithm, including the BKZ-2.0 improvements (extreme enumeration pruning, pre-processing of blocks, early termination). Additionally, Slide reduction and self dual BKZ are supported.

It also includes a floating-point implementation of the Kannan-Fincke-Pohst algorithm that finds a shortest non-zero lattice vector. For the same task, the GaussSieve algorithm is also available in `fpLLL`. Finally, it contains a variant of the enumeration algorithm that computes a lattice vector closest to a given vector belonging to the real span of the lattice.

- Author: Damien Stehlé
- Contact: Damien Stehlé
- URL: <https://github.com/fplll/fplll>

6.2. Gfun

generating functions package

KEYWORD: Symbolic computation

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

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

6.3. GNU-MPFR

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

FUNCTIONAL DESCRIPTION: GNU MPFR is an efficient arbitrary-precision floating-point library with well-defined semantics (copying the good ideas from the IEEE 754 standard), in particular correct rounding in 5 rounding modes. It provides about 80 mathematical functions, in addition to utility functions (assignments, conversions...). Special data (Not a Number, infinities, signed zeros) are handled like in the IEEE 754 standard. GNU MPFR is based on the mpn and mpz layers of the GMP library.

- Participants: Guillaume Hanrot, Paul Zimmermann, Philippe Théveny and Vincent Lefèvre
- Contact: Vincent Lefèvre
- Publications: [Correctly Rounded Arbitrary-Precision Floating-Point Summation - Optimized Binary64 and Binary128 Arithmetic with GNU MPFR](#) - [Évaluation rapide de fonctions hypergéométriques](#) - [Arbitrary Precision Error Analysis for computing \$\zeta\(s\)\$ with the Cohen-Olivier algorithm: Complete description of the real case and preliminary report on the general case](#) - [MPFR: A Multiple-Precision Binary Floating-Point Library with Correct Rounding](#). - [The Generic Multiple-Precision Floating-Point Addition With Exact Rounding \(as in the MPFR Library\)](#)
- URL: <https://www.mpfr.org/>

6.4. Sipe

KEYWORDS: Floating-point - Correct Rounding

FUNCTIONAL DESCRIPTION: Sipe is a mini-library in the form of a C header file, to perform radix-2 floating-point computations in very low precisions with correct rounding, either to nearest or toward zero. The goal of such a tool is to do proofs of algorithms/properties or computations of tight error bounds in these precisions by exhaustive tests, in order to try to generalize them to higher precisions. The currently supported operations are addition, subtraction, multiplication (possibly with the error term), fused multiply-add/subtract (FMA/FMS), and miscellaneous comparisons and conversions. Sipe provides two implementations of these operations, with the same API and the same behavior: one based on integer arithmetic, and a new one based on floating-point arithmetic.

- Participant: Vincent Lefèvre
- Contact: Vincent Lefèvre
- Publications: [SIPE: Small Integer Plus Exponent](#) - [Sipe: a Mini-Library for Very Low Precision Computations with Correct Rounding](#)
- URL: <https://www.vinc17.net/research/sipe/>

6.5. LinBox

KEYWORD: Exact linear algebra

FUNCTIONAL DESCRIPTION: LinBox is an open-source C++ template library for exact, high-performance linear algebra computations. It is considered as the reference library for numerous computations (such as linear system solving, rank, characteristic polynomial, Smith normal forms,...) over finite fields and integers with dense, sparse, and structured matrices.

- Participants: Clément Pernet and Thierry Gautier
- Contact: Clément Pernet
- URL: <http://linalg.org/>

6.6. HPLLL

KEYWORDS: Euclidean Lattices - Computer algebra system (CAS)

FUNCTIONAL DESCRIPTION: Software library for linear algebra and Euclidean lattice problems

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

CASH Team

6. New Software and Platforms

6.1. DCC

DPN C Compiler

KEYWORDS: Polyhedral compilation - Automatic parallelization - High-level synthesis

FUNCTIONAL DESCRIPTION: Dcc (Data-aware process network C compiler) analyzes a sequential regular program written in C and generates an equivalent architecture of parallel computer as a communicating process network (Data-aware Process Network, DPN). Internal communications (channels) and external communications (external memory) are automatically handled while fitting optimally the characteristics of the global memory (latency and throughput). The parallelism can be tuned. Dcc has been registered at the APP ("Agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria license.

- Participants: Alexandru Plesco and Christophe Alias
- Contact: Christophe Alias

6.2. PoCo

Polyhedral Compilation Library

KEYWORDS: Polyhedral compilation - Automatic parallelization

FUNCTIONAL DESCRIPTION: PoCo (Polyhedral Compilation Library) is a compilation framework allowing to develop parallelizing compilers for regular programs. PoCo features many state-of-the-art polyhedral program analysis and a symbolic calculator on execution traces (represented as convex polyhedra). PoCo has been registered at the APP ("agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria licence.

- Participant: Christophe Alias
- Contact: Christophe Alias

6.3. MPPcodegen

Source-to-source loop tiling based on MPP

KEYWORDS: Source-to-source compiler - Polyhedral compilation

FUNCTIONAL DESCRIPTION: MPPcodegen applies a monoparametric tiling to a C program enriched with pragmas specifying the tiling and the scheduling function. The tiling can be generated by any convex polyhedron and translation functions, it is not necessarily a partition. The result is a C program depending on a scaling factor (the parameter). MPPcodegen relies on the MPP mathematical library to tile the iteration sets.

- Partner: Colorado State University
- Contact: Christophe Alias
- URL: <http://foobar.ens-lyon.fr/mppcodegen/>

CONVECS Project-Team

5. New Software and Platforms

5.1. CADP Pro

Construction and Analysis of Distributed Processes

KEYWORDS: Formal methods - Verification

FUNCTIONAL DESCRIPTION: CADP (*Construction and Analysis of Distributed Processes* – formerly known as *CAESAR/ALDEBARAN Development Package*) [4] is a toolbox for protocols and distributed systems engineering.

In this toolbox, we develop and maintain the following tools:

- CAESAR.ADT [40] is a compiler that translates LOTOS abstract data types into C types and C functions. The translation involves pattern-matching compiling techniques and automatic recognition of usual types (integers, enumerations, tuples, etc.), which are implemented optimally.
- CAESAR [46], [45] is a compiler that translates LOTOS processes into either C code (for rapid prototyping and testing purposes) or finite graphs (for verification purposes). The translation is done using several intermediate steps, among which the construction of a Petri net extended with typed variables, data handling features, and atomic transitions.
- OPEN/CAESAR [41] is a generic software environment for developing tools that explore graphs on the fly (for instance, simulation, verification, and test generation tools). Such tools can be developed independently of any particular high level language. In this respect, OPEN/CAESAR plays a central role in CADP by connecting language-oriented tools with model-oriented tools. OPEN/CAESAR consists of a set of 16 code libraries with their programming interfaces, such as:
 - CAESAR_GRAPH, which provides the programming interface for graph exploration,
 - CAESAR_HASH, which contains several hash functions,
 - CAESAR_SOLVE, which resolves Boolean equation systems on the fly,
 - CAESAR_STACK, which implements stacks for depth-first search exploration, and
 - CAESAR_TABLE, which handles tables of states, transitions, labels, etc.

A number of on-the-fly analysis tools have been developed within the OPEN/CAESAR environment, among which:

- BISIMULATOR, which checks bisimulation equivalences and preorders,
- CUNCTATOR, which performs steady-state simulation of continuous-time Markov chains,
- DETERMINATOR, which eliminates stochastic nondeterminism in normal, probabilistic, or stochastic systems,
- DISTRIBUTOR, which generates the graph of reachable states using several machines,
- EVALUATOR, which evaluates MCL formulas,
- EXECUTOR, which performs random execution,
- EXHIBITOR, which searches for execution sequences matching a given regular expression,
- GENERATOR, which constructs the graph of reachable states,
- PROJECTOR, which computes abstractions of communicating systems,
- REDUCTOR, which constructs and minimizes the graph of reachable states modulo various equivalence relations,

- SIMULATOR, XSIMULATOR, and OCIS, which enable interactive simulation, and
- TERMINATOR, which searches for deadlock states.
- BCG (*Binary Coded Graphs*) is both a file format for storing very large graphs on disk (using efficient compression techniques) and a software environment for handling this format. BCG also plays a key role in CADP as many tools rely on this format for their inputs/outputs. The BCG environment consists of various libraries with their programming interfaces, and of several tools, such as:
 - BCG_CMP, which compares two graphs,
 - BCG_DRAW, which builds a two-dimensional view of a graph,
 - BCG_EDIT, which allows the graph layout produced by BCG_DRAW to be modified interactively,
 - BCG_GRAPH, which generates various forms of practically useful graphs,
 - BCG_INFO, which displays various statistical information about a graph,
 - BCG_IO, which performs conversions between BCG and many other graph formats,
 - BCG_LABELS, which hides and/or renames (using regular expressions) the transition labels of a graph,
 - BCG_MIN, which minimizes a graph modulo strong or branching equivalences (and can also deal with probabilistic and stochastic systems),
 - BCG_STEADY, which performs steady-state numerical analysis of (extended) continuous-time Markov chains,
 - BCG_TRANSIENT, which performs transient numerical analysis of (extended) continuous-time Markov chains, and
 - XTL (*eXecutable Temporal Language*), which is a high level, functional language for programming exploration algorithms on BCG graphs. XTL provides primitives to handle states, transitions, labels, *successor* and *predecessor* functions, etc.

For instance, one can define recursive functions on sets of states, which allow evaluation and diagnostic generation fixed point algorithms for usual temporal logics (such as HML [49], CTL [37], ACTL [38], etc.) to be defined in XTL.
- PBG (*Partitioned BCG Graph*) is a file format implementing the theoretical concept of *Partitioned LTS* [44] and providing a unified access to a graph partitioned in fragments distributed over a set of remote machines, possibly located in different countries. The PBG format is supported by several tools, such as:
 - PBG_CP, PBG_MV, and PBG_RM, which facilitate standard operations (copying, moving, and removing) on PBG files, maintaining consistency during these operations,
 - PBG_MERGE (formerly known as BCG_MERGE), which transforms a distributed graph into a monolithic one represented in BCG format,
 - PBG_INFO, which displays various statistical information about a distributed graph.
- The connection between explicit models (such as BCG graphs) and implicit models (explored on the fly) is ensured by OPEN/CAESAR-compliant compilers, e.g.:
 - BCG_OPEN, for models represented as BCG graphs,
 - CAESAR.OPEN, for models expressed as LOTOS descriptions,
 - EXP.OPEN, for models expressed as communicating automata,
 - FSP.OPEN, for models expressed as FSP [53] descriptions,
 - LNT.OPEN, for models expressed as LNT descriptions, and
 - SEQ.OPEN, for models represented as sets of execution traces.

The CADP toolbox also includes TGV (*Test Generation based on Verification*), which has been developed by the VERIMAG laboratory (Grenoble) and Inria Rennes – Bretagne-Atlantique.

The CADP tools are well-integrated and can be accessed easily using either the EUCALYPTUS graphical interface or the SVL [42] scripting language. Both EUCALYPTUS and SVL provide users with an easy and uniform access to the CADP tools by performing file format conversions automatically whenever needed and by supplying appropriate command-line options as the tools are invoked.

- Participants: Hubert Garavel, Frédéric Lang, Radu Mateescu and Wendelin Serwe
- Contact: Hubert Garavel
- URL: <http://cadp.inria.fr/>

5.2. TRAIAN

KEYWORDS: Compilation - LOTOS NT

FUNCTIONAL DESCRIPTION: TRAIAN is a compiler for translating LOTOS NT descriptions into C programs, which will be used for simulation, rapid prototyping, verification, and testing.

The current version of TRAIAN, which handles LOTOS NT types and functions only, has useful applications in compiler construction [43], being used in all recent compilers developed by CONVECS.

- Participants: Hubert Garavel, Frédéric Lang and Wendelin Serwe
- Contact: Hubert Garavel
- URL: <http://convecs.inria.fr/software/traian/>

CORSE Project-Team

6. New Software and Platforms

6.1. Verde

KEYWORDS: Debug - Verification

FUNCTIONAL DESCRIPTION: Interactive Debugging with a traditional debugger can be tedious. One has to manually run a program step by step and set breakpoints to track a bug.

i-RV is an approach to bug fixing that aims to help developers during their Interactive Debugging sessions using Runtime Verification.

Verde is the reference implementation of i-RV.

- Participants: Kevin Pouget, Ylies Falcone, Raphael Jakse and Jean-François Méhaut
- Contact: Raphael Jakse
- Publication: [Interactive Runtime Verification - When Interactive Debugging meets Runtime Verification](#)
- URL: <https://gitlab.inria.fr/monitoring/verde>

6.2. Mickey

KEYWORDS: Dynamic Analysis - Performance analysis - Profiling - Polyhedral compilation

FUNCTIONAL DESCRIPTION: Mickey is a set of tools for profiling based performance debugging for compiled binaries. It uses a dynamic binary translator to instrument arbitrary programs as they are being run to reconstruct the control flow and track data dependencies. This information is then fed to a polyhedral optimizer that proposes structured transformations for the original code.

Mickey can handle both inter- and intra-procedural control and data flow in a unified way, thus enabling inter-procedural structured transformations. It is based on QEMU to allow for portability, both in terms of targeted CPU architectures, but also in terms of programming environment and the use of third-party libraries for which no source code is available.

- Partner: STMicroelectronics
- Contact: Fabian Gruber

6.3. Platforms

6.3.1. Grid'5000

Grid'5000 is a large-scale and versatile testbed for experiment-driven research in all areas of computer science, with a focus on parallel and distributed computing including Cloud, HPC and Big Data. It provides access to a large amount of resources: 12000 cores, 800 compute-nodes grouped in homogeneous clusters, and featuring various technologies (GPU, SSD, NVMe, 10G and 25G Ethernet, Infiniband, Omni-Path) and advanced monitoring and measurement features for traces collection of networking and power consumption, providing a deep understanding of experiments. It is highly reconfigurable and controllable. Researchers can experiment with a fully customized software stack thanks to bare-metal deployment features, and can isolate their experiment at the networking layer advanced monitoring and measurement features for traces collection of networking and power consumption, providing a deep understanding of experiments designed to support Open Science and reproducible research, with full traceability of infrastructure and software changes on the testbed. Frédéric Desprez is director of the GIS GRID5000.

6.3.2. SILECS

Frédéric Desprez is co-PI with Serge Fdida (Université Sorbonne) of the SILECS infrastructure (IR ministère) which goal is to provide an experimental platform for experimental computer Science (Internet of things, clouds, hpc, big data, ...). This new infrastructure is based on two existing infrastructures, Grid'5000 and FIT.

DATASPHERE Team

6. New Software and Platforms

6.1. DNS data analysis

Data analytics tools for DNS data analysis were developed in a cooperation with ICT, Chinese Academy of Sciences in the frame of the thesis of Jingxiu SU [8].

6.1.1. BGP Geopolitics

An observatory of global BGP connectivity has been developed that is used to monitor and detect in real time BGP level attacks. In addition, a set of tools were developed to analyse the structure of information propagation over social networks.

6.1.2. Atlas of Data

A platform to visualize data flows over the planet is under construction. It can be accessed online at <https://theatlasofdata.earth/>.

PRIVATICS Project-Team

5. New Software and Platforms

5.1. FECFRAME

FEC Framework following RFC 6363 specifications (<https://datatracker.ietf.org/doc/rfc6363/>)

KEYWORDS: Error Correction Code - Content delivery protocol - Robust transmission

FUNCTIONAL DESCRIPTION: This software implements the FECFRAME IETF standard (RFC 6363) co-authored by V. Roca, and is compliant with 3GPP specifications for mobile terminals. It enables the simultaneous transmission of multimedia flows to one or several destinations, while being robust to packet erasures that happen on wireless networks (e.g., 4G or Wifi). This software relies on the OpenFEC library (the open-source <http://openfec.org> version or the commercial version) that provides the erasure correction codes (or FEC) and thereby offer robustness in front of packet erasures.

- Participant: Vincent Roca
- Contact: Vincent Roca

5.2. Mobilitics

FUNCTIONAL DESCRIPTION: Mobilitics is a joint project, started in 2012 between Inria and CNIL, which targets privacy issues on smartphones. The goal is to analyze the behavior of smartphones applications and their operating system regarding users private data, that is, the time they are accessed or sent to third party companies usually neither with user's awareness nor consent.

In the presence of a wide range of different smartphones available in terms of operating systems and hardware architecture, Mobilitics project focuses actually its study on the two mostly used mobile platforms, IOS (Iphone) and Android. Both versions of the Mobilitics software: (1) capture any access to private data, any modification (e.g., ciphering or hashing of private data), or transmission of data to remote locations on the Internet, (2) store these events in a local database on the phone for offline analysis, and (3) provide the ability to perform an in depth database analysis in order to identify personal information leakage.

- Authors: Jagdish Achara, James-Douglass Lefruit, Claude Castelluccia, Franck Baudot, Geoffrey Delcroix, Gwendal Le Grand, Stéphane Petitcolas and Vincent Roca
- Contact: Claude Castelluccia

5.3. MyTrackingChoices

KEYWORDS: Privacy - User control

FUNCTIONAL DESCRIPTION: This extension lets you control how you are being tracked on the Internet. It allows you to choose the categories (e.g., health, adult) of the websites where you don't want to be tracked on. When you browse the web, your visited webpages will be categorized on the fly and, depending on your choices, the extension will block the trackers (webpage by webpage) or not.

Existing anti-tracking (Ghostery, Disconnect etc.) and ad-blocking (AdBlock Plus etc.) tools block almost ALL trackers and as a result, ads. This has a negative impact on the Internet economy because free services/content on the Internet are fuelled by ads. As a result, websites are starting to block access to their content if they detect use of Ad-blockers or they ask users to move to a subscription-based model (where users have to pay to get access to the website).

This extension is testing another approach: It is trying to find a trade-off between privacy and economy, that would allow users to protect their privacy while still accessing to free content.

It is based on the assumption that most people are not against advertisements, but want to keep control over their data. We believe that some sites are more sensitive than others. In fact, most people don't want to be tracked on "sensitive" websites (for example related to religion, health,...), but don't see any problem to be tracked on less sensitive ones (such as news, sport,...). This extension allows you to take control and specify which on which categories of sites you don't want to be tracked on! Furthermore, the extension also gives you the option to block the trackers on specific websites.

- Contact: Claude Castelluccia
- URL: <https://addons.mozilla.org/FR/firefox/addon/mytrackingchoices/>

5.4. OMEN+

FUNCTIONAL DESCRIPTION: Omen+ is a password cracker following our previous work. It is used to guess possible passwords based on specific information about the target. It can also be used to check the strength of user password by effectively looking at the similarity of that password with both usual structures and information relative to the user, such as his name, birth date...

It is based on a Markov analysis of known passwords to build guesses. The previous work Omen needs to be cleaned in order to be scaled to real problems and to be distributed or transferred to the security community (maintainability): eventually it will become an open source software. The main challenge of Omen+ is to optimize the memory consumption.

- Participants: Claude Castelluccia and Pierre Rouveyrol
- Contact: Claude Castelluccia

5.5. OPENFEC

KEYWORD: Error Correction Code

FUNCTIONAL DESCRIPTION: OpenFEC is a C-language implementation of several Application-Level Forward Erasure Correction (AL-FEC) codecs, namely: Reed-Solomon (RFC 5510), LDPC-Staircase (RFC 5170) codes, and RLC (<https://datatracker.ietf.org/doc/draft-ietf-tsvwg-rlc-fec-scheme/>). Two versions are available: an open-source, unsupported version (<http://openfec.org>), and an advanced version commercialized by the Expway SME.

RELEASE FUNCTIONAL DESCRIPTION: Added support of RLC codes (Random Linear Codes), based on a sliding encoding window.

- Participants: Christophe Neumann, Belkacem Teibi, Jérôme Lacan, Jonathan Detchart, Julien Laboure, Kevin Chaumont, Mathieu Cunche and Vincent Roca
- Partner: Expway
- Contact: Vincent Roca
- URL: <http://openfec.org/>

SPADES Project-Team

5. New Software and Platforms

5.1. pyCPA_TWCA

Analysis tool for weakly-hard real-time systems

KEYWORDS: Real time - Scheduling analyses

FUNCTIONAL DESCRIPTION: pyCPA_TWCA is a pyCPA plugin for Typical Worst-Case Analysis. pyCPA is an open-source Python implementation of Compositional Performance Analysis developed at TU Braunschweig, which allows in particular response-time analysis. pyCPA_TWCA is an extension of that tool that is co-developed by Sophie Quinton and Zain Hammadeh at TU Braunschweig. It allows in particular the computation of weakly-hard guarantees for real-time tasks, i.e. number of deadline misses out of a sequence of executions. So far, pyCPA_TWCA is restricted to uniprocessor systems of independent tasks. pyCPA_TWCA can handle the following scheduling policies: Fixed Priority Preemptive, Fixed Priority Non-Preemptive, Weighted Round-Robin, Earliest Deadline First.

- Contact: Sophie Quinton

5.2. CertiCAN

Certifier of CAN bus analysis results

KEYWORDS: Certification - CAN bus - Real time - Static analysis

FUNCTIONAL DESCRIPTION: CertiCAN is a tool, produced using the Coq proof assistant, allowing the formal certification of the correctness of CAN bus analysis results. Result certification is a process that is lightweight and flexible compared to tool certification, which makes it a practical choice for industrial purposes. The analysis underlying CertiCAN, which is based on a combined use of two well-known CAN analysis techniques, is computationally efficient. Experiments demonstrate that CertiCAN is able to certify the results of RTaW-Pegase, an industrial CAN analysis tool, even for large systems. Furthermore, CertiCAN can certify the results of any other RTA tool for the same analysis and system model (periodic tasks with offsets in transactions).

