RESEARCH CENTER

FIELD

Activity Report 2018

Section Software

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ALGORITHMICS, PROGRAMMING, SOFTWARE AND ARCHITECTURE

APPLIED MATHEMATICS, COMPUTATION AND SIMULATION

DIGITAL HEALTH, BIOLOGY AND EARTH

NETWORKS, SYSTEMS AND SERVICES, DISTRIBUTED COMPUTING

PERCEPTION, COGNITION AND INTERACTION

ANTIQUE Project-Team

5. New Software and Platforms

5.1. APRON

SCIENTIFIC DESCRIPTION: The APRON library is intended to be a common interface to various underlying libraries/abstract domains and to provide additional services that can be implemented independently from the underlying library/abstract domain, as shown by the poster on the right (presented at the SAS 2007 conference. You may also look at:
FUNCTIONAL DESCRIPTION: The Apron library is dedicated to the static analysis of the numerical variables of a program by abstract interpretation. Its goal is threefold: provide ready-to-use numerical abstractions under a common API for analysis implementers, encourage the research in numerical abstract domains by providing a platform for integration and comparison of domains, and provide a teaching and demonstration tool to disseminate knowledge on abstract interpretation.

- Participants: Antoine Miné and Bertrand Jeannet
- Contact: Antoine Miné
- URL: http://apron.cri.ensmp.fr/library/

5.2. Astrée

The AstréeA Static Analyzer of Asynchronous Software
KEYWORDS: Static analysis - Static program analysis - Program verification - Software Verification - Abstraction
SCIENTIFIC DESCRIPTION: Astrée analyzes structured C programs, with complex memory usages, but without dynamic memory allocation nor recursion. This encompasses many embedded programs as found in earth transportation, nuclear energy, medical instrumentation, and aerospace applications, in particular synchronous control/command. The whole analysis process is entirely automatic.

Astrée discovers all runtime errors including:

undefined behaviors in the terms of the ANSI C99 norm of the C language (such as division by 0 or out of bounds array indexing),

any violation of the implementation-specific behavior as defined in the relevant Application Binary Interface (such as the size of integers and arithmetic overflows),

any potentially harmful or incorrect use of C violating optional user-defined programming guidelines (such as no modular arithmetic for integers, even though this might be the hardware choice),

failure of user-defined assertions.
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Astrée is a static analyzer for sequential programs based on abstract interpretation. The Astrée static analyzer aims at proving the absence of runtime errors in programs written in the C programming language.

- Participants: Antoine Miné, Jérôme Feret, Laurent Mauborgne, Patrick Cousot, Radhia Cousot and Xavier Rival
- Partners: CNRS - ENS Paris - AbsInt Angewandte Informatik GmbH
- Contact: Patrick Cousot
- URL: http://www.astree.ens.fr/

5.3. AstréeA

The AstréeA Static Analyzer of Asynchronous Software
KEYWORDS: Static analysis - Static program analysis
SCIENTIFIC DESCRIPTION: AstréeA analyzes C programs composed of a fixed set of threads that communicate through a shared memory and synchronization primitives (mutexes, FIFOs, blackboards, etc.), but without recursion nor dynamic creation of memory, threads nor synchronization objects. AstréeA assumes a real-time scheduler, where thread scheduling strictly obeys the fixed priority of threads. Our model follows the ARINC 653 OS specification used in embedded industrial aeronautic software. Additionally, AstréeA employs a weakly-consistent memory semantics to model memory accesses not protected by a mutex, in order to take into account soundly hardware and compiler-level program transformations (such as optimizations). AstréeA checks for the same run-time errors as Astrée , with the addition of data-races.
FUNCTIONAL DESCRIPTION: AstréeA is a static analyzer prototype for parallel software based on abstract interpretation. The AstréeA prototype is a fork of the Astrée static analyzer that adds support for analyzing parallel embedded C software.

- Participants: Antoine Miné, Jérôme Feret, Patrick Cousot, Radhia Cousot and Xavier Rival
- Partners: CNRS - ENS Paris - AbsInt Angewandte Informatik GmbH
- Contact: Patrick Cousot
- URL: http://www.astreea.ens.fr/

5.4. ClangML

KEYWORD: Compilation
FUNCTIONAL DESCRIPTION: ClangML is an OCaml binding with the Clang front-end of the LLVM compiler suite. Its goal is to provide an easy to use solution to parse a wide range of C programs, that can be called from static analysis tools implemented in OCaml, which allows to test them on existing programs written in C (or in other idioms derived from C) without having to redesign a front-end from scratch. ClangML features an interface to a large set of internal AST nodes of Clang , with an easy to use API. Currently, ClangML supports all C language AST nodes, as well as a large part of the C nodes related to C++ and Objective-C.

- Participants: Devin Mccoughlin, François Berenger and Pippijn Van Steenhoven
- Contact: Xavier Rival
- URL: https://github.com/Antique-team/clangml/tree/master/clang

5.5. FuncTion

SCIENTIFIC DESCRIPTION: FuncTion is based on an extension to liveness properties of the framework to analyze termination by abstract interpretation proposed by Patrick Cousot and Radhia Cousot. FuncTion infers ranking functions using piecewise-defined abstract domains. Several domains are available to partition the ranking function, including intervals, octagons, and polyhedra. Two domains are also available to represent the value of ranking functions: a domain of affine ranking functions, and a domain of ordinal-valued ranking functions (which allows handling programs with unbounded non-determinism).

FUNCTIONAL DESCRIPTION: FuncTion is a research prototype static analyzer to analyze the termination and functional liveness properties of programs. It accepts programs in a small non-deterministic imperative language. It is also parameterized by a property: either termination, or a recurrence or a guarantee property (according to the classification by Manna and Pnueli of program properties). It then performs a backward static analysis that automatically infers sufficient conditions at the beginning of the program so that all executions satisfying the conditions also satisfy the property.

- Participants: Antoine Miné and Caterina Urban
- Contact: Caterina Urban
- URL: http://www.di.ens.fr/~urban/FuncTion.html

5.6. HOO

Heap Abstraction for Open Objects

FUNCTIONAL DESCRIPTION: JSAna with HOO is a static analyzer for JavaScript programs. The primary component, HOO, which is designed to be reusable by itself, is an abstract domain for a dynamic language heap. A dynamic language heap consists of open, extensible objects linked together by pointers. Uniquely, HOO abstracts these extensible objects, where attribute/field names of objects may be unknown. Additionally, it contains features to keeping precise track of attribute name/value relationships as well as calling unknown functions through desynchronized separation.

As a library, HOO is useful for any dynamic language static analysis. It is designed to allow abstractions for values to be easily swapped out for different abstractions, allowing it to be used for a wide-range of dynamic languages outside of JavaScript.

- Participant: Arlen Cox
- Contact: Arlen Cox

5.7. MemCAD

The MemCAD static analyzer

KEYWORDS: Static analysis - Abstraction

FUNCTIONAL DESCRIPTION: MemCAD is a static analyzer that focuses on memory abstraction. It takes as input C programs, and computes invariants on the data structures manipulated by the programs. It can also verify memory safety. It comprises several memory abstract domains, including a flat representation, and two graph abstractions with summaries based on inductive definitions of data-structures, such as lists and trees and several combination operators for memory abstract domains (hierarchical abstraction, reduced product). The purpose of this construction is to offer a great flexibility in the memory abstraction, so as to either make very efficient static analyses of relatively simple programs, or still quite efficient static analyses of very involved pieces of code. The implementation consists of over 30 000 lines of ML code, and relies on the ClangML front-end. The current implementation comes with over 300 small size test cases that are used as regression tests.

- Participants: Antoine Toubhans, François Berenger, Huisong Li and Xavier Rival
- Contact: Xavier Rival
- URL: http://www.di.ens.fr/~rival/memcad.html

5.8. KAPPA

A rule-based language for modeling interaction networks

KEYWORDS: Systems Biology - Modeling - Static analysis - Simulation - Model reduction

SCIENTIFIC DESCRIPTION: OpenKappa is a collection of tools to build, debug and run models of biological pathways. It contains a compiler for the Kappa Language, a static analyzer (for debugging models), a simulator, a compression tool for causal traces, and a model reduction tool.

FUNCTIONAL DESCRIPTION: Kappa is provided with the following tools: - a compiler - a stochastic simulator - a static analyzer - a trace compression algorithm - an ODE generator.

RELEASE FUNCTIONAL DESCRIPTION: On line UI, Simulation is based on a new data-structure (see ESOP 2017), New abstract domains are available in the static analyzer (see SASB 2016), Local traces (see TCBB 2018), Reasoning on polymers (see SASB 2018).

- Participants: Jean Krivine, Jérôme Feret, Kim Quyen Ly, Pierre Boutillier, Russ Harmer, Vincent Danos and Walter Fontana
- Partners: ENS Lyon - Université Paris-Diderot - HARVARD Medical School
- Contact: Jérôme Feret
- URL: http://www.kappalanguage.org/

5.9. QUICr

FUNCTIONAL DESCRIPTION: QUICr is an OCaml library that implements a parametric abstract domain for sets. It is constructed as a functor that accepts any numeric abstract domain that can be adapted to the interface and produces an abstract domain for sets of numbers combined with numbers. It is relational, flexible, and tunable. It serves as a basis for future exploration of set abstraction.

- Participant: Arlen Cox
- Contact: Arlen Cox

5.10. LCertify

KEYWORD: Compilation

SCIENTIFIC DESCRIPTION: The compilation certification process is performed automatically, thanks to a prover designed specifically. The automatic proof is done at a level of abstraction which has been defined so that the result of the proof of equivalence is strong enough for the goals mentioned above and so that the proof obligations can be solved by efficient algorithms.

FUNCTIONAL DESCRIPTION: Abstract interpretation, Certified compilation, Static analysis, Translation validation, Verifier. The main goal of this software project is to make it possible to certify automatically the compilation of large safety critical software, by proving that the compiled code is correct with respect to the source code: When the proof succeeds, this guarantees semantic equivalence. Furthermore, this approach should allow to meet some domain specific software qualification criteria (such as those in DO-178 regulations for avionics software), since it allows proving that successive development levels are correct with respect to each other i.e., that they implement the same specification. Last, this technique also justifies the use of source level static analyses, even when an assembly level certification would be required, since it establishes separately that the source and the compiled code are equivalent.ntees that no compiler bug did cause incorrect code to be generated.

- Participant: Xavier Rival
- Partners: CNRS - ENS Paris
- Contact: Xavier Rival
- URL: http://www.di.ens.fr/~rival/lcertify.html

5.11. Zarith

FUNCTIONAL DESCRIPTION: Zarith is a small (10K lines) OCaml library that implements arithmetic and logical operations over arbitrary-precision integers. It is based on the GNU MP library to efficiently implement arithmetic over big integers. Special care has been taken to ensure the efficiency of the library also for small integers: small integers are represented as Caml unboxed integers and use a specific C code path. Moreover, optimized assembly versions of small integer operations are provided for a few common architectures.

Zarith is currently used in the Astrée analyzer to enable the sound analysis of programs featuring 64-bit (or larger) integers. It is also used in the Frama-C analyzer platform developed at CEA LIST and Inria Saclay.

- Participants: Antoine Miné, Pascal Cuoq and Xavier Leroy
- Contact: Antoine Miné
- URL: http://forge.ocamlcore.org/projects/zarith

AOSTE2 Team

6. New Software and Platforms

6.1. SynDEx

KEYWORDS: Distributed - Optimization - Real time - Embedded systems - Scheduling analyses
SCIENTIFIC DESCRIPTION: SynDEx is a system level CAD software implementing the AAA methodology for rapid prototyping and for optimizing distributed real-time embedded applications. It is developed in OCaML.

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

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

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

Finally, real-time distributed embedded code can be automatically generated for dedicated distributed real-time executives, possibly calling services of resident real-time operating systems such as Linux/RTAI or Osek for instance. These executives are deadlock-free, based on off-line scheduling policies. Dedicated executives induce minimal overhead, and are built from processor-dependent executive kernels. To this date, executives kernels are provided for: TMS320C40, PIC18F2680, i80386, MC68332, MPC555, i80C196 and Unix/Linux workstations. Executive kernels for other processors can be achieved at reasonable cost following these examples as patterns.
FUNCTIONAL DESCRIPTION: Software for optimising the implementation of embedded distributed real-time applications and generating efficient and correct by construction code
NEWS OF THE YEAR: We improved the distribution and scheduling heuristics to take into account the needs of co-simulation.

- Participant: Yves Sorel
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- URL: http://www.syndex.org

6.2. EVT Kopernic

KEYWORDS: Embedded systems - Worst Case Execution Time - Real-time application - Statistics
SCIENTIFIC DESCRIPTION: The EVT-Kopernic tool is an implementation of the Extreme Value Theory (EVT) for the problem of the statistical estimation of worst-case bounds for the execution time of a program on a processor. Our implementation uses the two versions of EVT - GEV and GPD - to propose two independent methods of estimation. Their results are compared and only results that are sufficiently close allow to validate an estimation. Our tool is proved predictable by its unique choice of block (GEV) and threshold (GPD) while proposant reproducible estimations.

FUNCTIONAL DESCRIPTION: EVT-Kopernic is tool proposing a statistical estimation for bounds on worst-case execution time of a program on a processor. The estimator takes into account dependences between execution times by learning from the history of execution, while dealing also with cases of small variability of the execution times.

NEWS OF THE YEAR: Any statistical estimator should come with an representative measurement protocole based on the processus of composition, proved correct. We propose the first such principle of composition while using a Bayesien modeling taking into account iteratively different measurement models. The composition model has been described in a patent submitted this year with a scientific publication under preparation.

- Participants: Adriana Gogonel and Liliana Cucu
- Contact: Adriana Gogonel
- URL: http://inria-rscript.serveftp.com/

6.3. LoPhT-manycore

Logical to Physical Time compiler for many cores

KEYWORDS: Real time - Compilation - Task scheduling - Automatic parallelization

SCIENTIFIC DESCRIPTION: Lopht is a system-level compiler for embedded systems, whose objective is to fully automate the implementation process for certain classes of embedded systems. Like in a classical compiler (e.g. gcc), its input is formed of two objects. The first is a program providing a platform-indepedent description of the functionality to implement and of the non-functional requirements it must satisfy (e.g. real-time, partitioning). This is provided under the form of a data-flow synchronous program annotated with non-functional requirements. The second is a description of the implementation platform, defining the topology of the platform, the capacity of its elements, and possibly platform-dependent requirements (e.g. allocation).

From these inputs, Lopht produces all the C code and configuration information needed to allow compilation and execution on the physical target platform. Implementations are correct by construction Resulting implementations are functionally correct and satisfy the non-functional requirements. Lopht-manycore is a version of Lopht targeting shared-memory many-core architectures.

The algorithmic core of Lopht-manycore is formed of timing analysis, allocation, scheduling, and code generation heuristics which rely on four fundamental choices. 1) A static (off-line) real-time scheduling approach where allocation and scheduling are represented using time tables (also known as scheduling or reservation tables). 2) Scalability, attained through the use of low-complexity heuristics for all synthesis and associated analysis steps. 3) Efficiency (of generated implementations) is attained through the use of precise representations of both functionality and the platform, which allow for fine-grain allocation of resources such as CPU, memory, and communication devices such as network-on-chip multiplexers. 4) Full automation, including that of the timing analysis phase.

The last point is characteristic to Lopht-manycore. Existing methods for schedulability analysis and real-time software synthesis assume the existence of a high-level timing characterization that hides much of the hardware complexity. For instance, a common hypothesis is that synchronization and interference costs are accounted for in the duration of computations. However, the high-level timing characterization is seldom (if ever) soundly derived from the properties of the platform and the program. In practice, large margins (e.g. 100%) with little formal justification are added to computation durations to account for hidden hardware complexity. Lopht-manycore overcomes this limitation. Starting from the worst-case execution time (WCET) estimations of computation operations and from a precise and safe timing model of the platform, it maintains a precise timing accounting throughout the mapping process. To do this, timing accounting must take into account all details of allocation, scheduling, and code generation, which in turn must satisfy specific hypotheses.

FUNCTIONAL DESCRIPTION: Accepted input languages for functional specifications include dialects of Lustre such as Heptagon and Scade v4. To ensure the respect of real-time requirements, Lopht-manycore pilots the use of the worst-case execution time (WCET) analysis tool (ait from AbsInt). By doing this, and by using a precise timing model for the platform, Lopht-manycore eliminates the need to adjust the WCET values through the addition of margins to the WCET values that are usually both large and without formal safety guarantees. The output of Lopht-manycore is formed of all the multi-threaded C code and configuration information needed to allow compilation, linking/loading, and real-time execution on the target platform.

NEWS OF THE YEAR: In the framework of the ITEA3 ASSUME project we have extended the Lopht-manycore to allow multiple cores to access the same memory bank at the same time. To do this, the timing accounting of Lopht has been extended to take into account memory access interferences during the allocation and scheduling process. Lopht now also pilots the aiT static WCET analysis tool from AbsInt by generating the analysis scripts, thus ensuring the consistency between the hypotheses made by Lopht and the way timing analysis is performed by aiT. As a result, we are now able to synthesize code for the computing clusters of the Kalray MPPA256 platform. Lopht-manycore is evaluated on avionics case studies in the perspective of increasing its technology readiness level for this application class.

- Participants: Dumitru Potop-Butucaru and Keryan Didier
- Contact: Dumitru Potop-Butucaru

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

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

AROMATH Project-Team

5. New Software and Platforms

5.1. Platforms

5.1.1. Axl

KEYWORDS: Algorithm , CAD , Numerical algorithm , Geometric algorithms

SCIENTIFIC DESCRIPTION

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

FUNCTIONAL DESCRIPTION

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

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

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

5.1.2. Skelton

KEYWORDS: Algorithm, Numerical algorithm, Geometric algorithm, Scaffolding, Implicit surface, Mesh generation

SCIENTIFIC DESCRIPTION

Skelton is a C++ library for skeleton-based modeling with convolution surfaces. It supports skeletons made of line segments and arcs of circle, including circular splines, and features an anisotropic extension to circular splines. The library can generate a quad dominant mesh that surrounds, and follows, the structure of the skeleton. The mesh is generated with an advanced scaffolding algorithm that works for skeletons of any topology.

FUNCTIONAL DESCRIPTION

Skelton is a multi-platform C++ library distributed as source code. It provides a class hierarchy for creating and manipulating geometric objects generated with anisotropic convolution. It can take the skeleton as an input file or defined directly by the user. The library supports an improved version of convolution surfaces and permits the design of anisotropic surfaces. The scaffolding algorithm can be used independently of the implicit surface definition. The library has a command line interface that controls most of the functionality. The user can subclass elements of the library for extended behavior.

- Participants: Alvaro Fuentes, Evelyne Hubert.
- Contacts: Alvaro Fuentes, Evelyne Hubert.
- URL: https://gitlab.inria.fr/afuentes/Skelton

CAIRN Project-Team

6. New Software and Platforms

6.1. Gecos

Generic Compiler Suite
KEYWORDS: Source-to-source compiler - Model-driven software engineering - Retargetable compilation
SCIENTIFIC DESCRIPTION: The Gecos (Generic Compiler Suite) project is a source-to-source compiler infrastructure developed in the Cairn group since 2004. It was designed to enable fast prototyping of program analysis and transformation for hardware synthesis and retargetable compilation domains.

Gecos is Java based and takes advantage of modern model driven software engineering practices. It uses the Eclipse Modeling Framework (EMF) as an underlying infrastructure and takes benefits of its features to make it easily extensible. Gecos is open-source and is hosted on the Inria gforge.

The Gecos infrastructure is still under very active development, and serves as a backbone infrastructure to projects of the group. Part of the framework is jointly developed with Colorado State University and between 2012 and 2015 it was used in the context of the FP7 ALMA European project. The Gecos infrastructure is currently used by the EMMTRIX start-up, a spin-off from the ALMA project which aims at commercializing the results of the project, and in the context of the H2020 ARGO European project.
FUNCTIONAL DESCRIPTION: GeCoS provides a programme transformation toolbox facilitating parallelisation of applications for heterogeneous multiprocessor embedded platforms. In addition to targeting programmable processors, GeCoS can regenerate optimised code for High Level Synthesis tools.

- Participants: Tomofumi Yuki, Thomas Lefeuvre, Imèn Fassi, Mickael Dardaillon, Ali Hassan El Moussawi and Steven Derrien
- Partner: Université de Rennes 1
- Contact: Steven Derrien
- URL: http://gecos.gforge.inria.fr

6.2. ID-Fix

Infrastructure for the Design of Fixed-point systems
KEYWORDS: Energy efficiency - Dynamic range evaluation - Accuracy optimization - Fixed-point arithmetic - Analytic Evaluation - Embedded systems - Code optimisation
SCIENTIFIC DESCRIPTION: The different techniques proposed by the team for fixed-point conversion are implemented on the ID.Fix infrastructure. The application is described with a C code using floating-point data types and different pragmas, used to specify parameters (dynamic, input/output word-length, delay operations) for the fixed-point conversion. This tool determines and optimizes the fixed-point specification and then, generates a C code using fixed-point data types (ac_fixed) from Mentor Graphics. The infrastructure is made-up of two main modules corresponding to the fixed-point conversion (ID.Fix-Conv) and the accuracy evaluation (ID.Fix-Eval).
FUNCTIONAL DESCRIPTION: ID.Fix focuses on computational precision accuracy and can provide an optimised specification using fixed point arithmetic from a C source code with floating point data types. Fixed point arithmetic is very widely used in embedded systems as it provides better performance and is much more energy efficient. ID.Fix used an analytic programme model which means it can explore more solutions and thereby produce much more efficient code.

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- Partner: Université de Rennes 1
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- URL: http://idfix.gforge.inria.fr

6.3. Platforms

6.3.1. Zyggie: a Wireless Body Sensor Network Platform

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

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

FUNCTIONAL DESCRIPTION: The Zyggie sensor platform was developed to create an autonomous Wireless Body Sensor Network (WBSN) with the capabilities of monitoring body movements. The Zyggie platform is part of the BoWI project funded by CominLabs. Zyggie is composed of a processor, a radio transceiver and different sensors including an Inertial Measurement Unit (IMU) with 3-axis accelerometer, gyrometer, and magnetometer. Zyggie is used for evaluating data fusion algorithms, low power computing algorithms, wireless protocols, and body channel characterization in the BoWI project.

The Zyggie V2 prototype (see Figure 2) includes the following features: a 32-bit micro-controller to manage a custom MAC layer and process quaternions based on IMU measures, and an UWB radio from DecaWave to measure distances between nodes with Time of Flight (ToF).

- Participants: Arnaud Carer and Olivier Sentieys
- Partners: Lab-STICC, Université de Rennes 1
- Contact: Olivier Sentieys
- URL: https://bowi.cominlabs.u-bretagneloire.fr/zyggie-wbsn-platform

Figure 2. CAIRN's Ziggie platform for WBSN

6.3.2. E-methodHW: an automatic tool for the evaluation of polynomial and rational function approximations

KEYWORDS: function approximation, FPGA hardware implementation generator

SCIENTIFIC DESCRIPTION: E-methodHW is an open source C/C++ prototype tool written to exemplify what kind of numerical function approximations can be developed using a digit recurrence evaluation scheme for polynomials and rational functions.

FUNCTIONAL DESCRIPTION: E-methodHW provides a complete design flow from choice of mathematical function operator up to optimised VHDL code that can be readily deployed on an FPGA. The use of the E-method allows the user great flexibility if targeting high throughput applications.

- Participants: Silviu-Ioan Filip, Matei Istoan
- Partners: Université de Rennes 1, Imperial College London
- Contact: Silviu-Ioan Filip
- URL: https://github.com/sfilip/emethod

6.3.3. Hybrid-DBT

KEYWORDS: Dynamic Binary Translation, hardware acceleration, VLIW processor, RISC-V

SCIENTIFIC DESCRIPTION: Hybrid-DBT is a hardware/software Dynamic Binary Translation (DBT) framework capable of translating RISC-V binaries into VLIW binaries. Since the DBT overhead has to be as small as possible, our implementation takes advantage of hardware acceleration for performance critical stages (binary translation, dependency analysis and instruction scheduling) of the flow. Thanks to hardware acceleration, our implementation is two orders of magnitude faster than a pure software implementation and enable an overall performance improvements by 23% on average, compared to a native RISC-V execution.

- Participants: Simon Rokicki, Steven Derrien
- Partners: Université de Rennes 1
- URL: https://github.com/srokicki/HybridDBT

6.3.4. Comet

KEYWORDS: Processor core, RISC-V instruction-set architecture

SCIENTIFIC DESCRIPTION: Comet is a RISC-V pipelined processor with data/instruction caches, fully developed using High-Level Synthesis. The behavior of the core is defined in a small C code which is then fed into a HLS tool to generate the RTL representation. Thanks to this design flow, the C description can be used as a fast and cycle-accurate simulator, which behaves exactly like the final hardware. Moreover, modifications on the core can be done easily at the C level. Figure 3 depicts the place and route of a Comet core in a 28nm FDSOI technology.