- Contact: Xiaojie Guo

ELAN Team

5. New Software and Platforms

5.1. Argus-distribution

KEYWORDS: Frictional contact - Cloth dynamics - Mesh adaptation

SCIENTIFIC DESCRIPTION: The Argus-distribution software exactly replicates all the results published in the SIGGRAPH 2018 paper entitled "An Implicit Frictional Contact Solver for Adaptive Cloth Simulation", by Li et al. This paper presents the first method able to account for cloth contact with exact Coulomb friction, treating both cloth self-contacts and contacts occurring between the cloth and an underlying character. The key contribution is to observe that for a nodal system like cloth, the frictional contact problem may be formulated based on velocities as primary variables, without having to compute the costly Delassus operator. Then, by reversing the roles classically played by the velocities and the contact impulses, conical complementarity solvers of the literature can be adapted to solve for compatible velocities at nodes. To handle the full complexity of cloth dynamics scenarios, this base algorithm has been extended in two ways: first, towards the accurate treatment of frictional contact at any location of the cloth, through an adaptive node refinement strategy, second, towards the handling of multiple constraints at each node, through the duplication of constrained nodes and the adding of pin constraints between duplicata. This method allows to handle the complex cloth-cloth and cloth-body interactions in full-size garments with an unprecedented level of realism compared to former methods, while maintaining reasonable computational timings. allows to simulate cloth dynamics subject to frictional contact.

FUNCTIONAL DESCRIPTION: Adaptive cloth simulation in the presence of frictional contact. Reference software for the paper "An Implicit Frictional Contact Solver for Adaptive Cloth Simulation", Li et al. 2018, ACM Transactions on Graphics (SIGGRAPH'18).

- Participants: Jie Li, Gilles Daviet, Rahul Narain, Florence Descoubes, Matthew Overby, George Brown and Laurence Boissieux
- Partners: Department of Computer Science and Engineering, University of Minnesota - IIT Delhi
- Contact: Florence Descoubes
- Publication: [An Implicit Frictional Contact Solver for Adaptive Cloth Simulation](#)
- URL: http://www-users.cselabs.umn.edu/~lix4611/contact_friction.html

MISTIS Project-Team

6. New Software and Platforms

6.1. BOLD model FIT

KEYWORDS: Functional imaging - FMRI - Health

SCIENTIFIC DESCRIPTION: Physiological and biophysical models have been proposed to link neuronal activity to the Blood Oxygen Level-Dependent (BOLD) signal in functional MRI (fMRI). Those models rely on a set of parameter values that are commonly estimated using gradient-based local search methods whose initial values are taken from the literature. In some applications, interesting insight into the brain physiology or physiopathology can be gained from an estimation of the model parameters from measured BOLD signals. In this work we focus on the extended Balloon model and propose the estimation of 15 parameters using seven different approaches: three versions of the Expectation Maximization Gauss-Newton (EM/GN) approach (the *de facto* standard in the neuroscientific community) and four metaheuristics (Particle Swarm Optimization (PSO), Differential Evolution (DE), Real-Coded Genetic Algorithms (GA), and a Memetic Algorithm (MA) combining EM/GN and DE). To combine both the ability to escape local optima and to incorporate prior knowledge, we derive the target function from Bayesian modeling. The general behavior of these algorithms is analyzed and compared, providing very promising results on challenging real and synthetic fMRI data sets involving rats with epileptic activity. These stochastic optimizers provided a better performance than EM/GN in terms of distance to the ground truth in 4 out of 6 synthetic data sets and a better signal fitting in 12 out of 12 real data sets. Non-parametric statistical tests showed the existence of statistically significant differences between the real data results obtained by DE and EM/GN. Finally, the estimates obtained from DE for these parameters seem both more realistic and more stable or at least as stable across sessions as the estimates from EM/GN. This is the largest comparison of optimizers for the estimation of biophysical parameters in BOLD fMRI

FUNCTIONAL DESCRIPTION: This Matlab toolbox performs the automatic estimation of biophysical parameters using the extended Balloon model and BOLD fMRI data. It takes as input a MAT file and provides as output the parameter estimates achieved by using stochastic optimization

NEWS OF THE YEAR: The main differences with our previous work: 1) we also use synthetic data, 2) we use stochastic GN and MCMC+DE, 3) We evaluate results not only in physiological terms but also comparing fitness function values. Also changes were made to allow running on the cluster via MPI

- Participants: Pablo Mesejo Santiago, Florence Forbes and Jan Warnking
- Partner: University of Granada, Spain
- Contact: Pablo Mesejo Santiago
- Publication: [A differential evolution-based approach for fitting a nonlinear biophysical model to fMRI BOLD data](#)
- URL: <https://hal.archives-ouvertes.fr/hal-01221115v2/>

6.2. PyHRF

KEYWORDS: Medical imaging - Health - Brain - IRM - Neurosciences - Statistic analysis - FMRI

SCIENTIFIC DESCRIPTION: Functional Magnetic Resonance Imaging (fMRI) is a neuroimaging technique that allows the non-invasive study of brain function. It is based on the hemodynamic variations induced by changes in cerebral synaptic activity following sensory or cognitive stimulation. The measured signal depends on the variation of blood oxygenation level (BOLD signal) which is related to brain activity: a decrease in deoxyhemoglobin concentration induces an increase in BOLD signal. The BOLD signal is delayed with respect to changes in synaptic activity, which can be modeled as a convolution with the Hemodynamic Response Function (HRF) whose exact form is unknown and fluctuates with various parameters such as age, brain region or physiological conditions. In this work we propose to analyze fMRI data using a Joint Detection-Estimation (JDE) approach. It jointly detects cortical activation and estimates the HRF. In contrast to existing tools, PyHRF estimates the HRF instead of considering it as a given constant in the entire brain.

FUNCTIONAL DESCRIPTION: As part of fMRI data analysis, PyHRF provides a set of tools for addressing the two main issues involved in intra-subject fMRI data analysis : (i) the localization of cerebral regions that elicit evoked activity and (ii) the estimation of the activation dynamics also referenced to as the recovery of the Hemodynamic Response Function (HRF). To tackle these two problems, PyHRF implements the Joint Detection-Estimation framework (JDE) which recovers parcel-level HRFs and embeds an adaptive spatio-temporal regularization scheme of activation maps.

NEWS OF THE YEAR: The framework to perform software tests has been further developed. Some unitary tests have been set.

- Participants: Aina Frau Pascual, Christine Bakhous, Florence Forbes, Jaime Eduardo Arias Almeida, Laurent Risser, Lotfi Chaari, Philippe Ciuciu, Solveig Badillo, Thomas Perret and Thomas Vincent
- Partners: CEA - NeuroSpin
- Contact: Florence Forbes
- Publications: [Frontiers in Neuroinformatics Flexible multivariate hemodynamics fMRI data analyses and simulations with PyHRF - Fast joint detection-estimation of evoked brain activity in event-related fMRI using a variational approach - A Bayesian Non-Parametric Hidden Markov Random Model for Hemodynamic Brain Parcellation](#)
- URL: <http://pyhrf.org>

6.3. xLLiM

High dimensional locally linear mapping

KEYWORDS: Clustering - Regression

SCIENTIFIC DESCRIPTION: Building a regression model for the purpose of prediction is widely used in all disciplines. A large number of applications consists of learning the association between responses and predictors and focusing on predicting responses for the newly observed samples. In this work, we go beyond simple linear models and focus on predicting low-dimensional responses using high-dimensional covariates when the associations between responses and covariates are non-linear.

FUNCTIONAL DESCRIPTION: This is an R package available on the CRAN at <https://cran.r-project.org/web/packages/xLLiM/index.html>

xLLiM provides a tool for non linear mapping (non linear regression) using a mixture of regression model and an inverse regression strategy. The methods include the GLLiM model (Deleforge et al (2015)) based on Gaussian mixtures and a robust version of GLLiM, named SLLiM (see Perthame et al (2016)) based on a mixture of Generalized Student distributions.

NEWS OF THE YEAR: A new Hierarchical version of GLLiM has been developed in collaboration with University of Michigan, USA.

- Participants: Antoine Deleforge, Emeline Perthame and Florence Forbes
- Partner: University of Michigan, Ann Arbor, USA
- Contact: Florence Forbes
- Publications: [Inverse regression approach to robust nonlinear high-to-low dimensional mapping - High-Dimensional Regression with Gaussian Mixtures and Partially-Latent Response Variables](#)
- URL: <https://cran.r-project.org/web/packages/xLLiM/index.html>

6.4. MMST

Mixtures of Multiple Scaled Student T distributions

KEYWORDS: Health - Statistics - Brain MRI - Medical imaging - Robust clustering

SCIENTIFIC DESCRIPTION: A new family of multivariate heavy-tailed distributions that allow variable marginal amounts of tailweight is proposed and implemented. The originality comes from introducing multidimensional instead of univariate scale variables for the mixture of scaled Gaussian family of distributions. In contrast to most existing approaches, the derived distributions can account for a variety of shapes and have a simple tractable form with a closed-form probability density function whatever the dimension. We provide maximum likelihood estimation of the parameters and illustrate their modelling flexibility.

FUNCTIONAL DESCRIPTION: The package implements mixtures of so-called multiple scaled Student distributions, which are generalisation of multivariate Student T distribution allowing different tails in each dimension. Typical applications include Robust clustering to analyse data with possible outliers. In this context, the model and package have been used on large data sets of brain MRI to segment and identify brain tumors. Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

RELEASE FUNCTIONAL DESCRIPTION: Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

NEWS OF THE YEAR: Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

- Participants: Alexis Arnaud, Darren Wraith, Florence Forbes, Steven Quinito Masnada and Stéphane Despréaux
- Partner: Institut des Neurosciences Grenoble
- Contact: Florence Forbes
- Publications: [A new family of multivariate heavy-tailed distributions with variable marginal amounts of tailweights: Application to robust clustering - Fully Automatic Lesion Localization and Characterization: Application to Brain Tumors Using Multiparametric Quantitative MRI Data](#)
- URL: <https://team.inria.fr/mistis/software/>

NANO-D Project-Team

5. New Software and Platforms

5.1. SAMSON

Software for Adaptive Modeling and Simulation Of Nanosystems

KEYWORDS: Bioinformatics - Simulation - Nanosystems - Structural Biology - Chemistry

SCIENTIFIC DESCRIPTION: Please refer to <https://www.samson-connect.net>

FUNCTIONAL DESCRIPTION: SAMSON is a software platform for real-time modelling and simulation of natural or artificial nanosystems. The objective is to make SAMSON a generic application for computer-aided design of nanosystems, similar to existing applications for macrosystem prototyping (CATIA, SolidWorks, etc.).

- Contact: Stéphane Redon
- URL: <http://nano-d.inrialpes.fr/software/>

5.2. DockTrina

A novel protein docking method for modeling the 3D structures of nonsymmetrical triangular trimers

FUNCTIONAL DESCRIPTION: DockTrina is a novel protein docking method for modeling the 3D structures of nonsymmetrical triangular trimers. The method takes as input pair-wise contact predictions from a rigid body docking program. It then scans and scores all possible combinations of pairs of monomers using a very fast root mean square deviation (RMSD) test (see below). Finally, it ranks the predictions using a scoring function which combines triples of pair-wise contact terms and a geometric clash penalty term. The overall approach takes less than 2 min per complex on a modern desktop computer.

- Contact: Sergey Grudinin
- URL: <https://team.inria.fr/nano-d/software/docktrina/>

5.3. HermiteFit

A new docking algorithm for rapid fitting atomic structures into cryo-EM density maps

FUNCTIONAL DESCRIPTION: HermiteFit is a new docking algorithm for rapid fitting atomic structures into cryo-EM density maps using 3D orthogonal Hermite functions. HermiteFit uses the cross-correlation or the Laplacian-filtered cross-correlation as the fitting criterion. HermiteFit exhaustively rotates the protein density in the Hermite space and then converts the expansion coefficients into the Fourier space for the subsequent fast FFT-based correlation computations.

- Partners: IBS - FZJ Juelich
- Contact: Sergey Grudinin
- URL: <https://team.inria.fr/nano-d/software/hermitefit/>

5.4. Knodle

KNOWledge-Driven Ligand Extractor

KEYWORDS: Bioinformatics - Machine learning

FUNCTIONAL DESCRIPTION: KNOWledge-Driven Ligand Extractor is a software library for the recognition of atomic types, their hybridization states and bond orders in the structures of small molecules. Its prediction model is based on nonlinear Support Vector Machines. The process of bond and atom properties perception is divided into several steps. At the beginning, only information about the coordinates and elements for each atom is available :

Connectivity is recognized. A search of rings is performed to find the Smallest Set of Smallest Rings (SSSR). Atomic hybridizations are predicted by the corresponding SVM model. Bond orders are predicted by the corresponding SVM model. Aromatic cycles are found. Atomic types are set in obedience to the functional groups. Some bonds are reassigned during this stage.

- Participants: Maria Kadukova and Sergey Grudinin
- Partner: MIPT Moscow
- Contact: Sergey Grudinin
- Publication: [Knodle: A Support Vector Machines-Based Automatic Perception of Organic Molecules from 3D Coordinates](#)
- URL: <https://team.inria.fr/nano-d/software/Knodle/>

5.5. RigidRMSD

A library for rapid computations of the root mean square deviations (RMSDs) corresponding to a set of rigid body transformations of a coordinate vector

KEYWORD: Bioinformatics

FUNCTIONAL DESCRIPTION: RigidRMSD is a library for rapid computations of the root mean square deviations (RMSDs) corresponding to a set of rigid body transformations of a coordinate vector (which can be a molecule in PDB format, for example). Calculation of the RMSD splits into two steps:

Initialization, which is linear in the number of vector entities (or particles in a rigid body). RMSD computation, which is computed in constant time for a single rigid-body spatial transformation (rotation + translation). This step uses the inertia tensor and the the center of mass computed on the first step. Initialization step is performed only once. It makes RigidRMSD particularly useful when computing multiple RMSDs, since each new RMSD calculation takes only constant time.

- Participants: Petr Popov and Sergey Grudinin
- Contact: Sergey Grudinin
- Publication: [Rapid determination of RMSDs corresponding to macromolecular rigid body motions](#)
- URL: <https://team.inria.fr/nano-d/software/rigidrmsd/>

5.6. SAMSON-Drug-design

KEYWORDS: Algorithm - Nanosystems - Structural Biology - Bioinformatics - Chemistry - 3D modeling - Molecular simulation

FUNCTIONAL DESCRIPTION: Arap Interpolation Path : Generate interpolation path between two protein structures by the As-Rigid-As-Possible principle from computer graphics

Ligand unbinding search : Find ligand unbinding pathway with the ART-RRT method. The method uses the T-RRT method from robotics for efficiently searching low-energy paths and the ARAP modeling method from computer graphics for handling flexible motions of the ligand and reducing the number of the dimensions of the search space.

Protein Path search : Find protein conformational transition paths between two given conformations with the ART-RRT method. The method uses the T-RRT method from robotics for searching low-energy paths and the As-Rigid-As-Possible (ARAP) methods from computer graphics for handling the flexibility of the protein and reducing the number of the dimensions of the search space.

- Authors: Leonard Jaillet, Minh Khoa Nguyen and Jocelyn Gaté
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.7. DeepSymmetry

KEYWORDS: Bioinformatics - 3D modeling - Machine learning - Neural networks

FUNCTIONAL DESCRIPTION: DeepSymmetry is a method based on three-dimensional (3D) convolutional networks that detects structural repetitions in proteins and their density maps. It identifies tandem repeat proteins, proteins with internal symmetries, their symmetry order, and also the corresponding symmetry axes.

- Participants: Guillaume Pages and Sergey Grudinin
- Contact: Sergey Grudinin
- Publication: [DeepSymmetry : Using 3D convolutional networks for identification of tandem repeats and internal symmetries in protein structures](#)
- URL: <https://team.inria.fr/nano-d/software/deepsymmetry/>

5.8. SAMSON-ARAP-Planner

KEYWORDS: 3D - Algorithm - Nanosystems - Bioinformatics - Structural Biology - Chemistry

FUNCTIONAL DESCRIPTION: ARAP planner combines the ARAP method from computer graphics with T-RRT exploration method from robotics for efficiently finding low-energy paths in high-dimensional energy landscapes.

- Authors: Leonard Jaillet and Minh Khoa Nguyen
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.9. SAMSON-Hydrocarbons

KEYWORDS: Algorithm - Quantum chemistry - Chemistry - Nanosystems - 3D - 3D modeling

FUNCTIONAL DESCRIPTION: Interactive quantum chemistry : This SAMSON Element demonstrates interactive quantum chemistry for small molecules at the ASED-MO level of theory. Choose the ASED-MO (atom superposition and electron delocalization) interaction model when adding a simulator through the 'Simulation' menu. The SAMSON Element also includes an App that makes it possible to visualize how the electron density evolves during interactive simulation.

Brenner interaction model : This SAMSON Element contains an adaptive implementation of the Brenner interaction model. Interaction models are one of the five model categories that are used to model nanosystems in SAMSON, along with structural models (for geometry and topology), dynamical models (to represent degrees of freedom), visual models (for visual representations) and property models (to represent properties). The Brenner interaction model is a reactive bond-order potential for hydrocarbon systems. This adaptive implementation makes it possible to interactively simulate large systems. Choose this interaction model when adding a simulator through the 'Simulation' menu.

- Author: Maël Bosson
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.10. SAMSON-RDKit

KEYWORDS: 2D - 3D - Chemistry - Algorithm - 3D modeling - Structural Biology - Bioinformatics

FUNCTIONAL DESCRIPTION: Based on the RDKit open-source libraries, convert and manage SMILES codes in the SAMSON platform. The RDKit-SMILES Manager element allows you to easily import files (.smi or .txt) containing several SMILES codes or add each code separately. 2D conformation of each code will then be generated and you can save them into svg or png files. Using a checkbox you will be able to select the codes that you want to convert into 3D structures and add them directly into the SAMSON data graph node as structural model. For more information about using this SAMSON Element, please visit <https://documentation.samson-connect.net/using-the-rdkit-smiles-manager/>.

- Author: Yassine Naimi
- Partner: Inria
- Contact: Stéphane Redon
- URL: <https://samson-connect.net/app/main?key=element&uuid=ce09650a-c071-4e84-1f6a-b8706937d5c1>

5.11. SAMSON-GROMACS

KEYWORDS: Algorithm - Materials - Chemistry - Bioinformatics - Structural Biology - Nanosystems - 3D modeling - 3-order

FUNCTIONAL DESCRIPTION: This SAMSON Element wraps GROMACS 5.1 force fields and setup tools. Use the "GROMACS setup" app (in the App menu), which wraps the pdb2gmx tool, to generate a structural model suitable for simulation (i.e. add hydrogens, etc.). Then, apply a simulator from the Simulation menu and choose "GROMACS force field" to add a GROMACS interaction model suitable for interactive minimization and simulation (no periodic boundary conditions). Note that, at the moment, at most one structural model should be selected (or in the document, when the selection is empty), and that bond lengths are not yet constrained in this version. This may be combined with the Twister editor to perform large-scale modifications of the structure, and the secondary structure visual model for interactively updated secondary structure prediction. Future updates of this SAMSON Element will wrap more GROMACS tools. Source code for this SAMSON Element will be made available at <https://gforge.inria.fr/projects/elements/>.

- Authors: Stéphane Redon, Minh Khoa Nguyen and Yassine Naimi
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.12. SAMSON-Essentials

KEYWORDS: 3D - C++ - OpenGL - Molecular surface - Molecular simulation - Structural Biology - Chemistry - 3D modeling - Bioinformatics - Nanosystems

FUNCTIONAL DESCRIPTION: A set of SAMSON Elements that adds essential features to SAMSON such as import / export of models, import / export of documents, generators, simulators, editors, scripting, app as well as software integrations (autodock vina).

- Authors: Stéphane Redon, Jocelyn Gaté, Guillaume Pages, Dmitriy Marin, Svetlana Artemova, Himani Singhal, Marc Aubert, Marc Piuze and Clement Beitone
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.13. Samson-base

KEYWORDS: Bioinformatics - Simulation - Nanosystems - Structural Biology - Chemistry

- Participants: Evelyne Altariba, Jocelyn Gaté, Noëlle Le Delliou and Stéphane Redon
- Contact: Stéphane Redon

5.14. SAMSON-Connect

KEYWORDS: Web Application - Software platform - Web

FUNCTIONAL DESCRIPTION: SAMSON, SAMSON Elements and the SAMSON Software Development Kit are distributed via the SAMSON Connect website.[2] The site acts as a repository for the SAMSON Elements being uploaded by developers, and users of SAMSON choose and add Elements from SAMSON Connect.

- Authors: Stéphane Redon, Mohamed Yengui and Jocelyn Gaté
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.15. SAMSON-Updater

KEYWORDS: Webservices - Web Application

FUNCTIONAL DESCRIPTION: Web service to ensure communication between SAMSON and SAMSON-Connect. Features: Add / remove new items to SAMSON if they have been added / deleted on SAMON-Connect Update SAMSON or SAMSON-Elements Authenticate users ...

- Authors: Mohamed Yengui and Jocelyn Gaté
- Partner: Inria
- Contact: Stéphane Redon

5.16. SAMSON-VariouS-tools

SAMSON-VariouS-toolsrere

KEYWORDS: 3D - 3D modeling - Chemistry - Algorithm - Bioinformatics - Nanosystems - Structural Biology

FUNCTIONAL DESCRIPTION: Cluster Game : This element has been made in order to help students discover the Lennard Jones interactions. It is a game in which the goal is to optimize the atoms' placement. Contains eight levels and five tutorial levels.

Atoms Selector : This SAMSON element allows selection of atoms in the active document according to a user-provided expression with the usage of NSL-like variables (NSL - Node Specification Language), standard mathematical and logical operations. Parsing and evaluation of expressions is done with the usage of C++ Mathematical Expression Parsing And Evaluation Library 'exprtck' by Arash Partow (<https://github.com/ArashPartow/exprtck>)

Simple Script : This SAMSON element allows modification of some parameters of atoms using scripting language, standard mathematical and logical operations, and NSL-like variables (NSL - Node Specification Language). The script is applied to each atom independently. Parsing and evaluation of the script is done with the usage of C++ Mathematical Expression Parsing And Evaluation Library 'exprtck' by Arash Partow (<https://github.com/ArashPartow/exprtck>)

Bond Angle Distribution : This App will compute the bond angle distribution of the selected atoms. The result and its image can then be exported.

Bond Distortion Visualisation : This App permits to visualize with colors the distortion of a molecular or crystallic structure. The angle distortion, the bond distortion and the projected bond distortion can be represented with colors on bonds and atoms.

Frame axis : Basic visual model to show cartesian axis. Open a new visual model and select "Frame axis" to see the frame axis as arrows, lines or both.

Radial Distribution Function : This app computes and draws the radial distribution function of a selection.
- Compute the crossed-RDF by selecting 2 different sets of atoms.
- Follow the evolution of the RDF by selecting a simulator.

Adaptive Lennard-Jones : An interaction model to compute the forces with an adaptive version of Lennard-Jones potential. The update of forces is done by storing all the position, and at each position update, subtracting previous pair forces, then adding new ones. If both pair particles were frozen by restraining dynamical model, the update is useless and so not done.

STL File Importer : Reads Stereolithography (.stl) binary and ASCII files. Spawns carbon atoms at the intersections of vertices to create quickly new original atomic configurations. Many STL files are available online to generate thousands of new configurations.

StyleSheet Viewer : An app for internal developers to test their skin/styles ...

Animation Player : Create animation from a list of conformations in SAMSON Document view There are 3 play modes: loop, only 1 time, or continuous back-forth. The user can change the frame order by drag and drop in the frame list.

Internal Coordinate Editor : This editor rotate the molecule by defining rotation axis and rotation angle. The user define the rotation axis (represented by an arrow in the view) by clicking on one atom and drag it to the second atom. The rotation angle is defined by the small GUI windows. The editor will try to rotate all the atoms after the head of the arrow and in between the tail and head of the arrow

RMSD : This app calculates RMSD between 2 structures. If it is an amino acid chains, a sequence alignment of the structures is needed (in fasta format). The fasta format has to be obtained from external sources. If it is not a protein, the app will try to match atoms one by one in both structures.

Trajectory Importer : This app import selected pdb files (hold Ctrl + Mouse click for multiple selection) as a trajectory. The result is one single structural model and a list of conformations in SAMSON Document View

Open Babel connector : This app allows users to use Open Babel from inside SAMSON

ARPS demo : This SAMSON Element features a demonstration of ARPS: Adaptively Restrained Particle Simulations, an adaptive simulation technique able to focus computations on the most mobile degrees of freedom. In this demo, a collision cascade may be simulated with various degrees of precision by changing the restrained dynamics threshold and the full dynamics threshold. For example, 0 0 produces a classical, non-adaptive simulation, while 0.625 and 0.7 result in a 10 times speedup in this example (without the graphics overhead). Click on 2D Shock to generate the example, enter the simplification parameters, and press start to simulate the collision cascade. Undo and redo make it possible to zoom on and compare simulations. Please refer to "S. Artemova and S. Redon. Adaptively restrained particle simulations. Physical review letters, 2012" for more details.

Hydrogen bond finder : Find hydrogen bonds in a given structure. The bonds is detected by specifying a threshold distance. Bonds are displayed by yellow lines.

Lennard-Jones model : This SAMSON Element contains a Lennard-Jones interaction model that may be used for several purposes: teaching, learning about van der Waals interactions, developing optimization algorithms, looking for minimum energy Lennard-Jones clusters through interactive simulation, etc. Add this force field to a group of atoms (the atom types do not matter) via the 'Simulation' menu.

Catalogue : BETA version. Bunch of structures easy to load, with images.

Catalogue Generator : BETA. Generator for the Catalogue module.

SAMSON Basic Tutorial : Tutorial for SAMSON : Basic fonctionnalités. Learn how to create, move and delete an atom, and then create a basic molecule thanks to a step-by-step guide. Experiment in sandbox mode. Test your mastery of SAMSON's tools with 4 speed challenges. The following elements are required : SAMSON Editors, Periodic table, Basic importers. Currently only available in french.

SAMSON Courses : BETA. Module with a custom display, depending on the entry files

SAMSON Courses Creator : BETA. Generator for SAMSON Course module

Charts : A SAMSON Element to allow user plotting something from SAMSON datas interactively

Leap : A driver to control SAMSON with the Leap motion controller

- Authors: Mohamed Nadhir Ben Hadj Abdellatif, Svetlana Artemova, Clement Beitone, Jocelyn Gaté, Dmitriy Marin, Pierre Mehaye, Minh Khoa Nguyen, Guillaume Pages, Stéphane Redon, François Rousse and Joachim Woerly-Moussier
- Partner: Inria
- Contact: Stéphane Redon

5.17. SAMSON-Crystal-Study-Pack

KEYWORDS: Algorithm - Nanosystems - 3D - 3D modeling - Physical simulation

FUNCTIONAL DESCRIPTION: CrystalConstrainer : Constrains borders of a crystal. The crystal should be aligned on xyz axes. The margin defines the maximum distance to the bonding box border for which atoms are constrained. Can use the current positions as constrained pos or some fixed one. Can constrain each pair of plans separately or by couples (e.g. XY)

CrystalProber : Get some statistics about a crystal. Compute for now the X, Y and Z lattice parameters. Can remove a margin to discard atoms at the border

CrystalRigidityProber : Analyze some crystal properties related to the rigidity and based on forces, such as the Young modulus, Poisson's ration, elastic constants, stiffness, etc.

Keating : Implement the Keating force field. Compute energy and forces according to positions. Follows anikin2011keating

nonharmonic Keating : Develop a nonharmonic Keating model as proposed in Rucker1995anharmonic. As parameter file it uses a .nhk extension. As parameters, it require a nu and theta0 value in addition to the equilibrium distances for each atom type. Also, it requires a0 distances for pairwise atoms, in addition to the alpha and beta parameters.

generalized harmonic Keating : Develop a generalized harmonic Keating force field as proposed in mojica2010modélisation. This model generalizes to atoms of columns III and V of the periodic table. The systems are anisotropics, with specific bond lengths and angles when involving the z direction.

CrystalCharacterizer : Provides functionalities to characterise a crystal.

CrystalVisualizer : Provides functionalities to visualize a crystal. Choose the pointing direction of the eye, according to some representative directions of the crystal mesh. Choose the orientation in the camera planer.

- Author: Leonard Jaillet
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.18. SAMSON-Materials

KEYWORDS: Algorithm - Materials - 3D - 3D modeling - Nanosystems

FUNCTIONAL DESCRIPTION: Crystal Creator : This SAMSON Elements enables to generate crystals. It contains a SAMSON App to write a unit cell and a SAMSON importer to read CIF format files. Once a unit cell is written or imported, it can be repeated in the directions of the lattice vectors to create a whole crystal. Each repetition is not a mere copy but is generated again so that the defects and the impurities are modeled. A functionality of the associated property model permits to cut the crystal with the Miller indices and expose the important crystalic planes.

Orbital Free DFT : This App computes the electron density of an atomic system. It comes with an interaction model to minimize the atomic structure and a visual model to appreciate the result of computations. The scheme used is the orbital-free DFT, and the pseudo-potential available restrains its use to only 9 elements : Li, Mg, Al, Si, P, Ga, In and Sb.

- Author: François Rousse
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.19. SAMSON-Planner-Tools

KEYWORDS: 3D - Algorithm - 3D modeling - Molecular simulation - Chemistry - Planning

FUNCTIONAL DESCRIPTION: A set of SAMSON Elements that adds planning features to SAMSON.

- Author: Leonard Jaillet
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

5.20. SAMSON-HEX

KEYWORD: Algorithm

FUNCTIONAL DESCRIPTION: Sampling and Docking using the Hex algorithm developed by Dave Ritchie in SAMSON. Docking solutions can be easily displayed and clustered.

- Authors: Sergey Grudin, Emilie Neveu and Yassine Naimi
- Partner: Inria
- Contact: Stéphane Redon
- URL: <https://www.samson-connect.net/>

5.21. SAMSON-UFF

KEYWORDS: Algorithm - Bioinformatics - 3D - 3D modeling - Nanosystems - Molecular simulation

FUNCTIONAL DESCRIPTION: Universal Force Field : This SAMSON Element contains a new implementation of the Universal Force Field, with automatic structure perception. In order to use this interaction model, add a simulator to the document from the Simulation menu, and choose "Universal Force Field". The property window of the interaction model makes it possible to customize the perception and setup the interaction model (e.g. choose the cutoff), and displays the various energy types and the total energy.

Interactive Modeling Universal Force Field : It is an extension of UFF that combines the possibility to significantly modify molecular structures (as with reactive force fields) with a broad diversity of supported systems thanks to the universality of UFF. Such an extension lets the user easily build and edit molecular systems interactively while being guided by physics based inter-atomic forces.

- Authors: Leonard Jaillet and Svetlana Artemova
- Partner: Inria
- Contact: Stéphane Redon
- URL: <https://samson-connect.net/app/main?key=element&uuid=8cbdc8b1-59e1-6459-d68f-b840275dd5e9>

5.22. SAMSON-Normal-modes

KEYWORDS: Algorithm - Bioinformatics - Structural Biology - 3-order - 3D modeling - Nanosystems

FUNCTIONAL DESCRIPTION: Normal mode analysis advanced : This SAMSON Element computes the nonlinear normal modes of a molecular system (protein, RNA, DNA) very quickly using the NOLB algorithm developed by Alexandre Hoffmann and Sergei Grudinin (J. Chem. Theory Comput., 2017, 13 (5), pp 2123-2134, DOI: 10.1021 / acs.jctc.7b00197.). The user indicates the desired number of modes, the interactions cutoff distance and the potential function. For now, the elastic network model potential is the one that is available. In the output, each mode is represented by a slider. The user can visualize the motion of each mode independently by moving its corresponding slider manually or by checking its checkbox and then pressing on the play button. Also, the user can visualize the motion of a combination of modes selecting them before playing the motion. The transformations used in this motion can be set to linear or nonlinear and the amplitude of the motion can be increased/decreased by changing the scaling factor. During this motion, the user can activate a real time minimization using one of the provided algorithms (steepest descent, conjugated gradient or LBGF) and defined values of minimization steps and minimization tolerance. Finally, the user can either save/export a given conformation of the structure or the entire displayed trajectory by going into the "Save Frames" tabulation of the SAMSON element. Please visit <https://blog.samson-connect.net/computing-non-linear-normal-modes-of-biomolecules/> for a tutorial.

Normal mode analysis : A light version of the previous element

- Authors: Sergey Grudinin, Alexandre Hoffmann and Yassine Naimi
- Partner: Inria
- Contact: Sergey Grudinin
- URL: <http://samson-connect.net>

5.23. SAMSON-SAXS

KEYWORDS: Algorithm - Bioinformatics - Structural Biology - Nanosystems - 3D - 3D modeling

FUNCTIONAL DESCRIPTION: The Pepsi-SAXS module rapidly computes small-angle X-ray scattering profiles. It is based on the spherical harmonics expansion method and interactively updates the fits if the molecular structure is modified. Multi-threading is currently only supported for Linux & macOS.

- Authors: Sergey Grudinin, Mariya Garkavenko and Mohamed Nadhir Ben Hadj Abdellatif
- Partner: Inria
- Contact: Sergey Grudinin
- URL: <https://samson-connect.net/app/main?key=element&uuid=844be03b-cab2-4420-464b-6f0f9384bc4a>

5.24. Ananas

Analytical Analyzer of Symmetries

KEYWORDS: Bioinformatics - Structural Biology

FUNCTIONAL DESCRIPTION: Analytical Analyzer of Symmetries is a software for detection and assessment of the quality of symmetry in a protein assembly.

This software can : Detect the best axes of symmetry for any symmetry group in an assembly containing the right amount of chains, Provide the symmetry-aware RMSD for these axes, Detect the best axis of symmetry for cyclic assemblies with missing subunits, Compute the axes of symmetry with user-provided correspondences.

- Participants: Guillaume Pages and Sergey Grudinin
- Contact: Sergey Grudinin
- Publications: [Analytical symmetry detection in protein assemblies. I. Cyclic symmetries](#) - [Analytical symmetry detection in protein assemblies. II. Dihedral and Cubic symmetries](#)
- URL: <https://team.inria.fr/nano-d/software/ananas/>

5.25. Pepsi-SAXS

KEYWORDS: Bioinformatics - Structural Biology - Data modeling

FUNCTIONAL DESCRIPTION: Pepsi-SAXS (PEPSI stands for Polynomial Expansions of Protein Structures and Interactions) is new implementation of the multipole-based scheme initially proposed by Stuhrmann (Stuhrmann, 1970). Overall, our method is significantly faster with a similar accuracy compared to Crysol, FoXS, and the 3D-Zernike implementation from the SAS2tbx package.

- Participant: Sergey Grudinin
- Partner: MIPT Moscow
- Contact: Sergey Grudinin
- Publication: [Pepsi-SAXS : an adaptive method for rapid and accurate computation of small-angle X-ray scattering profiles](#)
- URL: <https://team.inria.fr/nano-d/software/pepsi-saxs/>

5.26. NOLB

NON-Linear rigid Block NMA method

KEYWORDS: Structural Biology - Bioinformatics - Elasticity - Proteins - Motion analysis

FUNCTIONAL DESCRIPTION: It's a new conceptually simple and computationally efficient method for non-linear normal mode analysis of macromolecules.

- Participants: Sergey Grudinin and Alexandre Hoffmann
- Contact: Sergey Grudinin
- Publications: [NOLB: Nonlinear Rigid Block Normal Mode Analysis Method - RapidRMSD: Rapid determination of RMSDs corresponding to motions of flexible molecules](#)
- URL: <https://team.inria.fr/nano-d/software/nolb-normal-modes/>

5.27. SBROD

KEYWORDS: Bioinformatics - Machine learning

FUNCTIONAL DESCRIPTION: Smooth orientation-dependent scoring function (SBROD) for coarse-grained protein quality assessment uses only the conformation of the protein backbone, and hence it can be applied to scoring the coarse-grained protein models.

The workflow of SBROD consists in two stages. First, the method extracts features from each protein model in the dataset. Then, the scoring function assigns a score to each processed protein model depending on its features extracted at the first stage. Figure above schematically shows the workflow of SBROD. Here, four types of inter-atomic interactions, described in details below, are taken into account when extracting the features. After these features have been extracted and preprocessed, a Ridge Regression model is trained on them to predict the GDT-TS of protein models.

- Participants: Mikhail Karasikov, Guillaume Pages and Sergey Grudinin
- Contact: Sergey Grudinin
- Publication: [Smooth orientation-dependent scoring function for coarse-grained protein quality assessment](#)
- URL: <https://team.inria.fr/nano-d/software/sbrod/>

5.28. Ornate

KEYWORDS: Bioinformatics - Machine learning - Neural networks

FUNCTIONAL DESCRIPTION: Oriented Routed Neural network with Automatic Typing is a method for protein quality assessment. Ornat is a residue-wise scoring method. It first constructs a three dimensional map representing the structure of the residue, and its neighborhood.

- Participants: Guillaume Pages, BENOIT CHARMETTANT and Sergey Grudin
- Contact: Sergey Grudin
- Publication: [Protein model quality assessment using 3D oriented convolutional neural networks](#)
- URL: <https://team.inria.fr/nano-d/software/ornate/>

5.29. SAMSON-AR-LAMMPS

KEYWORDS: Algorithm - Molecular simulation - 3D modeling

- Authors: Sémého Edoh, Krishna Kant Singh and Dmitriy Marin
- Partner: Inria
- Contact: Stéphane Redon
- URL: <http://samson-connect.net>

NECS Project-Team

6. New Software and Platforms

6.1. GTL

Grenoble Traffic Lab

FUNCTIONAL DESCRIPTION: The Grenoble Traffic Lab (GTL) initiative, led by the NeCS team, is a real-time traffic data Center (platform) that collects traffic road infrastructure information in real-time with minimum latency and fast sampling periods. The main elements of the GTL are: a real-time data-base, a show room, and a calibrated micro-simulator of the Grenoble South Ring. Sensed information comes from a dense wireless sensor network deployed on Grenoble South Ring, providing macroscopic traffic signals such as flows, velocities, densities, and magnetic signatures. This sensor network was set in place in collaboration with Inria spin-off Karrus-ITS, local traffic authorities (DIR-CE, CG38, La Metro), and specialized traffic research centers. In addition to real data, the project also uses simulated data, in order to validate models and to test the ramp-metering, the micro-simulator is a commercial software (developed by TSS AIMSUN ©). More details at <http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php>

- Participants: Alain Kibangou, Andres Alberto Ladino Lopez, Anton Andreev, Carlos Canudas-De-Wit, Dominik Pisarski, Enrico Lovisari, Fabio Morbidi, Federica Garin, Hassen Fourati, Iker Bellicot, Maria Laura Delle Monache, Paolo Frasca, Pascal Bellemain, Pietro Grandinetti, Rémi Piotaix, Rohit Singhal and Vadim Bertrand
- Contact: Carlos Canudas-De-Wit
- URL: <http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php>

6.2. Benchmarks Attitude Smartphones

KEYWORDS: Experimentation - Motion analysis - Sensors - Performance analysis - Smartphone

SCIENTIFIC DESCRIPTION: We investigate the precision of attitude estimation algorithms in the particular context of pedestrian navigation with commodity smartphones and their inertial/magnetic sensors. We report on an extensive comparison and experimental analysis of existing algorithms. We focus on typical motions of smartphones when carried by pedestrians. We use a precise ground truth obtained from a motion capture system. We test state-of-the-art attitude estimation techniques with several smartphones, in the presence of magnetic perturbations typically found in buildings. We discuss the obtained results, analyze advantages and limits of current technologies for attitude estimation in this context. Furthermore, we propose a new technique for limiting the impact of magnetic perturbations with any attitude estimation algorithm used in this context. We show how our technique compares and improves over previous works.

- Participants: Hassen Fourati, Nabil Layaïda, Pierre Genevès and Thibaud Michel
- Partner: GIPSA-Lab
- Contact: Pierre Genevès
- URL: <http://tyrex.inria.fr/mobile/benchmarks-attitude/>

TRIPOP Team

5. New Software and Platforms

5.1. Platforms: SICONOS

5.1.1. Platform A : SICONOS

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

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

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

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

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

AIRSEA Project-Team

5. New Software and Platforms

5.1. AGRIF

Adaptive Grid Refinement In Fortran

KEYWORD: Mesh refinement

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

NEWS OF THE YEAR: In 2017, the multiresolution capabilities of the AGRIF software have been extended to be able to treat a much larger number of grids. In particular, the load balancing algorithms have been greatly improved.

- Participants: Roland Patoum and Laurent Debreu
- Contact: Laurent Debreu
- Publications: [Numerical and experimental approach for a better physical description of submesoscale processes : A north-western Mediterranean Sea case - AGRIF: Adaptive Grid Refinement in Fortran](#)
- URL: <http://www-ljk.imag.fr/MOISE/AGRIF>

5.2. BALAISE

Bibliothèque d'Assimilation Lagrangienne Adaptée aux Images Séquencées en Environnement

KEYWORDS: Multi-scale analysis - Data assimilation - Optimal control

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

- Contact: Patrick Vidard

5.3. NEMOVAR

Variational data assimilation for NEMO

KEYWORDS: Oceanography - Data assimilation - Adjoint method - Optimal control

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

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

5.4. Sensitivity

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

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

BEAGLE Project-Team

6. New Software and Platforms

6.1. aevol

Artificial Evolution

KEYWORDS: Bioinformatics - Genomics - Evolution

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

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

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

RELEASE FUNCTIONAL DESCRIPTION: Fix compilation error on Mac (tr1 included in std). The new mac compiler includes the tr1 directly in std which caused a compilation error. This issue was specific to aevol-4.4.1

- Participants: Antoine Frénoy, Bérénice Batut, Carole Knibbe, David Parsons, Dusan Misevic, Guillaume Beslon, Jonathan Rouzaud-Cornabas and Vincent Liard
- Partners: UCBL Lyon 1 - INSERM - Université Paris-Descartes - Insa de Lyon
- Contact: Guillaume Beslon
- URL: <http://www.aevol.fr/>

6.2. DeCoSTAR

KEYWORDS: Bioinformatics - Evolution

FUNCTIONAL DESCRIPTION: DeCoSTAR reconstructs ancestral genomes and improves the assembly of extant genomes. It takes as input a set of gene trees, a species tree and adjacency relations between extant genes. It outputs ancestral genes, adjacencies between extant and ancestral genes, and a statistical support associated to each inferred adjacency.

NEWS OF THE YEAR: Publication of the software with several test sets in Genome Biology and Evolution

- Participants: Eric Tannier and Wandrille Duchemin
- Contact: Eric Tannier
- Publication: [hal-01503766](https://hal.archives-ouvertes.fr/hal-01503766)
- URL: <http://pbil.univ-lyon1.fr/software/DeCoSTAR/>

6.3. Evo2Sim

Evolution of Evolution Simulator

KEYWORDS: Bioinformatics - Biology - Evolution

FUNCTIONAL DESCRIPTION: In the context of the EvoEvo european project we developed an integrated model of microorganisms evolution. This model extends the evolutionary models developed in the team (Aevol and R-Aevol) by adding a metabolic level and an ecosystem level. It includes the genomic, genetic and metabolic levels.

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

6.4. evowave

KEYWORDS: Data stream - Clustering - Evolution - Wireless network

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

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

6.5. FluoBacTracker

KEYWORDS: Bioinformatics - Biology - Biomedical imaging

SCIENTIFIC DESCRIPTION: FluoBacTracker is an ImageJ plugin allowing the segmentation and tracking of growing bacterial cells from time-lapse microscopy movies. The segmentation and tracking algorithms used by FluoBacTracker have been developed by Lionel Moisan and colleagues at Université Paris Descartes.

FUNCTIONAL DESCRIPTION: FluoBacTracker has the following functionalities: 1) Select regions of interest in images of microcolonies 2) Denoise and renormalize the images 3) Identify each cells in each image (segmentation) 4) Follow cells through the whole movie (tracking), including the detection of cells washed out from a microfluidics channel 5) Detect divisions and construct cell lineage of the population

NEWS OF THE YEAR: Version 2 of FluoBacTracker also allows the analysis of microscopy of bacteria growing in a microfluidics device called "mother machine".

- Participants: Hugues Berry, Cyril Dutrieux, Hidde De Jong, Charles Kervrann, David Parsons and Magali Vangkeosay
- Partners: Université Descartes - UGA
- Contact: Hugues Berry
- URL: <http://fluobacktracker.inrialpes.fr>

6.6. Tewep

Simulator of the dynamics of Transposable Elements Within Expanding Populations

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

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

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

6.7. Treerecs

KEYWORDS: Bioinformatics - Biology - Computational biology

SCIENTIFIC DESCRIPTION: The reconciliation between gene trees and species trees is a modern method of molecular phylogeny, which does not yet have its standard software, as for example phylogeny from DNA or amino acid sequences. Treerecs has this ambition, incorporating the classic functionalities of reconciliation: annotating the vertices of a gene tree with the tops of a species tree, rooting and correcting the gene tree. Rooting and correction are calculated to minimize the number of duplications and losses in reconciliation. Medium-sized solutions are randomly sampled according to a uniform law. A likelihood can then be calculated using probabilistic methods. In addition, Treerecs is integrated into a standard software ecosystem of phylogeny, bio ++, ALE, Seaview, and has a graphical interface. Some original features are implemented, such as the possibility of combining two types of likelihoods, the one calculated from the sequences and the one calculated from the reconciliations, the possibility of estimating the costs of the evolutionary events, the possibility of exploring the space of trees according to a joined likelihood.