- Participants: Simon Rokicki, Steven Derrien, Olivier Sentieys, Davide Pala, Joseph Paturel
- Partners: Université de Rennes 1
- URL: https://gitlab.inria.fr/srokicki/Comet

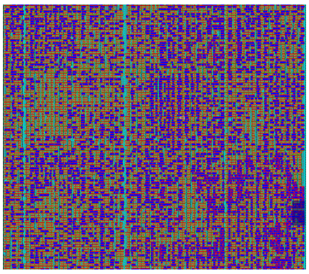

Figure 3. Floorplan of the Comet core (150μm$\times$150μm in a 28nm FDSOI technology)

CAMUS Team

6. New Software and Platforms

6.1. APOLLO

Automatic speculative POLyhedral Loop Optimizer
KEYWORD: Automatic parallelization
FUNCTIONAL DESCRIPTION: APOLLO is dedicated to automatic, dynamic and speculative parallelization of loop nests that cannot be handled efficiently at compile-time. It is composed of a static part consisting of specific passes in the LLVM compiler suite, plus a modified Clang frontend, and a dynamic part consisting of a runtime system. It can apply on-the-fly any kind of polyhedral transformations, including tiling, and can handle nonlinear loops, as while-loops referencing memory through pointers and indirections.

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

6.2. Clan

A Polyhedral Representation Extraction Tool for C-Based High Level Languages
KEYWORD: Polyhedral compilation
FUNCTIONAL DESCRIPTION: Clan is a free software and library which translates some particular parts of high level programs written in C, C++ or Java into a polyhedral representation called OpenScop. This representation may be manipulated by other tools to, e.g., achieve complex analyses or program restructurations (for optimization, parallelization or any other kind of manipulation). It has been created to avoid tedious and error-prone input file writing for polyhedral tools (such as CLooG, LeTSeE, Candl etc.). Using Clan, the user has to deal with source codes based on C grammar only (as C, C++ or Java). Clan is notably the frontend of the two major high-level compilers Pluto and PoCC.

- Participants: Cédric Bastoul and Imèn Fassi
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/clan/

6.3. Clay

Chunky Loop Alteration wizardrY
FUNCTIONAL DESCRIPTION: Clay is a free software and library devoted to semi-automatic optimization using the polyhedral model. It can input a high-level program or its polyhedral representation and transform it according to a transformation script. Classic loop transformations primitives are provided. Clay is able to check for the legality of the complete sequence of transformation and to suggest corrections to the user if the original semantics is not preserved.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/clay/

6.4. CLooG

Code Generator in the Polyhedral Model

FUNCTIONAL DESCRIPTION: CLooG is a free software and library to generate code (or an abstract syntax tree of a code) for scanning Z-polyhedra. That is, it finds a code (e.g. in C, FORTRAN...) that reaches each integral point of one or more parameterized polyhedra. CLooG has been originally written to solve the code generation problem for optimizing compilers based on the polyhedral model. Nevertheless it is used now in various area e.g. to build control automata for high-level synthesis or to find the best polynomial approximation of a function. CLooG may help in any situation where scanning polyhedra matters. While the user has full control on generated code quality, CLooG is designed to avoid control overhead and to produce a very effective code. CLooG is widely used (including by GCC and LLVM compilers), disseminated (it is installed by default by the main Linux distributions) and considered as the state of the art in polyhedral code generation.

RELEASE FUNCTIONAL DESCRIPTION: It mostly solves building and offers a better OpenScop support.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://www.cloog.org

6.5. OpenScop

A Specification and a Library for Data Exchange in Polyhedral Compilation Tools

FUNCTIONAL DESCRIPTION: OpenScop is an open specification that defines a file format and a set of data structures to represent a static control part (SCoP for short), i.e., a program part that can be represented in the polyhedral model. The goal of OpenScop is to provide a common interface to the different polyhedral compilation tools in order to simplify their interaction. To help the tool developers to adopt this specification, OpenScop comes with an example library (under 3-clause BSD license) that provides an implementation of the most important functionalities necessary to work with OpenScop.

- Participant: Cédric Bastoul
- Contact: Cédric Bastoul
- URL: http://icps.u-strasbg.fr/people/bastoul/public_html/development/openscop/

6.6. ORWL

Ordered Read-Write Lock

KEYWORDS: Task scheduling - Deadlock detection

FUNCTIONAL DESCRIPTION: ORWL is a reference implementation of the Ordered Read-Write Lock tools. The macro definitions and tools for programming in C99 that have been implemented for ORWL have been separated out into a toolbox called P99.

- Participants: Jens Gustedt, Mariem Saied and Stéphane Vialle
- Contact: Jens Gustedt
- Publications: Iterative Computations with Ordered Read-Write Locks - Automatic, Abstracted and Portable Topology-Aware Thread Placement - Resource-Centered Distributed Processing of Large Histopathology Images - Automatic Code Generation for Iterative Multi-dimensional Stencil Computations

6.7. musl

KEYWORDS: Standards - Library

SCIENTIFIC DESCRIPTION: musl provides consistent quality and implementation behavior from tiny embedded systems to full-fledged servers. Minimal machine-specific code means less chance of breakage on minority architectures and better success with “write once run everywhere” C development.

musl's efficiency is unparalleled in Linux libc implementations. Designed from the ground up for static linking, musl carefully avoids pulling in large amounts of code or data that the application will not use. Dynamic linking is also efficient, by integrating the entire standard library implementation, including threads, math, and even the dynamic linker itself into a single shared object, most of the startup time and memory overhead of dynamic linking have been eliminated.
FUNCTIONAL DESCRIPTION: We participate in the development of musl, a re-implementation of the C library as it is described by the C and POSIX standards. It is lightweight, fast, simple, free, and strives to be correct in the sense of standards-conformance and safety. Musl is production quality code that is mainly used in the area of embedded devices. It gains more market share also in other areas, e.g. there are now Linux distributions that are based on musl instead of Gnu LibC.

- Participant: Jens Gustedt
- Contact: Jens Gustedt
- URL: http://www.musl-libc.org/

6.8. Modular C

KEYWORDS: Programming language - Modularity
FUNCTIONAL DESCRIPTION: The change to the C language is minimal since we only add one feature, composed identifiers, to the core language. Our modules can import other modules as long as the import relation remains acyclic and a module can refer to its own identifiers and those of the imported modules through freely chosen abbreviations. Other than traditional C include, our import directive ensures complete encapsulation between modules. The abbreviation scheme allows to seamlessly replace an imported module by another one with an equivalent interface. In addition to the export of symbols, we provide parameterized code injection through the import of "snippets". This implements a mechanism that allows for code reuse, similar to X macros or templates. Additional features of our proposal are a simple dynamic module initialization scheme, a structured approach to the C library and a migration path for existing software projects.

- Author: Jens Gustedt
- Contact: Jens Gustedt
- Publications: Modular C - Arbogast: Higher order automatic differentiation for special functions with Modular C - Futex based locks for C11's generic atomics
- URL: http://cmod.gforge.inria.fr/

6.9. arbogast

KEYWORD: Automatic differentiation
SCIENTIFIC DESCRIPTION: This high-level toolbox for the calculus with Taylor polynomials is named after L.F.A. Arbogast (1759-1803), a French mathematician from Strasbourg (Alsace), for his pioneering work in derivation calculus. Its modular structure ensures unmatched efficiency for computing higher order Taylor polynomials. In particular it permits compilers to apply sophisticated vector parallelization to the derivation of nearly unmodified application code.
FUNCTIONAL DESCRIPTION: Arbogast is based on a well-defined extension of the C programming language, Modular C, and places itself between tools that proceed by operator overloading on one side and by rewriting, on the other. The approach is best described as contextualization of C code because it permits the programmer to place his code in different contexts – usual math or AD – to reinterpret it as a usual C function or as a differential operator. Because of the type generic features of modern C, all specializations can be delegated to the compiler.

- Author: Jens Gustedt
- Contact: Jens Gustedt
- Publications: Arbogast: Higher order automatic differentiation for special functions with Modular C - Arbogast – Origine d'un outil de dérivation automatique
- URL: https://gforge.inria.fr/projects/arbo

6.10. CFML

Interactive program verification using characteristic formulae
KEYWORDS: Coq - Software Verification - Deductive program verification - Separation Logic
FUNCTIONAL DESCRIPTION: The CFML tool supports the verification of OCaml programs through interactive Coq proofs. CFML proofs establish the full functional correctness of the code with respect to a specification. They may also be used to formally establish bounds on the asymptotic complexity of the code. The tool is made of two parts: on the one hand, a characteristic formula generator implemented as an OCaml program that parses OCaml code and produces Coq formulae, and, on the other hand, a Coq library that provides notations and tactics for manipulating characteristic formulae interactively in Coq.

- Participants: Arthur Charguéraud, Armaël Guéneau and François Pottier
- Contact: Arthur Charguéraud
- URL: http://www.chargueraud.org/softs/cfml/

6.11. SPETABARU

SPEculative TAsk-BAsed RUntime system
KEYWORDS: HPC - Parallel computing - Task-based algorithm
FUNCTIONAL DESCRIPTION: SPETABARU is a task-based runtime system for multi-core architectures that includes speculative execution models. It is a pure C++11 product without external dependency. It uses advanced meta-programming and allows for an easy customization of the scheduler. It is also capable to generate execution traces in SVG to better understand the behavior of the applications.

- Contact: Bérenger Bramas
- URL: https://gitlab.inria.fr/bramas/spetabaru

CARAMBA Project-Team

6. New Software and Platforms

6.1. Belenios

Belenios - Verifiable online voting system
KEYWORD: E-voting
FUNCTIONAL DESCRIPTION: Belenios is an open-source online voting system that provides confidentiality and verifiability. End-to-end verifiablity relies on the fact that the ballot box is public (voters can check that their ballots have been received) and on the fact that the tally is publicly verifiable (anyone can recount the votes). Confidentiality relies on the encryption of the votes and the distribution of the decryption key.

Belenios builds upon Helios, a voting protocol used in several elections. The main design enhancement of Belenios vs. Helios is that the ballot box can no longer add (fake) ballots, due to the use of credentials. Moreover, Belenios includes a practical threshold decryption system that allows splitting the decryption key among several authorities.
NEWS OF THE YEAR: Since 2015, it has been used by CNRS for remote election among its councils (more than 30 elections every year) and since 2016, it has been used by Inria to elect representatives in the “comités de centre” of each Inria center. In 2018, it has been used to organize about 250 elections (not counting test elections). Belenios is typically used for elections in universities as well as in associations. This goes from laboratory councils (e.g. Irisa, Cran), scientific societies (e.g. SMAI) to various associations (e.g. FFBS - Fédération Française de Baseball et Softball, or SRFA - Société du Rat Francophone et de ses Amateurs).

In total in 2018, more than 13000 ballots have been cast using the voting platform Belenios.

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

6.2. CADO-NFS

Crible Algébrique: Distribution, Optimisation - Number Field Sieve
KEYWORDS: Cryptography - Number theory
FUNCTIONAL DESCRIPTION: CADO-NFS is a complete implementation in C/C++ of the Number Field Sieve (NFS) algorithm for factoring integers and computing discrete logarithms in finite fields. It consists in various programs corresponding to all the phases of the algorithm, and a general script that runs them, possibly in parallel over a network of computers.
NEWS OF THE YEAR: The main program for relation collection now supports composite "special-q", and also parallelizes better. The memory footprint of the central step of linear algebra has been reduced, and the parallelism of this step has been improved.

- Participants: Pierrick Gaudry, Emmanuel Thomé and Paul Zimmermann
- Contact: Emmanuel Thomé
- URL: http://cado-nfs.gforge.inria.fr/

6.3. rrspace

RIemann-Roch spaces
KEYWORD: Riemann-Roch spaces

FUNCTIONAL DESCRIPTION: The software rrspace implements an algorithm for computing a basis of the Riemann-Roch space associated to a divisor on a curve defined over a finite field. It also implements an algorithm for computing the group law in the Jacobian of such curves. The main algorithm is a variant of Brill-Noether's approach, designed during Aude Le Gluher's Master thesis.

- Participants: Pierre-Jean Spaenlehauer and Aude Le Gluher
- Contact: Pierre-Jean Spaenlehauer
- URL: https://gitlab.inria.fr/pspaenle/rrspace

6.4. Platforms

6.4.1. Platform: computational resources

The computational resources of Caramba have increased significantly in 2018. On the one hand, the CPER «CyberEntreprises» (French Ministry of Research, Région Grand Est, Inria, CNRS) funded the acquisition of a 64-node, 2,048-core cluster called `grvingt`. This cluster is installed in the Inria facility. Other slightly older hardware (a medium-size cluster called `grcinq` from 2013, funded by ANR, and a special machine funded by the aforementioned CPER grant) was moved in the same location to form a coherent platform with about 3,000 cpu cores, 100 TB of storage, and specific machines for RAM-demanding computation. As a whole, this platform provides an excellent support for the computational part of the work done in Caramba. This platform is also embedded in the larger Grid'5000/Silecs platform (and accessible as a normal resource within this platform). Technical administration is done by the Grid'5000 staff.

CASCADE Project-Team (section vide)

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/

CELTIQUE Project-Team

4. New Software and Platforms

4.1. CompcertSSA

KEYWORDS: Optimizing compiler - Formal methods - Proof assistant - SSA
FUNCTIONAL DESCRIPTION: CompcertSSA is built on top of the Compcert verified C compiler, by adding a middle-end based on the SSA form (Static Single Assignment) : conversion to SSA, SSA-based optimizations, and destruction of SSA.

- Participants: Sandrine Blazy, Delphine Demange, Yon Fernandez De Retana, David Pichardie and Leo Stefanesco
- Contact: Delphine Demange
- Publications: Mechanizing conventional SSA for a verified destruction with coalescing - Validating Dominator Trees for a Fast, Verified Dominance Test - A Formally Verified SSA-based Middle-end - Formal Verification of an SSA-based Middle-end for CompCert - Verifying Fast and Sparse SSA-based Optimizations in Coq.
- URL: http://compcertssa.gforge.inria.fr/

4.2. Jacal

JAvaCard AnaLyseur
KEYWORDS: JavaCard - Certification - Static program analysis - AFSCM
FUNCTIONAL DESCRIPTION: Jacal is a JAvaCard AnaLyseur developed on top of the SAWJA platform. This proprietary software verifies automatically that Javacard programs conform with the security guidelines issued by the AFSCM (Association Française du Sans Contact Mobile). Jacal is based on the theory of abstract interpretation and combines several object-oriented and numeric analyses to automatically infer sophisticated invariants about the program behaviour. The result of the analysis is thereafter harvest to check that it is sufficient to ensure the desired security properties.

- Participants: David Pichardie, Delphine Demange, Frédéric Besson and Thomas Jensen
- Contact: Thomas Jensen

4.3. Javalib

KEYWORDS: Library - Java - Ocaml
FUNCTIONAL DESCRIPTION: Javalib is an efficient library to parse Java .class files into OCaml data structures, thus enabling the OCaml programmer to extract information from class files, to manipulate and to generate valid .class files.

- Participants: David Pichardie, Frédéric Besson, Laurent Guillo, Laurent Hubert, Nicolas Barré, Pierre Vittet and Tiphaine Turpin
- Contact: David Pichardie
- URL: http://sawja.inria.fr/

4.4. JSCert

Certified JavaScript

FUNCTIONAL DESCRIPTION: The JSCert project aims to really understand JavaScript. JSCert itself is a mechanised specification of JavaScript, written in the Coq proof assistant, which closely follows the ECMAScript 5 English standard. JSRef is a reference interpreter for JavaScript in OCaml , which has been proved correct with respect to JSCert and tested with the Test 262 test suite.

- Participants: Alan Schmitt and Martin Bodin
- Partner: Imperial College London
- Contact: Alan Schmitt
- URL: http://jscert.org/

4.5. SAWJA

Static Analysis Workshop for Java
KEYWORDS: Security - Software - Code review - Smart card
SCIENTIFIC DESCRIPTION: Sawja is a library written in OCaml, relying on Javalib to provide a high level representation of Java bytecode programs. It name comes from Static Analysis Workshop for JAva. Whereas Javalib is dedicated to isolated classes, Sawja handles bytecode programs with their class hierarchy and with control flow algorithms.

Moreover, Sawja provides some stackless intermediate representations of code, called JBir and A3Bir. The transformation algorithm, common to these representations, has been formalized and proved to be semantics-preserving.

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

Version: 1.5

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

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

4.6. Timbuk

KEYWORDS: Automated deduction - Ocaml - Program verification - Tree Automata - Term Rewriting Systems
FUNCTIONAL DESCRIPTION: Timbuk is a tool designed to compute or over-approximate sets of terms reachable by a given term rewriting system. The libray also provides an OCaml toplevel with all usual functions on Bottom-up Nondeterministic Tree Automata.

- Participant: Thomas Genet
- Contact: Thomas Genet
- URL: http://people.irisa.fr/Thomas.Genet/timbuk/index.html

4.7. jsexplain

JSExplain
KEYWORDS: JavaScript - Compilation - Standards - Debug - Interpreter

FUNCTIONAL DESCRIPTION: JSExplain is a reference interpreter for JavaScript that closely follows the specification and that produces execution traces. These traces may be interactively investigated in a browser, with an interface that displays not only the code and the state of the interpreter, but also the code and the state of the interpreted program. Conditional breakpoints may be expressed with respect to both the interpreter and the interpreted program. In that respect, JSExplain is a double-debugger for the specification of JavaScript.

- Partner: Imperial College London
- Contact: Alan Schmitt
- Publication: JSExplain: A Double Debugger for JavaScript
- URL: https://github.com/jscert/jsexplain

CIDRE Project-Team

5. New Software and Platforms

5.1. Blare

To detect intrusion using information flows
KEYWORDS: Cybersecurity - Intrusion Detection Systems (IDS) - Data Leakage Protection
SCIENTIFIC DESCRIPTION: Blare implements our approach of illegal information flow detection for a single node (Android and Linux kernel, JVM) and a set of nodes (monitoring of flows between linux machines).
FUNCTIONAL DESCRIPTION: Blare IDS is a set of tools that implements our approach to illegal information flow detection for a single node and a set of nodes.
NEWS OF THE YEAR: During this year, Laurent Georget has modified the implementation of Blare in order to correctly monitor the kernel system calls with LSM hooks. He add also ported this new version of Blare to the Lollipop Android emulator.

- Partner: CentraleSupélec
- Contact: Frédéric Tronel
- Publications: Information Flow Tracking for Linux Handling Concurrent System Calls and Shared Memory - Verifying the Reliability of Operating System-Level Information Flow Control Systems in Linux - Monitoring both OS and program level information flows to detect intrusions against network servers - Experimenting a Policy-Based HIDS Based on an Information Flow Control Model - Introducing reference flow control for intrusion detection at the OS level - Blare Tools: A Policy-Based Intrusion Detection System Automatically Set by the Security Policy - Diagnosing intrusions in Android operating system using system flow graph - Intrusion detection in distributed systems, an approach based on taint marking - BSPL: A Language to Specify and Compose Fine-grained Information Flow Policies - Information Flow Policies vs Malware - A taint marking approach to confidentiality violation detection - Designing information flow policies for Android's operating system - Information Flow Control for Intrusion Detection derived from MAC Policy - Flow based interpretation of access control: Detection of illegal information flows - A taint marking approach to confidentiality violation detection
- URL: http://www.blare-ids.org

5.2. GNG

Security Supervision by Alert Correlation
KEYWORDS: Intrusion Detection Systems (IDS) - SIEM
SCIENTIFIC DESCRIPTION: GNG is an intrusion detection system that correlates different sources (such as different logs) in order to identify attacks against the system. The attack scenarios are defined using the Attack Description Langage (ADeLe) proposed by our team, and are internally translated to attack recognition automatons. GNG intends to define time efficient algorithms based on these automatons to recognize complex attack scenarios.

- Partner: CentraleSupélec
- Contact: Eric Totel
- Publication: A Language Driven Intrusion Detection System for Events and Alerts Correlation
- URL: http://www.rennes.supelec.fr/ren/perso/etotel/GNG/index.html

5.3. GroddDroid

KEYWORDS: Android - Detection - Malware

SCIENTIFIC DESCRIPTION: GroddDroid automates the dynamic analysis of a malware. When a piece of suspicious code is detected, groddDroid interacts with the user interface and eventually forces the execution of the identified code. Using Blare (Information Flow Monitor), GroddDroid monitors how an execution contaminates the operating system. The output of GroddDroid can be visualized in an web browser. GroddDroid is used by the Kharon software.
FUNCTIONAL DESCRIPTION: GroddDroid 1 - locates suspicious code in Android application 2 - computes execution paths towards suspicious code 3 - forces executions of suspicious code 4 - automate the execution of a malware or a regular Android application
NEWS OF THE YEAR: In 2017, GroddDroid has integrated the work of Mourad Leslous, who have implemented GFinder. GPFinder improves the computation of control flow paths by taking into account the Android framework. The end of the year has been used to clean the code and to improves the graphical interface.

- Partners: CentraleSupélec - Insa Centre Val-de-Loire
- Contact: Valérie Viet Triem Tong
- Publications: Kharon dataset: Android malware under a microscope - GroddDroid: a Gorilla for Triggering Malicious Behaviors - GPFinder: Tracking the Invisible in Android Malware - Information flows at OS level unmask sophisticated Android malware
- URL: http://kharon.gforge.inria.fr/grodddroid.html

5.4. Kharon

KEYWORDS: Android - Malware - Dynamic Analysis
FUNCTIONAL DESCRIPTION: Kharon is a software for managing Android application analysis. Kharon uses the results of the GroddDroid software. The user can submit one or several applications to Kharon and get a graph of the innformation flows that occured at system level and that have been caused by the application.

Kharon is used in the Kharon platform for the analysis of malicious applications. This platform is deployed at the high security laboratory (LHS) of Rennes.

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

5.5. StarLord

KEYWORDS: Security - SIEM
FUNCTIONAL DESCRIPTION: In the domain of security event visualisation, we have developed a prototype called StarLord. Basically, this software is able to parse heterogeneous logs, and to extract from each line of logs a set of security objects. Moreover, some of these objects appears in several lines of different logs. These lines are thus linked by the sharing of one or more security objects. When we analyse the lines of logs, we are thus able to generate graphs that represents the links between the different objects discovered in the logs. These graphs are thus displayed in 3D in order for the administrator to investigate easily the relations between the logs and the relations between the logs and some particular indicators of compromission. The tool permits to discover visually the activity of an attacker on the supervised system.

- Authors: Ludovic Mé, Eric Totel, Nicolas Prigent and Laetitia Leichtnam
- Contact: Eric Totel
- Publication: STARLORD: Linked Security Data Exploration in a 3D Graph

5.6. SpecCert

KEYWORDS: Formal methods - Coq

FUNCTIONAL DESCRIPTION: SpecCert is a framework for specifying and verifying Hardware-based Security Enforcement (HSE) mechanisms against hardware architecture models. HSE mechanisms form a class of security enforcement mechanism such that a set of trusted software components relies on hardware functions to enforce a security policy.

- Participant: Thomas Letan
- Partners: ANSSI - CentraleSupélec
- Contact: Guillaume Hiet
- Publications: SpecCert: Specifying and Verifying Hardware-based Security Enforcement - SpecCert: Specifying and Verifying Hardware-based Software Enforcement
- URL: https://github.com/lethom/speccert

5.7. HardBlare

KEYWORDS: Intrusion Detection Systems (IDS) - FPGA - Static analysis
FUNCTIONAL DESCRIPTION: HardBlare is a hardware/software framework to implement hardware DIFC on Xilinx Zynq Platform. HardBlare consists of three components : 1) the VHDL code of the coprocessor, 2) a modified LLVM compiler to compute the static analysis, and 3) a dedicated Linux kernel. This last component is a specific version of the Blare monitor.

- Partners: CentraleSupélec - Lab-STICC
- Contact: Guillaume Hiet
- Publications: ARMHEx: A hardware extension for DIFT on ARM-based SoCs - ARMHEx: a framework for efficient DIFT in real-world SoCs - ARMHEx: embedded security through hardware-enhanced information flow tracking - HardBlare: a Hardware-Assisted Approach for Dynamic Information Flow Tracking - A portable approach for SoC-based Dynamic Information Flow Tracking implementations - Towards a hardware-assisted information flow tracking ecosystem for ARM processors - HardBlare: an efficient hardware-assisted DIFC for non-modified embedded processors

5.8. Conductor

KEYWORDS: Intrusion Detection Systems (IDS) - Static analysis - Instrumentation
FUNCTIONAL DESCRIPTION: Conductor contains three main components: a static analysis to extract the expected behavior of the target, an instrumentation module to add instructions to the target's code in order to send messages to the co-processor, and an intrusion detection engine executed on the co-processor. The latter processes the messages sent by the instrumented target, describing its current behavior. This behavior is then compared against the expected behavior previously extracted by the static analysis.

- Participants: Ronny Chevalier, Guillaume Hiet, Maugan Villatel and David Plaquin
- Partners: CentraleSupélec - HP Labs
- Contact: Ronny Chevalier
- Publication: Co-processor-based Behavior Monitoring: Application to the Detection of Attacks Against the System Management Mode

5.9. Platforms

5.9.1. Kharon platform

The Kharon platform is under development in the LHS of Rennes and should be ready to use in the beginning of 2018. This experimental platform aims to analyze Android malware using a set of software developed by the CIDRE team. Software that are involved are:

- The Blare IDS http://www.blare-ids.org/, and in particular the AndroBlare version, for tracking information flows of malware;
- The GroddDroid software http://kharon.gforge.inria.fr/grodddroid.html, for manipulating the malware statically and dynamically;
- The GPFinder software http://kharon.gforge.inria.fr/gpfinder.html, for computing paths in the malware's control flow;
- The kharon software that handles the orchestration of a bunch of malware, the server and a set of smartphones.

The Kharon platform will be used for analysing malware as soon as they appear in the wild. The analysis results will be stored for further experiments and statistics.

COMETE Project-Team

5. New Software and Platforms

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

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

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

The library's development continued in 2018 with several new added features. 82 new commits were pushed to the project's git repository during this year. The new functionality was directly applied to the exeperimental results of several publications of the team (QEST'18, Entropy'18, POST'18, CSF'18).

- Contact: Konstantinos Chatzikokolakis
- URL: https://github.com/chatziko/libqif

5.2. F-BLEAU

KEYWORDS: Information leakage - Machine learning - Privacy
FUNCTIONAL DESCRIPTION: F-BLEAU is a tool for estimating the leakage of a system about its secrets in a black-box manner (i.e., by only looking at examples of secret inputs and respective outputs). It considers a generic system as a black-box, taking secret inputs and returning outputs accordingly, and it measures how much the outputs "leak" about the inputs.

F-BLEAU is based on the equivalence between estimating the error of a Machine Learning model of a specific class and the estimation of information leakage.

This code was also used for the experiments of a paper under submission, on the following evaluations: Gowalla, e-passport, and side channel attack to finite field exponentiation.

RELEASE FUNCTIONAL DESCRIPTION: First F-BLEAU release. Supports frequentist and k-NN estimates with several parameters, and it allows stopping according to delta-convergence criteria.

- Contact: Konstantinos Chatzikokolakis
- URL: https://github.com/gchers/fbleau

5.3. Location Guard

KEYWORDS: Privacy - Geolocation - Browser Extensions
SCIENTIFIC DESCRIPTION: The purpose of Location Guard is to implement obfuscation techniques for achieving location privacy, in a an easy and intuitive way that makes them available to the general public. Various modern applications, running either on smartphones or on the web, allow third parties to obtain the user's location. A smartphone application can obtain this information from the operating system using a system call, while web application obtain it from the browser using a JavaScript call.

FUNCTIONAL DESCRIPTION: Websites can ask the browser for your location (via JavaScript). When they do so, the browser first asks your permission, and if you accept, it detects your location (typically by transmitting a list of available wifi access points to a geolocation provider such as Google Location Services, or via GPS if available) and gives it to the website.

Location Guard is a browser extension that intercepts this procedure. The permission dialog appears as usual, and you can still choose to deny. If you give permission, then Location Guard obtains your location and adds "random noise" to it, creating a fake location. Only the fake location is then given to the website.

Location Guard is by now a stable tool with a large user base. No new features were added in 2018, however the tool is still actively maintained, and several issues have beed fixed during this year (new geocoder API, manual installation method for Opera users, etc).

- Participants: Catuscia Palamidessi, Konstantinos Chatzikokolakis, Marco Stronati, Miguel Andrés and Nicolas Bordenabe
- Contact: Konstantinos Chatzikokolakis
- URL: https://github.com/chatziko/location-guard

5.4. dspacenet

Distributed-Spaces Network.
KEYWORDS: Social networks - Distributed programming
FUNCTIONAL DESCRIPTION: DSpaceNet is a tool for social networking based on multi-agent spatial and timed concurrent constraint language.

I - The fundamental structure of DSPaceNet is that of *space*: A space may contain

(1) spatial-mobile-reactive tcc programs, and (2) other spaces.

Furthermore, (3) each space belongs to a given agent. Thus, a space of an agent j within the space of agent i means that agent i allows agent j to use a computation sub-space within its space.

II - The fundamental operation of DSPaceNet is that of *program posting*: In each time unit, agents can post spatial-mobile-reactive tcc programs in the spaces they are allowed to do so (ordinary message posting corresponds to the posting of tell processes). Thus, an agent can for example post a watchdog tcc process to react to messages in their space, e.g. whenever (*happy b*frank*) do tell("thank you!"). More complex mobile programs are also allowed (see below).

The language of programs is a spatial mobile extension of tcc programs:

$P, Q ... := tell(c) | whencdoP || nextP | P || Q | unlesscnextP | [P]\_i | \uparrow \_iP | recX.P$

computation of timed processes proceeds as in tcc. The spatial construct [P]_i runs P in the space of agent i and the mobile process uparrow_i P, extrudes P from the space of i. By combining space and mobility, arbitrary processes can be moved from one a space into another. For example, one could send a trojan watchdog to another space for spying for a given message and report back to one's space.

III- Constraint systems can be used to specify advance text message deduction, arithmetic deductions, scheduling, etc.

IV - Epistemic Interpretation of spaces can be used to derive whether they are users with conflicting/inconsistent information, or whether a group of agents may be able to deduce certain message.

V - The scheduling of agent requests for program posts, privacy settings, friendship lists are handled by an external interface. For example, one could use type systems to check whether a program complies with privacy settings (for example checking that the a program does not move other program into a space it is not allowed into).

- Partner: Pontificia Universidad Javeriana Cali
- Contact: Frank Valencia
- URL: http://www.dspacenet.com

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 developpers during their Interactive Debbugging 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.

DATASHAPE Project-Team

6. New Software and Platforms

6.1. GUDHI

Geometric Understanding in Higher Dimensions

KEYWORDS: Computational geometry - Topology

SCIENTIFIC DESCRIPTION: The current release of the GUDHI library includes: – Data structures to represent, construct and manipulate simplicial and cubical complexes. – Algorithms to compute simplicial complexes from point cloud data. – Algorithms to compute persistent homology and multi-field persistent homology. – Simplification methods via implicit representations.

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

NEWS OF THE YEAR: - Cover complex - Representation of persistence diagrams - Cech complex - weighted periodic 3d alpha-complex - sparse Rips complex - debian / docker / conda-forge packages

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

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/.

DEDUCTEAM Project-Team

6. New Software and Platforms

6.1. Autotheo

KEYWORD: Automated deduction
SCIENTIFIC DESCRIPTION: Transformation of axiomatic theories into rewriting systems that can be used by iProverModulo.
FUNCTIONAL DESCRIPTION: Autotheo is a tool that transforms axiomatic theories into polarized rewriting systems, thus making them usable in iProverModulo. It supports several strategies to orient the axioms, some of them being proved to be complete, in the sense that ordered polarized resolution modulo the resulting systems is refutationally complete, some others being merely heuristics. In practice, Autotheo takes a TPTP input file and produces an input file for iProverModulo.
NEWS OF THE YEAR: Maintenance.

- Participant: Guillaume Burel
- Partner: ENSIIE
- Contact: Guillaume Burel
- Publication: Consistency Implies Cut Admissibility
- URL: http://www.ensiie.fr/~guillaume.burel/blackandwhite_autotheo.html.en

6.2. CoLoR

Coq Library on Rewriting and termination
KEYWORDS: Coq - Formalisation
FUNCTIONAL DESCRIPTION: CoLoR is a Coq library on rewriting theory and termination. It provides many definitions and theorems on various mathematical structures (quasi-ordered sets, relations, ordered semi-rings, etc.), data structures (lists, vectors, matrices, polynomials, finite graphs), term structures (strings, first-order terms, lambda-terms, etc.), transformation techniques (dependency pairs, semantic labeling, etc.) and (non-)termination criteria (polynomial and matrix interpretations, recursive path ordering, computability closure, etc.).

- Authors: Frédéric Blanqui and Sébastien Hinderer
- Contact: Frédéric Blanqui
- Publications: CoLoR: a Coq library on well-founded rewrite relations and its application to the automated verification of termination certificates - Automated Verification of Termination Certificates - CoLoR: a Coq library on rewriting and termination
- URL: http://color.inria.fr/

6.3. Coqine

Coq In dEdukti
KEYWORDS: Higher-order logic - Formal methods - Proof
FUNCTIONAL DESCRIPTION: CoqInE is a plugin for the Coq software translating Coq proofs into Dedukti terms. It provides a Dedukti signature file faithfully encoding the underlying theory of Coq (or a sufficiently large subset of it). Current development is mostly focused on implementing support for Coq universe polymorphism. The generated ouput is meant to be type-checkable using the latest version of Dedukti.

- Contact: Guillaume Burel
- URL: http://www.ensiie.fr/~guillaume.burel/blackandwhite_coqInE.html.en

6.4. Dedukti

KEYWORD: Logical Framework
FUNCTIONAL DESCRIPTION: Dedukti is a proof-checker for the LambdaPi-calculus modulo. As it can be parametrized by an arbitrary set of rewrite rules, defining an equivalence relation, this calculus can express many different theories. Dedukti has been created for this purpose: to allow the interoperability of different theories.

Dedukti's core is based on the standard algorithm for type-checking semi-full pure type systems and implements a state-of-the-art reduction machine inspired from Matita's and modified to deal with rewrite rules.

Dedukti's input language features term declarations and definitions (opaque or not) and rewrite rule definitions. A basic module system allows the user to organize his project in different files and compile them separately.

Dedukti features matching modulo beta for a large class of patterns called Miller's patterns, allowing for more rewriting rules to be implemented in Dedukti.
NEWS OF THE YEAR: There has been a new release 2.6 in 2018. This release provides a better control on module loading, and a better log of rewrite steps.

- Participants: François Thiré, Gaspard Ferey, Guillaume Genestier and Rodolphe Lepigre
- Contact: François Thiré
- Publications: Dedukti:un vérificateur de preuves universel - Rewriting Modulo β in the $\lambda\Pi$-Calculus Modulo - Expressing theories in the $\lambda\Pi$-calculus modulo theory and in the Dedukti system
- URL: https://deducteam.github.io/

6.5. Holide

KEYWORD: Proof
FUNCTIONAL DESCRIPTION: Holide translates HOL proofs to Dedukti[OT] proofs, using the OpenTheory standard (common to HOL Light and HOL4). Dedukti[OT] being the encoding of OpenTheory in Dedukti.

- Contact: Guillaume Burel
- URL: http://deducteam.gforge.inria.fr/holide/

6.6. HOT

Higher-Order Termination
FUNCTIONAL DESCRIPTION: HOT is an automated termination prover for higher-order rewriting, based on the notion of computability closure.

- Contact: Frédéric Blanqui
- URL: http://rewriting.gforge.inria.fr/hot.html

6.7. iProver Modulo

KEYWORDS: Automated deduction - Automated theorem proving
SCIENTIFIC DESCRIPTION: Integration of ordered polarized resolution modulo theory into the prover iProver.
FUNCTIONAL DESCRIPTION: iProver Modulo is an extension of the automated theorem prover iProver originally developed by Konstantin Korovin at the University of Manchester. It implements ordered polarized resolution modulo theory, a refinement of the resolution method based on deduction modulo theory. It takes as input a proposition in predicate logic and a clausal rewriting system defining the theory in which the formula has to be proved. Normalization with respect to the term rewriting rules is performed very efficiently through translation into OCaml code, compilation and dynamic linking. Experiments have shown that ordered polarized resolution modulo dramatically improves proof search compared to using raw axioms.

NEWS OF THE YEAR: Maintenance of Dedukti output

- Participant: Guillaume Burel
- Partner: ENSIIE
- Contact: Guillaume Burel
- Publications: A Shallow Embedding of Resolution and Superposition Proofs into the ??-Calculus Modulo - Experimenting with deduction modulo
- URL: https://github.com/gburel/iProverModulo

6.8. mSAT

KEYWORD: Propositional logic

FUNCTIONAL DESCRIPTION: mSAT is a modular, proof-producing, SAT and SMT core based on Alt-Ergo Zero, written in OCaml. The solver accepts user-defined terms, formulas and theory, making it a good tool for experimenting. This tool produces resolution proofs as trees in which the leaves are user-defined proof of lemmas.

- Contact: Guillaume Bury
- Publication: mSAT:An OCaml SAT Solver
- URL: https://github.com/Gbury/mSAT

6.9. Rainbow

Termination certificate verifier

KEYWORDS: Demonstration - Code generation - Verification

FUNCTIONAL DESCRIPTION: Rainbow is a set of tools for automatically verifying the correctness of termination certificates expressed in the CPF format used in the annual international competition of termination tools. It contains: a tool xsd2coq for generating Coq data types for representing XML files valid with respect to some XML Schema, a tool xsd2ml for generating OCaml data types and functions for parsing XML files valid with respect to some XML Schema, a tool for translating a CPF file into a Coq script, and a standalone Coq certified tool for verifying the correctness of a CPF file.

- Author: Frédéric Blanqui
- Contact: Frédéric Blanqui
- Publications: Automated verification of termination certificates - Automated verification of termination certificates
- URL: http://color.inria.fr/rainbow.html

6.10. Krajono

KEYWORD: Proof

FUNCTIONAL DESCRIPTION: Krajono translates Matita proofs into Dedukti[CiC] (encoding of CiC in Dedukti) terms.

- Contact: François Thiré

6.11. archsat

KEYWORDS: Automated theorem proving - First-order logic - Propositional logic

FUNCTIONAL DESCRIPTION: Archsat is an automated theorem prover aimed at studying the integration of first-order theorem prover technologies, such as rewriting, into SMT solvers.

- Contact: Guillaume Bury
- URL: https://gforge.inria.fr/projects/archsat

6.12. lrat2dk

KEYWORDS: Automated theorem proving - Proof

FUNCTIONAL DESCRIPTION: Take as input a SAT proof trace in LRAT format, which can be obtained from the de facto standard format DRAT using drat-trim. Output a proof checkable by Dedukti, in a shallow encoding of propositional logic.

- Participant: Guillaume Burel
- Partner: ENSIIE
- Contact: Guillaume Burel
- URL: https://github.com/gburel/lrat2dk

6.13. ekstrakto

KEYWORDS: TPTP - TSTP - Proof assistant - Dedukti

FUNCTIONAL DESCRIPTION: Extracting TPTP problems from a TSTP trace. Proof reconstruction in Dedukti from TSTP trace.

- Contact: Mohamed Yacine El Haddad
- URL: https://github.com/elhaddadyacine/ekstrakto

6.14. SizeChangeTool

KEYWORDS: Rewriting systems - Proof assistant - Termination

FUNCTIONAL DESCRIPTION: A termination-checker for higher-order rewriting with dependent types. Took part in the Termination Competition 2018 (http://termination-portal.org/wiki/Termination_Competition_2018) in the "Higher-Order Rewriting (union Beta)" category.

- Partner: Mines ParisTech
- Contact: Guillaume Genestier
- URL: https://github.com/Deducteam/SizeChangeTool

GAIA Team

6. New Software and Platforms

6.1. ADHOMFI

Adaptive Homogeneous Filtering
KEYWORDS: Automatic differentiation - Filtering
FUNCTIONAL DESCRIPTION: allows to reconstruct a signal based on derivatives estimation and to filter high amplitude and wide frequencies spectrum perturbations.

- Contact: Denis Efimov

6.2. Platforms

6.2.1. BLINEIDE library

We have released the first version of the BLINEIDE library. BLINEIDE stands for Bibliothèques Lilloises dédiées à l'Intégration Numérique des Équations Intégro-Différentielles. It is an open source C library dedicated to the numerical integration of systems of integro-differential equations. for more details, see https://pro.univ-lille.fr/francois-boulier/logiciels/blineide.

GALLINETTE Project-Team

5. New Software and Platforms

5.1. Coq

The Coq Proof Assistant

KEYWORDS: Proof - Certification - Formalisation

SCIENTIFIC DESCRIPTION: Coq is an interactive proof assistant based on the Calculus of (Co-)Inductive Constructions, extended with universe polymorphism. This type theory features inductive and co-inductive families, an impredicative sort and a hierarchy of predicative universes, making it a very expressive logic. The calculus allows to formalize both general mathematics and computer programs, ranging from theories of finite structures to abstract algebra and categories to programming language metatheory and compiler verification. Coq is organised as a (relatively small) kernel including efficient conversion tests on which are built a set of higher-level layers: a powerful proof engine and unification algorithm, various tactics/decision procedures, a transactional document model and, at the very top an IDE.

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

RELEASE FUNCTIONAL DESCRIPTION: Coq version 8.8.2 contains the result of refinements and stabilization of features and deprecations, cleanups of the internals of the system along with a few new features.

Summary of changes:

Kernel: fix a subject reduction failure due to allowing fixpoints on non-recursive values (#407), by Matthieu Sozeau. Handling of evars in the VM (#935) by Pierre-Marie Pédrot.

Notations: many improvements on recursive notations and support for destructuring patterns in the syntax of notations by Hugo Herbelin.

Proof language: tacticals for profiling, timing and checking success or failure of tactics by Jason Gross. The focusing bracket { supports single-numbered goal selectors, e.g. 2:{, (#6551) by Théo Zimmermann.

Vernacular: cleanup of definition commands (#6653) by Vincent Laporte and more uniform handling of the Local flag (#1049), by Maxime Dénès. Experimental Show Extraction command (#6926) by Pierre Letouzey. Coercion now accepts Prop or Type as a source (#6480) by Arthur Charguéraud. Export modifier for options allowing to export the option to modules that Import and not only Require a module (#6923), by Pierre-Marie Pédrot.

Universes: many user-level and API level enhancements: qualified naming and printing, variance annotations for cumulative inductive types, more general constraints and enhancements of the minimization heuristics, interaction with modules by Gaëtan Gilbert, Pierre-Marie Pédrot and Matthieu Sozeau.

Library: Decimal Numbers library (#6599) by Pierre Letouzey and various small improvements.

Documentation: a large community effort resulted in the migration of the reference manual to the Sphinx documentation tool. The new documentation infrastructure (based on Sphinx) is by Clément Pit-Claudel. The migration was coordinated by Maxime Dénès and Paul Steckler, with some help of Théo Zimmermann during the final integration phase. The 14 people who ported the manual are Calvin Beck, Heiko Becker, Yves Bertot, Maxime Dénès, Richard Ford, Pierre Letouzey, Assia Mahboubi, Clément Pit-Claudel, Laurence Rideau, Matthieu Sozeau, Paul Steckler, Enrico Tassi, Laurent Théry, Nikita Zyuzin.

Tools: experimental -mangle-names option to coqtop/coqc for linting proof scripts (#6582), by Jasper Hugunin. Main changes:

Critical soundness bugs were fixed between versions 8.8.0 and 8.8.2, and a PDF version of the reference manual was made available. The Windows installer also includes many more external packages that can be individually selected for installation.

On the implementation side, the dev/doc/changes.md file documents the numerous changes to the implementation and improvements of interfaces. The file provides guidelines on porting a plugin to the new version.

More information can be found in the CHANGES file. Feedback and bug reports are extremely welcome.

Distribution Installers for Windows 32 bits (i686), Windows 64 bits (x8_64) and macOS are available. They come bundled with CoqIDE. Windows binaries now include the Bignums library.

Complete sources of the files installed by the Windows installers are made available, to comply with license requirements.
NEWS OF THE YEAR: Version 8.8.0 was released in April 2018 and version 8.8.2 in September 2018. This is the third release of Coq developed on a time-based development cycle. Its development spanned 6 months from the release of Coq 8.7 and was based on a public road-map. It attracted many external contributions. Code reviews and continuous integration testing were systematically used before integration of new features, with an important focus given to compatibility and performance issues.

The main advances in this version are cleanups and fixes in the many different components of the system, ranging from low level kernel fixes to advances in the support of notations and tacticals for selecting goals. A large community effort was made to move the documentation to the Sphinx format, providing a more accessible online ressource to users.

- Participants: Abhishek Anand, C. J. Bell, Yves Bertot, Frédéric Besson, Tej Chajed, Pierre Courtieu, Maxime Denes, Julien Forest, Emilio Jesús Gallego Arias, Gaëtan Gilbert, Benjamin Grégoire, Jason Gross, Hugo Herbelin, Ralf Jung, Matej Kosik, Sam Pablo Kuper, Xavier Leroy, Pierre Letouzey, Assia Mahboubi, Cyprien Mangin, Érik Martin-Dorel, Olivier Marty, Guillaume Melquiond, Pierre-Marie Pédrot, Benjamin C. Pierce, Lars Rasmusson, Yann Régis-Gianas, Lionel Rieg, Valentin Robert, Thomas Sibut-Pinote, Michael Soegtrop, Matthieu Sozeau, Arnaud Spiwack, Paul Steckler, George Stelle, Pierre-Yves Strub, Enrico Tassi, Hendrik Tews, Laurent Théry, Amin Timany, Vadim Zaliva and Théo Zimmermann
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Matthieu Sozeau
- Publication: The Coq Proof Assistant, version 8.8.0
- URL: http://coq.inria.fr/

5.2. Math-Components

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

RELEASE FUNCTIONAL DESCRIPTION: The library includes 16 more theory files, covering in particular field and Galois theory, advanced character theory, and a construction of algebraic numbers.

- Participants: Alexey Solovyev, Andrea Asperti, Assia Mahboubi, Cyril Cohen, Enrico Tassi, François Garillot, Georges Gonthier, Ioana Pasca, Jeremy Avigad, Laurence Rideau, Laurent Théry, Russell O'Connor, Sidi Ould Biha, Stéphane Le Roux and Yves Bertot
- Contact: Assia Mahboubi
- URL: http://math-comp.github.io/math-comp/

5.3. Ssreflect

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

- Participants: Assia Mahboubi, Cyril Cohen, Enrico Tassi, Georges Gonthier, Laurence Rideau, Laurent Théry and Yves Bertot
- Contact: Yves Bertot
- URL: http://math-comp.github.io/math-comp/

5.4. Ltac2

KEYWORDS: Coq - Proof assistant
FUNCTIONAL DESCRIPTION: A replacement for Ltac, the tactic language of Coq.

- Contact: Pierre-Marie Pédrot

GALLIUM Project-Team

6. New Software and Platforms

6.1. Compcert

The CompCert formally-verified C compiler

KEYWORDS: Compilers - Formal methods - Deductive program verification - C - Coq

FUNCTIONAL DESCRIPTION: CompCert is a compiler for the C programming language. Its intended use is the compilation of life-critical and mission-critical software written in C and meeting high levels of assurance. It accepts most of the ISO C 99 language, with some exceptions and a few extensions. It produces machine code for the ARM, PowerPC, RISC-V, and x86 architectures. What sets CompCert C apart from any other production compiler, is that it is formally verified to be exempt from miscompilation issues, using machine-assisted mathematical proofs (the Coq proof assistant). In other words, the executable code it produces is proved to behave exactly as specified by the semantics of the source C program. This level of confidence in the correctness of the compilation process is unprecedented and contributes to meeting the highest levels of software assurance. In particular, using the CompCert C compiler is a natural complement to applying formal verification techniques (static analysis, program proof, model checking) at the source code level: the correctness proof of CompCert C guarantees that all safety properties verified on the source code automatically hold as well for the generated executable.

RELEASE FUNCTIONAL DESCRIPTION: Novelties include a formally-verified type checker for CompCert C, a more careful modeling of pointer comparisons against the null pointer, algorithmic improvements in the handling of deeply nested struct and union types, much better ABI compatibility for passing composite values, support for GCC-style extended inline asm, and more complete generation of DWARF debugging information (contributed by AbsInt).

- Participants: Xavier Leroy, Sandrine Blazy, Jacques-Henri Jourdan, Sylvie Boldo and Guillaume Melquiond
- Partner: AbsInt Angewandte Informatik GmbH
- Contact: Xavier Leroy
- URL: http://compcert.inria.fr/

6.2. Diy

Do It Yourself

KEYWORD: Parallelism

FUNCTIONAL DESCRIPTION: The diy suite provides a set of tools for testing shared memory models: the litmus tool for running tests on hardware, various generators for producing tests from concise specifications, and herd, a memory model simulator. Tests are small programs written in x86, Power or ARM assembler that can thus be generated from concise specification, run on hardware, or simulated on top of memory models. Test results can be handled and compared using additional tools.