FUNCTIONAL DESCRIPTION: Treerecs takes as minimum input a gene tree and a species tree. It "reconciles" them, that is, it annotates gene tree nodes with events and assign them to species tree nodes. Biologically, it is a reconstruction of the gene history, given the species history, in terms of duplications, speciations, losses.

With the appropriate options Treerecs can root and correct the gene tree.

NEWS OF THE YEAR: Release of a 0.1 stable version

- Participants: Nicolas Comte, David Parsons, Eric Tannier and Benoît Morel
- Partner: Laboratoire de Biométrie et Biologie Evolutive (LBBE) - UMR CNRS 5558
- Contact: Eric Tannier

6.8. EvoMove

KEYWORDS: Music - Improvisation - Clustering - Evolution - Evolutionary Algorithms

FUNCTIONAL DESCRIPTION: EvoMove uses data from Inertial Measurement Units carried by dancers. It classifies these data in a non-supervised way to recognise "moves" and from these triggers music samples that accompany the dancers.

- Contact: Guillaume Beslon

DRACULA Project-Team

4. New Software and Platforms

4.1. CelDyn

KEYWORDS: Modeling - Bioinformatics - Biology

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

- Participants: Alen Tosenberger, Laurent Pujo-Menjouet, Nikolai Bessonov and Vitaly Volpert
- Contact: Vitaly Volpert

ERABLE Project-Team

5. New Software and Platforms

5.1. C3Part/Isofun

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: The C3PART / ISOFUN package implements a generic approach to the local alignment of two or more graphs representing biological data, such as genomes, metabolic pathways or protein-protein interactions, in order to infer a functional coupling between them.

- Participants: Alain Viari, Anne Morgat, Frédéric Boyer, Marie-France Sagot and Yves-Pol Deniérou
- Contact: Alain Viari
- URL: <http://www.inrialpes.fr/helix/people/viari/lxgraph/index.html>

5.2. Cassis

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: Implements methods for the precise detection of genomic rearrangement breakpoints.

- Participants: Christian Baudet, Christian Gautier, Claire Lemaitre, Eric Tannier and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: <http://pbil.univ-lyon1.fr/software/Cassis/>

5.3. Coala

CO-evolution Assessment by a Likelihood-free Approach

KEYWORDS: Bioinformatics - Evolution

SCIENTIFIC DESCRIPTION: Despite an increasingly vaster literature on cophylogenetic reconstructions for studying host-parasite associations, understanding the common evolutionary history of such systems remains a problem that is far from being solved. Many of the most used algorithms do the host-parasite reconciliation analysis using an event-based model, where the events include in general (a subset of) cospeciation, duplication, loss, and host-switch. All known event-based methods then assign a cost to each type of event in order to find a reconstruction of minimum cost. The main problem with this approach is that the cost of the events strongly influence the reconciliation obtained.

To deal with this problem, we developed an algorithm, called Coala, for estimating the frequency of the events based on an approximate Bayesian computation approach.

FUNCTIONAL DESCRIPTION: COALA stands for “COevolution Assessment by a Likelihood-free Approach”. It is thus a likelihood-free method for the co-phylogeny reconstruction problem which is based on an Approximate Bayesian Computation (ABC) approach.

- Participants: Beatrice Donati, Blerina Sinimeri, Catherine Matias, Christian Baudet, Christian Gautier, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinimeri
- URL: <http://coala.gforge.inria.fr/>

5.4. CSC

KEYWORDS: Genomics - Algorithm

FUNCTIONAL DESCRIPTION: Given two sequences x and y , CSC (which stands for Circular Sequence Comparison) finds the cyclic rotation of x (or an approximation of it) that minimises the blockwise q -gram distance from y .

- Contact: Nadia Pisanti
- URL: <https://github.com/solonas13/csc>

5.5. Cycads

KEYWORDS: Systems Biology - Bioinformatics

FUNCTIONAL DESCRIPTION: Annotation database system to ease the development and update of enriched BIOCYC databases. CYCADS allows the integration of the latest sequence information and functional annotation data from various methods into a metabolic network reconstruction. Functionalities will be added in future to automate a bridge to metabolic network analysis tools, such as METEXPLORE. CYCADS was used to produce a collection of more than 22 arthropod metabolism databases, available at ACYPICYC (<http://acypicyc.cycadsys.org>) and ARTHROPODACYC (<http://arthropodacyc.cycadsys.org>). It will continue to be used to create other databases (newly sequenced organisms, Aphid biotypes and symbionts...).

- Participants: Augusto Vellozo, Hubert Charles, Marie-France Sagot and Stefano Colella
- Contact: Hubert Charles
- URL: <http://www.cycadsys.org/>

5.6. DBGWAS

KEYWORDS: Graph algorithmics - Genomics

FUNCTIONAL DESCRIPTION:DBGWAS is a tool for quick and efficient bacterial GWAS. It uses a compacted De Bruijn Graph (cDBG) structure to represent the variability within all bacterial genome assemblies given as input. Then cDBG nodes are tested for association with a phenotype of interest and the resulting associated nodes are then re-mapped on the cDBG. The output of DBGWAS consists of regions of the cDBG around statistically significant nodes with several informations related to the phenotypes, offering a representation helping in the interpretation. The output can be viewed with any modern web browser, and thus easily shared.

- Contact: Leandro Ishi Soares De Lima
- URL: <https://gitlab.com/leosl/dbgwas>

5.7. Eucalypt

KEYWORDS: Bioinformatics - Evolution

FUNCTIONAL DESCRIPTION:EUCALYPT stands for “EnUmerator of Coevolutionary Associations in PoLYnomial-Time delay”. It is an algorithm for enumerating all optimal (possibly time-unfeasible) mappings of a symbiont tree unto a host tree.

- Participants: Beatrice Donati, Blerina Sinimeri, Christian Baudet, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinimeri
- URL: <http://eucalypt.gforge.inria.fr/>

5.8. Fast-SG

KEYWORDS: Genomics - Algorithm - NGS

FUNCTIONAL DESCRIPTION:FAST-SG enables the optimal hybrid assembly of large genomes by combining short and long read technologies.

- Contact: Alex Di Genova
- URL: <https://github.com/adigenova/fast-sg>

5.9. Gobbolino-Touché

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: 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.

- Participants: Etienne Birmelé, Fabien Jourdan, Ludovic Cottret, Marie-France Sagot, Paulo Vieira Milreu, Pierluigi Crescenzi, Vicente Acuna Aguayo and Vincent Lacroix
- Contact: Marie-France Sagot
- URL: <http://gforge.inria.fr/projects/gobbolino>

5.10. HapCol

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: A fast and memory-efficient DP approach for haplotype assembly from long reads that works until 25x coverage and solves a constrained minimum error correction problem exactly.

- Contact: Nadia Pisanti
- URL: <http://hapcol.algolab.eu/>

5.11. HgLib

HyperGraph Library

KEYWORDS: Graph algorithmics - Hypergraphs

FUNCTIONAL DESCRIPTION: The open-source library hglib is dedicated to model hypergraphs, which are a generalisation of graphs. In an **undirected** hypergraph, an hyperedge contains any number of vertices. A **directed** hypergraph has hyperarcs which connect several tail and head vertices. This library, which is written in C++, allows to associate user defined properties to vertices, to hyperedges/hyperarcs and to the hypergraph itself. It can thus be used for a wide range of problems arising in operations research, computer science, and computational biology.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Participants: Martin Wannagat, David Parsons, Arnaud Mary and Irene Ziska
- Contact: Arnaud Mary
- URL: <https://gitlab.inria.fr/kirikomics/hglib>

5.12. KissDE

KEYWORDS: Bioinformatics - NGS

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

RELEASE FUNCTIONAL DESCRIPTION: This new version improved the recall and made more precise the size of the effect computation.

- Participants: Camille Marchet, Aurélie Siberchicot, Audric Cologne, Clara Benoît-Pilven, Janice Kielbassa, Lilia Brinza and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: <http://kisssplice.prabi.fr/tools/kissDE/>

5.13. KisSplice

KEYWORDS: Bioinformatics - Bioinformatics search sequence - Genomics - NGS

FUNCTIONAL DESCRIPTION: Enables to analyse RNA-seq data with or without a reference genome. It is an exact local transcriptome assembler, which can identify SNPs, indels and alternative splicing events. It can deal with an arbitrary number of biological conditions, and will quantify each variant in each condition.

RELEASE FUNCTIONAL DESCRIPTION: Improvements : KissReads module has been modified and sped up, with a significant impact on run times. Parameters : `-timeout` default now at 10000: in big datasets, recall can be increased while run time is a bit longer. Bugs fixed : Reads containing only 'N': the graph construction was stopped if the file contained a read composed only of 'N's. This is was a silence bug, no error message was produced. Problems compiling with new versions of MAC OSX (10.8+): KisSplice is now compiling with the new default C++ compiler of OSX 10.8+.

- Participants: Alice Julien-Laferrière, Leandro Ishi Soares De Lima, Vincent Miele, Rayan Chikhi, Pierre Peterlongo, Camille Marchet, Gustavo Akio Tominaga Sacomoto, Marie-France Sagot and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: <http://kisssplice.prabi.fr/>

5.14. KisSplice2RefGenome

KEYWORDS: Bioinformatics - NGS - Transcriptomics

FUNCTIONAL DESCRIPTION: KISSPLICE identifies variations in RNA-seq data, without a reference genome. In many applications however, a reference genome is available. KISSPLICE2REFGENOME enables to facilitate the interpretation of the results of KISSPLICE after mapping them to a reference genome.

- Participants: Audric Cologne, Camille Marchet, Camille Sessegolo, Alice Julien-Laferrière and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: <http://kisssplice.prabi.fr/tools/kiss2refgenome/>

5.15. KisSplice2RefTranscriptome

KEYWORDS: Bioinformatics - NGS - Transcriptomics

FUNCTIONAL DESCRIPTION: KISSPLICE2REFTRANSCRIPTOME enables to combine the output of KISSPLICE with the output of a full length transcriptome assembler, thus allowing to predict a functional impact for the positioned SNPs, and to intersect these results with condition-specific SNPs. Overall, starting from RNA-seq data only, we obtain a list of condition-specific SNPs stratified by functional impact.

- Participants: Helene Lopez Maestre, Mathilde Boutigny and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: <http://kisssplice.prabi.fr/tools/kiss2rt/>

5.16. MetExplore

KEYWORDS: Systems Biology - Bioinformatics

SCIENTIFIC DESCRIPTION: MetExplore stores metabolic networks of 160 organisms into a relational database. Information about metabolic networks mainly come from BioCyc-like databases. Two BioCyc-like databases contain information about several organisms: PlantCyc and MetaCyc. MetExplore contains also the information about metabolites stored in Metabolome.jp. Note that there is no information about reactions in this database and is only useful to identify compounds from masses. Several genome-scale models designed for Flux Balance Analysis have also been imported into MetExplore. The table below gives details about the sources of the metabolic networks present in MetExplore.

FUNCTIONAL DESCRIPTION: Web-server that allows to build, curate and analyse genome-scale metabolic networks. METEXPLORE is also able to deal with data from metabolomics experiments by mapping a list of masses or identifiers onto filtered metabolic networks. Finally, it proposes several functions to perform Flux Balance Analysis (FBA). The web-server is mature, it was developed in PHP, JAVA, Javascript and Mysql. METEXPLORE was started under another name during Ludovic Cottret's PhD in Bamboo, and is now maintained by the METEXPLORE group at the Inra of Toulouse.

- Participants: Fabien Jourdan, Hubert Charles, Ludovic Cottret and Marie-France Sagot
- Contact: Fabien Jourdan
- URL: <https://metexplore.toulouse.inra.fr/index.html/>

5.17. Mirinho

KEYWORDS: Bioinformatics - Computational biology - Genomics - Structural Biology

FUNCTIONAL DESCRIPTION: Predicts, at a genome-wide scale, microRNA candidates.

- Participants: Christian Gautier, Christine Gaspin, Cyril Fournier, Marie-France Sagot and Susan Higashi
- Contact: Marie-France Sagot
- URL: <http://mirinho.gforge.inria.fr/>

5.18. Momo

Multi-Objective Metabolic mixed integer Optimization

KEYWORDS: Metabolism - Metabolic networks - Multi-objective optimisation

FUNCTIONAL DESCRIPTION: MOMO is a multi-objective mixed integer optimisation approach for enumerating knockout reactions leading to the overproduction and/or inhibition of specific compounds in a metabolic network.

- Contact: Marie-France Sagot
- URL: <http://momo-sysbio.gforge.inria.fr>

5.19. MultiPus

KEYWORDS: Systems Biology - Algorithm - Graph algorithmics - Metabolic networks - Computational biology

SCIENTIFIC DESCRIPTION: Synthetic biology has boomed since the early 2000s when it started being shown that it was possible to efficiently synthesise compounds of interest in a much more rapid and effective way by using other organisms than those naturally producing them. However, to thus engineer a single organism, often a microbe, to optimise one or a collection of metabolic tasks may lead to difficulties when attempting to obtain a production system that is efficient, or to avoid toxic effects for the recruited microorganism. The idea of using instead a microbial consortium has thus started being developed in the last decade. This was motivated by the fact that such consortia may perform more complicated functions than could single populations and be more robust to environmental fluctuations. Success is however not always guaranteed. In particular, establishing which consortium is best for the production of a given compound or set thereof remains a great challenge. The algorithm MultiPus is based on an initial model that enables to propose a consortium to synthetically produce compounds that are either exogenous to it, or are endogenous but where interaction among the species in the consortium could improve the production line.

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

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

5.20. Pitufolandia

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: The algorithms in PITUFOLANDIA (PITUFO / PITUFINA / PAPAITUFO) are designed to solve the minimal precursor set problem, which consists in finding all minimal sets of precursors (usually, nutrients) in a metabolic network that are able to produce a set of target metabolites.

- Contact: Marie-France Sagot
- URL: <http://gforge.inria.fr/projects/pitufo/>

5.21. Sasita

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION:SASITA is a software for the exhaustive enumeration of minimal precursor sets in metabolic networks.

- Contact: Marie-France Sagot
- URL: <http://sasita.gforge.inria.fr/>

5.22. Savage

KEYWORDS: Algorithm - Genomics

FUNCTIONAL DESCRIPTION: Reconstruction of viral quasi species without using a reference genome.

- Contact: Alexander Schonhuth
- URL: <https://bitbucket.org/jbaaijens/savage>

5.23. Smile

KEYWORDS: Bioinformatics - Genomic sequence

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

- Participant: Marie-France Sagot
- Contact: Marie-France Sagot

5.24. Rime

KEYWORDS: Bioinformatics - Genomics - Sequence alignment

FUNCTIONAL DESCRIPTION: Detects long similar fragments occurring at least twice in a set of biological sequences.

- Contact: Nadia Pisanti

5.25. Totoro & Kotoura

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: Both TOTORO and KOTOURA decipher the reaction changes during a metabolic transient state, using measurements of metabolic concentrations. These are called metabolic hyperstories. TOTORO (for TOpological analysis of Transient metabOlic RespOnse) is based on a qualitative measurement of the concentrations in two steady-states to infer the reaction changes that lead to the observed differences in metabolite pools in both conditions. In the currently available release, a pre-processing and a post-processing steps are included. After the post-processing step, the solutions can be visualised using DINGHY (<http://dinghy.gforge.inria.fr>). KOTOURA (for Kantitative analysis Of Transient metabOlic and regUlatory Response And control) infers quantitative changes of the reactions using information on measurement of the metabolite concentrations in two steady-states.

- Contact: Marie-France Sagot
- URL: <http://hyperstories.gforge.inria.fr/>

5.26. WhatsHap

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: WHATSHAP is a DP approach for haplotype assembly from long reads that works until 20x coverage and solves the minimum error correction problem exactly. PWHATSHAP is a parallelisation of the core dynamic programming algorithm of WHATSHAP.

- Contact: Nadia Pisanti
- URL: <https://bitbucket.org/whatschap/whatschap>

IBIS Project-Team

5. New Software and Platforms

5.1. WellFARE

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling

SCIENTIFIC DESCRIPTION: WellFARE is a Python library implementing linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. WellFARE form the computational core of the WellInverter web application.

FUNCTIONAL DESCRIPTION: As input, WellFARE reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various functions exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. WellFARE is the computational core of the web application WellInverter.

NEWS OF THE YEAR: Submission of a journal publication describing the new version of WellInverter and WellFARE

- Participants: Delphine Ropers, Hans Geiselmann, Hidde De Jong, Michel Page, Valentin Zulkower and Yannick Martin
- Partner: UGA
- Contact: Hidde De Jong
- Publication: [Robust reconstruction of gene expression profiles from reporter gene data using linear inversion](#)
- URL: <https://github.com/ibis-inria/welfare>

5.2. WellInverter

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling

SCIENTIFIC DESCRIPTION: WellInverter is a web application that implements linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. WellInverter makes the methods available to a broad audience of biologists and bioinformaticians. In particular, we have put in place a parallel computing architecture with a load balancer to distribute the analysis queries over several back-end servers, redesigned the graphical user interface, and developed a plug-in system for defining high-level routines for parsing data files produced by microplate readers from different manufacturers.

FUNCTIONAL DESCRIPTION: As input, WellInverter reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various modules exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. The computational core of the web application consists of the Python library WellFARE.

NEWS OF THE YEAR: Deployment of WellInverter on an Inria server and on the new cloud of the French Institute for Bioinformatics (see the web page for details). Submission of a journal article describing the new version of the application.

- Participants: Delphine Ropers, Hans Geiselmann, Hidde De Jong, Johannes Geiselmann, Michel Page, Valentin Zulkower and Yannick Martin
- Partner: UGA
- Contact: Hidde De Jong
- Publication: [Robust reconstruction of gene expression profiles from reporter gene data using linear inversion](#)
- URL: <https://team.inria.fr/ibis/wellinverter/>

5.3. FluoBacTracker

KEYWORDS: Bioinformatics - Biology - Biomedical imaging

SCIENTIFIC DESCRIPTION: FluoBacTracker is an ImageJ plugin allowing the segmentation and tracking of growing bacterial cells from time-lapse microscopy movies. The segmentation and tracking algorithms used by FluoBacTracker have been developed by Lionel Moisan and colleagues at Université Paris Descartes.

FUNCTIONAL DESCRIPTION: FluoBacTracker has the following functionalities: 1) Select regions of interest in images of microcolonies 2) Denoise and renormalize the images 3) Identify each cells in each image (segmentation) 4) Follow cells through the whole movie (tracking), including the detection of cells washed out from a microfluidics channel 5) Detect divisions and construct cell lineage of the population

NEWS OF THE YEAR: Version 2 of FluoBacTracker also allows the analysis of microscopy of bacteria growing in a microfluidics device called "mother machine".

- Participants: Hugues Berry, Cyril Dutrieux, Hidde De Jong, Charles Kervrann, David Parsons and Magali Vangkeosay
- Partners: Université Descartes - UGA
- Contact: Hugues Berry
- URL: <http://fluobacktracker.inrialpes.fr>

5.4. GNA

Genetic Network Analyzer

KEYWORDS: Model Checking - Bioinformatics - Gene regulatory networks - Qualitative simulation

SCIENTIFIC DESCRIPTION: Genetic Network Analyzer (GNA) is the implementation of methods for the qualitative modeling and simulation of gene regulatory networks developed in the IBIS project-team.

FUNCTIONAL DESCRIPTION: 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.

RELEASE FUNCTIONAL DESCRIPTION: (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.

NEWS OF THE YEAR: New mode of distribution from the IBIS web site.

- Participants: Hidde De Jong, Michel Page and Delphine Ropers
- Partner: UGA
- Contact: Hidde De Jong
- Publications: [Genetic Network Analyzer: A Tool for the Qualitative Modeling and Simulation of Bacterial Regulatory Networks - Piecewise linear approximations to model the dynamics of adaptation to osmotic stress by food-borne pathogens](#)
- URL: <http://www-helix.inrialpes.fr/gna>

MOSAIC Team

5. New Software and Platforms

5.1. treex

KEYWORDS: Graph algorithmics - Data structures - Combinatorics

SCIENTIFIC DESCRIPTION: Trees form an expanded family of combinatorial objects that offers a wide range of application fields, especially in biology, from plant modeling to blood vessels network analysis through study of lineages. Consequently, it is crucial for the team to develop numerical tools and algorithms for processing tree data, in particular to answer questions about the representation of biological organisms and their forms in silico.

treex is a Python 3 library dedicated to the manipulation of tree objects, whatever they are ordered or not, with or without quantitative or qualitative labels.

FUNCTIONAL DESCRIPTION: treex is a Python library for manipulating rooted trees. The trees can be ordered or not, with or without labels on their vertices.

The package provides a data structure for rooted trees as well as the following main functionalities: - Random generation algorithms - DAG compression for ordered or not, labeled or not, trees - Approximation algorithms for unordered trees - Edit distance for unordered labeled trees - Computation of coding processes (Harris path, Lukasiewicz walk and height process) - Visualization algorithms in Matplotlib or in LaTeX

Representations of trees. With treex, we aim to propose all the standard representations of trees as well as the one-to-one correspondences between them. Main coding processes (Harris path, Lukasiewicz walk, and height process), DAG representation, doubly-chained tree structures have been already coded. Standard exploration algorithms and editing methods have also been developed. Through these generic tools, treex enables the manipulation of trees from various application contexts.

Easy-to-use. We think that treex must be user-friendly to be adopted by collaborators from fields of biology. To this end, we develop high-level algorithms and provide an extensive documentation (with sphinx) as well as a simple installation method through conda.

Algorithms. The current version of treex provides edit distance algorithms, approximation algorithms (that can be used to control the complexity of the edit distance algorithms), and visualization algorithms (with an interface for TEX / LATEX and Matplotlib). A first statistical learning module is in progress.

RELEASE FUNCTIONAL DESCRIPTION: The first release of treex happened in the late 2018 after an intensive work to ease both installation and handling. A publication on treex is planned for the next early year. In addition, treex will be integrated in Gnomon in the following months.