- Participants: Jade Alglave and Luc Maranget
- Partner: University College London UK
- Contact: Luc Maranget
- URL: http://diy.inria.fr/

6.3. Menhir

KEYWORDS: Compilation - Context-free grammars - Parsing

FUNCTIONAL DESCRIPTION: Menhir is a LR(1) parser generator for the OCaml programming language. That is, Menhir compiles LR(1) grammar specifications down to OCaml code. Menhir was designed and implemented by François Pottier and Yann Régis-Gianas.

- Contact: François Pottier
- Publications: A Simple, Possibly Correct LR Parser for C11 - Reachability and Error Diagnosis in LR(1) Parsers

6.4. OCaml

KEYWORDS: Functional programming - Static typing - Compilation
FUNCTIONAL DESCRIPTION: The OCaml language is a functional programming language that combines safety with expressiveness through the use of a precise and flexible type system with automatic type inference. The OCaml system is a comprehensive implementation of this language, featuring two compilers (a bytecode compiler, for fast prototyping and interactive use, and a native-code compiler producing efficient machine code for x86, ARM, PowerPC and System Z), a debugger, a documentation generator, a compilation manager, a package manager, and many libraries contributed by the user community.

- Participants: Damien Doligez, Xavier Leroy, Fabrice Le Fessant, Luc Maranget, Gabriel Scherer, Alain Frisch, Jacques Garrigue, Marc Shinwell, Jeremy Yallop and Leo White
- Contact: Damien Doligez
- URL: https://ocaml.org/

6.5. PASL

KEYWORD: Parallel computing
FUNCTIONAL DESCRIPTION: PASL is a C++ library for writing parallel programs targeting the broadly available multicore computers. The library provides a high level interface and can still guarantee very good efficiency and performance, primarily due to its scheduling and automatic granularity control mechanisms.

- Participants: Arthur Charguéraud, Michael Rainey and Umut Acar
- Contact: Michael Rainey
- URL: http://deepsea.inria.fr/pasl/

6.6. ZENON

FUNCTIONAL DESCRIPTION: Zenon is an automatic theorem prover based on the tableaux method. Given a first-order statement as input, it outputs a fully formal proof in the form of a Coq proof script. It has special rules for efficient handling of equality and arbitrary transitive relations. Although still in the prototype stage, it already gives satisfying results on standard automatic-proving benchmarks.

Zenon is designed to be easy to interface with front-end tools (for example integration in an interactive proof assistant), and also to be retargeted to output scripts for different frameworks (for example, Isabelle and Dedukti).

- Author: Damien Doligez
- Contact: Damien Doligez
- URL: http://zenon-prover.org/

6.7. OPAM Builder

KEYWORDS: Ocaml - Continuous integration - Opam

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

- Partner: OCamlPro
- Contact: Fabrice Le Fessant
- URL: http://github.com/OCamlPro/opam-builder

6.8. TLAPS

TLA+ proof system

KEYWORD: Proof assistant

FUNCTIONAL DESCRIPTION: TLAPS is a platform for developing and mechanically verifying proofs about TLA+ specifications. The TLA+ proof language is hierarchical and explicit, allowing a user to decompose the overall proof into proof steps that can be checked independently. TLAPS consists of a proof manager that interprets the proof language and generates a collection of proof obligations that are sent to backend verifiers. The current backends include the tableau-based prover Zenon for first-order logic, Isabelle/TLA+, an encoding of TLA+ set theory as an object logic in the logical framework Isabelle, an SMT backend designed for use with any SMT-lib compatible solver, and an interface to a decision procedure for propositional temporal logic.

NEWS OF THE YEAR: Ioannis Filippidis joined the development team in November 2018 and started designing and implementing support for reasoning about TLA+'s ENABLED construct.

- Participants: Damien Doligez, Stephan Merz and IOANNIS FILIPPIDIS
- Contact: Stephan Merz
- URL: https://tla.msr-inria.inria.fr/tlaps/content/Home.html

6.9. CFML

Interactive program verification using characteristic formulae

KEYWORDS: Coq - Software Verification - Deductive program verification - Separation Logic

FUNCTIONAL DESCRIPTION: The CFML tool supports the verification of OCaml programs through interactive Coq proofs. CFML proofs establish the full functional correctness of the code with respect to a specification. They may also be used to formally establish bounds on the asymptotic complexity of the code. The tool is made of two parts: on the one hand, a characteristic formula generator implemented as an OCaml program that parses OCaml code and produces Coq formulae, and, on the other hand, a Coq library that provides notations and tactics for manipulating characteristic formulae interactively in Coq.

- Participants: Arthur Charguéraud, Armaël Guéneau and François Pottier
- Contact: Arthur Charguéraud
- URL: http://www.chargueraud.org/softs/cfml/

6.10. ldrgen

Liveness-driven random C code generator

KEYWORDS: Code generation - Randomized algorithms - Static program analysis

FUNCTIONAL DESCRIPTION: The ldrgen program is a generator of C code: On every call it generates a new random C function and prints it to the standard output. The generator is "liveness-driven", which means that it tries to avoid generating dead code: All the computations it generates are (in a certain, limited sense) actually used to compute the function's return value. This is achieved by generating the program backwards, in combination with a simultaneous liveness analysis that guides the random generator's choices.

- Participant: Gergö Barany
- Contact: Gergö Barany
- Publication: Liveness-Driven Random Program Generation
- URL: https://github.com/gergo-/ldrgen

GAMBLE Project-Team

6. New Software and Platforms

6.1. ISOTOP

Topology and geometry of planar algebraic curves
KEYWORDS: Topology - Curve plotting - Geometric computing
FUNCTIONAL DESCRIPTION: Isotop is a Maple software for computing the topology of an algebraic plane curve, that is, for computing an arrangement of polylines isotopic to the input curve. This problem is a necessary key step for computing arrangements of algebraic curves and has also applications for curve plotting. This software has been developed since 2007 in collaboration with F. Rouillier from Inria Paris - Rocquencourt.
NEWS OF THE YEAR: In 2018, an engineer from Inria Nancy (Benjamin Dexheimer) finished the implementation of the web server to improve the diffusion of our software.

- Participants: Luis Penaranda, Marc Pouget and Sylvain Lazard
- Contact: Marc Pouget
- Publications: Rational Univariate Representations of Bivariate Systems and Applications - Separating Linear Forms for Bivariate Systems - On The Topology of Planar Algebraic Curves - New bivariate system solver and topology of algebraic curves - Improved algorithm for computing separating linear forms for bivariate systems - Solving bivariate systems using Rational Univariate Representations - On the topology of planar algebraic curves - On the topology of real algebraic plane curves - Bivariate triangular decompositions in the presence of asymptotes - Separating linear forms and Rational Univariate Representations of bivariate systems
- URL: https://isotop.gamble.loria.fr/

6.2. SubdivisionSolver

KEYWORDS: Numerical solver - Polynomial or analytical systems
SCIENTIFIC DESCRIPTION: The goal underlying the developpement of RealSolver is the ability to solve large polynomial systems with certified results using adaptive multi-precision arithmetic for efficiency.

The software is based on a classic branch and bound algorithm using interval arithmetic: an initial box is subdivided until its sub-boxes are certified to contain either no solution or a unique solution of the input system. Evaluation is performed with a centered evaluation at order two, and existence and uniqueness of solutions is verified thanks to the Krawczyk operator.

RealSolver uses two implementations of interval arithmetic: the C++ boost library that provides a fast arithmetic when double precision is enough, and otherwise the C mpfi library that allows to work in arbitrary precision. Considering the subdivision process as a breadth first search in a tree, the boost interval arithmetic is used as deeply as possible before a new subdivision process using higher precision arithmetic is performed on the remaining forest.

The software is can be interfaced with sage and the library Fast_Polynomial that allows to solve systems of polynomials that are large in terms of degree, number of monomials and bit-size of coefficients.
FUNCTIONAL DESCRIPTION: The software RealSolver solves square systems of analytic equations on a compact subset of a real space. RealSolver is a subdivision solver using interval arithmetic and multiprecision arithmetic to achieve certified results. If the arithmetic precision required to isolate solutions is known, it can be given as an input parameter of the process, otherwise the precision is increased on-the-fly. In particular, RealSolver can be interfaced with the Fast_Polynomial library (https://bil.inria.fr/en/software/view/2423/tab#lA) to solve polynomial systems that are large in terms of degree, number of monomials and bit-size of coefficients.

NEWS OF THE YEAR: In 2018, Mohamed Eissa was recruited on a FastTrack contract for porting the code to python.

- Contact: Rémi Imbach

6.3. CGAL Package : 2D hyperbolic triangulations

KEYWORDS: Geometry - Delaunay triangulation - Hyperbolic space
FUNCTIONAL DESCRIPTION: This package implements the construction of Delaunay triangulations in the Poincaré disk model.
NEWS OF THE YEAR: This package has been submitted to the CGAL Editorial Board for future integration into the library.

- Participants: Mikhail Bogdanov, Olivier Devillers, Iordan Iordanov and Monique Teillaud
- Contact: Monique Teillaud
- Publication: Hyperbolic Delaunay Complexes and Voronoi Diagrams Made Practical
- URL: https://github.com/CGAL/cgal-public-dev/tree/Periodic_4_hyperbolic_triangulation_2-IIordanov

6.4. CGAL Package : 2D periodic hyperbolic triangulations

KEYWORDS: Geometry - Delaunay triangulation - Hyperbolic space
FUNCTIONAL DESCRIPTION: This module implements the computation of Delaunay triangulations of the Bolza surface.
NEWS OF THE YEAR: This package has been submitted to the CGAL Editorial Board for future integration into the library.

- Authors: Iordan Iordanov and Monique Teillaud
- Contact: Monique Teillaud
- Publication: Implementing Delaunay Triangulations of the Bolza Surface
- URL: https://github.com/CGAL/cgal-public-dev/tree/Periodic_4_hyperbolic_triangulation_2-IIordanov

6.5. CGAL package: 3D periodic mesh generation

KEYWORDS: Flat torus - CGAL - Geometry - Delaunay triangulation - Mesh generation - Tetrahedral mesh - Mesh
FUNCTIONAL DESCRIPTION: This package of CGAL (Computational Geometry Algorithms Library http://www.cgal.org) allows to build and handle volumic meshes of shapes described through implicit functional boundaries over the 3D flat torus whose fundamental domain is a cube.
NEWS OF THE YEAR: This new package has been released in CGAL 4.13

- Participants: Mikhail Bogdanov, Aymeric Pellé, Mael Rouxel-Labbe and Monique Teillaud
- Contact: Monique Teillaud
- Publications: CGAL periodic volume mesh generator - Periodic meshes for the CGAL library
- URL: https://doc.cgal.org/latest/Manual/packages.html#PkgPeriodic_3_mesh_3Summary

GRACE Project-Team

5. New Software and Platforms

5.1. ACTIS

Algorithmic Coding Theory in Sage
FUNCTIONAL DESCRIPTION: The aim of this project is to vastly improve the state of the error correcting library in Sage. The existing library does not present a good and usable API, and the provided algorithms are very basic, irrelevant, and outdated. We thus have two directions for improvement: renewing the APIs to make them actually usable by researchers, and incorporating efficient programs for decoding, like J. Nielsen's CodingLib, which contains many new algorithms.

- Partner: Technical University Denmark
- Contact: Daniel Augot

5.2. DECODING

KEYWORD: Algebraic decoding
FUNCTIONAL DESCRIPTION: Decoding is a standalone C library. Its primary goal is to implement Guruswami–Sudan list decoding-related algorithms, as efficiently as possible. Its secondary goal is to give an efficient tool for the implementation of decoding algorithms (not necessarily list decoding algorithms) and their benchmarking.

- Participant: Guillaume Quintin
- Contact: Daniel Augot

5.3. Fast Compact Diffie-Hellman

KEYWORD: Cryptography
FUNCTIONAL DESCRIPTION: A competitive, high-speed, open implementation of the Diffie–Hellman protocol, targeting the 128-bit security level on Intel platforms. This download contains Magma files that demonstrate how to compute scalar multiplications on the x-line of an elliptic curve using endomorphisms. This accompanies the EuroCrypt 2014 paper by Costello, Hisil and Smith, the full version of which can be found here: http://eprint.iacr.org/2013/692 . The corresponding SUPERCOP-compatible crypto_dh application can be downloaded from http://hhisil.yasar.edu.tr/files/hisil20140318compact.tar.gz .

- Participant: Benjamin Smith
- Contact: Benjamin Smith
- URL: http://research.microsoft.com/en-us/downloads/ef32422a-af38-4c83-a033-a7aafbc1db55/

5.4. CADO-NFS

Crible Algébrique: Distribution, Optimisation - Number Field Sieve
KEYWORDS: Cryptography - Number theory
FUNCTIONAL DESCRIPTION: CADO-NFS is a complete implementation in C/C++ of the Number Field Sieve (NFS) algorithm for factoring integers and computing discrete logarithms in finite fields. It consists in various programs corresponding to all the phases of the algorithm, and a general script that runs them, possibly in parallel over a network of computers.
NEWS OF THE YEAR: The main program for relation collection now supports composite "special-q", and also parallelizes better. The memory footprint of the central step of linear algebra has been reduced, and the parallelism of this step has been improved.

- Participants: Pierrick Gaudry, Emmanuel Thomé and Paul Zimmermann
- Contact: Emmanuel Thomé
- URL: http://cado-nfs.gforge.inria.fr/

HYCOMES Project-Team

5. New Software and Platforms

5.1. Demodocos

Demodocos (Examples to Generic Scenario Models Generator)
KEYWORDS: Surgical process modelling - Net synthesis - Process mining
SCIENTIFIC DESCRIPTION: Demodocos is used to construct a Test and Flip net (Petri net variant) from a collection of instances of a given procedure. The tool takes as input either standard XES log files (a standard XML file format for process mining tools) or a specific XML file format for surgical applications. The result is a Test and Flip net and its marking graph. The tool can also build a #SEVEN scenario for integration into a virtual reality environment. The scenario obtained corresponds to the generalization of the input instances, namely the instances synthesis enriched with new behaviors respecting the relations of causality, conflicts and competition observed.

Demodocos is a synthesis tool implementing a linear algebraic polynomial time algorithm. Computations are done in the Z/2Z ring. Test and Flip nets extend Elementary Net Systems by allowing test to zero, test to one and flip arcs. The effect of flip arcs is to complement the marking of the place. While the net synthesis problem has been proved to be NP hard for Elementary Net Systems, thanks to flip arcs, the synthesis of Test and Flip nets can be done in polynomial time. Test and flip nets have the required expressivity to give concise and accurate representations of surgical processes (models of types of surgical operations). Test and Flip nets can express causality and conflict relations. The tool takes as input either standard XES log files (a standard XML file format for process mining tools) or a specific XML file format for surgical applications. The output is a Test and Flip net, solution of the following synthesis problem: Given a finite input language (log file), compute a net, which language is the least language in the class of Test and Flip net languages, containing the input language.
FUNCTIONAL DESCRIPTION: The tool Demodocos allows to build a generic model for a given procedure from some examples of instances of this procedure. The generated model can take the form of a graph, a Test 'n Flip net or a SEVEN scenario (intended for integration into a virtual reality environment).

The classic use of the tool is to apply the summary operation to a set of files describing instances of the target procedure. Several file formats are supported, including the standard XES format for log events. As output, several files are generated. These files represent the generic procedure in different forms, responding to varied uses.

This application is of limited interest in the case of an isolated use, out of context and without a specific objective when using the model generated. It was developed as part of a research project focusing in particular on surgical procedures, and requiring the generation of a generic model for integration into a virtual reality training environment. It is also quite possible to apply the same method in another context.

- Participants: Aurélien Lamercerie and Benoît Caillaud
- Contact: Benoît Caillaud
- Publication: Surgical Process Mining with Test and Flip Net Synthesis
- URL: http://www.irisa.fr/prive/Benoit.Caillaud/Benoit_Caillauds_Professional_homepage/Software/Entries/2017/12/31_Demodocos__A_test_and_flip_net_synthesis_tool_for_maintenance_and_surgical_process_
html

5.2. MICA

Model Interface Compositional Analysis Library
KEYWORDS: Modal interfaces - Contract-based desing

SCIENTIFIC DESCRIPTION: In Mica, systems and interfaces are represented by extension. However, a careful design of the state and event heap enables the definition, composition and analysis of reasonably large systems and interfaces. The heap stores states and events in a hash table and ensures structural equality (there is no duplication). Therefore complex data-structures for states and events induce a very low overhead, as checking equality is done in constant time.

Thanks to the Inter module and the mica interactive environment, users can define complex systems and interfaces using Ocaml syntax. It is even possible to define parameterized components as Ocaml functions.
FUNCTIONAL DESCRIPTION: Mica is an Ocaml library implementing the Modal Interface algebra. The purpose of Modal Interfaces is to provide a formal support to contract based design methods in the field of system engineering. Modal Interfaces enable compositional reasoning methods on I/O reactive systems.

- Participant: Benoît Caillaud
- Contact: Benoît Caillaud
- URL: http://www.irisa.fr/s4/tools/mica/

5.3. TnF-C++

FUNCTIONAL DESCRIPTION: TnF-C++ is a robust and portable re-implementation of Flipflop, developed in 2014 and integrated in the S3PM toolchain. Both software have been designed in the context of the S3PM project on surgical procedure modeling and simulation,

- Contact: Benoît Caillaud

KAIROS Team

6. New Software and Platforms

6.1. VerCors

VERification of models for distributed communicating COmponants, with safety and Security
KEYWORDS: Software Verification - Specification language - Model Checking
FUNCTIONAL DESCRIPTION: The VerCors tools include front-ends for specifying the architecture and behaviour of components in the form of UML diagrams. We translate these high-level specifications, into behavioural models in various formats, and we also transform these models using abstractions. In a final step, abstract models are translated into the input format for various verification toolsets. Currently we mainly use the various analysis modules of the CADP toolset.

RELEASE FUNCTIONAL DESCRIPTION: It includes integrated graphical editors for GCM component architecture descriptions, UML classes, interfaces, and state-machines. The user diagrams can be checked using the recently published validation rules from, then the corresponding GCM components can be executed using an automatic generation of the application ADL, and skeletons of Java files.

Experimental version (2018) also includes algorithm for computing the symbolic semantics of Open Systems

- Participants: Antonio Cansado, Bartlomiej Szejna, Eric Madelaine, Ludovic Henrio, Marcela Rivera, Nassim Jibai, Oleksandra Kulankhina and Siqi Li
- Partner: East China Normal University Shanghai (ECNU)
- Contact: Eric Madelaine
- URL: https://team.inria.fr/scale/software/vercors/

6.2. TimeSquare

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

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

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

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

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

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

* a generation of the whole state space of a specification (if finite of course) in order to enable model checking of temporal properties on it
FUNCTIONAL DESCRIPTION: TimeSquare is a software environment for the modeling and analysis of timing constraints in embedded systems. It relies specifically on the Time Model of the Marte UML profile, and more accurately on the associated Clock Constraint Specification Language (CCSL) for the expression of timing constraints.

- Participants: Benoît Ferrero, Charles André, Frédéric Mallet, Julien Deantoni and Nicolas Chleq
- Contact: Julien Deantoni
- URL: http://timesquare.inria.fr

6.3. GEMOC Studio

KEYWORDS: DSL - Language workbench - Model debugging
SCIENTIFIC DESCRIPTION: The language workbench put together the following tools seamlessly integrated to the Eclipse Modeling Framework (EMF):

- Melange, a tool-supported meta-language to modularly define executable modeling languages with execution functions and data, and to extend (EMF-based) existing modeling languages. - MoCCML, a tool-supported meta-language dedicated to the specification of a Model of Concurrency and Communication (MoCC) and its mapping to a specific abstract syntax and associated execution functions of a modeling language. - GEL, a tool-supported meta-language dedicated to the specification of the protocol between the execution functions and the MoCC to support the feedback of the data as well as the callback of other expected execution functions. - BCOoL, a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models. - Sirius Animator, an extension to the model editor designer Sirius to create graphical animators for executable modeling languages.
FUNCTIONAL DESCRIPTION: The GEMOC Studio is an eclipse package that contains components supporting the GEMOC methodology for building and composing executable Domain-Specific Modeling Languages (DSMLs). It includes the two workbenches: The GEMOC Language Workbench: intended to be used by language designers (aka domain experts), it allows to build and compose new executable DSMLs. The GEMOC Modeling Workbench: intended to be used by domain designersto create, execute and coordinate models conforming to executable DSMLs. The different concerns of a DSML, as defined with the tools of the language workbench, are automatically deployed into the modeling workbench. They parametrize a generic execution framework that provide various generic services such as graphical animation, debugging tools, trace and event managers, timeline, etc.

- Participants: Didier Vojtisek, Dorian Leroy, Erwan Bousse, Fabien Coulon and Julien Deantoni
- Partners: IRIT - ENSTA - I3S - OBEO - Thales TRT
- Contact: Benoît Combemale
- URL: http://gemoc.org/studio.html

6.4. BCOol

BCOoL
KEYWORDS: DSL - Language workbench - Behavior modeling - Model debugging - Model animation
FUNCTIONAL DESCRIPTION: BCOoL is a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models.