NEWS OF THE YEAR: The first release of treex happened in the late 2018 after an intensive work to ease both installation and handling. A publication on treex is planned for the next early year. In addition, treex will be integrated in Gnomon in the following months.

- Participants: Romain Azais, Guillaume Cerutti, Didier Gemmerle and FLORIAN INGELS
- Contact: Romain Azais
- URL: <https://gitlab.inria.fr/azais/treex>

5.2. Gnomon

KEYWORDS: 4D - Modelization and numerical simulations - Finite element modelling - Computational biology - Data visualization

SCIENTIFIC DESCRIPTION: Gnomon is a user-friendly computer platform developed by the Mosaic team for seamless simulation of form development *in silico*. It is intended to be a major tool for the team members to develop, integrate and share their models, algorithms and tools. In Gnomon, a developing form is represented at any time by a central data-structure that contains topological, geometric, genetic and physiological information and that represents the state of the growing form. Flexible components (plugins) make it possible to up-load or to create such data-structures, to program their development, to analyze, visualize them and interact with them in 3D+time.

FUNCTIONAL DESCRIPTION: Gnomon is developed based on the past experience of the team with the OpenAlea platform, but moving towards a more scalable software engineering solution based on the dtk kernel developed by the group of software engineers (SED) from the Sophia-Antipolis Inria Center. Gnomon development uses extensively an agile methodology and emphasizes three main aspects:

Deployable and extensible software architecture. The Gnomon platform is intended to become a perennial common resource for the members of the team as well as a tool to easily diffuse our methods to collaborators. It is a plugin-based architecture, relying on the dtk meta-platform developed by the SED at Inria Sophia-Antipolis. dtk eases the conception of a high-level C++ environment inside which added-value components are injected autonomously by the team members as Python plugins wrapping our scientific libraries. A significant effort is put on the packaging and deployability of this software (using conda), adding up unit testing, continuous integration and cross-platform installation.

Exploration of forms. The environment will provide tools to create and visualize forms, and explore them in space and time. Building on the algorithmic resources developed by the team for image sequences of multicellular tissues, user-friendly interfaces are being designed for the exploration of such structures. This gives the user the possibility to reconstruct computational representations from experimental data in an intuitive way, and to explore these spatio-temporal data in an interactive and visual manner.

Integrated form simulation framework. Within a general framework for the modeling of dynamical systems that the team is developing, a core component is the mechanical simulation engine that will handle the resolution of physical equations controlling form development. We want the simulation framework to be integrated within the Gnomon platform in a nearly transparent way for the user. To achieve this, we develop a high-level interface for a generic differential equation solver based on the *fenics* FEM library. Mapping the general concepts of morphogenesis modeling to this engine will allow the user to specify behavior rules of the system at high-level and easily design simulation scenarios directly in the Gnomon application.

Gnomon project organization:

- Project leader: Christophe Godin
- Software development coordinator: Guillaume Cerutti
- DTK backend coordinator: Thibaud Kloczko
- Plugin coordinators: Jonathan Legrand (TimageTK), treex (Romain Azais), Olivier Ali (Mechanics), Frédéric Boudon (L-Systems).
- Diffusion to end-users: Teva Vernoux

This work is part of the *Gnomon* ADT project supported by the Inria centers of Grenoble Rhône-Alpes and Sophia-Antipolis Méditerranée.

RELEASE FUNCTIONAL DESCRIPTION: A first, fully functional, prototype of the Gnomon software platform, dedicated to the modeling and simulation of plant and animal morphogenesis, was developed during a series of intensive coding sessions in Lyon and Sophia-Antipolis. This new concept of platform dedicated to the study of morphogenesis was presented in November 2018 to a panel of modelers and biologists at the RDP lab, who will contribute next year to the further testing and refining the platform. This prototype is a clear milestone and results from a strong collaboration between the Inria software engineering group from Sophia-Antipolis (who provides the software architecture kernel - DTK)) and the Mosaic team and is supported by Inria (Action de Développement Technologique, ADT).

NEWS OF THE YEAR: A first, fully functional, prototype of the Gnomon software platform, dedicated to the modeling and simulation of plant and animal morphogenesis, was developed during a series of intensive coding sessions in Lyon and Sophia-Antipolis. This new concept of platform dedicated to the study of morphogenesis was presented in November 2018 to a panel of modelers and biologists at the RDP lab, who will contribute next year to the further testing and refining the platform. This prototype is a clear milestone and results from a strong collaboration between the Inria software engineering group from Sophia-Antipolis (who provides the software architecture kernel - DTK)) and the Mosaic team and is supported by Inria (Action de Développement Technologique, ADT).

- Participants: Olivier Ali, Frédéric Boudon, Guillaume Cerutti, FLORIAN GACON, Christophe Godin, Jonathan Legrand and Grégoire Malandain
- Contact: Christophe Godin

5.3. TimageTK: a Python package for image processing of multicellular architectures

Participants: Frédéric Boudon [External Collaborator], Guillaume Cerutti, Christophe Godin, Jonathan Legrand, Grégoire Malandain [External Collaborator].

- Related Research Works: **RA1** (*Representations of forms in silico*) & **RA2** (*Data-driven models*) & **RA3** (*Plasticity and robustness of forms*)
- Related Key Modeling Challenges: **KMC3** (*Realistic integrated digital models*)

Processing images of multicellular tissue architectures in plants and animals present difficult computational challenges, notably when dealing with heterogeneous data sources, temporal data. As for now, only limited computational tools exist to analyze these types of images efficiently. Based on our initial experience with the development of MARS-ALT, a pipeline for segmenting and tracking cell lineages, we have recently redesigned our software in order to develop a new high-level Python package named Tissue image ToolKit (TimageTK).

C/Python library. TimageTK is written in Python and is largely built on top of a C library (VT) developed by the Morpheme Inria team. Part of the C library was developed for MARS-ALT software by the Morpheme team. TimageTK provides high-level wrapping of these algorithms with additional functionalities directly written in Python, such as cell tracking.

Well documented, high-level image processing. TimageTK offer high-level methods, where few parameters are required to tune algorithms. They offer a safer use of function through well documented class methods. For experts in image processing, low-level functions and wrappings of C-functions are still accessible.

Easy deployment. TimageTK has simple and robust installation procedure based on conda (Conda is a package and environment management system that runs on Windows, macOS and Linux and allows to get rid of most installation issues, such as compilation or dependency errors). For now only macOSX and Linux version are packaged (x64 architecture) using Inria continuous integration tools.

Continuous integration. Using Inria continuous integration tools, TimageTK is regularly released through conda packaging mechanism. We also make use of these resources to regularly generate (sphinx) and publish updates in the documentation.

Compatibility with Gnomon. TimageTK is based on data structures representing images that are fully compatible with Gnomon. This makes it possible to use TimageTK as a plugin of the Gnomon software.

NUMED Project-Team

4. New Software and Platforms

4.1. Bingham flows

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

- Contact: Emmanuel Grenier

4.2. OptimChemo

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

- Participants: Ehouarn Maguet, Emmanuel Grenier, Paul Vigneaux and Violaine Louvet
- Contact: Emmanuel Grenier

4.3. SETIS

KEYWORDS: Health - DICOM - Medical imaging - Drug development

FUNCTIONAL DESCRIPTION: SETIS software is a GUI allowing to treat DICOM medical images to extract pathological data. These data can then be exported and used in a SAEM software (including Monolix (Inria & Lixoft)) for the parameters' estimation of models in the context of population approaches. As an example SETIS can be used to segment and compute the tumor size of a patients from MRI scans taken at different times. The software is sufficiently general to be used in various situations by clinicians (already done by colleagues in Lyon Hospital).

- Participants: Ehouarn Maguet and Paul Vigneaux
- Partner: ENS Lyon
- Contact: Paul Vigneaux

4.4. SIMPHYT

KEYWORDS: Bioinformatics - Cancer - Drug development

FUNCTIONAL DESCRIPTION: SimPHYt is an implementation in Python of the low grad glioma model. The aim is to predict the evolution of the glioma size of patients.

- Participant: Benjamin Ribba
- Contact: Benjamin Ribba

4.5. SITLOG

- Participants: Benjamin Ribba and Morgan Martinet
- Contact: Emmanuel Grenier

4.6. VAXSIMSTAB

KEYWORDS: Bioinformatics - Health - Drug development

FUNCTIONAL DESCRIPTION: VAXSIMSTAB is a modeler stability prediction of vaccine software.

- Participants: Benjamin Ribba, Emmanuel Grenier and Vincent Calvez
- Contact: Benjamin Ribba

STEPP Project-Team

5. New Software and Platforms

5.1. Software tools for the TRANUS LUTI Model

KEYWORDS: Urban planning - Transport model - LUTI

FUNCTIONAL DESCRIPTION: This year, we have consolidated and extended our software tools for the TRANUS LUTI model, thanks to support by Inria allowing to hire an engineer for one year Emna Jribi (ADT TRACAV project). Various tasks have been accomplished, concerning three types of functionality, these are as follows. First, calibration of TRANUS. The software implementation of our methods for calibrating the TRANUS land-use component has been cleaned up. It has been encapsulated such as to be seamlessly integrated within the TRANUS workflow (consisting of a sequence of executables, exchanging data through binary and other files). Second, graphical user interfaces to facilitate the repeated execution of TRANUS executables, for generating reports on results or for the exploration of the space of some critical model parameters. Third, we have continued to work on the embedding of TRANUS within the open source QGIS platform (a widely used Geographic Information System).

- Participants: Emna Jribi, Thomas Capelle and Peter Sturm
- Contact: Peter Sturm
- URL: <https://gitlab.inria.fr/tranus>

5.2. USAT

Urban Sprawl Analysis Toolkit

KEYWORDS: Urban sprawl - Urban planning

FUNCTIONAL DESCRIPTION: This software allows to calculate and analyse indices of urban sprawl from open data (OpenStreetMap), aimed to be used by urban scientists and urban planners. A spatialized version of indices measuring the accessibility, dispersion and land use mix is calculated. The implemented methods are described in [9].

- Participants: Luciano Gervasoni, Serge Fenet and Peter Sturm
- Partner: LIRIS
- Contact: Peter Sturm
- URL: <https://github.com/lgervasoni/urbansprawl>

5.3. USAT WEB

Urban Sprawl Analysis Toolkit Web-service

KEYWORDS: Urban planning - Urban sprawl

FUNCTIONAL DESCRIPTION: This is a web-service on top of the software USAT described above. The web-service will allow any user to select a region of interest and to launch the calculation and display of sprawl indices using USAT. It is in the process of being hosted on the HPC platform of IN2P3, after which it will be made open to the public. The source code for this web-service is already available at the below site.

The web-service is described in [10].

- Participants: Lucas Rezakhanlou, Peter Sturm, Luciano Gervasoni and Serge Fenet
- Contact: Peter Sturm
- Publication: [USAT \(Urban Sprawl Analysis Toolkit\) : une plateforme web d'analyse de l'étalement urbain à partir de données massives ouvertes](#)
- URL: <https://gitlab.inria.fr/lrezakha/usat-web>

5.4. InterfacesTRANUS

FUNCTIONAL DESCRIPTION: This software contains two interfaces dedicated to facilitating the usage of the TRANUS integrated land use and transport model+software. The first interface is dedicated to enabling the execution of the TRANUS binary programs without the need to use the console or the TRANUS GUI. The second interface provides an aid for calibrating a TRANUS model, by interactively exploring ranges of different parameters of a TRANUS model and visualising model outputs across these ranges.

- Participants: Julien Armand, Peter Sturm and Thomas Capelle
- Contact: Peter Sturm
- URL: https://gitlab.inria.fr/tranus/TRANUS_Interfaces

5.5. LUM_OSM

Land Use Mix calculation from OpenStreepMap data

FUNCTIONAL DESCRIPTION: The software uses Mapzen Metro Extracts to retrieve the OpenStreetMap data of a given region in the PostgreSQL format. Afterwards, a continuous representation of residential and activity land uses is created. Finally, a GIS output containing the degree of land use mixture is calculated by means of using the land uses maps. The implemented approach is documented in the paper "A framework for evaluating urban land use mix from crowd-sourcing data", <http://hal.inria.fr/hal-01396792>

- Participants: Luciano Gervasoni, Marti Bosch Padros, Peter Sturm and Serge Fenet
- Partners: EPFL - Ecole Polytechnique Fédérale de Lausanne - LIRIS
- Contact: Peter Sturm
- URL: <http://github.com/martibosch/landusemix>

5.6. QGIS_Tranus_Reports

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

- Participants: Fausto Lo Feudo, Huu Phuoc Nguyen, Patricio Inzaghi, Peter Sturm and Thomas Capelle
- Contact: Peter Sturm
- URL: https://gitlab.inria.fr/tranus/QGIS_Tranus_Reports

5.7. Comptabilité Ecologique

FUNCTIONAL DESCRIPTION: Databases, database handling tools and data visualization tools (on the web-site). Databases include socio-economic and environmental datasets. Visualization tools include interactive piecharts, maps and Sankey diagrams.

- Participants: Jean-Yves Courtonne and Pierre-Yves Longaretti
- Contact: Jean-Yves Courtonne
- URL: <http://www.eco-data.fr>

AGORA Project-Team

6. New Software and Platforms

6.1. TAPASCologne

Travel and Activity PAtterns Simulation Cologne

KEYWORDS: Mobility - Traces

FUNCTIONAL DESCRIPTION: TAPASCologne is an initiative by the Institute of Transportation Systems at the German Aerospace Center (ITS-DLR), aimed at reproducing, with the highest level of realism possible, car traffic in the greater urban area of the city of Cologne, in Germany.

To that end, different state-of-art data sources and simulation tools are brought together, so to cover all of the specific aspects required for a proper characterization of vehicular traffic:

The street layout of the Cologne urban area is obtained from the OpenStreetMap (OSM) database, The microscopic mobility of vehicles is simulated with the Simulation of Urban Mobility (SUMO) software, The traffic demand information on the macroscopic traffic flows across the Cologne urban area (i.e., the O/D matrix) is derived through the Travel and Activity PAtterns Simulation (TAPAS) methodology, The traffic assignment of the vehicular flows described by the TAPASCologne O/D matrix over the road topology is performed by means of Gawron's dynamic user assignment algorithm.

- Participants: Marco Fiore and Razvan Stanica
- Contact: Marco Fiore
- URL: <http://kolntrace.project.citi-lab.fr/#download>

6.2. Sense in the City

KEYWORDS: Sensors - Sensors network - Wireless Sensor Networks

FUNCTIONAL DESCRIPTION: Sense in the city is a lightweight experimentation platform for wireless sensor networks in development. The main objective of this platform is to be easily transferable and deployable on the field. It allows a simplified deployment of the code running on the sensors and the collection of logs generated by the instrumentation of the code on a centralized database. In the early stage of the platform, the sensors are powered by small PCs, e.g. Raspberry Pis, but we are investigating the integration of energy harvesting capabilities such as solar panels.

- Participants: Hervé Rivano and Khaled Boussetta
- Contact: Khaled Boussetta

6.3. PrivaMovApp

KEYWORD: Crowd-sensing

FUNCTIONAL DESCRIPTION: Agora is leading the development of an Android application for user data collection purposes. The application is based on the Funf framework, and is currently available on Google Play.

- Participants: Stéphane D'alu, Hervé Rivano, Razvan Stanica and SOLOHAJA RABENJAMINA
- Contact: Razvan Stanica

6.4. WSNet

KEYWORD: Network simulator

FUNCTIONAL DESCRIPTION: WSNet is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalability, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation. We still hope to find the proper resource to make WSNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem and Fabrice Valois
- Partner: CEA-LETI
- Contact: Guillaume Chelius
- URL: <https://gforge.inria.fr/projects/wsnet-3/>

6.5. Platforms

6.5.1. PPAIR Plateforme LoRa - Campus Connecté

The project aims at providing a platform that offers connectivity through a long-range, low-energy network to smart objects. The platform uses LoRa technology, which offers a wide connectivity, covering the entire INSA Lyon campus and providing a data collection service to all campus users. The main purpose of the LoRa plateforme is: (i) research (researchers can use it for studying reliability and capacity problems, privacy related challenges, etc.), and (ii) teaching (several courses from INSA, especially in the Telecom department can use this platform as a pedagogical tool).

Part of the software is mutualized with the University of Paris 13, where a LoRaWan testbed project is under deployment at the campus of Villetaneuse. This project, is supported by a local BQR and is led by Khaled Boussetta. The mutualization of the software tools will allow us to conduct multi sites experiments, at Lyon and at Paris.

6.5.2. UrPolSens Platform

We designed from scratch an energy efficient air pollution sensor network using Atmega micro-controllers and electrochemical air pollution probes. The micro-controller is integrated into a lab-designed printed circuit which includes among others: a high precision ADC, a micro-SD card reader and a radio communication module. The designed nodes measure the nitrogen dioxide (NO₂) pollutant in addition to temperature and humidity and transmit data using LoRa to a gateway, which is connected to our servers using a 4G connection. The sensors are also equipped with solar panels in order to extend their lifetime when their batteries are drained. Our platform had been operational in the downtown of the Lyon city with 12 sensor nodes deployed in the Garibaldi street from mid-July to Mid-October 2018.

AVALON Project-Team

6. New Software and Platforms

6.1. MAD

Madeus Application Deployer

KEYWORDS: Automatic deployment - Distributed Software - Component models - Cloud computing

SCIENTIFIC DESCRIPTION: MAD is a Python implementation of the Madeus deployment model for multi-component distributed software. Precisely, it allows to: 1. describe the deployment process and the dependencies of distributed software components in accordance with the Madeus model, 2. describe an assembly of components, resulting in a functional distributed software, 3. automatically deploy the component assembly of distributed software following the operational semantics of Madeus.

RELEASE FUNCTIONAL DESCRIPTION: Initial submission with basic functionalities of MAD

NEWS OF THE YEAR: Operational prototype.

- Participants: Christian Pérez, Dimitri Pertin, H  l  ne Coullon and Maverick Chardet
- Partners: IMT Atlantique - LS2N - LIP
- Contact: H  l  ne Coullon
- Publications: [Madeus: A formal deployment model - Behavioral interfaces for reconfiguration of component models](#)

6.2. DIET

Distributed Interactive Engineering Toolbox

KEYWORDS: Scheduling - Clusters - Grid - Cloud - HPC - Middleware - Data management.

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

RELEASE FUNCTIONAL DESCRIPTION: - Upgrade to support Cmake 3.3 and later - Update workflow unit tests to take the results of the execution into account - DIET workflow engine was improved

NEWS OF THE YEAR: Work on the next DIET release (DIET 2.11) New DIET Webboard based on Angular Two news biological application platform based on DIET (Aevol and Wasabi) Rutgers University (NJ, USA) Collaboration

- Participants: Joel Faubert, Hadrien Croubois, Abdelkader Amar, Arnaud Lefray, Aur  lien Bouteiller, Benjamin Isnard, Daniel Balouek, Eddy Caron, Eric Bois, Fr  d  ric Desprez, Fr  d  ric Lombart, Ga  l Le Mahec, Guillaume Verger, Huaxi Zhang, Jean-Marc Nicod, Jonathan Rouzaud-Cornabas, Lamiel Toch, Maurice Faye, Peter Frauenkron, Philippe Combes, Philippe Laurent, Rapha  l Bolze and Yves Caniou
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - Sysfera
- Contact: Eddy Caron
- URL: <http://graal.ens-lyon.fr/diet/>

6.3. SimGrid

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

SCIENTIFIC DESCRIPTION: SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments. The simulation engine uses algorithmic and implementation techniques toward the fast simulation of large systems on a single machine. The models are theoretically grounded and experimentally validated. The results are reproducible, enabling better scientific practices.

Its models of networks, cpus and disks are adapted to (Data)Grids, P2P, Clouds, Clusters and HPC, allowing multi-domain studies. It can be used either to simulate algorithms and prototypes of applications, or to emulate real MPI applications through the virtualization of their communication, or to formally assess algorithms and applications that can run in the framework.

The formal verification module explores all possible message interleavings in the application, searching for states violating the provided properties. We recently added the ability to assess liveness properties over arbitrary and legacy codes, thanks to a system-level introspection tool that provides a finely detailed view of the running application to the model checker. This can for example be leveraged to verify both safety or liveness properties, on arbitrary MPI code written in C/C++/Fortran.

NEWS OF THE YEAR: There were 3 major releases in 2018: The public API was sanitized (with compatibility wrappers in place). Th documentation was completely overhauled. Our continuous integration was greatly improved (45 Proxy Apps + BigDFT + StarPU + BatSim now tested nightly). Some kernel headers are now installed, allowing external plugins. Allow dynamic replay of MPI apps, controlled by S4U actors. Port the MPI trace replay engine to C++, fix visualization (+ the classical bug fixes and doc improvement).

- Participants: Adrien Lèbre, Arnaud Legrand, Augustin Degomme, Florence Perronnin, Frédéric Suter, Jean-Marc Vincent, Jonathan Pastor, Luka Stanisic and Martin Quinson
- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson
- URL: <https://simgrid.org/>

6.4. Kwapi

KiloWatt API

KEYWORD: Power monitoring

FUNCTIONAL DESCRIPTION: Kwapi is a software framework dealing with energy monitoring of large scale infrastructures through heterogeneous energy sensors. Kwapi has been designed inside the FSN XLCloud project for Openstack infrastructures. Through the support of Hemera Inria project, kwapi has been extended and deployed in production mode to support easy and large scale energy profiling of the Grid5000 resources. Kwapi now supports high frequency powermeters of the Grid5000 Lyon platform.

RELEASE FUNCTIONAL DESCRIPTION: - many bugfixes - multiprocessing instead of multithreading - many optimizations

- Participants: François Rossigneux, Jean-Patrick Gelas, Laurent Lefèvre, Laurent Pouilloux, Simon Delamare and Matthieu Imbert
- Contact: Laurent Lefèvre
- URL: <https://launchpad.net/kwapi>

6.5. execo

KEYWORDS: Toolbox - Deployment - Orchestration - Python

FUNCTIONAL DESCRIPTION: Execo offers a Python API for asynchronous control of local or remote, standalone or parallel, unix processes. It is especially well suited for quickly and easily scripting workflows of parallel/distributed operations on local or remote hosts: automate a scientific workflow, conduct computer science experiments, perform automated tests, etc. The core python package is execo. The execo_g5k package provides a set of tools and extensions for the Grid5000 testbed. The execo_engine package provides tools to ease the development of computer sciences experiments.

RELEASE FUNCTIONAL DESCRIPTION: - misc python3 support fixes - basic documentation for wheezy compatible package build - remove some debug outputs - fix crash in processes conductor in some situations - improve/fix process stdout/stderr handlers - fix ge_cluste_networ equipments - add a FAQ

- Participants: Florent Chuffart, Laurent Pouilloux and Matthieu Imbert
- Contact: Matthieu Imbert
- URL: <http://execo.gforge.inria.fr>

6.6. SeeDep

Seed based Deployment

KEYWORDS: Reproducibility - Deployment - Cloud

SCIENTIFIC DESCRIPTION: SeeDep aims at devising a new way where researchers can communicate in a comprehensive and accurate way the experimentation set-up used in their work. It lies on two components: (i) a public algorithm that generates experimentation networks, and (ii) a generation key (i.e. a seed) that can be shared which specifies the said network. Therefore, researchers only need to share (in their paper for instance) the “generation key” that corresponds to their experimentation network. With such key, any other researcher/professional will be able to re-generate a comprehensive and accurate model of the same network.

FUNCTIONAL DESCRIPTION: SeeDep is a framework aiming at generating, reproducing and deploying experiments set-up on different Cloud platforms.

- Participants: Cyril Seguin and Eddy Caron
- Partner: Nokia Bell Labs
- Contact: Eddy Caron

6.7. libkomp

Runtime system libkomp

KEYWORDS: HPC - Multicore - OpenMP

FUNCTIONAL DESCRIPTION: libKOMP is a runtime support for OpenMP compatible with différent compiler: GNU gcc/gfortran, Intel icc/ifort or clang/llvm. It is based on source code initially developed by Intel for its own OpenMP runtime, with extensions from Kaapi software (task representation, task scheduling). Moreover it contains an OMPT module for recording trace of execution.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Contact: Thierry Gautier
- URL: <http://gitlab.inria.fr/openmp/libkomp>

6.8. Platform: Grid'5000

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

FUNCTIONAL DESCRIPTION

The Grid'5000 experimental platform is a scientific instrument to support computer science research related to distributed systems, including parallel processing, high performance computing, cloud computing, operating systems, peer-to-peer systems and networks. It is distributed on 10 sites in France and Luxembourg, including Lyon. Grid'5000 is a unique platform as it offers to researchers many and varied hardware resources and a complete software stack to conduct complex experiments, ensure reproducibility and ease understanding of results. In 2018, a new generation of high speed wattmeters has been deployed on the Lyon site. They allow energy monitoring with up to 50 measurements per second. In parallel, a new version of kwapi (software stack for energy monitoring) has been proposed and redesigned.

- Contact: Laurent Lefèvre
- URL: <https://www.grid5000.fr/>

6.9. Platform: Leco

Participants: Thierry Gautier, Laurent Lefèvre, Christian Perez.

FUNCTIONAL DESCRIPTION

The LECO experimental platform is a new medium size scientific instrument funded by DRRT to investigate research related to BigData and HPC. It is located in Grenoble as part of the the HPCDA computer managed by UMS GRICAD. The platform has been deployed in 2018 and was available for experiment since the summer. All the nodes of the platform are instrumented to capture the energy consumption and data are available through the Kwapi software.

- Contact: Thierry Gautier

6.10. Platform: SILECS

Participants: Laurent Lefèvre, Simon Delamare, Christian Perez.

The SILECS infrastructure (IR ministère) aims at providing an experimental platform for experimental computer Science (Internet of things, clouds, hpc, big data, *etc.*). This new infrastructure is based on two existing infrastructures, Grid'5000 and FIT.

- Contact: Christian Perez
- URL: <https://www.silecs.net/>

CTRL-A Project-Team

5. New Software and Platforms

5.1. Heptagon

KEYWORDS: Compilers - Synchronous Language - Controller synthesis

FUNCTIONAL DESCRIPTION: Heptagon is an experimental language for the implementation of embedded real-time reactive systems. It is developed inside the Synchronics large-scale initiative, in collaboration with Inria Rhones-Alpes. It is essentially a subset of Lucid Synchronic, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierarchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

The current version of the compiler includes the following features: - Inclusion of discrete controller synthesis within the compilation: the language is equipped with a behavioral contract mechanisms, where assumptions can be described, as well as an "enforce" property part. The semantics of this latter is that the property should be enforced by controlling the behaviour of the node equipped with the contract. This property will be enforced by an automatically built controller, which will act on free controllable variables given by the programmer. This extension has been named BZR in previous works. - Expression and compilation of array values with modular memory optimization. The language allows the expression and operations on arrays (access, modification, iterators). With the use of location annotations, the programmer can avoid unnecessary array copies.

- Participants: Adrien Guatto, Brice Gelineau, Cédric Pasteur, Eric Rutten, Gwenaël Delaval, Léonard Gérard and Marc Pouzet
- Partners: UGA - ENS Paris - Inria - LIG
- Contact: Gwenaël Delaval
- URL: <http://heptagon.gforge.inria.fr>

DANTE Project-Team

6. New Software and Platforms

6.1. GraSP

Graph Signal Processing

KEYWORDS: Matlab - LaTeX - Graph - Graph visualization - Signal processing - GNU Octave

FUNCTIONAL DESCRIPTION: Matlab / GNU Octave toolbox to manipulate and visualize signals on graphs.

LaTeX package to draw signals.

- Contact: Benjamin Girault

6.2. IoT-LAB aggregation-tools

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB aggregation-tools allow aggregating data results from many nodes at a time. It connects to several tcp connections and handle the received data.

- Participant: Gaetan Harter
- Contact: Eric Fleury
- URL: <https://github.com/iot-lab/aggregation-tools>

6.3. IoT-LAB cli-tools

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB cli-tools provide a basic set of operations for managing IoT-LAB experiments from the command-line.

- Participants: Frédéric Saint-Marcel and Gaetan Harter
- Contact: Eric Fleury
- URL: <https://github.com/iot-lab/cli-tools>

6.4. IoT-LAB gateway

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB software embedded on a IoT-LAB gateway node new generation provides the local management of the experiment on that node. It is a software bridge between the IoT-LAB server, the user open node and the control node.

- Contact: Frédéric Saint-Marcel
- URL: <https://github.com/iot-lab/iot-lab-gateway>

6.5. IoT-LAB robots

KEYWORDS: Internet of things - Robotics

FUNCTIONAL DESCRIPTION: IoT-LAB robots is an embedded robot controller on a Turtlebot2 providing the IoT-LAB node mobility functionality

- Partner: Université de Strasbourg
- Contact: Julien Vandaële
- URL: <https://github.com/iot-lab/>

6.6. Queueing Systems

FUNCTIONAL DESCRIPTION: This tool aims at providing a simple web interface to promote the use of our proposed solutions to numerically solve classical queueing systems.

- Participants: Alexandre Brandwajn and Thomas Begin
- Contact: Thomas Begin
- URL: <http://queueing-systems.ens-lyon.fr/>

6.7. WSNNet

KEYWORD: Network simulator

FUNCTIONAL DESCRIPTION: WSNNet is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalability, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation. We still hope to find the proper resource to make WSNNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem and Fabrice Valois
- Partner: CEA-LETI
- Contact: Guillaume Chelius
- URL: <https://gforge.inria.fr/projects/wsnet-3/>

DATAMOVE Project-Team

5. New Software and Platforms

5.1. FlowVR

SCIENTIFIC DESCRIPTION: FlowVR adopts the "data-flow" paradigm, where your application is divided as a set of components exchanging messages (think of it as a directed graph). FlowVR enables to encapsulate existing codes in components, interconnect them through data channels, and deploy them on distributed computing resources. FlowVR takes care of all the heavy lifting such as application deployment and message exchange.

The base entity, called a module or component, is an autonomous process, potentially multi-threaded with tools like OpenMP, TBB, or deferring computations to a GPU or Xeon Phi. This module processes data coming from input ports and write data on output ports. A module has no global insight on where the data comes from or goes to. The programming interface is designed to limit code refactoring, easing turning an existing code into a FlowVR component. The three main functions are:

wait(): Blocking function call that waits for the availability of new messages on input ports. get(): Retrieve a handle to access the message received at the previous wait() call on a given input port. put(): Notify FlowVR that a new message on a given output port is ready for dispatch. FlowVR manages data transfers. Intra-node communications between two components take place through a shared memory segment, avoiding copies. Once the sender has prepared the data in a shared memory segment, it simply handles a pointer to the destination that can directly access them. Inter-node communications extend this mechanism, FlowVR taking care of packing and transferring the data from the source shared memory segment to the destination shared memory segment.

Assembling components to build an application consists in writing a Python script, instantiate it according to the target machine. FlowVR will process it and prepare everything so that in one command line you can deploy and start your application.

FUNCTIONAL DESCRIPTION: FlowVR adopts the "data-flow" paradigm, where your application is divided as a set of components exchanging messages (think of it as a directed graph). FlowVR enables to encapsulate existing codes in components, interconnect them through data channels, and deploy them on distributed computing resources. FlowVR takes care of all the heavy lifting such as application deployment and message exchange.

- Participants: Bruno Raffin, Clément Ménier, Emmanuel Melin, Jean Denis Lesage, Jérémie Allard, Jérémy Jaussaud, Matthieu Dreher, Sébastien Limet, Sophie Robert and Valérie Gourantou
- Contact: Bruno Raffin
- URL: <http://flowvr.sf.net>

5.2. OAR

KEYWORDS: HPC - Cloud - Clusters - Resource manager - Light grid

SCIENTIFIC DESCRIPTION: This batch system is based on a database (PostgreSQL (preferred) or MySQL), a script language (Perl) and an optional scalable administrative tool (e.g. Taktuk). It is composed of modules which interact mainly via the database and are executed as independent programs. Therefore, formally, there is no API, the system interaction is completely defined by the database schema. This approach eases the development of specific modules. Indeed, each module (such as schedulers) may be developed in any language having a database access library.

FUNCTIONAL DESCRIPTION: OAR is a versatile resource and task manager (also called a batch scheduler) for HPC clusters, and other computing infrastructures (like distributed computing experimental testbeds where versatility is a key).

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

5.3. MELISSA

Modular External Library for In Situ Statistical Analysis

KEYWORD: Sensitivity Analysis

FUNCTIONAL DESCRIPTION: Melissa is an in situ solution for sensitivity analysis. It implements iterative algorithms to compute spatio-temporal statistic fields over results of large scale sensitivity studies. Melissa relies on a client/server architecture, composed of three main modules:

Melissa Server: an independent parallel executable. It receives data from the simulations, updates iterative statistics as soon as possible, then throw data away. Melissa API: a shared library to be linked within the simulation code. It mainly transmit simulation data to Melissa Server at each timestep. The simulations of the sensitivity analysis become the clients of Melissa Server. Melissa Launcher: A Python script in charge of generating and managing the whole global sensitivity analysis.

- Authors: Théophile Terraz, Bruno Raffin, Alejandro Ribes and Bertrand Iooss
- Partner: Edf
- Contact: Bruno Raffin
- Publications: [In Situ Statistical Analysis for Parametric Studies - Melissa: Large Scale In Transit Sensitivity Analysis Avoiding Intermediate Files](#)
- URL: <https://melissa-sa.github.io>

5.4. Platforms

5.4.1. Grid'5000 (<https://www.grid5000.fr/>) and Meso Center Ciment (<https://ciment.ujf-grenoble.fr>)

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

POLARIS Project-Team

6. New Software and Platforms

6.1. Framesoc

FUNCTIONAL DESCRIPTION: Framesoc is the core software infrastructure of the SoC-Trace project. It provides a graphical user environment for execution-trace analysis, featuring interactive analysis views as Gantt charts or statistics views. It provides also a software library to store generic trace data, play with them, and build other analysis tools (e.g., Ocelotl).

- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Guillaume Huard
- URL: <http://soctrace-inria.github.io/framesoc/>

6.2. GameSeer

FUNCTIONAL DESCRIPTION: GameSeer is a tool for students and researchers in game theory that uses Mathematica to generate phase portraits for normal form games under a variety of (user-customizable) evolutionary dynamics. The whole point behind GameSeer is to provide a dynamic graphical interface that allows the user to employ Mathematica's vast numerical capabilities from a simple and intuitive front-end. So, even if you've never used Mathematica before, you should be able to generate fully editable and customizable portraits quickly and painlessly.

- Contact: Panayotis Mertikopoulos
- URL: <http://mescal.imag.fr/membres/panayotis.mertikopoulos/publications.html>

6.3. marmoteCore

Markov Modeling Tools and Environments - the Core

KEYWORDS: Modeling - Stochastic models - Markov model

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

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

- Participants: Alain Jean-Marie, Hlib Mykhailenko, Benjamin Briot, Franck Quessette, Issam Rabhi, Jean-Marc Vincent and Jean-Michel Fourneau
- Partner: UVSQ
- Contact: Alain Jean-Marie
- Publications: [marmoteCore: a Markov Modeling Platform](#) - [marmoteCore: a software platform for Markov modeling](#)
- URL: <http://marmotecore.gforge.inria.fr/>

6.4. Moca

Memory Organisation Cartography and Analysis

KEYWORDS: High-Performance Computing - Performance analysis

- Contact: David Beniamine
- URL: <https://github.com/dbeniamine/MOCA>

6.5. Ocelotl

Multidimensional Overviews for Huge Trace Analysis

FUNCTIONAL DESCRIPTION: Ocelotl is an innovative visualization tool, which provides overviews for execution trace analysis by using a data aggregation technique. This technique enables to find anomalies in huge traces containing up to several billions of events, while keeping a fast computation time and providing a simple representation that does not overload the user.

- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Jean-Marc Vincent
- URL: <http://soctrace-inria.github.io/ocelotl/>

6.6. PSI

Perfect Simulator

FUNCTIONAL DESCRIPTION: Perfect simulator is a simulation software of markovian models. It is able to simulate discrete and continuous time models to provide a perfect sampling of the stationary distribution or directly a sampling of functional of this distribution by using coupling from the past. The simulation kernel is based on the CFTP algorithm, and the internal simulation of transitions on the Aliasing method.

- Contact: Jean-Marc Vincent
- URL: <http://psi.gforge.inria.fr/>

6.7. SimGrid

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

SCIENTIFIC DESCRIPTION: SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments. The simulation engine uses algorithmic and implementation techniques toward the fast simulation of large systems on a single machine. The models are theoretically grounded and experimentally validated. The results are reproducible, enabling better scientific practices.

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The formal verification module explores all possible message interleavings in the application, searching for states violating the provided properties. We recently added the ability to assess liveness properties over arbitrary and legacy codes, thanks to a system-level introspection tool that provides a finely detailed view of the running application to the model checker. This can for example be leveraged to verify both safety or liveness properties, on arbitrary MPI code written in C/C++/Fortran.

NEWS OF THE YEAR: There were 3 major releases in 2018: The public API was sanitized (with compatibility wrappers in place). Th documentation was completely overhauled. Our continuous integration was greatly improved (45 Proxy Apps + BigDFT + StarPU + BatSim now tested nightly). Some kernel headers are now installed, allowing external plugins. Allow dynamic replay of MPI apps, controlled by S4U actors. Port the MPI trace replay engine to C++, fix visualization (+ the classical bug fixes and doc improvement).

- Participants: Adrien Lèbre, Arnaud Legrand, Augustin Degomme, Florence Perronnin, Frédéric Suter, Jean-Marc Vincent, Jonathan Pastor, Luka Stanic and Martin Quinson
- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson
- URL: <https://simgrid.org/>

6.8. Tabarnac

Tool for Analyzing the Behavior of Applications Running on NUMA Architecture

KEYWORDS: High-Performance Computing - Performance analysis - NUMA

- Contact: David Beniamine
- URL: <https://dbeniamine.github.io/Tabarnac/>

ROMA Project-Team

6. New Software and Platforms

6.1. MUMPS

A Multifrontal Massively Parallel Solver

KEYWORDS: High-Performance Computing - Direct solvers - Finite element modelling

FUNCTIONAL DESCRIPTION: MUMPS is a software library to solve large sparse linear systems ($AX=B$) on sequential and parallel distributed memory computers. It implements a sparse direct method called the multifrontal method. It is used worldwide in academic and industrial codes, in the context numerical modeling of physical phenomena with finite elements. Its main characteristics are its numerical stability, its large number of features, its high performance and its constant evolution through research and feedback from its community of users. Examples of application fields include structural mechanics, electromagnetism, geophysics, acoustics, computational fluid dynamics. MUMPS is developed by INPT(ENSEEIH)-IRIT, Inria, CERFACS, University of Bordeaux, CNRS and ENS Lyon. In 2014, a consortium of industrial users has been created (<http://mumps-consortium.org>).

RELEASE FUNCTIONAL DESCRIPTION: MUMPS versions 5.1.0, 5.1.1 and 5.1.2, all released in 2017 include many new features and improvements. The two main new features are Block Low-Rank compression, decreasing the complexity of sparse direct solvers for various types of applications, and selective 64-bit integers, allowing to process matrices with more than 2 billion entries. Several new features have been developed in 2017 and 2018 that are included in some MUMPS versions provided to partners for experimentation (e.g. in the context of industrial contracts). These features will appear in the future public versions, starting with MUMPS 5.2.0.

- Participants: Gilles Moreau, Abdou Guermouche, Alfredo Buttari, Aurélie Fevre, Bora Uçar, Chiara Puglisi, Clément Weisbecker, Emmanuel Agullo, François-Henry Rouet, Guillaume Joslin, Jacko Koster, Jean-Yves L'Excellent, Marie Durand, Maurice Bremond, Mohamed Sid-Lakhdar, Patrick Amestoy, Philippe Combes, Stéphane Pralet, Theo Mary and Tzvetomila Slavova
- Partners: Université de Bordeaux - CNRS - CERFACS - ENS Lyon - INPT - IRIT - Université de Lyon - Université de Toulouse - LIP
- Contact: Jean-Yves L'Excellent
- URL: <http://mumps-solver.org/>

SOCRATE Project-Team

5. New Software and Platforms

5.1. fftweb

KEYWORDS: Experimentation - Data visualization - SDR (Software Defined Radio)

FUNCTIONAL DESCRIPTION: fftweb is a real-time spectral (FFT) visualization of one or several signal, embedded in a web page. The FFT is computed in a GNURadio block, then sent to a gateway server, which serves the web page, associated javascripts, and signal websockets. The end user only has to use the GNURadio block and the web page, and doesn't need to bother about the internal details of the system. fftweb has been developed specially for the CorteXlab testbed but with minor adaptations, it can be used in other contexts, and also can be used to draw more generic real-time graphs, not only FFTs. Technologies: GNURadio, python, python-gevent, Javascript, D3JS

- Contact: Matthieu Imbert

5.2. FloPoCo

Floating-Point Cores, but not only

KEYWORD: Synthesizable VHDL generator

FUNCTIONAL DESCRIPTION: The purpose of the open-source FloPoCo project is to explore the many ways in which the flexibility of the FPGA target can be exploited in the arithmetic realm.

NEWS OF THE YEAR: FloPoCo has been enhanced in 2019 with a last-bit accurate IIR filter generator and a generator of parallel FFT cores, among others.

- Participants: Florent Dupont De Dinechin and Luc Forget
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - UPVD
- Contact: Florent Dupont De Dinechin
- URL: <http://flopoco.gforge.inria.fr/>

5.3. minus

KEYWORDS: Experimentation - SDR (Software Defined Radio)

FUNCTIONAL DESCRIPTION: Minus is an experiment control system able to control, the whole lifecycle of a radio experiment in CorteXlab or any other testbed inspired by it. Minus controls and automates the whole experiment process starting from node power cycling, experiment deployment, experiment start and stop, and results collection and transfer. Minus is also capable of managing multiple queues of experiments which are executed simultaneously in the testbed.

- Contact: Matthieu Imbert

5.4. WiPlan

FUNCTIONAL DESCRIPTION: WiPlan is a software including an Indoor propagation engine and a wireless LAN optimization suite, which has been registered by INSA-Lyon. The heart of this software is the propagation simulation core relying on an original method, MR-FDPF (multi-resolution frequency domain ParFlow), proposed by JM Gorce in 2001 and further extended. The discrete ParFlow equations are translated in the Fourier domain providing a large linear system, solved in two steps taking advantage of a multi-resolution approach. The first step computes a cell-based tree structure referred to as the pyramid. In the second phase, a radiating source is simulated, taking advantage of the pre-processed pyramidal structure. Using of a full-space discrete simulator instead of classical ray-tracing techniques is a challenge due to the inherent high computation requests. However, we have shown that the use of a multi-resolution approach allows the main computational load to be restricted to a pre-processing phase. Extensive works have been done to make predictions more realistic.

- Contact: Tanguy Risset

5.5. Sytare

KEYWORDS: Embedded systems - Operating system - Non volatile memory

FUNCTIONAL DESCRIPTION: Sytare is an embedded operating system targeting tiny platforms with intermittent power. In order to make power failures transparent for the application, the system detects imminent failures and saves a checkpoint of program state to non-volatile memory. Hardware peripherals are also made persistent without requiring developer attention.

- Authors: Tristan Delizy, Gautier Berthou, Guillaume Salagnac, Kevin Marquet and Tanguy Risset
- Contact: Guillaume Salagnac
- Publication: [Peripheral State Persistence For Transiently Powered Systems](#)
- URL: <https://hal.inria.fr/hal-01460699>

Chroma Project-Team

6. New Software and Platforms

6.1. kinetics

FUNCTIONAL DESCRIPTION: Software computing decision support strategies and decision-making

- Contact: Jilles Dibangoye

6.2. VI-SFM

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

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

6.3. Ground Elevation and Occupancy Grid Estimator (GEOG - Estimator)

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: GEOG-Estimator is a system of joint estimation of the shape of the ground, in the form of a Bayesian network of constrained elevation nodes, and the ground-obstacle classification of a pointcloud. Starting from an unclassified 3D pointcloud, it consists of a set of expectation-maximization methods computed in parallel on the network of elevation nodes, integrating the constraints of spatial continuity as well as the influence of 3D points, classified as ground-based or obstacles. Once the ground model is generated, the system can then construct a occupation grid, taking into account the classification of 3D points, and the actual height of these impacts. Mainly used with lidars (Velodyne64, Quanergy M8, IBEO Lux), the approach can be generalized to any type of sensor providing 3D pointclouds. On the other hand, in the case of lidars, free space information between the source and the 3D point can be integrated into the construction of the grid, as well as the height at which the laser passes through the area (taking into account the height of the laser in the sensor model). The areas of application of the system spread across all areas of mobile robotics, it is particularly suitable for unknown environments. GEOG-Estimator was originally developed to allow optimal integration of 3D sensors in systems using 2D occupancy grids, taking into account the orientation of sensors, and indefinite forms of grounds. The ground model generated can be used directly, whether for mapping or as a pre-calculation step for methods of obstacle recognition or classification. Designed to be effective (real-time) in the context of embedded applications, the entire system is implemented on Nvidia graphics card (in Cuda), and optimized for Tegra X2 embedded boards. To ease interconnections with the sensor outputs and other perception modules, the system is implemented using ROS (Robot Operating System), a set of opensource tools for robotics.