- Participants: Julien Deantoni, Matias Vara Larsen, Benoît Combemale and Didier Vojtisek
- Contact: Julien Deantoni
- URL: http://www.gemoc.org

6.5. myMed

Framework for building social networks executable on web browsers, android and apple platforms
KEYWORDS: Framework - Peer-to-peer. - NoSQL - Mobile application - Social network - Publish-subscribe

SCIENTIFIC DESCRIPTION: [EN] myMed : an ad hoc framework to execute homogeneous social networks. The explosion of different Open Social Networks (OSN) "running" in the internet arena has changed the habits of mostly all of us. There are OSN almost for everything, from cooperative work, car pooling, healthcare, friendship, love, affairs, healthcare, information, gaming, etc. In almost all of the cases, there are no two OSN that are built by the same software producer, and - quite often - mostly of them work on a competitive basis, and - for many different reasons (business, privacy, politics, etc.) - they are not open source and they are hosted by their private servers. The interactions between those OSN is very little, since the Application Programming Interfaces (API) - if existing - are very weak and limited to access to the friends lists or to access OSN X with the password of OSN Y. Even worst, the possibility of programming or at least interconnecting common features (e.g. search on different data bases, link user names and passwords, chat, access to common data bases etc.) between different OSN advance slowly. The most used practice of interconnecting OSN is based on a form of "asymmetric viral communication" where one can relay (or post or publish) a duplicated copy or a pointer of a record published by user A in OSN X into another OSN Y, provided user A have also an account on OSN Y, and de facto forbidding in mostly cases the inverse operation, aka subscribing for a different user B on OSN Y to any publication of user A on OSN X even if user B does not have an account on OSN X. As such, the well know paradigm of Publish/Subscribe at the basis of many CSCW applications cannot be fully exploited inter social networks, leaving only their use intra social network, the latter use being of less impact in coordination and cooperation. Beside of the "business needs" of OSNs, the myMed (www.mymed.fr) meta-social network represents an important step toward the natural interconnections of social applications. This paper introduce the concept and the original structure of the myMed experimental system, as it was conceived as a common effort between five academic sites (Inria, Polytechnic of Turin, University of Turin, University of Piedmont Oriental, University of Nice Sophia Antipolis) and few local startups. myMed is an open source project, which facilitate and accelerate the development of ad hoc social applications (called in myMed jargon "sociapps") running over an heterogeneous "Plateau" of platforms, such as PCs, Smartphones and Tablets running iOS and Android. myMed provides a rich framework for publishing, searching and subscribing to content: the engine is built on top of a distributed noSQL database. In its current version, it provides high scalability and fault tolerance. The myMed framework allows you to easily build social web applications: it features geolocalization, points of interest in charts, buddy lists, profile management, content/user reputation, built-in cooperation and coordination among different OSN running on it, proto OSN store, etc. A short description of the framework can be found in the appendix of this paper. In a nutshell the myMed framework is composed of: • a Software Development Kit (SDK) to develop fixed and mobile web sociapps, running on many Web browsers but also natively on Smartphones and Tablets equipped with Android or iOS. Sociapps, by their name, must have a strong social flavor (open social networks, closed social networks, enterprise social networks, micro/nano social networks and so on). Thanks to the rich, general-purpose, catalog of modules in the framework, every module can be freely used without interfering with other sociapps, in a true "Lego" fashion. The program is distributed under the Apache V2 free license. The TTM ("Time To Market") envisaged to develop a sociapp using the myMed SDK can be estimated from 1 to 3 months employing 1 or 2 senior programmers. • A "cloud" to execute the "sociapps" represented by a "backbone" of 50PCs, distributed through the "AlpMed" EuroRegion following some precise efficiency criteria (as example the presence of Internet running on optical fibers). Part of those PCs have a double function: o ensure the good behavior of all the running sociapps, and o offer services other than those offered by myMed, such as a web browser, an open-source Office suite, a private disk of little size, logically separated from the noSQL space that can be used by others users (we call this "an elastic usage of the myMed cloud PC"). Those PCs can be accessed via a private login and password generated by the framework on demand. The operating systems running on those PC (Ubuntu myMed Edition, UME) is also open source and it is based on a customized version of the Ubuntu operating system. To guarantee the quality of the execution of the sociapps, we require that all machines belonging to the backbone are constantly running (on state). • A little collection of "proof of concept" sociapps to validate, experiment, and testing the development kit and the execution cloud. These sociapps have been conceived with the precious help of the "Civil society" of the EuroRegion "AlpMed" (States, Regions, Prefectures, Associations, Chambers of Commerce, Municipalities, Universities, etc.) that have played a role of "maitre d'oeuvre" (or experts) in a given "applicative domain". The quasi totality of the sociapps are available on the myMed web platform at the address http://www.mymed.fr/?action=login but also on the most common mobile application stores, such as the Apple Store and the Google Play Store Markets. The myMed system is naturally divided into a backend and a frontend permitting a natural separation of concerns. The present and the future features of the myMed architecture together with the many open questions left open are: • myMed is distributed by construction and could be decentralized. The myMed backbone is based on a well-tested noSQL database, Cassandra, which can accommodate any number of users without any code changes. Machines can be classically concentrated on a data-center or – more interestingly – fully decentralized modulo a decent internet connection. Failures of one or many machines do not affect the running of the system, thanks to replication of the data on several servers. • myMed (should be) Easy to use. Start from the template, add or remove features, play with the design and the interface and you have an application ready to deploy on the myMed cloud and accessible to all myMed users via the proto store. • myMed is Extensible. myMed provides a modular architecture, since developers can easily install new modules and users can add or remove all the sociapps they like using the proto store. • myMed as a distributed Social Operating system? for many aspects myMed looks like an social operating system installed on a distributed and decentralize pull of PCs. Modifications of internal myMed modules would not affect the behavior of all sociapps using those modules. • myMed promotes collaboration and cooperation between OSN. The sharing of all social modules have the positive effect of greatly facilitate OSN interconnection • myMed users feature a two level profile. Having a myMed "basic profile" just give access to the store and to a "read only view" of each OSN X. For a full experience the user must fill the, so called, "extended profile" for OSN X which allows a full read/write access. • myMed and myMed sociapps can feature an ad hoc economical model? It is well know that economical models for OSN are quite often related to advertising, or buying intra OSN features. The myMed interconnectivity by construction, open a way to novel business models, like "the more you open the more you earn?" • myMed should feature an unique Human Computer Interface? a common template is provided to expert users that want to implement a proper OSN. Do they need to be compliant with some graphical chart? • myMed can run on different instances. Can different instances cooperate? As in higher-order languages, the same cooperation level featured between different OSNs running on one myMed instance can be applied on different myMed instances running on different hardware. This would be subject of a further evolution of inter-cooperation and connection of myMed instances and their OSN running inside it. A lot of care must be given in building coherent "meta basic profiles".

FUNCTIONAL DESCRIPTION: myMed is an experimental framework for implementing and deploying, on the top of a built-in cloud platform, many Open Social Networks (OSN) that could take advantage of sharing common software modules, hardware resources, making inter-communication and inter-interaction simpler and improving rapid development and deployement. myMed OSN are either accessible on web browsers and mobile platforms (android, ios). myMed is based on a peer-to-peer architecture and noSQL database technology. A number of experimental OSN are experimentally implemented and deployed to validate the framework : among them we mention myRiviera, myPaysduPaillon, mioConsolato, myBenevolat, myFondationSophiaAntipolis, myEurocin, myEurope, myAngel, ...

- Participants: Claudio Casetti, Luigi Liquori, Mariangiola Dezani and Mino Anglano
- Partners: Politecnico di Torino - Université de Nice Sophia Antipolis (UNS) - Università di Torino - Università del Piemonte Orientale
- Contact: Luigi Liquori
- URL: http://www.mymed.fr

6.6. JMaxGraph

KEYWORDS: Java - HPC - Graph algorithmics

FUNCTIONAL DESCRIPTION: JMaxGraph is a collection of techniques for the computation of large graphs on one single computer. The motivation for such a centralized computing platform originates in the constantly increasing efficiency of computers which now come with hundred gigabytes of RAM, tens of cores and fast drives. JMaxGraph implements a compact adjacency-table for the representation of the graph in memory. This data structure is designed to 1) be fed page by page, à-la GraphChi, 2) enable fast iteration, avoiding memory jumps as much as possible in order to benefit from hardware caches, 3) be tackled in parallel by multiple-threads. Also, JMaxGraph comes with a flexible and resilient batch-oriented middleware, which is suited to executing long computations on shared clusters. The first use-case of JMaxGraph allowed F. Giroire, T. Trolliet and S. Pérennes to count K2,2s, and various types of directed triangles in the Twitter graph of users (23G arcs, 400M vertices). The computation campaign took 4 days, using up to 400 cores in the NEF Inria cluster.

- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/software/?name=jmaxgraph

LFANT Project-Team

5. New Software and Platforms

5.1. APIP

Another Pairing Implementation in PARI
KEYWORDS: Cryptography - Computational number theory
SCIENTIFIC DESCRIPTION: Apip , Another Pairing Implementation in PARI, is a library for computing standard and optimised variants of most cryptographic pairings.

The following pairings are available: Weil, Tate, ate and twisted ate, optimised versions (à la Vercauteren–Hess) of ate and twisted ate for selected curve families.

The following methods to compute the Miller part are implemented: standard Miller double-and-add method, standard Miller using a non-adjacent form, Boxall et al. version, Boxall et al. version using a non-adjacent form.

The final exponentiation part can be computed using one of the following variants: naive exponentiation, interleaved method, Avanzi–Mihailescu's method, Kato et al.'s method, Scott et al.'s method.

Part of the library has been included into Pari/Gp proper.
FUNCTIONAL DESCRIPTION: APIP is a library for computing standard and optimised variants of most cryptographic pairings.

- Participant: Jérôme Milan
- Contact: Andreas Enge
- URL: http://www.lix.polytechnique.fr/~milanj/apip/apip.xhtml

5.2. AVIsogenies

Abelian Varieties and Isogenies
KEYWORDS: Computational number theory - Cryptography
FUNCTIONAL DESCRIPTION: AVIsogenies is a Magma package for working with abelian varieties, with a particular emphasis on explicit isogeny computation.

Its prominent feature is the computation of (l,l)-isogenies between Jacobian varieties of genus-two hyperelliptic curves over finite fields of characteristic coprime to l, practical runs have used values of l in the hundreds.

It can also be used to compute endomorphism rings of abelian surfaces, and find complete addition laws on them.

- Participants: Damien Robert, Gaëtan Bisson and Romain Cosset
- Contact: Damien Robert
- URL: http://avisogenies.gforge.inria.fr/

5.3. CM

KEYWORD: Arithmetic
FUNCTIONAL DESCRIPTION: The Cm software implements the construction of ring class fields of imaginary quadratic number fields and of elliptic curves with complex multiplication via floating point approximations. It consists of libraries that can be called from within a C program and of executable command line applications.

RELEASE FUNCTIONAL DESCRIPTION: Features - Precisions beyond 300000 bits are now supported by an addition chain of variable length for the -function. Dependencies - The minimal version number of Mpfr has been increased to 3.0.0, that of Mpc to 1.0.0 and that of Pari to 2.7.0.

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/cm/home.html

5.4. CMH

Computation of Igusa Class Polynomials
KEYWORDS: Mathematics - Cryptography - Number theory
FUNCTIONAL DESCRIPTION: Cmh computes Igusa class polynomials, parameterising two-dimensional abelian varieties (or, equivalently, Jacobians of hyperelliptic curves of genus 2) with given complex multiplication.

- Participants: Andreas Enge, Emmanuel Thomé and Regis Dupont
- Contact: Emmanuel Thomé
- URL: http://cmh.gforge.inria.fr

5.5. CUBIC

KEYWORD: Number theory
FUNCTIONAL DESCRIPTION: Cubic is a stand-alone program that prints out generating equations for cubic fields of either signature and bounded discriminant. It depends on the Pari library. The algorithm has quasi-linear time complexity in the size of the output.

- Participant: Karim Belabas
- Contact: Karim Belabas
- URL: http://www.math.u-bordeaux.fr/~belabas/research/software/cubic-1.2.tgz

5.6. Euclid

KEYWORD: Number theory
FUNCTIONAL DESCRIPTION: Euclid is a program to compute the Euclidean minimum of a number field. It is the practical implementation of the algorithm described in [38] . Some corresponding tables built with the algorithm are also available. Euclid is a stand-alone program depending on the PARI library.

- Participants: Jean-Paul Cerri and Pierre Lezowski
- Contact: Jean-Paul Cerri
- URL: http://www.math.u-bordeaux1.fr/~plezowsk/euclid/index.php

5.7. KleinianGroups

KEYWORDS: Computational geometry - Computational number theory
FUNCTIONAL DESCRIPTION: KleinianGroups is a Magma package that computes fundamental domains of arithmetic Kleinian groups.

- Participant: Aurel Page
- Contact: Aurel Page
- URL: http://www.normalesup.org/~page/Recherche/Logiciels/logiciels-en.html

5.8. GNU MPC

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: Mpc is a C library for the arithmetic of complex numbers with arbitrarily high precision and correct rounding of the result. It is built upon and follows the same principles as Mpfr. The library is written by Andreas Enge, Philippe Théveny and Paul Zimmermann.

RELEASE FUNCTIONAL DESCRIPTION: Fixed `mp\_pow`, see http://lists.gforge.inria.fr/pipermail/mpc-discuss/2014-October/001315.html - `\#18257`: Switched to libtool 2.4.5.

- Participants: Andreas Enge, Mickaël Gastineau, Paul Zimmermann and Philippe Théveny
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/

5.9. MPFRCX

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: Mpfrcx is a library for the arithmetic of univariate polynomials over arbitrary precision real (Mpfr) or complex (Mpc) numbers, without control on the rounding. For the time being, only the few functions needed to implement the floating point approach to complex multiplication are implemented. On the other hand, these comprise asymptotically fast multiplication routines such as Toom-Cook and the FFT.

RELEASE FUNCTIONAL DESCRIPTION: - new function `produc\_an\_hecke` - improved memory consumption for unbalanced FFT multiplications

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: http://www.multiprecision.org/mpfrcx/home.html

5.10. PARI/GP

KEYWORD: Computational number theory

FUNCTIONAL DESCRIPTION: Pari/Gp is a widely used computer algebra system designed for fast computations in number theory (factorisation, algebraic number theory, elliptic curves, modular forms ...), but it also contains a large number of other useful functions to compute with mathematical entities such as matrices, polynomials, power series, algebraic numbers, etc., and many transcendental functions.

- Participants: Andreas Enge, Hamish Ivey-Law, Henri Cohen and Karim Belabas
- Partner: CNRS
- Contact: Karim Belabas
- URL: http://pari.math.u-bordeaux.fr/

MARELLE Project-Team

5. New Software and Platforms

5.1. Coq

The Coq Proof Assistant
KEYWORDS: Proof - Certification - Formalisation
SCIENTIFIC DESCRIPTION: Coq is an interactive proof assistant based on the Calculus of (Co-)Inductive Constructions, extended with universe polymorphism. This type theory features inductive and co-inductive families, an impredicative sort and a hierarchy of predicative universes, making it a very expressive logic. The calculus allows to formalize both general mathematics and computer programs, ranging from theories of finite structures to abstract algebra and categories to programming language metatheory and compiler verification. Coq is organised as a (relatively small) kernel including efficient conversion tests on which are built a set of higher-level layers: a powerful proof engine and unification algorithm, various tactics/decision procedures, a transactional document model and, at the very top an IDE.
FUNCTIONAL DESCRIPTION: Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

RELEASE FUNCTIONAL DESCRIPTION: Coq version 8.8.2 contains the result of refinements and stabilization of features and deprecations, cleanups of the internals of the system along with a few new features.

Summary of changes:

Kernel: fix a subject reduction failure due to allowing fixpoints on non-recursive values (#407), by Matthieu Sozeau. Handling of evars in the VM (#935) by Pierre-Marie Pédrot.

Notations: many improvements on recursive notations and support for destructuring patterns in the syntax of notations by Hugo Herbelin.

Proof language: tacticals for profiling, timing and checking success or failure of tactics by Jason Gross. The focusing bracket { supports single-numbered goal selectors, e.g. 2:{, (#6551) by Théo Zimmermann.

Vernacular: cleanup of definition commands (#6653) by Vincent Laporte and more uniform handling of the Local flag (#1049), by Maxime Dénès. Experimental Show Extraction command (#6926) by Pierre Letouzey. Coercion now accepts Prop or Type as a source (#6480) by Arthur Charguéraud. Export modifier for options allowing to export the option to modules that Import and not only Require a module (#6923), by Pierre-Marie Pédrot.

Universes: many user-level and API level enhancements: qualified naming and printing, variance annotations for cumulative inductive types, more general constraints and enhancements of the minimization heuristics, interaction with modules by Gaëtan Gilbert, Pierre-Marie Pédrot and Matthieu Sozeau.

Library: Decimal Numbers library (#6599) by Pierre Letouzey and various small improvements.

Documentation: a large community effort resulted in the migration of the reference manual to the Sphinx documentation tool. The new documentation infrastructure (based on Sphinx) is by Clément Pit-Claudel. The migration was coordinated by Maxime Dénès and Paul Steckler, with some help of Théo Zimmermann during the final integration phase. The 14 people who ported the manual are Calvin Beck, Heiko Becker, Yves Bertot, Maxime Dénès, Richard Ford, Pierre Letouzey, Assia Mahboubi, Clément Pit-Claudel, Laurence Rideau, Matthieu Sozeau, Paul Steckler, Enrico Tassi, Laurent Théry, Nikita Zyuzin.

Tools: experimental -mangle-names option to coqtop/coqc for linting proof scripts (#6582), by Jasper Hugunin. Main changes:

Critical soundness bugs were fixed between versions 8.8.0 and 8.8.2, and a PDF version of the reference manual was made available. The Windows installer also includes many more external packages that can be individually selected for installation.

On the implementation side, the dev/doc/changes.md file documents the numerous changes to the implementation and improvements of interfaces. The file provides guidelines on porting a plugin to the new version.

More information can be found in the CHANGES file. Feedback and bug reports are extremely welcome.

Distribution Installers for Windows 32 bits (i686), Windows 64 bits (x8_64) and macOS are available. They come bundled with CoqIDE. Windows binaries now include the Bignums library.

Complete sources of the files installed by the Windows installers are made available, to comply with license requirements.
NEWS OF THE YEAR: Version 8.8.0 was released in April 2018 and version 8.8.2 in September 2018. This is the third release of Coq developed on a time-based development cycle. Its development spanned 6 months from the release of Coq 8.7 and was based on a public road-map. It attracted many external contributions. Code reviews and continuous integration testing were systematically used before integration of new features, with an important focus given to compatibility and performance issues.

The main advances in this version are cleanups and fixes in the many different components of the system, ranging from low level kernel fixes to advances in the support of notations and tacticals for selecting goals. A large community effort was made to move the documentation to the Sphinx format, providing a more accessible online ressource to users.

- Participants: Abhishek Anand, C. J. Bell, Yves Bertot, Frédéric Besson, Tej Chajed, Pierre Courtieu, Maxime Denes, Julien Forest, Emilio Jesús Gallego Arias, Gaëtan Gilbert, Benjamin Grégoire, Jason Gross, Hugo Herbelin, Ralf Jung, Matej Kosik, Sam Pablo Kuper, Xavier Leroy, Pierre Letouzey, Assia Mahboubi, Cyprien Mangin, Érik Martin-Dorel, Olivier Marty, Guillaume Melquiond, Pierre-Marie Pédrot, Benjamin C. Pierce, Lars Rasmusson, Yann Régis-Gianas, Lionel Rieg, Valentin Robert, Thomas Sibut-Pinote, Michael Soegtrop, Matthieu Sozeau, Arnaud Spiwack, Paul Steckler, George Stelle, Pierre-Yves Strub, Enrico Tassi, Hendrik Tews, Laurent Théry, Amin Timany, Vadim Zaliva and Théo Zimmermann
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Matthieu Sozeau
- Publication: The Coq Proof Assistant, version 8.8.0
- URL: http://coq.inria.fr/

5.2. Easycrypt

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

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

5.3. ELPI

Embeddable Lambda Prolog Interpreter
KEYWORDS: Constraint Programming - Programming language - Higher-order logic
SCIENTIFIC DESCRIPTION: The programming language has the following features

- Native support for variable binding and substitution, via an Higher Order Abstract Syntax (HOAS) embedding of the object language. The programmer needs not to care about De Bruijn indexes.

- Native support for hypothetical context. When moving under a binder one can attach to the bound variable extra information that is collected when the variable gets out of scope. For example when writing a type-checker the programmer needs not to care about managing the typing context.

- Native support for higher order unification variables, again via HOAS. Unification variables of the meta-language (lambdaProlog) can be reused to represent the unification variables of the object language. The programmer does not need to care about the unification-variable assignment map and cannot assign to a unification variable a term containing variables out of scope, or build a circular assignment.

- Native support for syntactic constraints and their meta-level handling rules. The generative semantics of Prolog can be disabled by turning a goal into a syntactic constraint (suspended goal). A syntactic constraint is resumed as soon as relevant variables gets assigned. Syntactic constraints can be manipulated by constraint handling rules (CHR).

- Native support for backtracking. To ease implementation of search.

- The constraint store is extensible. The host application can declare non-syntactic constraints and use custom constraint solvers to check their consistency.

- Clauses are graftable. The user is free to extend an existing program by inserting/removing clauses, both at runtime (using implication) and at "compilation" time by accumulating files.

Most of these feature come with lambdaProlog. Constraints and propagation rules are novel in ELPI.
FUNCTIONAL DESCRIPTION: ELPI implements a variant of lambdaProlog enriched with Constraint Handling Rules, a programming language well suited to manipulate syntax trees with binders and unification variables.

ELPI is a research project aimed at providing a programming platform for the so called elaborator component of an interactive theorem prover.

ELPI is designed to be embedded into larger applications written in OCaml as an extension language. It comes with an API to drive the interpreter and with an FFI for defining built-in predicates and data types, as well as quotations and similar goodies that come in handy to adapt the language to the host application.

RELEASE FUNCTIONAL DESCRIPTION: First public release
NEWS OF THE YEAR: First public release

- Participant: Claudio Sacerdoti Coen
- Contact: Enrico Tassi
- Publications: ELPI: fast, Embeddable, λProlog Interpreter - Implementing Type Theory in Higher Order Constraint Logic Programming
- URL: https://github.com/lpcic/elpi/

5.4. Math-Components

Mathematical Components library
KEYWORD: Proof assistant
FUNCTIONAL DESCRIPTION: The Mathematical Components library is a set of Coq libraries that cover the prerequiste for the mechanization of the proof of the Odd Order Theorem.

RELEASE FUNCTIONAL DESCRIPTION: The library includes 16 more theory files, covering in particular field and Galois theory, advanced character theory, and a construction of algebraic numbers.

- Participants: Alexey Solovyev, Andrea Asperti, Assia Mahboubi, Cyril Cohen, Enrico Tassi, François Garillot, Georges Gonthier, Ioana Pasca, Jeremy Avigad, Laurence Rideau, Laurent Théry, Russell O'Connor, Sidi Ould Biha, Stéphane Le Roux and Yves Bertot
- Contact: Assia Mahboubi
- URL: http://math-comp.github.io/math-comp/

5.5. Semantics

KEYWORDS: Semantic - Programming language - Coq
FUNCTIONAL DESCRIPTION: A didactical Coq development to introduce various semantics styles. Shows how to derive an interpreter, a verifier, or a program analyser from formal descriptions, and how to prove their consistency.

This is a library for the Coq system, where the description of a toy programming language is presented. The value of this library is that it can be re-used in classrooms to teach programming language semantics or the Coq system. The topics covered include introductory notions to domain theory, pre and post-conditions, abstract interpretation, and the proofs of consistency between all these point of views on the same programming language. Standalone tools for the object programming language can be derived from this development.

- Participants: Christine Paulin and Yves Bertot
- Contact: Yves Bertot
- URL: http://www-sop.inria.fr/members/Yves.Bertot/proofs/semantics_survey.tgz

5.6. Ssreflect

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

- Participants: Assia Mahboubi, Cyril Cohen, Enrico Tassi, Georges Gonthier, Laurence Rideau, Laurent Théry and Yves Bertot
- Contact: Yves Bertot
- URL: http://math-comp.github.io/math-comp/

5.7. AutoGnP

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

- Participants: Benjamin Grégoire, Gilles Barthe and Pierre-Yves Strub
- Contact: Gilles Barthe
- URL: https://github.com/ZooCrypt/AutoGnP

MEXICO Project-Team

6. New Software and Platforms

6.1. COSMOS

KEYWORD: Model Checker

FUNCTIONAL DESCRIPTION: COSMOS is a statistical model checker for the Hybrid Automata Stochastic Logic (HASL). HASL employs Linear Hybrid Automata (LHA), a generalization of Deterministic Timed Automata (DTA), to describe accepting execution paths of a Discrete Event Stochastic Process (DESP), a class of stochastic models which includes, but is not limited to, Markov chains. As a result HASL verification turns out to be a unifying framework where sophisticated temporal reasoning is naturally blended with elaborate reward-based analysis. COSMOS takes as input a DESP (described in terms of a Generalized Stochastic Petri Net), an LHA and an expression Z representing the quantity to be estimated. It returns a confidence interval estimation of Z, recently, it has been equipped with functionalities for rare event analysis.

It is easy to generate and use a C code for discrete Simulink models (using only discrete blocks, which are sampled at fixed intervals) using MathWorks tools. However, it limits the expressivity of the models. In order to use more diverse Simulink models and control the flow of a multi-model simulation (with Discrete Event Stochastic Processes) we developed a Simulink Simulation Engine embedded into Cosmos.

COSMOS is written in C++

- Participants: Benoît Barbot, Hilal Djafri, Marie Duflot-Kremer, Paolo Ballarini and Serge Haddad
- Contact: Benoît Barbot
- URL: http://www.lsv.ens-cachan.fr/~barbot/cosmos/

6.2. CosyVerif

FUNCTIONAL DESCRIPTION: CosyVerif is a platform dedicated to the formal specification and verification of dynamic systems. It allows to specify systems using several formalisms (such as automata and Petri nets), and to run verification tools on these models.

- Participants: Alban Linard, Fabrice Kordon, Laure Petrucci and Serge Haddad
- Partners: LIP6 - LSV - LIPN (Laboratoire d'Informatique de l'Université Paris Nord)
- Contact: Serge Haddad
- URL: http://www.cosyverif.org/

6.3. Mole

FUNCTIONAL DESCRIPTION: Mole computes, given a safe Petri net, a finite prefix of its unfolding. It is designed to be compatible with other tools, such as PEP and the Model-Checking Kit, which are using the resulting unfolding for reachability checking and other analyses. The tool Mole arose out of earlier work on Petri nets.

- Participant: Stefan Schwoon
- Contact: Stefan Schwoon
- URL: http://www.lsv.ens-cachan.fr/~schwoon/tools/mole/

MOCQUA Team

6. New Software and Platforms

6.1. Software

6.1.1. FiatLux

- Participants: Nazim Fatès, Nicolas Gauville

FiatLux is a simulation program for cellular automata and discrete dynamical systems. It is developed by Nazim Fatès ; the project is currently available at the Inria GForge. The program is published with the CeCILL license. New features have been implemented in 2018, as for example the possibility to define some systems directly in the software by writing the local transition rules in Java. These features were mostly added by Nicolas Gauville, a Master's student who was an intern in the team.

OURAGAN Team

6. New Software and Platforms

6.1. ISOTOP

Topology and geometry of planar algebraic curves
KEYWORDS: Topology - Curve plotting - Geometric computing
FUNCTIONAL DESCRIPTION: Isotop is a Maple software for computing the topology of an algebraic plane curve, that is, for computing an arrangement of polylines isotopic to the input curve. This problem is a necessary key step for computing arrangements of algebraic curves and has also applications for curve plotting. This software has been developed since 2007 in collaboration with F. Rouillier from Inria Paris - Rocquencourt.
NEWS OF THE YEAR: In 2018, an engineer from Inria Nancy (Benjamin Dexheimer) finished the implementation of the web server to improve the diffusion of our software.

- Participants: Luis Penaranda, Marc Pouget and Sylvain Lazard
- Contact: Marc Pouget
- Publications: Rational Univariate Representations of Bivariate Systems and Applications - Separating Linear Forms for Bivariate Systems - On The Topology of Planar Algebraic Curves - New bivariate system solver and topology of algebraic curves - Improved algorithm for computing separating linear forms for bivariate systems - Solving bivariate systems using Rational Univariate Representations - On the topology of planar algebraic curves - On the topology of real algebraic plane curves - Bivariate triangular decompositions in the presence of asymptotes - Separating linear forms and Rational Univariate Representations of bivariate systems
- URL: https://isotop.gamble.loria.fr/

6.2. RS

FUNCTIONAL DESCRIPTION: Real Roots isolation for algebraic systems with rational coefficients with a finite number of Complex Roots

- Participant: Fabrice Rouillier
- Contact: Fabrice Rouillier
- URL: https://team.inria.fr/ouragan/software/

6.3. A NewDsc

A New Descartes
KEYWORD: Scientific computing
FUNCTIONAL DESCRIPTION: Computations of the real roots of univariate polynomials with rational coefficients.

- Authors: Fabrice Rouillier, Alexander Kobel and Michael Sagraloff
- Partner: Max Planck Institute for Software Systems
- Contact: Fabrice Rouillier
- URL: https://anewdsc.mpi-inf.mpg.de

6.4. SIROPA

KEYWORDS: Robotics - Kinematics

FUNCTIONAL DESCRIPTION: Library of functions for certified computations of the properties of articulated mechanisms, particularly the study of their singularities

- Authors: Damien Chablat, Fabrice Rouillier, Guillaume Moroz and Philippe Wenger
- Partner: LS2N
- Contact: Guillaume Moroz
- URL: http://siropa.gforge.inria.fr/

6.5. MPFI

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: MPFI is a C library based on MPFR and GMP for multi precision floating point arithmetic.

- Contact: Fabrice Rouillier
- URL: http://mpfi.gforge.inria.fr

PACAP Project-Team

6. New Software and Platforms

6.1. ATMI

KEYWORDS: Analytic model - Chip design - Temperature
SCIENTIFIC DESCRIPTION: Research on temperature-aware computer architecture requires a chip temperature model. General purpose models based on classical numerical methods like finite differences or finite elements are not appropriate for such research, because they are generally too slow for modeling the time-varying thermal behavior of a processing chip.

ATMI (Analytical model of Temperature in MIcroprocessors) is an ad hoc temperature model for studying thermal behaviors over a time scale ranging from microseconds to several minutes. ATMI is based on an explicit solution to the heat equation and on the principle of superposition. ATMI can model any power density map that can be described as a superposition of rectangle sources, which is appropriate for modeling the microarchitectural units of a microprocessor.
FUNCTIONAL DESCRIPTION: ATMI is a library for modelling steady-state and time-varying temperature in microprocessors. ATMI uses a simplified representation of microprocessor packaging.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/pacap/software/atmi/

6.2. HEPTANE

KEYWORDS: IPET - WCET - Performance - Real time - Static analysis - Worst Case Execution Time
SCIENTIFIC DESCRIPTION: WCET estimation

The aim of Heptane is to produce upper bounds of the execution times of applications. It is targeted at applications with hard real-time requirements (automotive, railway, aerospace domains). Heptane computes WCETs using static analysis at the binary code level. It includes static analyses of microarchitectural elements such as caches and cache hierarchies.
FUNCTIONAL DESCRIPTION: In a hard real-time system, it is essential to comply with timing constraints, and Worst Case Execution Time (WCET) in particular. Timing analysis is performed at two levels: analysis of the WCET for each task in isolation taking account of the hardware architecture, and schedulability analysis of all the tasks in the system. Heptane is a static WCET analyser designed to address the first issue.

- Participants: Benjamin Lesage, Loïc Besnard, Damien Hardy, François Joulaud, Isabelle Puaut and Thomas Piquet
- Partner: Université de Rennes 1
- Contact: Isabelle Puaut
- URL: https://team.inria.fr/pacap/software/heptane/

6.3. tiptop

KEYWORDS: Instructions - Cycles - Cache - CPU - Performance - HPC - Branch predictor
SCIENTIFIC DESCRIPTION: Tiptop is a new simple and flexible user-level tool that collects hardware counter data on Linux platforms (version 2.6.31+) and displays them in a way simple to the Linux "top" utility. The goal is to make the collection of performance and bottleneck data as simple as possible, including simple installation and usage. No privilege is required, any user can run tiptop.

Tiptop is written in C. It can take advantage of libncurses when available for pseudo-graphic display. Installation is only a matter of compiling the source code. No patching of the Linux kernel is needed, and no special-purpose module needs to be loaded.

Current version is 2.3.1, released October 2017. Tiptop has been integrated in major Linux distributions, such as Fedora, Debian, Ubuntu.

FUNCTIONAL DESCRIPTION: Today's microprocessors have become extremely complex. To better understand the multitude of internal events, manufacturers have integrated many monitoring counters. Tiptop can be used to collect and display the values from these performance counters very easily. Tiptop may be of interest to anyone who wants to optimise the performance of their HPC applications.

- Participant: Erven Rohou
- Contact: Erven Rohou
- URL: http://tiptop.gforge.inria.fr

6.4. PADRONE

KEYWORDS: Legacy code - Optimization - Performance analysis - Dynamic Optimization

FUNCTIONAL DESCRIPTION: Padrone is new platform for dynamic binary analysis and optimization. It provides an API to help clients design and develop analysis and optimization tools for binary executables. Padrone attaches to running applications, only needing the executable binary in memory. No source code or debug information is needed. No application restart is needed either. This is especially interesting for legacy or commercial applications, but also in the context of cloud deployment, where actual hardware is unknown, and other applications competing for hardware resources can vary. The profiling overhead is minimum.

- Participants: Emmanuel Riou and Erven Rohou
- Contact: Erven Rohou
- URL: https://team.inria.fr/pacap/software/padrone

6.5. If-memo

KEYWORD: Performance

SCIENTIFIC DESCRIPTION: We propose a linker based technique for enabling software memorizing of any dynamically linked pure function by function interception and we illustrate our framework using a set of computationally expensive pure functions - the transcendental functions. Our technique does not need the availability of source code and thus can even be applied to commercial applications as well as applications with legacy codes. As far as users are concerned, enabling memoization is as simple as setting an environment variable. Our framework does not make any specific assumptions about the underlying architecture or compiler too-chains, and can work with a variety of current architectures.

FUNCTIONAL DESCRIPTION: If-memo is a linker-based technique for enabling software memorizing of any dynamically linked pure function by function interception. Typically, this framework is useful to intercept the computationally expensive pure functions - the transcendental functions from the math library. Our technique does not need the availability of source code and thus can even be applied to commercial applications as well as applications with legacy codes. As far as users are concerned, enabling memoization is as simple as setting an environment variable. Our framework does not make any specific assumptions about the underlying architecture or compiler too-chains, and can work with a variety of current architectures.

- Participants: Arjun Suresh and Erven Rohou
- Contact: Erven Rohou
- URL: https://team.inria.fr/pacap/software/if-memo/

6.6. Simty

KEYWORDS: GPU - Softcore - FPGA - SIMT - Multi-threading - RISC-V

FUNCTIONAL DESCRIPTION: Simty is a massively multi-threaded processor core that dynamically assembles SIMD instructions from scalar multi-thread code. It runs the RISC-V (RV32-I) instruction set. Unlike existing SIMD or SIMT processors like GPUs, Simty takes binaries compiled for general-purpose processors without any instruction set extension or compiler changes. Simty is described in synthesizable VHDL.

- Author: Sylvain Collange
- Contact: Sylvain Collange
- URL: https://gforge.inria.fr/projects/simty

6.7. Barra

KEYWORDS: GPU - GPGPU - Tesla ISA - Debug - Computer architecture - Performance - Profiling - Simulator - HPC - CUDA

SCIENTIFIC DESCRIPTION: Research on throughput-oriented architectures demands accurate and representative models of GPU architectures in order to be able to evaluate new architectural ideas, explore design spaces and characterize applications. The Barra project is a simulator of the NVIDIA Tesla GPU architecture.

Barra builds upon knowledge acquired through micro-benchmarking, in order to provide a baseline model representative of industry practice. The simulator provides detailed statistics to identify optimization opportunities and is fully customizable to experiment ideas of architectural modifications. Barra incorporates both a functional model and a cycle-level performance model.

FUNCTIONAL DESCRIPTION: Barra is a Graphics Processing Unit (GPU) architecture simulator. It simulates NVIDIA CUDA programs at the assembly language level. Barra is a tool for research on computer architecture, and can also be used to debug, profile and optimize CUDA programs at the lowest level.

RELEASE FUNCTIONAL DESCRIPTION: Version 0.5.10 introduces: Timing model, Tesla-like architecture model, Fermi-like architecture model, New per-PC control-flow divergence management, Support for Simultaneous branch and warp interweaving, Support for Affine vector cache.

- Participants: Alexandre Kouyoumdjian, David Defour, Fabrice Mouhartem and Sylvain Collange
- Partners: ENS Lyon - UPVD
- Contact: Sylvain Collange
- URL: http://barra.gforge.inria.fr/

6.8. Memoization

KEYWORDS: Optimization - Pure function - Memoization

FUNCTIONAL DESCRIPTION: Memoization is a technique used at runtime that consists in caching results of pure functions and retrieving them instead of computing it when the arguments repeat. It can be applied to C and C++ programs. To be memoized, the interface of a pure function (or a method) must verify the following properties: (1) the function/method has at most four arguments of same type T, (2) the function/method returns a data of type T, (3) T is either 'double', 'float', or 'int'.

The memoization operation of a function/method is controlled by several parameters: the size of the internal table (number of entries), the replacement policy to be used in case of index conflict (whether the value of the table must be replaced or not), an approximation threshold that allows to not distinguish very close values). It is also possible to initialize the table with the content of a file, and to save the content of the table to a file at the end of the execution (the data may be used as input for a future execution).

- Participants: Loïc Besnard, Imane Lasri and Erven Rohou
- Contact: Loïc Besnard

6.9. FiPlib

KEYWORDS: Compilation - Approximate computing - Fixed-point representation

FUNCTIONAL DESCRIPTION: FiPlib is a C++ library that provides type definition and conversion operations for computations in fixed-point representation. Basic arithmetic as well as logical operations are transparently supported thanks to operator overloading. FiPlib also provides optimized implementations of the transcendental math functions of libm. For convenient integration, FiPlib is released as C++ header files only. Optionally, FiPlib can detect overflows and compute errors compared to floating point representation.

- Participants: Pierre Le Meur, Imane Lasri and Erven Rohou
- Contact: Erven Rohou

6.10. sigmask

KEYWORDS: Compilation - Side-channel - Masking - Security - Embedded systems
SCIENTIFIC DESCRIPTION: Sigmask is a compiler plugin based on the LLVM infrastructure that automatically protects secret information in programs, such as encryption keys, against side-channel attacks. The programmer annotates their source code to highlight variables containing sensitive data. The compiler automatically analyzes the program and computes all memory locations potentially derived from the secret. It then applies a masking scheme to avoid information leakage. Sigmask provides several schemes: OSDM (Orthogonal Direct Sum Masking), IP (Inner Product) Masking, and simple random bit masking. The programmer may also provide their own masking scheme through a well-defined API.

- Participants: Nicolas Kiss, Damien Hardy and Erven Rohou
- Contact: Erven Rohou

PARKAS Project-Team

5. New Software and Platforms

5.1. Cmmtest

FUNCTIONAL DESCRIPTION: Cmmtest is a tool for hunting concurrency compiler bugs. The Cmmtest tool performs random testing of C and C++ compilers against the C11/C++11 memory model. A test case is any well-defined, sequential C program, for each test case, cmmtest:

compiles the program using the compiler and compiler optimisations that are being tested,

runs the compiled program in an instrumented execution environment that logs all memory accesses to global variables and synchronisations,

compares the recorded trace with a reference trace for the same program, checking if the recorded trace can be obtained from the reference trace by valid eliminations, reorderings and introductions.

Cmmtest identified several mistaken write introductions and other unexpected behaviours in the latest release of the gcc compiler. These have been promptly fixed by the gcc developers.

- Participants: Anirudh Kumar, Francesco Zappa Nardelli, Pankaj More, Pankaj Pawan, Pankaj Prateek Kewalramani and Robin Morisset
- Contact: Francesco Zappa Nardelli
- URL: http://www.di.ens.fr/~zappa/projects/cmmtest/

5.2. GCC

KEYWORDS: Compilation - Polyhedral compilation
FUNCTIONAL DESCRIPTION: The GNU Compiler Collection includes front ends for C, C++, Objective-C, Fortran, Java, Ada, and Go, as well as libraries for these languages (libstdc++, libgcj,...). GCC was originally written as the compiler for the GNU operating system. The GNU system was developed to be 100

- Participants: Albert Cohen, Feng Li, Nhat Minh Le, Riyadh Baghdadi and Tobias Grosser
- Contact: Albert Cohen
- URL: http://gcc.gnu.org/

5.3. 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 Synchrone, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

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

5.4. isl

FUNCTIONAL DESCRIPTION: isl is a library for manipulating sets and relations of integer points bounded by linear constraints. Supported operations on sets include intersection, union, set difference, emptiness check, convex hull, (integer) affine hull, integer projection, transitive closure (and over-approximation), computing the lexicographic minimum using parametric integer programming. It includes an ILP solver based on generalized basis reduction, and a new polyhedral code generator. isl also supports affine transformations for polyhedral compilation, and increasingly abstract representations to model source and intermediate code in a polyhedral framework.

- Participants: Albert Cohen, Sven Verdoolaege and Tobias Grosser
- Contact: Sven Verdoolaege
- URL: http://freshmeat.net/projects/isl

5.5. Lem

lightweight executable mathematics

FUNCTIONAL DESCRIPTION: Lem is a lightweight tool for writing, managing, and publishing large scale semantic definitions. It is also intended as an intermediate language for generating definitions from domain-specific tools, and for porting definitions between interactive theorem proving systems (such as Coq, HOL4, and Isabelle). As such it is a complementary tool to Ott. Lem resembles a pure subset of Objective Caml, supporting typical functional programming constructs, including top-level parametric polymorphism, datatypes, records, higher-order functions, and pattern matching. It also supports common logical mechanisms including list and set comprehensions, universal and existential quantifiers, and inductively defined relations. From this, Lem generates OCaml, HOL4, Coq, and Isabelle code.

- Participants: Francesco Zappa Nardelli, Peter Sewell and Scott Owens
- Contact: Francesco Zappa Nardelli
- URL: http://www.cl.cam.ac.uk/~pes20/lem/

5.6. Lucid Synchrone

FUNCTIONAL DESCRIPTION: Lucid Synchrone is a language for the implementation of reactive systems. It is based on the synchronous model of time as provided by Lustre combined with features from ML languages. It provides powerful extensions such as type and clock inference, type-based causality and initialization analysis and allows to arbitrarily mix data-flow systems and hierarchical automata or flows and valued signals.

RELEASE FUNCTIONAL DESCRIPTION: The language is still used for teaching and in our research but we do not develop it anymore. Nonetheless, we have integrated several features from Lucid Synchrone in new research prototypes described below. The Heptagon language and compiler are a direct descendent of it. The new language Zélus for hybrid systems modeling borrows many features originaly introduced in Lucid Synchrone.

- Contact: Marc Pouzet
- URL: http://www.di.ens.fr/~pouzet/lucid-synchrone/

5.7. Lucy-n

Lucy-n: an n-synchronous data-flow programming language

FUNCTIONAL DESCRIPTION: Lucy-n is a language to program in the n-synchronous model. The language is similar to Lustre with a buffer construct. The Lucy-n compiler ensures that programs can be executed in bounded memory and automatically computes buffer sizes. Hence this language allows to program Kahn networks, the compiler being able to statically compute bounds for all FIFOs in the program.

- Participants: Adrien Guatto, Albert Cohen, Louis Mandel and Marc Pouzet
- Contact: Albert Cohen
- URL: https://www.lri.fr/~mandel/lucy-n/

5.8. Ott

FUNCTIONAL DESCRIPTION: Ott is a tool for writing definitions of programming languages and calculi. It takes as input a definition of a language syntax and semantics, in a concise and readable ASCII notation that is close to what one would write in informal mathematics. It generates output:

a LaTeX source file that defines commands to build a typeset version of the definition,

a Coq version of the definition,

an Isabelle version of the definition, and

a HOL version of the definition.

Additionally, it can be run as a filter, taking a LaTeX/Coq/Isabelle/HOL source file with embedded (symbolic) terms of the defined language, parsing them and replacing them by typeset terms.

The main goal of the Ott tool is to support work on large programming language definitions, where the scale makes it hard to keep a definition internally consistent, and to keep a tight correspondence between a definition and implementations. We also wish to ease rapid prototyping work with smaller calculi, and to make it easier to exchange definitions and definition fragments between groups. The theorem-prover backends should enable a smooth transition between use of informal and formal mathematics.

- Participants: Francesco Zappa Nardelli, Peter Sewell and Scott Owens
- Contact: Francesco Zappa Nardelli
- URL: http://www.cl.cam.ac.uk/~pes20/ott/

5.9. PPCG

FUNCTIONAL DESCRIPTION: PPCG is our source-to-source research tool for automatic parallelization in the polyhedral model. It serves as a test bed for many compilation algorithms and heuristics published by our group, and is currently the best automatic parallelizer for CUDA and OpenCL (on the Polybench suite).

- Participants: Albert Cohen, Riyadh Baghdadi, Sven Verdoolaege and Tobias Grosser
- Contact: Sven Verdoolaege
- URL: http://freshmeat.net/projects/ppcg

5.10. ReactiveML

FUNCTIONAL DESCRIPTION: ReactiveML is a programming language dedicated to the implementation of interactive systems as found in graphical user interfaces, video games or simulation problems. ReactiveML is based on the synchronous reactive model due to Boussinot, embedded in an ML language (OCaml).

The Synchronous reactive model provides synchronous parallel composition and dynamic features like the dynamic creation of processes. In ReactiveML, the reactive model is integrated at the language level (not as a library) which leads to a safer and a more natural programming paradigm.

- Participants: Cédric Pasteur, Guillaume Baudart and Louis Mandel
- Contact: Guillaume Baudart

5.11. SundialsML

Sundials/ML
KEYWORDS: Simulation - Mathematics - Numerical simulations
SCIENTIFIC DESCRIPTION: Sundials/ML is a comprehensive OCaml interface to the Sundials suite of numerical solvers (CVODE, CVODES, IDA, IDAS, KINSOL). Its structure mostly follows that of the Sundials library, both for ease of reading the existing documentation and for adapting existing source code, but several changes have been made for programming convenience and to increase safety, namely:

solver sessions are mostly configured via algebraic data types rather than multiple function calls,

errors are signalled by exceptions not return codes (also from user-supplied callback routines),

user data is shared between callback routines via closures (partial applications of functions),

vectors are checked for compatibility (using a combination of static and dynamic checks), and

explicit free commands are not necessary since OCaml is a garbage-collected language.
FUNCTIONAL DESCRIPTION: Sundials/ML is a comprehensive OCaml interface to the Sundials suite of numerical solvers (CVODE, CVODES, IDA, IDAS, KINSOL, ARKODE).

RELEASE FUNCTIONAL DESCRIPTION: Adds support for v3.1.x of the Sundials Suite of numerical solvers.

Notably this release adds support for the new generic matrix and linear solver interfaces. The OCaml interface changes but the library is backward compatible with Sundials 2.7.0.

OCaml 4.02.3 or greater is now required and optionally OCamlMPI 1.03.

* New Sundials.Matrix and Sundials.LinearSolver modules. * Better treatment of integer type used for matrix indexing. * Refactor Dls and Sls modules into Sundials.Matrix. * Add confidence intervals to performance graph. * Miscellaneous improvements to configure script. * Potential incompatibility: changes to some label names: com_fn -> comm, ite_type -> iter. * Untangle the ARKODE mass-solver interface from the Jacobian interface.

- Participants: Jun Inoue, Marc Pouzet and Timothy Bourke
- Partner: UPMC
- Contact: Marc Pouzet
- URL: http://inria-parkas.github.io/sundialsml/

5.12. Zelus

SCIENTIFIC DESCRIPTION: The Zélus implementation has two main parts: a compiler that transforms Zélus programs into OCaml programs and a runtime library that orchestrates compiled programs and numeric solvers. The runtime can use the Sundials numeric solver, or custom implementations of well-known algorithms for numerically approximating continuous dynamics.

FUNCTIONAL DESCRIPTION: Zélus is a new programming language for hybrid system modeling. It is based on a synchronous language but extends it with Ordinary Differential Equations (ODEs) to model continuous-time behaviors. It allows for combining arbitrarily data-flow equations, hierarchical automata and ODEs. The language keeps all the fundamental features of synchronous languages: the compiler statically ensure the absence of deadlocks and critical races, it is able to generate statically scheduled code running in bounded time and space and a type-system is used to distinguish discrete and logical-time signals from continuous-time ones. The ability to combines those features with ODEs made the language usable both for programming discrete controllers and their physical environment.

- Participants: Marc Pouzet and Timothy Bourke
- Contact: Marc Pouzet

PARSIFAL Project-Team

6. New Software and Platforms

6.1. Abella

FUNCTIONAL DESCRIPTION: Abella is an interactive theorem prover for reasoning about computations given as relational specifications. Abella is particuarly well suited for reasoning about binding constructs.

- Participants: Dale Miller, Gopalan Nadathur, Kaustuv Chaudhuri, Mary Southern, Matteo Cimini, Olivier Savary-Bélanger and Yuting Wang
- Partner: Department of Computer Science and Engineering, University of Minnesota
- Contact: Kaustuv Chaudhuri
- URL: http://abella-prover.org/

6.2. Bedwyr

Bedwyr - A proof search approach to model checking
KEYWORD: Model Checker
FUNCTIONAL DESCRIPTION: Bedwyr is a generalization of logic programming that allows model checking directly on syntactic expressions that possibly contain bindings. This system, written in OCaml, is a direct implementation of two recent advances in the theory of proof search.

It is possible to capture both finite success and finite failure in a sequent calculus. Proof search in such a proof system can capture both may and must behavior in operational semantics. Higher-order abstract syntax is directly supported using term-level lambda-binders, the nabla quantifier, higher-order pattern unification, and explicit substitutions. These features allow reasoning directly on expressions containing bound variables.

The distributed system comes with several example applications, including the finite pi-calculus (operational semantics, bisimulation, trace analyses, and modal logics), the spi-calculus (operational semantics), value-passing CCS, the lambda-calculus, winning strategies for games, and various other model checking problems.

- Participants: Dale Miller, Quentin Heath and Roberto Blanco Martinez
- Contact: Dale Miller
- URL: http://slimmer.gforge.inria.fr/bedwyr/

6.3. Checkers

Checkers - A proof verifier
KEYWORDS: Proof - Certification - Verification
FUNCTIONAL DESCRIPTION: Checkers is a tool in Lambda-prolog for the certification of proofs. Checkers consists of a kernel which is based on LKF and is based on the notion of ProofCert.

- Participants: Giselle Machado Nogueira Reis, Marco Volpe and Tomer Libal
- Contact: Tomer Libal
- URL: https://github.com/proofcert/checkers

6.4. Psyche

Proof-Search factorY for Collaborative HEuristics

FUNCTIONAL DESCRIPTION: Psyche is a modular platform for automated or interactive theorem proving, programmed in OCaml and built on an architecture (similar to LCF) where a trusted kernel interacts with plugins. The kernel offers an API of proof-search primitives, and plugins are programmed on top of the API to implement search strategies. This architecture is set up for pure logical reasoning as well as for theory-specific reasoning, for various theories.

RELEASE FUNCTIONAL DESCRIPTION: It is now equipped with the machinery to handle quantifiers and quantifier-handling techniques. Concretely, it uses meta-variables to delay the instantiation of existential variables, and constraints on meta-variables are propagated through the various branches of the search-space, in a way that allows local backtracking. The kernel, of about 800 l.o.c., is purely functional.

- Participants: Assia Mahboubi, Jean-Marc Notin and Stéphane Graham-Lengrand
- Contact: Stéphane Graham-Lengrand
- URL: http://www.lix.polytechnique.fr/~lengrand/Psyche/

6.5. Maetning

FUNCTIONAL DESCRIPTION: Mætning is an automated theorem prover for intuitionistic predicate logic that is designed to disprove non-theorems.