- Authors: Amaury Nègre, Lukas Rummelhard, Lukas Rummelhard, Jean-Alix David and Christian Laugier
- Contact: Christian Laugier

6.4. CMCDOT

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: CMCDOT is a Bayesian filtering system for dynamic occupation grids, allowing parallel estimation of occupation probabilities for each cell of a grid, inference of velocities, prediction of the risk of collision and association of cells belonging to the same dynamic object. Last generation of a suite of Bayesian filtering methods developed in the Inria eMotion team, then in the Inria Chroma team (BOF, HSBOF, ...), it integrates the management of hybrid sampling methods (classical occupancy grids for static parts, particle sets for parts dynamics) into a Bayesian unified programming formalism, while incorporating elements resembling the Dempster-Shafer theory (state "unknown", allowing a focus of computing resources). It also offers a projection system of the estimated scene in the near future, to reference potential collisions with the ego-vehicle or any other element of the environment, as well as very low cost pre-segmentation of coherent dynamic spaces (taking into account speeds). It takes as input instantaneous occupation grids generated by sensor models for different sources, the system is composed of a ROS package, to manage the connectivity of I/O, which encapsulates the core of the embedded and optimized application on GPU Nvidia (Cuda), allowing real-time analysis of the direct environment on embedded boards (Tegra X1, X2). ROS (Robot Operating System) is a set of open source tools to develop software for robotics. Developed in an automotive setting, these techniques can be exploited in all areas of mobile robotics, and are particularly suited to highly dynamic and uncertain environment management (eg urban scenario, with pedestrians, cyclists, cars, buses, etc.).

- Authors: Amaury Nègre, Lukas Rummelhard, Jean-Alix David and Christian Laugier
- Partners: CEA - CNRS
- Contact: Christian Laugier

6.5. cuda_grid_fusion

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: This module, directly implemented in ROS / Cuda, performs the merge of occupancy grids, defined in the format proposed in CMCDOT (probabilities integrating the "visibility" information of the cell, via the coefficients "unknown") thanks to an original method, allowing not only consistency with the rest of the system, but also a nuanced consideration of confidence criteria towards the various sources of information.

- Authors: Lukas Rummelhard and Jean-Alix David
- Contact: Lukas Rummelhard

6.6. cuda_laser_grid

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: This module generates occupation grids from "almost" planar lidar. The sensor model, as well as the outputs, have been modified, in order to be fully consistent with the CMCDOT and grid fusion module formats.

- Authors: Amaury Nègre, Lukas Rummelhard and Jean-Alix David
- Contact: Lukas Rummelhard

6.7. CMCDOT-Tools

KEYWORD: Robotics

FUNCTIONAL DESCRIPTION: Tools for CMCDOT Software

- Authors: Amaury Nègre, Lukas Rummelhard, Jean-Alix David, Mathias Perrollaz, Procopio Silveira-Stein, Jérôme Lussereau and Nicolas Vignard
- Contact: Jean-Alix David

6.8. DWA Planner on occupancy grid

Dynamic Window Approach Planner based on occupancy grid

KEYWORD: Navigation

FUNCTIONAL DESCRIPTION: This program considers : - a given target - an occupancy grid which represents the environment - the odometry of the vehicle With these data, it computes the commands for a safe navigation towards the target.

- Authors: Christian Laugier and Thomas Genevois
- Partner: CEA
- Contact: Christian Laugier

6.9. Zoe Simulation

Simulation of Inria's Renault Zoe in Gazebo environment

KEYWORD: Simulation

FUNCTIONAL DESCRIPTION: This simulation represents the Renault Zoe vehicle considering the realistic physical phenomena (friction, sliding, inertia, ...). The simulated vehicle embeds sensors similar to the ones of the actual vehicle. They provide measurement data under the same format. Moreover the software input/output are identical to the vehicle's. Therefore any program executed on the vehicle can be used with the simulation and reciprocally.

- Authors: Christian Laugier, Nicolas Turro and Thomas Genevois
- Contact: Christian Laugier

6.10. PedSim-ROS

FUNCTIONAL DESCRIPTION: Simulation of moving people and mobile robots that can detect agents around them. Integration of ROS mobile robots with the PedSim simulator.

- Contact: Jacques Saraydaryan

6.11. EKF Odom

EKF based localisation for vehicles

KEYWORDS: Localization - Autonomous Cars

FUNCTIONAL DESCRIPTION: This software fuses IMU data with wheel rotation or speed measurement inside an Extended Kalman Filter. It estimates the state position, orientation, speed, angular speed, acceleration.

- Authors: Thomas Genevois and Christian Laugier
- Contact: Christian Laugier
- URL: <https://team.inria.fr/chroma/en/>

6.12. Light Vehicle Simulation

Simulation of a light vehicle in Gazebo environment

KEYWORD: Simulation

FUNCTIONAL DESCRIPTION: This simulation represents a light vehicle considering the realistic physical phenomena (friction, sliding, inertia, ...). The simulated vehicle embeds sensors similar to the ones of the actual vehicle. They provide measurement data under the same format. Moreover the software input/output are identical to the vehicle's. Therefore any program executed on the vehicle can be used with the simulation and reciprocally.

- Authors: Thomas Genevois and Christian Laugier
- Contact: Christian Laugier
- URL: <https://team.inria.fr/chroma/en/>

6.13. CarHybridSim

Hybrid simulation for autonomous cars with high traffic

KEYWORDS: Simulation - Autonomous Cars

FUNCTIONAL DESCRIPTION: Open source tool for simulating autonomous vehicles in complex, high traffic, scenarios. The hybrid simulation fully integrates and synchronizes a microscopic, multi-modal traffic simulator and a complex 3D simulator.

- Contact: Mario Garzon Oviedo
- URL: https://github.com/marioney/hybrid_simulation

6.14. SimuDronesGR

Simulation of UAV fleets with Gazebo/ROS

KEYWORDS: Robotics - Simulation

FUNCTIONAL DESCRIPTION: The simulator includes the following functionality : 1) Simulation of the mechanical behavior of an Unmanned Aerial Vehicle : * Modeling of the body's aerodynamics with lift, drag and moment * Modeling of rotors' aerodynamics using the forces and moments' expressions from Philippe Martin's and Erwan Salaün's 2010 IEEE Conference on Robotics and Automation paper "The True Role of Accelerometer Feedback in Quadrotor Control". 2) Gives groundtruth informations : * Positions in East-North-Up reference frame * Linear velocity in East-North-Up and Front-Left-Up reference frames * Linear acceleration in East-North-Up and Front-Left-Up reference frames * Orientation from East-North-Up reference frame to Front-Left-Up reference frame (Quaternions) * Angular velocity of Front-Left-Up reference frame expressed in Front-Left-Up reference frame. 3) Simulation of the following sensors : * Inertial Measurement Unit with 9DoF (Accelerometer + Gyroscope + Orientation) * Barometer using an ISA model for the troposphere (valid up to 11km above Mean Sea Level) * Magnetometer with the earth magnetic field declination * GPS Antenna with a geodesic map projection.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Author: Vincent Le Doze
- Partner: Insa de Lyon
- Contact: Vincent Le Doze

IMAGINE Project-Team

6. New Software and Platforms

6.1. MyCF

My Corporis Fabrica

KEYWORDS: 3D modeling - Simulation - Health - Ontologies - Anatomy - Patientspecific - Medical imaging

FUNCTIONAL DESCRIPTION: Knowledge-based 3D anatomical modeling using MyCF The MyCF software eases the creation of 3D anatomical models for visualization and mechanical simulation. As input, the user provides a list of anatomical entities or functions to simulate, using keywords or navigating in reference 3D model. As output, she gets a 3D model ready to visualize, or to simulate.

- Participants: Ali Hamadi Dicko, Federico Ulliana, François Faure and Olivier Palombi
- Partner: Université Joseph-Fourier
- Contact: Olivier Palombi

6.2. Kino AI

Artificial intelligence for cinematography

KEYWORDS: Video analysis - Post-production

FUNCTIONAL DESCRIPTION: Kino AI is an implementation of the method described in our patent "automatic generation of cinematographic rushes using video processing". Starting from a single ultra high definition (UltraHD) recording of a live performance, we track and recognize all actors present on stage and generate one or more rushes suitable for cinematographic editing of a movie.

- Partner: IIIT Hyderabad
- Contact: Rémi Ronfard
- Publications: [Multi-Clip Video Editing from a Single Viewpoint - Zooming On All Actors: Automatic Focus+Context Split Screen Video Generation](#)

6.3. Platforms

6.3.1. AANALYSIS

AANALYSIS is a platform developed from 2015 to 2018 as a module of the SALOME platform and as a plugin of SHAPER (a software under development by EDF, CEA and OpenCascade). It processes CAD assemblies to derive symmetry properties, similarities of solids and groups of solids, interface features between solids and is operational on industrial models. The plugin version implements a shape similarity selection feature. The module is connected with a knowledge database MyProductFabrica developed in our group in partnership with GraphiK Inria team. It enables the automatic generation/annotation of functional knowledge from 3D geometry using 350 concepts, 90 relations and more than 100 inferences.

6.3.2. RUMBA

RUMBA is a next-generation 3D animation software targeted to professional animation studios, developed jointly by Mercenaries Engineering, TEAMTO and IMAGINE. Development was funded in part by FUI projects COLLODI 1 and COLLODI 2. RUMBA has been used in production by TEAMTO since 2017. RUMBA will be made commercially available to other animation studio by Mercenaries Engineering in 2019. We are using RUMBA as a platform for developing new algorithms in sketch-based animation, based on our previous work during Martin Guay's PhD thesis. This includes many improvements to allow those methods to work in a professional workflow.

6.3.3. SKY ENGINE

Sky Engine is a realtime game engine developed by Maxime Garcia as part of his PhD thesis, which incorporates several shape modeling and animation tools developed within the team. It is hoped that it will supersede Expressive as a platform for future integration of research results of the team involving real-time, story-driven shape modeling, animation and cinematography.

MAVERICK Project-Team

6. New Software and Platforms

6.1. Diffusion curves

KEYWORDS: Vector-based drawing - Shading

FUNCTIONAL DESCRIPTION: Diffusion Curves is a vector-based design tool for creating complex shaded images. This prototype is composed of the Windows binary, along with the required shader programs (ie. in source code).

- Participants: Adrien Bousseau, Alexandrina Orzan, David Salesin, Holger Winnemoeller, Joëlle Thollot and Pascal Barla
- Partners: CNRS - LJK - INP Grenoble - Université Joseph-Fourier
- Contact: Joëlle Thollot
- URL: <http://maverick.inria.fr/Publications/2008/OBWBTS08/index.php>

6.2. GigaVoxels

FUNCTIONAL DESCRIPTION: Gigavoxel is a software platform which goal is the real-time quality rendering of very large and very detailed scenes which couldn't fit memory. Performances permit showing details over deep zooms and walk through very crowded scenes (which are rigid, for the moment). The principle is to represent data on the GPU as a Sparse Voxel Octree which multiscale voxels bricks are produced on demand only when necessary and only at the required resolution, and kept in a LRU cache. User defined producer lays across CPU and GPU and can load, transform, or procedurally create the data. Another user defined function is called to shade each voxel according to the user-defined voxel content, so that it is user choice to distribute the appearance-making at creation (for faster rendering) or on the fly (for storageless thin procedural details). The efficient rendering is done using a GPU differential cone-tracing using the scale corresponding to the 3D-MIPmapping LOD, allowing quality rendering with one single ray per pixel. Data is produced in case of cache miss, and thus only whenever visible (accounting for view frustum and occlusion). Soft-shadows and depth-of-field is easily obtained using larger cones, and are indeed cheaper than unblurred rendering. Beside the representation, data management and base rendering algorithm themselves, we also worked on realtime light transport, and on quality prefiltering of complex data. Ongoing researches are addressing animation. GigaVoxels is currently used for the quality real-time exploration of the detailed galaxy in ANR RTIGE. Most of the work published by Cyril Crassin (and al.) during his PhD (see <http://maverick.inria.fr/Members/Cyril.Crassin/>) is related to GigaVoxels. GigaVoxels is available for Windows and Linux under the BSD-3 licence.

- Participants: Cyril Crassin, Eric Heitz, Fabrice Neyret, Jérémy Sinoir, Pascal Guehl and Prashant Goswami
- Contact: Fabrice Neyret
- URL: <http://gigavoxels.inrialpes.fr>

6.3. GRATIN

FUNCTIONAL DESCRIPTION: Gratin is a node-based compositing software for creating, manipulating and animating 2D and 3D data. It uses an internal direct acyclic multi-graph and provides an intuitive user interface that allows to quickly design complex prototypes. Gratin has several properties that make it useful for researchers and students. (1) it works in real-time: everything is executed on the GPU, using OpenGL, GLSL and/or Cuda. (2) it is easily programmable: users can directly write GLSL scripts inside the interface, or create new C++ plugins that will be loaded as new nodes in the software. (3) all the parameters can be animated using keyframe curves to generate videos and demos. (4) the system allows to easily exchange nodes, group of nodes or full pipelines between people.

- Participants: Pascal Barla and Romain Vergne
- Partner: UJF
- Contact: Romain Vergne
- URL: <http://gratin.gforge.inria.fr/>

6.4. HQR

High Quality Renderer

KEYWORDS: Lighting simulation - Materials - Plug-in

FUNCTIONAL DESCRIPTION: HQR is a global lighting simulation platform. HQR software is based on the photon mapping method which is capable of solving the light balance equation and of giving a high quality solution. Through a graphical user interface, it reads X3D scenes using the X3DToolkit package developed at Maverick, it allows the user to tune several parameters, computes photon maps, and reconstructs information to obtain a high quality solution. HQR also accepts plugins which considerably eases the development of new algorithms for global illumination, those benefiting from the existing algorithms for handling materials, geometry and light sources.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: <http://artis.imag.fr/~Cyril.Soler/HQR>

6.5. libylm

LibYLM

KEYWORD: Spherical harmonics

FUNCTIONAL DESCRIPTION: This library implements spherical and zonal harmonics. It provides the means to perform decompositions, manipulate spherical harmonic distributions and provides its own viewer to visualize spherical harmonic distributions.

- Author: Cyril Soler
- Contact: Cyril Soler
- URL: <https://launchpad.net/~csoler-users/+archive/ubuntu/ylm>

6.6. MobiNet

KEYWORDS: Co-simulation - Education - Programmation

FUNCTIONAL DESCRIPTION: The MobiNet software allows for the creation of simple applications such as video games, virtual physics experiments or pedagogical math illustrations. It relies on an intuitive graphical interface and language which allows the user to program a set of mobile objects (possibly through a network). It is available in public domain for Linux, Windows and MacOS.

- Participants: Fabrice Neyret, Franck Hétyroy-Wheeler, Joëlle Thollot, Samuel Hornus and Sylvain Lefebvre
- Partners: CNRS - LJK - INP Grenoble - Inria - IREM - Cies - GRAVIR
- Contact: Fabrice Neyret
- URL: <http://mobinet.imag.fr/index.en.html>

6.7. PLANTRAD

KEYWORDS: Bioinformatics - Biology

FUNCTIONAL DESCRIPTION: PlantRad is a software program for computing solutions to the equation of light equilibrium in a complex scene including vegetation. The technology used is hierarchical radiosity with clustering and instantiation. Thanks to the latter, PlantRad is capable of treating scenes with a very high geometric complexity (up to millions of polygons) such as plants or any kind of vegetation scene where a high degree of approximate self-similarity permits a significant gain in memory requirements.

- Participants: Cyril Soler, François Sillion and George Drettakis
- Contact: Cyril Soler

6.8. PROLAND

PROcedural LANDscape

KEYWORDS: Real time - 3D - Realistic rendering - Masses of data - Atmosphere - Ocean

FUNCTIONAL DESCRIPTION: The goal of this platform is the real-time quality rendering and editing of large landscapes. All features can work with planet-sized terrains, for all viewpoints from ground to space. Most of the work published by Eric Bruneton and Fabrice Neyret (see <http://evasion.inrialpes.fr/Membres/Eric.Bruneton/>) has been done within Proland and integrated in the main branch. Proland is available under the BSD-3 licence.

- Participants: Antoine Begault, Eric Bruneton, Fabrice Neyret and Guillaume Piolet
- Contact: Fabrice Neyret
- URL: <https://proland.inrialpes.fr/>

6.9. ShwarpIt

KEYWORD: Warping

FUNCTIONAL DESCRIPTION: ShwarpIt is a simple mobile app that allows you to manipulate the perception of shapes in images. Slide the ShwarpIt slider to the right to make shapes appear rounder. Slide it to the left to make shapes appear more flat. The Scale slider gives you control on the scale of the warping deformation.

- Contact: Georges-Pierre Bonneau
- URL: <http://bonneau.meylan.free.fr/ShwarpIt/ShwarpIt.html>

6.10. Vrender

FUNCTIONAL DESCRIPTION: The VRender library is a simple tool to render the content of an OpenGL window to a vectorial device such as Postscript, XFig, and soon SVG. The main usage of such a library is to make clean vectorial drawings for publications, books, etc.

In practice, VRender replaces the z-buffer based hidden surface removal of OpenGL by sorting the geometric primitives so that they can be rendered in a back-to-front order, possibly cutting them into pieces to solve cycles.

VRender is also responsible for the vectorial snapshot feature of the QGLViewer library.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: <http://artis.imag.fr/Software/VRender/>

6.11. X3D TOOLKIT

X3D Development pateform

FUNCTIONAL DESCRIPTION: X3DToolkit is a library to parse and write X3D files, that supports plugins and extensions.

- Participants: Gilles Debunne and Yannick Le Goc
- Contact: Cyril Soler
- URL: <http://artis.imag.fr/Software/X3D/>

MOEX Project-Team (section vide)

MORPHEO Project-Team

6. New Software and Platforms

6.1. 4D repository

KEYWORDS: 4D - Dynamic scene

FUNCTIONAL DESCRIPTION: This website hosts dynamic mesh sequences reconstructed from images captured using a multi-camera set up. Such mesh-sequences offer a new promising vision of virtual reality, by capturing real actors and their interactions. The texture information is trivially mapped to the reconstructed geometry, by back-projecting from the images. These sequences can be seen from arbitrary viewing angles as the user navigates in 4D (3D geometry + time) . Different sequences of human / non-human interaction can be browsed and downloaded from the data section.

- Contact: Edmond Boyer
- URL: <http://4drepository.inrialpes.fr/>

6.2. Lucy Viewer

KEYWORDS: Data visualization - 4D - Multi-Cameras

SCIENTIFIC DESCRIPTION: Lucy Viewer is an interactive viewing software for 4D models, i.e. dynamic three-dimensional scenes that evolve over time. Each 4D model is a sequence of meshes with associated texture information, in terms of images captured from multiple cameras at each frame. Such data is available from the 4D repository website hosted by Inria Grenoble.

With Lucy Viewer, the user can use the mouse to zoom in onto the 4D models, zoom out, rotate, translate and view from an arbitrary angle as the 4D sequence is being played. The texture information is read from the images at each frame in the sequence and applied onto the meshes. This helps the user visualize the 3D scene in a realistic manner. The user can also freeze the motion at a particular frame and inspect a mesh in detail. Lucy Viewer lets the user to also select a subset of cameras from which to apply texture information onto the meshes. The supported formats are meshes in .OFF format and associated images in .PNG or .JPG format.

FUNCTIONAL DESCRIPTION: Lucy Viewer is an interactive viewing software for 4D models, i.e. dynamic three-dimensional scenes that evolve over time. Each 4D model is a sequence of meshes with associated texture information, in terms of images captured from multiple cameras at each frame.

- Participants: Edmond Boyer, Jean-Sébastien Franco, Matthieu Armando and EYMERIC AMSE-LEM
- Contact: Edmond Boyer
- URL: <https://kinovis.inria.fr/lucyviewer/>

6.3. Shape Tracking

FUNCTIONAL DESCRIPTION: We are developing a software suite to track shapes over temporal sequences. The motivation is to provide temporally coherent 4D Models, i.e. 3D models and their evolutions over time , as required by motion related applications such as motion analysis. This software takes as input a temporal sequence of 3D models in addition to a template and estimate the template deformations over the sequence that fit the observed 3D models.

- Contact: Edmond Boyer

6.4. QuickCSG V2

KEYWORDS: 3D modeling - CAD - 3D reconstruction - Geometric algorithms

SCIENTIFIC DESCRIPTION: See the technical report "QuickCSG: Arbitrary and Faster Boolean Combinations of N Solids", Douze, Franco, Raffin.

The extension of the algorithm to self-intersecting meshes is described in "QuickCSG with self-intersections", a document inside the package.

FUNCTIONAL DESCRIPTION: QuickCSG is a library and command-line application that computes Boolean operations between polyhedra. The basic algorithm is described in the research report "QuickCSG: Arbitrary and Faster Boolean Combinations of N Solids", Douze, Franco, Raffin. The input and output polyhedra are defined as indexed meshes. In version 2, that was developed in the context of a software transfer contract, the meshes can be self-intersecting, in which case the inside and outside are defined by the non-zero winding rule. The operation can be any arbitrary Boolean function, including one that is defined as a CSG tree. The focus of QuickCSG is speed. Robustness to degeneracies is obtained by carefully applied random perturbations.

- Authors: Matthys Douze, Jean-Sébastien Franco and Bruno Raffin
- Contact: Jean-Sébastien Franco
- URL: <https://kinovis.inria.fr/quickcsg/>

6.5. CVTGenerator

KEYWORDS: Mesh - Centroidal Voronoi tessellation - Implicit surface

FUNCTIONAL DESCRIPTION: CVTGenerator is a program to build Centroidal Voronoi Tessellations of any 3D meshes and implicit surfaces.