- Contact: Kaustuv Chaudhuri
- URL: https://github.com/chaudhuri/maetning/

6.6. OCaml

KEYWORDS: Functional programming - Static typing - Compilation

FUNCTIONAL DESCRIPTION: The OCaml language is a functional programming language that combines safety with expressiveness through the use of a precise and flexible type system with automatic type inference. The OCaml system is a comprehensive implementation of this language, featuring two compilers (a bytecode compiler, for fast prototyping and interactive use, and a native-code compiler producing efficient machine code for x86, ARM, PowerPC and System Z), a debugger, a documentation generator, a compilation manager, a package manager, and many libraries contributed by the user community.

- Participants: Damien Doligez, Xavier Leroy, Fabrice Le Fessant, Luc Maranget, Gabriel Scherer, Alain Frisch, Jacques Garrigue, Marc Shinwell, Jeremy Yallop and Leo White
- Contact: Damien Doligez
- URL: https://ocaml.org/

PESTO Project-Team

6. New Software and Platforms

6.1. Akiss

AKISS - Active Knowledge in Security Protocols
KEYWORDS: Security - Verification
FUNCTIONAL DESCRIPTION: AKISS (Active Knowledge in Security Protocols) is a tool for verifying indistinguishability properties in cryptographic protocols, modelled as trace equivalence in a process calculus. Indistinguishability is used to model a variety of properties including anonymity properties, strong versions of confidentiality and resistance against offline guessing attacks, etc. AKISS implements a procedure to verify equivalence properties for a bounded number of sessions based on a fully abstract modelling of the traces of a bounded number of sessions of the protocols into first-order Horn clauses and a dedicated resolution procedure. The procedure can handle a large set of cryptographic primitives, namely those that can be modeled by an optimally reducing convergent rewrite system, as well as the exclusive or (xor) operator.

- Contact: Steve Kremer
- URL: https://github.com/akiss

6.2. Belenios

Belenios - Verifiable online voting system
KEYWORD: E-voting
FUNCTIONAL DESCRIPTION: Belenios is an open-source online voting system that provides confidentiality and verifiability. End-to-end verifiablity relies on the fact that the ballot box is public (voters can check that their ballots have been received) and on the fact that the tally is publicly verifiable (anyone can recount the votes). Confidentiality relies on the encryption of the votes and the distribution of the decryption key.

Belenios builds upon Helios, a voting protocol used in several elections. The main design enhancement of Belenios vs. Helios is that the ballot box can no longer add (fake) ballots, due to the use of credentials. Moreover, Belenios includes a practical threshold decryption system that allows splitting the decryption key among several authorities.
NEWS OF THE YEAR: Since 2015, it has been used by CNRS for remote election among its councils (more than 30 elections every year) and since 2016, it has been used by Inria to elect representatives in the “comités de centre” of each Inria center. In 2018, it has been used to organize about 250 elections (not counting test elections). Belenios is typically used for elections in universities as well as in associations. This goes from laboratory councils (e.g. Irisa, Cran), scientific societies (e.g. SMAI) to various associations (e.g. FFBS - Fédération Française de Baseball et Softball, or SRFA - Société du Rat Francophone et de ses Amateurs).

In total in 2018, more than 13000 ballots have been cast using the voting platform Belenios.

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

6.3. Deepsec

DEEPSEC - DEciding Equivalence Properties in SECurity protocols
KEYWORDS: Security - Verification

FUNCTIONAL DESCRIPTION: DEEPSEC (DEciding Equivalence Properties in SECurity protocols) is a tool for verifying indistinguishability properties in cryptographic protocols, modelled as trace equivalence in a process calculus. Indistinguishability is used to model a variety of properties including anonymity properties, strong versions of confidentiality and resistance against offline guessing attacks, etc. DEEPSEC implements a decision procedure to verify trace equivalence for a bounded number of sessions and cryptographic primitives modeled by a subterm convergent destructor rewrite system. The procedure is based on constraint solving techniques. The tool also implements state-of-the-art partial order reductions and allows to distribute the computation on multiple cores and multiple machines.

- Contact: Vincent Cheval
- URL: https://deepsec-prover.github.io/

6.4. Tamarin

TAMARIN prover

KEYWORDS: Security - Verification

FUNCTIONAL DESCRIPTION: The TAMARIN prover is a security protocol verification tool that supports both falsification and unbounded verification of security protocols specified as multiset rewriting systems with respect to (temporal) first-order properties and a message theory that models Diffie-Hellman exponentiation, bilinear pairing, multisets, and exclusive-or (XOR), combined with a user-defined convergent rewriting theory. Its main advantages are its ability to handle stateful protocols and its interactive proof mode. Moreover, it has been extended to verify equivalence properties. The tool is developed jointly by the PESTO team, the Institute of Information Security at ETH Zurich, and the University of Oxford. In a joint effort, the partners wrote and published a user manual in 2016, available from the Tamarin website.

- Contact: Jannik Dreier
- URL: http://tamarin-prover.github.io/

6.5. SAPIC

SAPIC: Stateful Applied Pi Calculus

KEYWORDS: Security - Verification

FUNCTIONAL DESCRIPTION: SAPIC is a plugin of the TAMARIN tool that translates protocols from a high-level protocol description language akin to the applied pi-calculus into multiset rewrite rules, that can then be analysed by the TAMARIN prover. TAMARIN has also been extended with dedicated heuristics that exploit the form of translated rules and favor termination.

SAPIC offers support for the analysis of protocols that include states, for example Hardware Security Tokens communicating with a possibly malicious user, or protocols that rely on databases. It also allows us to verify liveness properties and a notion of location and reporting used for modelling trusted execution environments. It has been successfully applied on several case studies including the Yubikey authentication protocol, and extensions of the PKCS#11 standard. SAPIC also includes support for verifying liveness properties, which are for instance important in fair exchange and contract signing protocols, as well as support for constructions useful when modelling isolated execution environments.

- Contact: Steve Kremer
- URL: http://sapic.gforge.inria.fr/

6.6. TypeEquiv

A type checker for privacy properties

KEYWORDS: Security - Cryptographic protocol - Privacy

FUNCTIONAL DESCRIPTION: TypeEquiv provides a (sound) type system for proving equivalence of protocols (to anaylse privacy properties such as vote privacy, anonymity, unlinkability), for both a bounded or an unbounded number of sessions and for the standard cryptographic primitives. TypeEquiv takes as input the specification of a pair of security protocols, written in a dialect of the applied-pi calculus, together with some type annotations. It checks whether the two protocols are in equivalence or not. The tool provides a significant speed-up compared with tools that decide equivalence of security protocols for a bounded number of sessions.

- Partner: Technische Universität Wien
- Contact: Véronique Cortier

PI.R2 Project-Team

5. New Software and Platforms

5.1. Coq

The Coq Proof Assistant
KEYWORDS: Proof - Certification - Formalisation
SCIENTIFIC DESCRIPTION: Coq is an interactive proof assistant based on the Calculus of (Co-)Inductive Constructions, extended with universe polymorphism. This type theory features inductive and co-inductive families, an impredicative sort and a hierarchy of predicative universes, making it a very expressive logic. The calculus allows to formalize both general mathematics and computer programs, ranging from theories of finite structures to abstract algebra and categories to programming language metatheory and compiler verification. Coq is organised as a (relatively small) kernel including efficient conversion tests on which are built a set of higher-level layers: a powerful proof engine and unification algorithm, various tactics/decision procedures, a transactional document model and, at the very top an IDE.
FUNCTIONAL DESCRIPTION: Coq provides both a dependently-typed functional programming language and a logical formalism, which, altogether, support the formalisation of mathematical theories and the specification and certification of properties of programs. Coq also provides a large and extensible set of automatic or semi-automatic proof methods. Coq's programs are extractible to OCaml, Haskell, Scheme, ...

RELEASE FUNCTIONAL DESCRIPTION: Coq version 8.8.2 contains the result of refinements and stabilization of features and deprecations, cleanups of the internals of the system along with a few new features.

Summary of changes:

Kernel: fix a subject reduction failure due to allowing fixpoints on non-recursive values (#407), by Matthieu Sozeau. Handling of evars in the VM (#935) by Pierre-Marie Pédrot.

Notations: many improvements on recursive notations and support for destructuring patterns in the syntax of notations by Hugo Herbelin.

Proof language: tacticals for profiling, timing and checking success or failure of tactics by Jason Gross. The focusing bracket { supports single-numbered goal selectors, e.g. 2:{, (#6551) by Théo Zimmermann.

Vernacular: cleanup of definition commands (#6653) by Vincent Laporte and more uniform handling of the Local flag (#1049), by Maxime Dénès. Experimental Show Extraction command (#6926) by Pierre Letouzey. Coercion now accepts Prop or Type as a source (#6480) by Arthur Charguéraud. Export modifier for options allowing to export the option to modules that Import and not only Require a module (#6923), by Pierre-Marie Pédrot.

Universes: many user-level and API level enhancements: qualified naming and printing, variance annotations for cumulative inductive types, more general constraints and enhancements of the minimization heuristics, interaction with modules by Gaëtan Gilbert, Pierre-Marie Pédrot and Matthieu Sozeau.

Library: Decimal Numbers library (#6599) by Pierre Letouzey and various small improvements.

Documentation: a large community effort resulted in the migration of the reference manual to the Sphinx documentation tool. The new documentation infrastructure (based on Sphinx) is by Clément Pit-Claudel. The migration was coordinated by Maxime Dénès and Paul Steckler, with some help of Théo Zimmermann during the final integration phase. The 14 people who ported the manual are Calvin Beck, Heiko Becker, Yves Bertot, Maxime Dénès, Richard Ford, Pierre Letouzey, Assia Mahboubi, Clément Pit-Claudel, Laurence Rideau, Matthieu Sozeau, Paul Steckler, Enrico Tassi, Laurent Théry, Nikita Zyuzin.

Tools: experimental -mangle-names option to coqtop/coqc for linting proof scripts (#6582), by Jasper Hugunin. Main changes:

Critical soundness bugs were fixed between versions 8.8.0 and 8.8.2, and a PDF version of the reference manual was made available. The Windows installer also includes many more external packages that can be individually selected for installation.

On the implementation side, the dev/doc/changes.md file documents the numerous changes to the implementation and improvements of interfaces. The file provides guidelines on porting a plugin to the new version.

More information can be found in the CHANGES file. Feedback and bug reports are extremely welcome.

Distribution Installers for Windows 32 bits (i686), Windows 64 bits (x8_64) and macOS are available. They come bundled with CoqIDE. Windows binaries now include the Bignums library.

Complete sources of the files installed by the Windows installers are made available, to comply with license requirements.
NEWS OF THE YEAR: Version 8.8.0 was released in April 2018 and version 8.8.2 in September 2018. This is the third release of Coq developed on a time-based development cycle. Its development spanned 6 months from the release of Coq 8.7 and was based on a public road-map. It attracted many external contributions. Code reviews and continuous integration testing were systematically used before integration of new features, with an important focus given to compatibility and performance issues.

The main advances in this version are cleanups and fixes in the many different components of the system, ranging from low level kernel fixes to advances in the support of notations and tacticals for selecting goals. A large community effort was made to move the documentation to the Sphinx format, providing a more accessible online ressource to users.

- Participants: Abhishek Anand, C. J. Bell, Yves Bertot, Frédéric Besson, Tej Chajed, Pierre Courtieu, Maxime Denes, Julien Forest, Emilio Jesús Gallego Arias, Gaëtan Gilbert, Benjamin Grégoire, Jason Gross, Hugo Herbelin, Ralf Jung, Matej Kosik, Sam Pablo Kuper, Xavier Leroy, Pierre Letouzey, Assia Mahboubi, Cyprien Mangin, Érik Martin-Dorel, Olivier Marty, Guillaume Melquiond, Pierre-Marie Pédrot, Benjamin C. Pierce, Lars Rasmusson, Yann Régis-Gianas, Lionel Rieg, Valentin Robert, Thomas Sibut-Pinote, Michael Soegtrop, Matthieu Sozeau, Arnaud Spiwack, Paul Steckler, George Stelle, Pierre-Yves Strub, Enrico Tassi, Hendrik Tews, Laurent Théry, Amin Timany, Vadim Zaliva and Théo Zimmermann
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Matthieu Sozeau
- Publication: The Coq Proof Assistant, version 8.8.0
- URL: http://coq.inria.fr/

5.2. Equations

KEYWORDS: Coq - Dependent Pattern-Matching - Proof assistant - Functional programming
SCIENTIFIC DESCRIPTION: Equations is a tool designed to help with the definition of programs in the setting of dependent type theory, as implemented in the Coq proof assistant. Equations provides a syntax for defining programs by dependent pattern-matching and well-founded recursion and compiles them down to the core type theory of Coq, using the primitive eliminators for inductive types, accessibility and equality. In addition to the definitions of programs, it also automatically derives useful reasoning principles in the form of propositional equations describing the functions, and an elimination principle for calls to this function. It realizes this using a purely definitional translation of high-level definitions to core terms, without changing the core calculus in any way, or using axioms.
FUNCTIONAL DESCRIPTION: Equations is a function definition plugin for Coq (supporting Coq 8.6 and 8.7), that allows the definition of functions by dependent pattern-matching and well-founded, mutual or nested structural recursion and compiles them into core terms. It automatically derives the clauses equations, the graph of the function and its associated elimination principle.

Equations is based on a simplification engine for the dependent equalities appearing in dependent eliminations that is also usable as a separate tactic, providing an axiom-free variant of dependent destruction. The main features of Equations include:

Dependent pattern-matching in the style of Agda/Epigram, with inaccessible patterns, with and where clauses. The use of the K axiom or a proof of K is configurable.

Support for well-founded recursion using by rec annotations, and automatic derivation of the subterm relation for inductive families.

Support for mutual and nested structural recursion using with and where auxilliary definitions, allowing to factor multiple uses of the same nested fixpoint definition. It proves the expected elimination principles for mutual and nested definitions.

Automatic generation of the defining equations as rewrite rules for every definition.

Automatic generation of the unfolding lemma for well-founded definitions (requiring only functional extensionality).

Automatic derivation of the graph of the function and its elimination principle. In case the automation fails to prove these principles, the user is asked to provide a proof.

A new dependent elimination tactic based on the same splitting tree compilation scheme that can advantageously replace dependent destruction and sometimes inversion as well. The as clause of dependent elimination allows to specify exactly the patterns and naming of new variables needed for an elimination.

A set of Derive commands for automatic derivation of constructions from an inductive type: its signature, no-confusion property, well-founded subterm relation and decidable equality proof, if applicable.
NEWS OF THE YEAR: Equations 1.0 was released in december this year, after 7 years of (non-continuous) development. It provides the first feature-full version of the software. It has been tried and tested on small to medium scale examples (available on the website). Equations was presented at the Type Theory Tools EUTypes meeting in January 2017 in Paris, and another demo/presentation will be given at PEPM 2018 in Los Angeles in January 2018.

- Participants: Matthieu Sozeau and Cyprien Mangin
- Contact: Matthieu Sozeau
- Publications: Equations reloaded - Equations for Hereditary Substitution in Leivant's Predicative System F: A Case Study - Equations: A Dependent Pattern-Matching Compiler
- URL: http://mattam82.github.io/Coq-Equations/

5.3. Rewr

Rewriting methods in algebra
KEYWORDS: Computer algebra system (CAS) - Rewriting systems - Algebra
FUNCTIONAL DESCRIPTION: Rewr is a prototype of computer algebra system, using rewriting methods to compute resolutions and homotopical invariants of monoids. The library implements various classical constructions of rewriting theory (such as completion), improved by experimental features coming from Garside theory, and allows homotopical algebra computations based on Squier theory. Specific functionalities have been developed for usual classes of monoids, such as Artin monoids and plactic monoids.
NEWS OF THE YEAR: Rewr has been extended with the experimental KGB completion algorithm, based on Knuth-Bendix completion procedure improved by techniques coming from Garside theory.

- Participants: Yves Guiraud and Samuel Mimram
- Contact: Yves Guiraud
- Publications: Higher-dimensional categories with finite derivation type - Higher-dimensional normalisation strategies for acyclicity - Coherent presentations of Artin monoids - A Homotopical Completion Procedure with Applications to Coherence of Monoids - Polygraphs of finite derivation type - Quadratic normalisation in monoids
- URL: http://www.lix.polytechnique.fr/Labo/Samuel.Mimram/rewr

5.4. Catex

KEYWORDS: LaTeX - String diagram - Algebra
FUNCTIONAL DESCRIPTION: Catex is a Latex package and an external tool to typeset string diagrams easily from their algebraic expression. Catex works similarly to Bibtex.
NEWS OF THE YEAR: It is now possible to add labels to objects and morphisms

- Participant: Yves Guiraud
- Contact: Yves Guiraud
- URL: https://www.irif.fr/~guiraud/catex/catex.zip

5.5. Cox

KEYWORDS: Computer algebra system (CAS) - Rewriting systems - Algebra
FUNCTIONAL DESCRIPTION: Cox is a Python library for the computation of coherent presentations of Artin monoids, with experimental features to compute the lower dimensions of the Salvetti complex.

- Participant: Yves Guiraud
- Contact: Yves Guiraud
- Publications: Coherent presentations of Artin monoids - A Homotopical Completion Procedure with Applications to Coherence of Monoids
- URL: https://www.irif.fr/~guiraud/cox/cox.zip

POLSYS Project-Team

5. New Software and Platforms

5.1. Epsilon

FUNCTIONAL DESCRIPTION: Epsilon is a library of functions implemented in Maple and Java for polynomial elimination and decomposition with (geometric) applications.

- Contact: Dongming Wang
- URL: http://wang.cc4cm.org/epsilon/index.html

5.2. FGb

KEYWORDS: Gröbner bases - Nonlinear system - Computer algebra
FUNCTIONAL DESCRIPTION: FGb is a powerful software for computing Gröbner bases. It includes the new generation of algorihms for computing Gröbner bases polynomial systems (mainly the F4, F5 and FGLM algorithms). It is implemented in C/C++ (approximately 250000 lines), standalone servers are available on demand. Since 2006, FGb is dynamically linked with Maple software (version 11 and higher) and is part of the official distribution of this software.

- Participant: Jean Charles Faugere
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/FGb/index.html

5.3. FGb Light

FUNCTIONAL DESCRIPTION: Gröbner basis computation modulo p (p is a prime integer of 16 bits).

- Participant: Jean-Charles Faugère
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/FGb/index.html

5.4. GBLA

FUNCTIONAL DESCRIPTION: GBLA is an open source C library for linear algebra specialized for eliminating matrices generated during Gröbner basis computations in algorithms like F4 or F5.

- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/~jcf/GBLA/index.html

5.5. HFEBoost

FUNCTIONAL DESCRIPTION: Public-key cryptography system enabling an authentification of dematerialized data.

- Authors: Jean-Charles Faugère and Ludovic Perret
- Partner: UPMC
- Contact: Jean-Charles Faugère
- URL: http://www-polsys.lip6.fr/Links/hfeboost.html

5.6. RAGlib

Real Algebraic Geometry library

FUNCTIONAL DESCRIPTION: RAGLib is a powerful library, written in Maple, dedicated to solving over the reals polynomial systems. It is based on the FGb library for computing Grobner bases. It provides functionalities for deciding the emptiness and/or computing sample points to real solution sets of polynomial systems of equations and inequalities. This library provides implementations of the state-of-the-art algorithms with the currently best known asymptotic complexity for those problems.

- Contact: Mohab Safey El Din
- URL: http://www-polsys.lip6.fr/~safey/RAGLib/

5.7. RealCertify

KEYWORDS: Polynomial or analytical systems - Univariate polynomial - Real solving
FUNCTIONAL DESCRIPTION: The package RealCertify aims at providing a full suite of hybrid algorithms for computing certificates of non-negativity based on numerical software for solving linear matrix inequalities. The module univsos handles the univariate case and the module multivsos is designed for the multivariate case.

- Contact: Mohab Safey El Din
- URL: https://gricad-gitlab.univ-grenoble-alpes.fr/magronv/RealCertify

5.8. SLV

FUNCTIONAL DESCRIPTION: SLV is a software package in C that provides routines for isolating (and subsequently refine) the real roots of univariate polynomials with integer or rational coefficients based on subdivision algorithms and on the continued fraction expansion of real numbers. Special attention is given so that the package can handle polynomials that have degree several thousands and size of coefficients hundrends of Megabytes. Currently the code consists of approx. 5000 lines.

- Contact: Elias Tsigaridas
- URL: http://www-polsys.lip6.fr/~elias/soft

5.9. SPECTRA

Semidefinite Programming solved Exactly with Computational Tools of Real Algebra
KEYWORD: Linear Matrix Inequalities
FUNCTIONAL DESCRIPTION: SPECTRA is a Maple library devoted to solving exactly Semi-Definite Programs. It can handle rank constraints on the solution. It is based on the FGb library for computing Gröbner bases and provides either certified numerical approximations of the solutions or exact representations thereof.

- Contact: Mohab Safey El Din
- URL: http://homepages.laas.fr/henrion/software/spectra/

PRIVATICS Project-Team

5. New Software and Platforms

5.1. FECFRAME

FEC Framework following RFC 6363 specifications (https://datatracker.ietf.org/doc/rfc6363/)
KEYWORDS: Error Correction Code - Content delivery protocol - Robust transmission
FUNCTIONAL DESCRIPTION: This sofware implements the FECFRAME IETF standard (RFC 6363) co-authored by V. Roca, and is compliant with 3GPP specifications for mobile terminals. It enables the simultaneous transmission of multimedia flows to one or several destinations, while being robust to packet erasures that happen on wireless networks (e.g., 4G or Wifi). This software relies on the OpenFEC library (the open-source http://openfec.org version or the commercial version) that provides the erasure correction codes (or FEC) and thereby offer robustness in front of packet erasures.

- Participant: Vincent Roca
- Contact: Vincent Roca

5.2. Mobilitcs

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

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

- Authors: Jagdish Achara, James-Douglass Lefruit, Claude Castelluccia, 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 transfered to the security community (maintainability): eventually it will become an open source software. The main challenge of Omen+ is to optimize the memory consumption.

- Participants: 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, Jérome Lacan, Jonathan Detchart, Julien Laboure, Kevin Chaumont, Mathieu Cunche and Vincent Roca
- Partner: Expway
- Contact: Vincent Roca
- URL: http://openfec.org/

PROSECCO Project-Team

6. New Software and Platforms

6.1. Cryptosense Analyzer

SCIENTIFIC DESCRIPTION: Cryptosense Analyzer (formerly known as Tookan) is a security analysis tool for cryptographic devices such as smartcards, security tokens and Hardware Security Modules that support the most widely-used industry standard interface, RSA PKCS#11. Each device implements PKCS#11 in a slightly different way since the standard is quite open, but finding a subset of the standard that results in a secure device, i.e. one where cryptographic keys cannot be revealed in clear, is actually rather tricky. Cryptosense Analyzer analyses a device by first reverse engineering the exact implementation of PKCS#11 in use, then building a logical model of this implementation for a model checker, calling a model checker to search for attacks, and in the case where an attack is found, executing it directly on the device. It has been used to find at least a dozen previously unknown flaws in commercially available devices.
FUNCTIONAL DESCRIPTION: Cryptosense Analyzer (formerly known as Tookan) is a security analysis tool for cryptographic devices such as smartcards,

- Participants: Graham Steel and Romain Bardou
- Contact: Graham Steel
- URL: https://cryptosense.com/

6.2. CryptoVerif

Cryptographic protocol verifier in the computational model
KEYWORDS: Security - Verification - Cryptographic protocol
FUNCTIONAL DESCRIPTION: CryptoVerif is an automatic protocol prover sound in the computational model. In this model, messages are bitstrings and the adversary is a polynomial-time probabilistic Turing machine. CryptoVerif can prove secrecy and correspondences, which include in particular authentication. It provides a generic mechanism for specifying the security assumptions on cryptographic primitives, which can handle in particular symmetric encryption, message authentication codes, public-key encryption, signatures, hash functions, and Diffie-Hellman key agreements. It also provides an explicit formula that gives the probability of breaking the protocol as a function of the probability of breaking each primitives, this is the exact security framework.
NEWS OF THE YEAR: Bruno Blanchet modified ProVerif and CryptoVerif to improve the compatibility between these two tools (see the section on ProVerif). This feature is released in CryptoVerif 2.00.

Bruno Blanchet implemented several extensions of CryptoVerif, in particular: 1) reworked the model of Diffie-Hellman key agreements, in particular to account for the absence of public key validation in popular Diffie-Hellman groups like Curve25519, which is used in many modern protocols, 2) support for the proof of indistinguishability between two games given by the user, 3) facilitate the interactive proofs. Program points, used for instance to insert case distinctions, can now be designated as the line that matches a regular expression, instead of using a number. This is much more stable in case the protocol model is slightly modified. Groups of variables can be designated as all variables that match a regular expression. These features are not released yet.