- Partner: INP Grenoble
- Contact: Li Wang
- URL: <http://cvt.gforge.inria.fr/>

6.6. Kinovis Platform

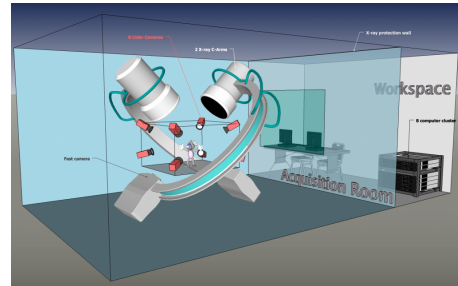
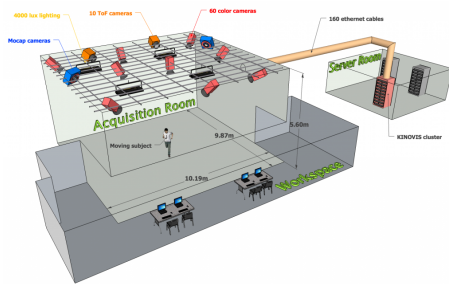


Figure 2. Kinovis platforms: on the left the Inria platform; on the right Grenoble Hospital platform.

Kinovis (<http://kinovis.inrialpes.fr/>) is a multi-camera acquisition project that was selected within the call for proposals "Equipements d'Excellence" of the program "Investissement d'Avenir" funded by the French government. The project involves 2 institutes: the Inria Grenoble Rhône-Alpes, the Université Joseph Fourier and 4 laboratories: the LJK (laboratoire Jean Kuntzmann - applied mathematics), the LIG (Laboratoire d'informatique de Grenoble - Computer Science), the Gipsa lab (Signal, Speech and Image processing) and the LADAF (Grenoble Hospitals - Anatomy). The Kinovis environment is composed of 2 complementary platforms (see Figure 2). A first platform located at Inria Grenoble with a 10mx10m acquisition surface is equipped with 68 color cameras and 20 IR motion capture (mocap) cameras. It is the evolution of the Grimage platform towards the production of better models of more complex dynamic scenes. A second platform located at Grenoble Hospitals (CHU), within the LADAF anatomy laboratory, is equipped with 10 color and 2 X-ray cameras to enable combined analysis of internal and external shape structures, such as skeletons and their surrounding bodies. Both platforms have already demonstrated their potential through a range of projects lead by the team and externally. Members of Morpheo are highly involved in this project. Edmond Boyer is coordinating this project, and Julien Pansiot is managing the technical resources of both platforms.

PERCEPTION Project-Team

5. New Software and Platforms

5.1. ECMPR

Expectation Conditional Maximization for the Joint Registration of Multiple Point Sets

FUNCTIONAL DESCRIPTION: Rigid registration of two or several point sets based on probabilistic matching between point pairs and a Gaussian mixture model

- Participants: Florence Forbes, Manuel Yguel and Radu Horaud
- Contact: Patrice Horaud
- URL: <https://team.inria.fr/perception/research/jrmpc/>

5.2. Mixcam

Reconstruction using a mixed camera system

KEYWORDS: Computer vision - 3D reconstruction

FUNCTIONAL DESCRIPTION: We developed a multiple camera platform composed of both high-definition color cameras and low-resolution depth cameras. This platform combines the advantages of the two camera types. On one side, depth (time-of-flight) cameras provide coarse low-resolution 3D scene information. On the other side, depth and color cameras can be combined such as to provide high-resolution 3D scene reconstruction and high-quality rendering of textured surfaces. The software package developed during the period 2011-2014 contains the calibration of TOF cameras, alignment between TOF and color cameras, TOF-stereo fusion, and image-based rendering. These software developments were performed in collaboration with the Samsung Advanced Institute of Technology, Seoul, Korea. The multi-camera platform and the basic software modules are products of 4D Views Solutions SAS, a start-up company issued from the PERCEPTION group.

- Participants: Clément Ménier, Georgios Evangelidis, Michel Amat, Miles Hansard, Patrice Horaud, Pierre Arquier, Quentin Pelorson, Radu Horaud, Richard Broadbridge and Soraya Arias
- Contact: Patrice Horaud
- URL: <https://team.inria.fr/perception/mixcam-project/>

5.3. NaoLab

Distributed middleware architecture for interacting with NAO

FUNCTIONAL DESCRIPTION: This software provides a set of libraries and tools to simplify the control of NAO robot from a remote machine. The main challenge is to make easy prototyping applications for NAO using C++ and Matlab programming environments. Thus NaoLab provides a prototyping-friendly interface to retrieve sensor data (video and sound streams, odometric data...) and to control the robot actuators (head, arms, legs...) from a remote machine. This interface is available on Naoqi SDK, developed by Aldebarab company, Naoqi SDK is needed as it provides the tools to access the embedded NAO services (low-level motor command, sensor data access...)

- Authors: Fabien Badeig, Quentin Pelorson and Patrice Horaud
- Contact: Patrice Horaud
- URL: <https://team.inria.fr/perception/research/naolab/>

5.4. Stereo matching and recognition library

KEYWORD: Computer vision

FUNCTIONAL DESCRIPTION: Library providing stereo matching components to rectify stereo images, to retrieve faces from left and right images, to track faces and method to recognise simple gestures

- Participants: Jan Cech, Jordi Sanchez-Riera, Radu Horaud and Soraya Arias
- Contact: Soraya Arias
- URL: <https://code.humavips.eu/projects/stereomatch>

5.5. Platforms

5.5.1. Audio-Visual Head Popeye+

In 2016 our audio-visual platform was upgraded from Popeye to Popeye+. Popeye+ has two high-definition cameras with a wide field of view. We also upgraded the software libraries that perform synchronized acquisition of audio signals and color images. Popeye+ has been used for several datasets.

Websites:

<https://team.inria.fr/perception/projects/popeye/>

<https://team.inria.fr/perception/projects/popeye-plus/>

<https://team.inria.fr/perception/avtrack1/>

<https://team.inria.fr/perception/avdiar/>

5.5.2. NAO Robots

The PERCEPTION team selected the companion robot NAO for experimenting and demonstrating various audio-visual skills as well as for developing the concept of social robotics that is able to recognize human presence, to understand human gestures and voice, and to communicate by synthesizing appropriate behavior. The main challenge of our team is to enable human-robot interaction in the real world.



Figure 2. The Popeye+ audio-visual platform (left) delivers high-quality, high-resolution and wide-angle images at 30FPS. The NAO prototype used by PERCEPTION in the EARS STREP project has a twelve-channel spherical microphone array synchronized with a stereo camera pair.

The humanoid robot NAO is manufactured by SoftBank Robotics Europe. Standing, the robot is roughly 60 cm tall, and 35cm when it is sitting. Approximately 30 cm large, NAO includes two CPUs. The first one, placed in the torso, together with the batteries, controls the motors and hence provides kinematic motions with 26 degrees of freedom. The other CPU is placed in the head and is in charge of managing the proprioceptive sensing, the communications, and the audio-visual sensors (two cameras and four microphones, in our case). NAO's on-board computing resources can be accessed either via wired or wireless communication protocols.

NAO's commercially available head is equipped with two cameras that are arranged along a vertical axis: these cameras are neither synchronized nor a significant common field of view. Hence, they cannot be used in combination with stereo vision. Within the EU project HUMAVIPS, Aldebaran Robotics developed a binocular camera system that is arranged horizontally. It is therefore possible to implement stereo vision algorithms on NAO. In particular, one can take advantage of both the robot's cameras and microphones. The cameras deliver VGA sequences of image pairs at 12 FPS, while the sound card delivers the audio signals arriving from all four microphones and sampled at 48 kHz. Subsequently, Aldebaran developed a second binocular camera system to go into the head of NAO v5.

In order to manage the information flow gathered by all these sensors, we implemented several middleware packages. In 2012 we implemented Robotics Services Bus (RSB) developed by the University of Bielefeld. Subsequently (2015-2016) the PERCEPTION team developed NAOLab, a middleware for hosting robotic applications in C, C++, Python and Matlab, using the computing power available with NAO, augmented with a networked PC. In 2017 we abandoned RSB and NAOLab and converted all our robotics software packages to ROS (Robotic Operating System).

Websites:

<https://team.inria.fr/perception/nao/>

<https://team.inria.fr/perception/research/naolab/>

PERVASIVE Project-Team

6. New Software and Platforms

6.1. Platforms

The AmiQual4Home Innovation Factory is an open research facility for innovation and experimentation with human-centered services based on the use of large-scale deployment of interconnected digital devices capable of perception, action, interaction and communication. The Innovation Factory is composed of a collection of workshops for rapid creation of prototypes, surrounded by a collection of living labs and supported by an industrial innovation and transfer service. Creation of the Innovation Factory has been made possible by a grant from French National programme Investissement d'avenir, together with substantial contributions of resources by Grenoble INP, Univ Joseph Fourier, UPMF, CNRS, Schneider Electric and the Communaute de Communes of Montbonnot. The objective is to provide the academic and industrial communities with an open platform to enable research on design, integration and evaluation of systems and services for smart habitats.

The AmiQual4Home Innovation Factory is a unique combination of three different innovation instruments:

1. Workshops for rapid prototyping of devices that embed perception, action, interaction and communication in ordinary objects based on the MIT FabLab model,
2. Facilities for real-world test and evaluation of devices and services organized as open Living Labs,
3. Resources for assisting students, researchers, entrepreneurs and industrial partners in creating new economic activities.

The AmiQual4Home Innovation Factory works with the Inovallee TARMAC technology incubator as well as the SAT Linksium to proved innovation and transfer services to enable students, researchers and local entrepreneurs to create and grow new commercial activities based on smart objects and services.

THOTH Project-Team

6. New Software and Platforms

6.1. LCR-Net

Localization-Classification-Regression Network for Human Pose

KEYWORDS: Object detection - Recognition of human movement

FUNCTIONAL DESCRIPTION: We propose an end-to-end architecture for joint 2D and 3D human pose estimation in natural images. Key to our approach is the generation and scoring of a number of pose proposals per image, which allows us to predict 2D and 3D pose of multiple people simultaneously. Our architecture contains 3 main components: 1) the pose proposal generator that suggests potential poses at different locations in the image, 2) a classifier that scores the different pose proposals, and 3) a regressor that refines pose proposals both in 2D and 3D.

- Participants: Grégory Rogez, Philippe Weinzaepfel and Cordelia Schmid
- Contact: Grégory Rogez
- Publication: [LCR-Net: Localization-Classification-Regression for Human Pose](#)
- URL: <https://thoth.inrialpes.fr/src/LCR-Net/>

6.2. CKN-seq

Convolutional Kernel Networks for Biological Sequences

KEYWORD: Bioinformatics

SCIENTIFIC DESCRIPTION: The growing amount of biological sequences available makes it possible to learn genotype-phenotype relationships from data with increasingly high accuracy. By exploiting large sets of sequences with known phenotypes, machine learning methods can be used to build functions that predict the phenotype of new, unannotated sequences. In particular, deep neural networks have recently obtained good performances on such prediction tasks, but are notoriously difficult to analyze or interpret. Here, we introduce a hybrid approach between kernel methods and convolutional neural networks for sequences, which retains the ability of neural networks to learn good representations for a learning problem at hand, while defining a well characterized Hilbert space to describe prediction functions. Our method outperforms state-of-the-art convolutional neural networks on a transcription factor binding prediction task while being much faster to train and yielding more stable and interpretable results.

FUNCTIONAL DESCRIPTION: CKN-Seq is a software package for predicting transcription factor binding sites. It was shipped with the BiorXiv preprint

D. Chen, L. Jacob, and J. Mairal. Predicting Transcription Factor Binding Sites with Convolutional Kernel Networks. 2017.

The software is implemented in PyTorch.

- Participants: Laurent Jacob, Dexiong Chen and Julien Mairal
- Partners: CNRS - UGA
- Contact: Julien Mairal
- Publication: [Biological Sequence Modeling with Convolutional Kernel Networks](#)
- URL: <https://gitlab.inria.fr/dchen/CKN-seq>

6.3. Loter

Loter: A software package to infer local ancestry for a wide range of species

KEYWORDS: Local Ancestry Inference - Bioinformatics

SCIENTIFIC DESCRIPTION: Admixture between populations provides opportunity to study biological adaptation and phenotypic variation. Admixture studies can rely on local ancestry inference for admixed individuals, which consists of computing at each locus the number of copies that originate from ancestral source populations. Loter is a software package that does not require any biological parameter besides haplotype data in order to make local ancestry inference available for a wide range of species.

FUNCTIONAL DESCRIPTION: Loter is a Python package for haplotype phasing and local ancestry inference.

NEWS OF THE YEAR: The software package was shipped with the biorxiv preprint T. Dias-Alves, J. Mairal, and M. Blum. Loter: A Software Package to Infer Local Ancestry for a Wide Range of Species. preprint BiorXiv. 2017

- Participants: Thomas Dias-Alves, Michael Blum and Julien Mairal
- Partners: UGA - CNRS
- Contact: Julien Mairal
- Publication: [Loter: A software package to infer local ancestry for a wide range of species](#)
- URL: <https://github.com/bcm-uga/Loter>

6.4. SPAMS

SParse Modeling Software

KEYWORDS: Signal processing - Machine learning

FUNCTIONAL DESCRIPTION: SPAMS is an open-source software package for sparse estimation

NEWS OF THE YEAR: The version 2.6.1 of the software package is now compatible with Python v3, R v3, comes with pre-compiled Matlab packages, and is now available on the conda and PyPi package managers.

- Participants: Ghislain Durif and Julien Mairal
- Contact: Julien Mairal
- URL: <http://spams-devel.gforge.inria.fr/>

6.5. LVO

Learning Video Object Segmentation with Visual Memory

KEYWORD: Video analysis

FUNCTIONAL DESCRIPTION: This is a public implementation of the method described in the following paper: Learning Video Object Segmentation with Visual Memory [ICCV 2017] (<https://hal.archives-ouvertes.fr/hal-01511145v2/document>).

This paper addresses the task of segmenting moving objects in unconstrained videos. We introduce a novel two-stream neural network with an explicit memory module to achieve this. The two streams of the network encode spatial and temporal features in a video sequence respectively, while the memory module captures the evolution of objects over time. The module to build a "visual memory" in video, i.e., a joint representation of all the video frames, is realized with a convolutional recurrent unit learned from a small number of training video sequences. Given a video frame as input, our approach assigns each pixel an object or background label based on the learned spatio-temporal features as well as the "visual memory" specific to the video, acquired automatically without any manually-annotated frames. The visual memory is implemented with convolutional gated recurrent units, which allows to propagate spatial information over time. We evaluate our method extensively on two benchmarks, DAVIS and Freiburg-Berkeley motion segmentation datasets, and show state-of-the-art results. For example, our approach outperforms the top method on the DAVIS dataset by nearly 6

- Participants: Karteek Alahari, Cordelia Schmid and Pavel Tokmakov
- Contact: Pavel Tokmakov
- Publication: [Learning Video Object Segmentation with Visual Memory](#)
- URL: <http://lear.inrialpes.fr/research/lvo/>

6.6. SURREAL

Learning from Synthetic Humans

KEYWORDS: Synthetic human - Segmentation - Neural networks

FUNCTIONAL DESCRIPTION: The SURREAL dataset consisting of synthetic videos of humans, and models trained on this dataset are released in this package. The code for rendering synthetic images of people and for training models is also included in the release.

- Participants: Gül Varol Simsekli, Xavier Martin, Ivan Laptev and Cordelia Schmid
- Contact: Gül Varol Simsekli
- Publication: [Learning from Synthetic Humans](#)
- URL: <http://www.di.ens.fr/willow/research/surreal/>

6.7. attn2d

Pervasive Attention

KEYWORDS: NLP - Deep learning - Machine translation

SCIENTIFIC DESCRIPTION: Pervasive attention : 2D Convolutional Networks for Sequence-to-Sequence Prediction

FUNCTIONAL DESCRIPTION: An open source PyTorch implementation of the pervasive attention model described in: Maha Elbayad, Laurent Besacier, and Jakob Verbeek. 2018. Pervasive Attention: 2D Convolutional Networks for Sequence-to-Sequence Prediction. In Proceedings of the 22nd Conference on Computational Natural Language Learning (CoNLL 2018)

- Participants: Maha Elbayad and Jakob Verbeek
- Contact: Maha Elbayad
- Publication: [Pervasive Attention: 2D Convolutional Neural Networks for Sequence-to-Sequence Prediction](#)
- URL: <https://github.com/elbayadm/attn2d>

TYREX Project-Team

5. New Software and Platforms

5.1. SPARQLGX

KEYWORDS: RDF - SPARQL - Distributed computing

SCIENTIFIC DESCRIPTION: SPARQL is the W3C standard query language for querying data expressed in RDF (Resource Description Framework). The increasing amounts of RDF data available raise a major need and research interest in building efficient and scalable distributed SPARQL query evaluators.

In this context, we propose and share SPARQLGX: our implementation of a distributed RDF datastore based on Apache Spark. SPARQLGX is designed to leverage existing Hadoop infrastructures for evaluating SPARQL queries. SPARQLGX relies on a translation of SPARQL queries into executable Spark code that adopts evaluation strategies according to (1) the storage method used and (2) statistics on data. Using a simple design, SPARQLGX already represents an interesting alternative in several scenarios.

FUNCTIONAL DESCRIPTION: This software system is an implementation of a distributed evaluator of SPARQL queries. It makes it possible to evaluate SPARQL queries on billions of triples distributed across multiple nodes in a cluster, while providing attractive performance figures.

RELEASE FUNCTIONAL DESCRIPTION: - Faster load routine which widely improves this phase performances by reading once the initial triple file and by partitioning data in the same time into the correct predicate files. - Improving the generated Scala-code of the translation process with mapValues. This technic allows not to break the partitioning of KeyValueRDD while applying transformations to the values instead of the traditional map that was done prior. - Merging and cleaning several scripts in bin/ such as for example `sgx-eval.sh` and `sde-eval.sh` - Improving the compilation process of `compile.sh` - Cleaner test scripts in tests/ - Offering the possibility of an easier deployment using Docker.

- Participants: Damien Graux, Thomas Calmant, Louis Jachiet, Nabil Layaïda and Pierre Genevès
- Contact: Pierre Genevès
- Publications: [Optimizing SPARQL query evaluation with a worst-case cardinality estimation based on statistics on the data](#) - [The SPARQLGX System for Distributed Evaluation of SPARQL Queries](#)
- URL: <https://github.com/tyrex-team/sparqlgx>

5.2. musparql

KEYWORDS: SPARQL - RDF - Property paths

FUNCTIONAL DESCRIPTION: reads a SPARQL request and translates it into an internal algebra. Rewrites the resulting term into many equivalent versions, then chooses one of them and executes it on a graph.

- Participant: Louis Jachiet
- Contact: Nabil Layaïda
- Publication: [Extending the SPARQL Algebra for the optimization of Property Paths](#)
- URL: <https://gitlab.inria.fr/tyrex/musparql>

5.3. MRB

Mixed Reality Browser

KEYWORDS: Augmented reality - Geolocation - Indoor geolocalisation - Smartphone

FUNCTIONAL DESCRIPTION: MRB displays PoI (Point of Interest) content remotely through panoramics with spatialized audio, or on-site by walking to the corresponding place, it can be used for indoor-outdoor navigation, with assistive audio technology for the visually impaired. It is the only browser of geolocalized data to use XML as a native format for PoIs, panoramics, 3D audio and to rely on HTML5 both for the iconic and full information content of PoIs. Positioning in MRB is based on a PDR library, written in C++ and Java and developed by the team, which provides the user's location in real time based on the interpretation of sensors. Three main modules have been designed to build this positioning system: (i) a pedometer that estimates the distance the user has walked and his speed, (ii) a motion manager that enables data set recording and simulation but also the creation of virtual sensors or filters (e.g gyroscope drift compensation, linear acceleration, altimeter), and (iii) a map-matching algorithm that provides a new location based on a given OpenStreetMap file description and the current user's trajectory.

- Participant: Thibaud Michel
- Contact: Nabil Layaïda
- Publications: [On Mobile Augmented Reality Applications based on Geolocation - Attitude Estimation for Indoor Navigation and Augmented Reality with Smartphones](#)
- URL: <http://tyrex.inria.fr/projects/mrb.html>

5.4. Benchmarks Attitude Smartphones

KEYWORDS: Experimentation - Motion analysis - Sensors - Performance analysis - Smartphone

SCIENTIFIC DESCRIPTION: We investigate the precision of attitude estimation algorithms in the particular context of pedestrian navigation with commodity smartphones and their inertial/magnetic sensors. We report on an extensive comparison and experimental analysis of existing algorithms. We focus on typical motions of smartphones when carried by pedestrians. We use a precise ground truth obtained from a motion capture system. We test state-of-the-art attitude estimation techniques with several smartphones, in the presence of magnetic perturbations typically found in buildings. We discuss the obtained results, analyze advantages and limits of current technologies for attitude estimation in this context. Furthermore, we propose a new technique for limiting the impact of magnetic perturbations with any attitude estimation algorithm used in this context. We show how our technique compares and improves over previous works.

- Participants: Hassen Fourati, Nabil Layaïda, Pierre Genevès and Thibaud Michel
- Partner: GIPSA-Lab
- Contact: Pierre Genevès
- URL: <http://tyrex.inria.fr/mobile/benchmarks-attitude/>

5.5. MedAnalytics

KEYWORDS: Big data - Predictive analytics - Distributed systems

FUNCTIONAL DESCRIPTION: We implemented a method for the automatic detection of at-risk profiles based on a fine-grained analysis of prescription data at the time of admission. The system relies on an optimized distributed architecture adapted for processing very large volumes of medical records and clinical data. We conducted practical experiments with real data of millions of patients and hundreds of hospitals. We demonstrated how the various perspectives of big data improve the detection of at-risk patients, making it possible to construct predictive models that benefit from volume and variety. This prototype implementation is described in the 2017 preprint available at: <https://hal.inria.fr/hal-01517087/document>.

- Participants: Pierre Genevès and Thomas Calmant
- Partner: CHU Grenoble
- Contact: Pierre Genevès
- Publication: [Scalable Machine Learning for Predicting At-Risk Profiles Upon Hospital Admission](#)

5.6. MuIR

Mu Intermediate Representation

KEYWORDS: Optimizing compiler - Querying

FUNCTIONAL DESCRIPTION: This is a prototype of an intermediate language representation, i.e. an implementation of algebraic terms, rewrite rules, query plans, cost model, query optimizer, and query evaluators (including a distributed evaluator of algebraic terms using Apache Spark).

- Contact: Pierre Genevès