- Participants: Bruno Blanchet and David Cadé
- Contact: Bruno Blanchet

- Publications: Composition Theorems for CryptoVerif and Application to TLS 1.3 - Composition Theorems for CryptoVerif and Application to TLS 1.3 - Proved Implementations of Cryptographic Protocols in the Computational Model - Proved Generation of Implementations from Computationally Secure Protocol Specifications - Verified Models and Reference Implementations for the TLS 1.3 Standard Candidate - Verified Models and Reference Implementations for the TLS 1.3 Standard Candidate - Symbolic and Computational Mechanized Verification of the ARINC823 Avionic Protocols - Automated Verification for Secure Messaging Protocols and Their Implementations: A Symbolic and Computational Approach
- URL: http://cryptoverif.inria.fr/

6.3. F*

FStar

KEYWORDS: Programming language - Software Verification

FUNCTIONAL DESCRIPTION: F* is a new higher order, effectful programming language (like ML) designed with program verification in mind. Its type system is based on a core that resembles System Fw (hence the name), but is extended with dependent types, refined monadic effects, refinement types, and higher kinds. Together, these features allow expressing precise and compact specifications for programs, including functional correctness properties. The F* type-checker aims to prove that programs meet their specifications using an automated theorem prover (usually Z3) behind the scenes to discharge proof obligations. Programs written in F* can be translated to OCaml, F#, or JavaScript for execution.

- Participants: Antoine Delignat-Lavaud, Catalin Hritcu, Cédric Fournet, Chantal Keller, Karthikeyan Bhargavan and Pierre-Yves Strub
- Contact: Catalin Hritcu
- URL: https://www.fstar-lang.org/

6.4. miTLS

KEYWORDS: Cryptographic protocol - Software Verification

FUNCTIONAL DESCRIPTION: miTLS is a verified reference implementation of the TLS protocol. Our code fully supports its wire formats, ciphersuites, sessions and connections, re-handshakes and resumptions, alerts and errors, and data fragmentation, as prescribed in the RFCs, it interoperates with mainstream web browsers and servers. At the same time, our code is carefully structured to enable its modular, automated verification, from its main API down to computational assumptions on its cryptographic algorithms.

- Participants: Alfredo Pironti, Antoine Delignat-Lavaud, Cédric Fournet, Jean-Karim Zinzindohoué, Karthikeyan Bhargavan, Pierre-Yves Strub and Santiago Zanella-Béguelin
- Contact: Karthikeyan Bhargavan
- URL: https://github.com/mitls/mitls-fstar

6.5. ProVerif

KEYWORDS: Security - Verification - Cryptographic protocol

FUNCTIONAL DESCRIPTION: ProVerif is an automatic security protocol verifier in the symbolic model (so called Dolev-Yao model). In this model, cryptographic primitives are considered as black boxes. This protocol verifier is based on an abstract representation of the protocol by Horn clauses. Its main features are:

It can verify various security properties (secrecy, authentication, process equivalences).

It can handle many different cryptographic primitives, specified as rewrite rules or as equations.

It can handle an unbounded number of sessions of the protocol (even in parallel) and an unbounded message space.

NEWS OF THE YEAR: Marc Sylvestre extended his interactive simulator of protocols modeled in ProVerif to simulate the semantics of biprocesses, used to prove observational equivalence between two processes. He also made minor improvements to this simulator and to the graphical display of attacks.

Bruno Blanchet modified ProVerif and CryptoVerif to improve the compatibility between these two tools. It is now possible for simple examples to use the same input file with both tools, for instance to try to find attacks in the symbolic model using ProVerif, and if no attack is found, then prove the protocol in the computational model using CryptoVerif. For more complex examples, the differences between the files to provide for each tool are considerably reduced. The cryptographic primitives are specified in distinct libraries, one for ProVerif and one for CryptoVerif, because the assumptions on primitives are very different in the symbolic and computational models. These features are released in ProVerif 2.00.

Vincent Cheval and Bruno Blanchet implemented several extensions of ProVerif: 1) support for integer counters, with incrementation and inequality tests, 2) lemmas and axioms to give intermediate results to ProVerif, which it exploits to help proving subsequent queries, by deriving additional information in the Horn clauses that it uses to perform the proofs, 3) proofs by induction on the length of the trace, by giving as lemma the property to prove, but obviously for strictly shorter traces. These features are not released yet.

- Participants: Bruno Blanchet, Marc Sylvestre and Vincent Cheval
- Contact: Bruno Blanchet
- Publications: Automated reasoning for equivalences in the applied pi calculus with barriers - Automated Reasoning for Equivalences in the Applied Pi Calculus with Barriers - Automated reasoning for equivalences in the applied pi calculus with barriers - Modeling and Verifying Security Protocols with the Applied Pi Calculus and ProVerif - Automatic Verification of Security Protocols in the Symbolic Model: The Verifier ProVerif - Verified Models and Reference Implementations for the TLS 1.3 Standard Candidate - Verified Models and Reference Implementations for the TLS 1.3 Standard Candidate - Automated Verification for Secure Messaging Protocols and Their Implementations: A Symbolic and Computational Approach - Symbolic and Computational Mechanized Verification of the ARINC823 Avionic Protocols - Symbolic and Computational Mechanized Verification of the ARINC823 Avionic Protocols
- URL: http://proverif.inria.fr/

6.6. HACL*

High Assurance Cryptography Library

KEYWORDS: Cryptography - Software Verification

FUNCTIONAL DESCRIPTION: HACL* is a formally verified cryptographic library in F*, developed by the Prosecco team at Inria Paris in collaboration with Microsoft Research, as part of Project Everest.

HACL stands for High-Assurance Cryptographic Library and its design is inspired by discussions at the HACS series of workshops. The goal of this library is to develop verified C reference implementations for popular cryptographic primitives and to verify them for memory safety, functional correctness, and secret independence.

- Contact: Karthikeyan Bhargavan
- URL: https://github.com/mitls/hacl-star

SECRET Project-Team

6. New Software and Platforms

6.1. CFS

FUNCTIONAL DESCRIPTION: Reference implementation of parallel CFS (reinforced version of the digital signature scheme CFS). Two variants are proposed, one with a « bit-packing » finite field arithmetic and an evolution with a « bit-slicing » finite-field arithmetic (collaboration with Peter Schwabe). For 80 bits of security the running time for producing one signature with the « bit-packing » variant is slightly above one second. This is high but was still the fastest so far. The evolution with the « bit-slicing » arithmetic produces the same signature in about 100 milliseconds.

- Participants: Grégory Landais and Nicolas Sendrier
- Contact: Nicolas Sendrier
- URL: https://gforge.inria.fr/projects/cfs-signature/

6.2. Collision Decoding

KEYWORDS: Algorithm - Binary linear code
FUNCTIONAL DESCRIPTION: Collision Decoding implements two variants of information set decoding : Stern-Dumer, and MMT. To our knowledge it is the best full-fledged open-source implementation of generic decoding of binary linear codes. It is the best generic attack against code-based cryptography.

- Participants: Grégory Landais and Nicolas Sendrier
- Contact: Nicolas Sendrier
- URL: https://gforge.inria.fr/projects/collision-dec/

6.3. ISDF

FUNCTIONAL DESCRIPTION: Implementation of the Stern-Dumer decoding algorithm, and of a varaint of the algorithm due to May, Meurer and Thomae.

- Participants: Grégory Landais and Nicolas Sendrier
- Contact: Anne Canteaut
- URL: https://gforge.inria.fr/projects/collision-dec/

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

SPECFUN Project-Team

6. New Software and Platforms

6.1. DynaMoW

Dynamic Mathematics on the Web
FUNCTIONAL DESCRIPTION: Programming tool for controlling the generation of mathematical websites that embed dynamical mathematical contents generated by computer-algebra calculations. Implemented in OCaml.

- Participants: Alexis Darrasse, Frédéric Chyzak and Maxence Guesdon
- Contact: Frédéric Chyzak
- URL: http://ddmf.msr-inria.inria.fr/DynaMoW/

6.2. ECS

Encyclopedia of Combinatorial Structures
FUNCTIONAL DESCRIPTION: On-line mathematical encyclopedia with an emphasis on sequences that arise in the context of decomposable combinatorial structures, with the possibility to search by the first terms in the sequence, keyword, generating function, or closed form.

- Participants: Alexis Darrasse, Frédéric Chyzak, Maxence Guesdon and Stéphanie Petit
- Contact: Frédéric Chyzak
- URL: http://ecs.inria.fr/

6.3. DDMF

Dynamic Dictionary of Mathematical Functions
FUNCTIONAL DESCRIPTION: Web site consisting of interactive tables of mathematical formulas on elementary and special functions. The formulas are automatically generated by OCaml and computer-algebra routines. Users can ask for more terms of the expansions, more digits of the numerical values, proofs of some of the formulas, etc.

- Participants: Alexandre Benoit, Alexis Darrasse, Bruno Salvy, Christoph Koutschan, Frédéric Chyzak, Marc Mezzarobba, Maxence Guesdon, Stefan Gerhold and Thomas Gregoire
- Contact: Frédéric Chyzak
- URL: http://ddmf.msr-inria.inria.fr/1.9.1/ddmf

6.4. Mgfun

multivariate generating functions package
FUNCTIONAL DESCRIPTION: The Mgfun Project is a collection of packages for the computer algebra system Maple, and is intended for the symbolic manipulation of a large class of special functions and combinatorial sequences (in one or several variables and indices) that appear in many branches of mathematics, mathematical physics, and engineering sciences. Members of the class satisfy a crucial finiteness property which makes the class amenable to computer algebra methods and enjoy numerous algorithmic closure properties, including algorithmic closures under integration and summation.

- Contact: Frédéric Chyzak
- URL: http://specfun.inria.fr/chyzak/mgfun.html

6.5. Ssreflect

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

- Participants: Assia Mahboubi, Cyril Cohen, Enrico Tassi, Georges Gonthier, Laurence Rideau, Laurent Théry and Yves Bertot
- Contact: Yves Bertot
- URL: http://math-comp.github.io/math-comp/

6.6. Math-Components

Mathematical Components library

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

RELEASE FUNCTIONAL DESCRIPTION: The library includes 16 more theory files, covering in particular field and Galois theory, advanced character theory, and a construction of algebraic numbers.

- Participants: Alexey Solovyev, Andrea Asperti, Assia Mahboubi, Cyril Cohen, Enrico Tassi, François Garillot, Georges Gonthier, Ioana Pasca, Jeremy Avigad, Laurence Rideau, Laurent Théry, Russell O'Connor, Sidi Ould Biha, Stéphane Le Roux and Yves Bertot
- Contact: Assia Mahboubi
- URL: http://math-comp.github.io/math-comp/

SUMO Project-Team

6. New Software and Platforms

6.1. Active Workspaces

KEYWORDS: Active workspace - Collaborative systems - Artifact centric workflow system
SCIENTIFIC DESCRIPTION: Tool for computer supported cooperative work where a user's workspace is given by an active structured repository containing the pending tasks together with information needed to perform the tasks. Communication between active workspaces is asynchronous using message passing. The tool is based on the model of guarded attribute grammars.

- Authors: Éric Badouel and Robert Nsaibirni
- Contact: Éric Badouel
- URL: http://people.rennes.inria.fr/Eric.Badouel/Research/ActiveWorkspaces.html

6.2. DAXML

KEYWORDS: XML - Web Services - Distributed Software - Active documents
SCIENTIFIC DESCRIPTION: DAXML is an interpreter and implementation of Distributed Active Documents, a formalism for data centric design of Web Services. This implementation is based on a REST framework, and can run on a network of machines connected to internet and equiped with JAVA.
FUNCTIONAL DESCRIPTION: This prototype interprets distributed Active XML documents. It can be used to deploy services defined as active documents over the web.

- Participants: Benoît Masson and Loïc Hélouët
- Contact: Loïc Hélouët
- URL: http://www.irisa.fr/sumo/Software/DAXML/

6.3. Sigali

FUNCTIONAL DESCRIPTION: Sigali is a model-checking tool that operates on ILTS (Implicit Labeled Transition Systems, an equational representation of an automaton), an intermediate model for discrete event systems. It offers functionalities for verification of reactive systems and discrete controller synthesis. The techniques used consist in manipulating the system of equations instead of the set of solutions, which avoids the enumeration of the state space. Each set of states is uniquely characterized by a predicate and the operations on sets can be equivalently performed on the associated predicates. Therefore, a wide spectrum of properties, such as liveness, invariance, reachability and attractivity, can be checked. Algorithms for the computation of predicates on states are also available. Sigali is connected with the Polychrony environment (Tea project-team) as well as the Matou environment (VERIMAG), thus allowing the modeling of reactive systems by means of Signal Specification or Mode Automata and the visualization of the synthesized controller by an interactive simulation of the controlled system.

- Contact: Hervé Marchand

6.4. SIMSTORS

Simulator for stochastic regulated systems
KEYWORDS: Simulation - Public transport - Stochastic models - Distributed systems

FUNCTIONAL DESCRIPTION: SIMSTORS is a software for the simulation of stochastic concurrent timed systems. The heart of the software is a variant of stochastic and timed Petri nets, whose execution is controlled by a regulation policy (a controller), or a predetermined theoretical schedule. The role of the regulation policy is to control the system to realize objectives or a schedule when it exists with the best possible precision. SIMSTORS is well adapted to represent systems with randomness, parallelism, tasks scheduling, and resources. It is currently in use within collaboration P22 with Asltom Transport, where it is used to model metro traffic and evaluate performance of regulation solutions. This software allows for step by step simulation, but also for efficient performance analysis of systems such as production cells or train systems. The initial implementation was released in 2015, and the software is protected by the APP.

In 2017, SIMSTORS has been extended along two main axes: on one hand, SIMSTORS models were extended to handle situations where shared resources can be occupied by more than one object (this is of paramount importance to represent conveyors, roads occupied by cars, or train tracks with smoothed scheduling allowing shared sections among trains) with priorities, constraint on their ordering and individual characteristics. This allows for instance to model vehicles with different speeds on a road, while handling safety distance constraints. On the other hand, SIMSTORS models were extended to allow control of stochastic nets based on decision rules that follow optimization schemes.

- Participants: Abd El Karim Kecir and Loïc Hélouët
- Contact: Loïc Hélouët
- URL: http://www.irisa.fr/sumo/Software/SIMSTORS/

TAMIS Project-Team

6. New Software and Platforms

6.1. GNUnet

KEYWORD: Distributed networks
SCIENTIFIC DESCRIPTION: The GNUnet project seeks to answer the question what a modern Internet architecture should look like for a society that care about security and privacy. We are considering all layers of the existing well-known Internet, but are also providing new and higher-level abstractions (such as voting protocols, Byzantine consensus, etc.) that are today solved in application-specific ways. Research questions include the desired functionality of the overall stack, protocol design for the various layers as well as implementation considerations, i.e. how to implement the design securely.
FUNCTIONAL DESCRIPTION: GNUnet is a framework for secure peer-to-peer networking that does not use any centralized or otherwise trusted services. Our high-level goal is to provide a strong free software foundation for a global network that provides security and in particular respects privacy.

GNUnet started with an idea for anonymous censorship-resistant file-sharing, but has grown to incorporate other applications as well as many generic building blocks for secure networking applications. In particular, GNUnet now includes the GNU Name System, a privacy-preserving, decentralized public key infrastructure.

- Participants: Alvaro Garcia Recuero, Florian Dold, Gabor Toth, Hans Grothoff, Jeffrey Paul Burdges and Sree Hrsha Totakura
- Partner: The GNU Project
- Contact: Sébastien Campion
- URL: https://gnunet.org/

6.2. PLASMA Lab

KEYWORDS: Energy - Statistics - Security - Runtime Analysis - Model Checker - Statistical - Model Checking - Aeronautics - Distributed systems
SCIENTIFIC DESCRIPTION: Statistical model checking (SMC) is a fast emerging technology for industrial scale verification and optimisation problems. SMC only requires an executable semantics and is not constrained by decidability. Therefore we can easily apply it to different modelling languages and logics. We have implemented in PLASMA Lab several advanced SMC algorithms that combine formal methods with statistical tests, which include techniques for rare events estimation and non-deterministic models. PLASMA Lab comes with a simulator plugin that allows to verify LLVM code.
FUNCTIONAL DESCRIPTION: PLASMA Lab is a compact, efficient and flexible platform for statistical model checking of stochastic models. PLASMA Lab includes simulators for PRISM models (Reactives Modules Language-RML) and Biological models. It also provides plugins that interface external simulators in order to support Matlab/Simulink, SytemC and LLVM . PLASMA Lab can be extended with new plugins to support other external simulators, and PLASMA Lab API can be used to embed the tool in other softwares. PLASMA Lab provide fast SMC algorithms, including advanced techniques for rare events simulation and nondeterministic models. These algorithms are designed in a distributed architecture to run large number of simulations on several computers, either on a local area network or grid. PLASMA Lab is implemented in Java with efficient data structures and low memory consumption.

NEWS OF THE YEAR: In 2018 Tania Richmond and Louis-Marie Traonouez have extended PLASMA Lab to propose statistical model checking analysis of discrete time Markov chains with unknown values (qDTMC). We have defined a new logic, called qBLTL, that extends the semantics of BLTL properties to take care of the unknown information in the path of the qDTMC. We have also adapted the model checking algorithm of probabilistic model checking of incomplete models to perform a three hypotheses test and provide bounds on the probability of errors of this test.

- Participants: Jean Quilbeuf, Louis-Marie Traonouez, Tania Richmond, Sean Sedwards, Benoît Boyer, Kevin Corre, Matthieu Simonin and Axel Legay
- Contact: Tania Richmond
- URL: https://project.inria.fr/plasma-lab/

6.3. Taler

GNU Taler
KEYWORD: Privacy
SCIENTIFIC DESCRIPTION: Taler is a Chaum-style digital payment system that enables anonymous payments while ensuring that entities that receive payments are auditable. In Taler, customers can never defraud anyone, merchants can only fail to deliver the merchandise to the customer, and payment service providers can be fully audited. All parties receive cryptographic evidence for all transactions, still, each party only receives the minimum information required to execute transactions. Enforcement of honest behavior is timely, and is at least as strict as with legacy credit card payment systems that do not provide for privacy.

The key technical contribution underpinning Taler is a new refresh protocol which allows fractional payments and refunds while maintaining untraceability of the customer and unlinkability of transactions. The refresh protocol combines an efficient cut-and-choose mechanism with a link step to ensure that refreshing is not abused for transactional payments.

We argue that Taler provides a secure digital currency for modern liberal societies as it is a flexible, libre and efficient protocol and adequately balances the state's need for monetary control with the citizen's needs for private economic activity.
FUNCTIONAL DESCRIPTION: Taler is a new electronic payment system. It includes an electronic wallet for customers, a payment backend for merchants and the main payment service provider logic called the exchange. Taler offers Chaum-style anonymous payments for citizens, and income-transparency for taxability.

- Participants: Florian Dold, Gabor Toth, Hans Grothoff, Jeffrey Paul Burdges and Marcello Stanisci
- Partner: The GNU Project
- Contact: Sébastien Campion
- URL: http://taler.net/

6.4. SimFI

Tool for Simulation Fault injection
KEYWORDS: Fault injection - Fault-tolerance
FUNCTIONAL DESCRIPTION: Fault injections are used to test the robust and security of systems. We have developed SimFI, a tool that can be used to simulate fault injection attacks against binary files. SimFI is lightweight utility designed to be integrated into larger environments as part of robustness testing and fault injection vulnerability detection.

- Contact: Nisrine Jafri
- URL: https://github.com/nisrine/Fault-Injection-Tool

6.5. DaD

Data-aware Defense

KEYWORD: Ransomware
FUNCTIONAL DESCRIPTION: DaD is a ransomware countermeasure based on a file system minifilter driver. It is a proof of concept and in its present condition cannot be used as a replacement of the existing antivirus solutions. DaD detects randomness of the data by monitoring the write operations on the file system. We monitor all the userland threads, and also the whole file system (i.e., not restricted to Documents). It blocks the threads that exceed a specific threshold. The malicious thread is not killed, we only block its next I/O operations.

- Participants: Aurélien Palisse and Jean-Louis Lanet
- Contact: Aurélien Palisse

6.6. MASSE

Modular Automated Syntactic Signature Extraction
KEYWORDS: Malware - Syntactic analysis
FUNCTIONAL DESCRIPTION: The Modular Automated Syntactic Signature Extraction (MASSE) architecture is a new integrated open source client-server architecture for syntactic malware detection and analysis based on the YARA, developed with Teclib'. MASSE includes highly effective automated syntactic malware detection rule generation for the clients based on a server-side modular malware detection system. Multiple techniques are used to make MASSE effective at detecting malware while keeping it from disrupting users and hindering reverse-engineering of its malware analysis by malware creators. MASSE integrates YARA in a distributed system able to detect malware on endpoint systems using YARA, analyze malware with multiple analysis techniques, automatically generate syntactic malware detection rules, and deploy the new rules to the endpoints. The MASSE architecture is freely available to companies and institutions as a complete, modular, self-maintained antivirus solution. Using MASSE, a security department can immediately update the rule database of the whole company, stopping an infection on its tracks and preventing future ones.

- Participants: Bruno Lebon, Olivier Zendra, Alexander Zhdanov and Fabrizio Biondi
- Contact: Bruno Lebon

6.7. BMA

Behavioral Malware Analysis
KEYWORDS: Artificial intelligence - Malware - Automatic Learning - Concolic Execution
FUNCTIONAL DESCRIPTION: Our approach is based on artificial intelligence. We use concolic analysis to extract behavioral signatures from binaries in a form of system call dependency graphs (SCDGs). Our software can do both supervised and unsupervised learning. The former learns the distinctive features of different malware families on a large training set in order to classify the new binaries as malware or cleanware according to their behavioural signatures. In the unsupervised learning the binaries are clustered according to their graph similarity. The toolchain is orchestrated by an experiment manager that allows to easily setup, launch and view results of all modules of the toolchain.

- Participants: Stefano Sebastio, Cassius De Oliveira Puodzius, Lamine Noureddine, Sébastien Campion, Jean Quilbeuf, Eduard Baranov and Thomas Given-Wilson
- Partner: Cisco
- Contact: Sébastien Campion
- URL: https://team.inria.fr/tamis/

6.8. PEPAC

PE PAcker Classifier. Version 1.4
KEYWORDS: Packer classification - Packer detection - Entropy - Machine learning - Feature selection - Portable Executable file - Obfuscation - Malware

FUNCTIONAL DESCRIPTION: This program takes a number of PE binary files and runs many packer detection and classification techniques on them, including YARA rules, PEiD rules, hash lists, and ML classifiers. The results are outputted to screen and dumped to disk on .json form.

This program is meant as a convenient way to compare the effectiveness of ML packer classifiers, but can also be used to detect and classify packing techniques in given binaries.

- Participants: Lamine Noureddine and Fabrizio Biondi
- Partner: Cisco
- Contact: Lamine Noureddine
- Publication: Effective, Efficient, and Robust Packing Detection and Classification

6.9. Arml

ARM to RML translator

KEYWORDS: Binary translation - ARM - RML

FUNCTIONAL DESCRIPTION: ArmL is an ARM to RML translator tool. ArmL tool takes as input an ARM executable binary, it produces as output a RML model.

- Contact: Nisrine Jafri

6.10. IoTMLT

IoT Modeling Language and tool

KEYWORDS: Internet of things - Modeling language - Cyber attack

SCIENTIFIC DESCRIPTION: We propose a framework to analyze security in IoT systems consisting of a formal languages for modeling IoT systems and of attack trees for modeling the possible attacks on the system. In our approach a malicious entity is present in the system, called the Attacker. The other IoT entities can inadvertently help the Attacker, by leaking their sensitive data. Equipped with the acquired knowledge the Attacker can then communicate with the IoT entities undetected. The attack tree provided with the model acts as a monitor: It observes the interactions the Attacker has with the system and detects when an attack is successful.

An IoT system is then analyzed using statistical model checking (SMC). The first method we use is Monte Carlo, which consists of sampling the executions of an IoT system and computing the probability of a successful attack based on the number of executions for which the attack was successful. However, the evaluation may be difficult if a successful attack is rare. We therefore propose a second SMC method, developed for rare events, called importance splitting. Both methods are proposed by Plasma, the SMC tool we use.

FUNCTIONAL DESCRIPTION: The IoT modeling language is a formal language and tool for specifying and enforcing security in IoT systems.

- Participants: Delphine Beaulaton, Ioana-Domnina Cristescu and Najah Ben Said
- Partner: Vérimag
- Contact: Delphine Beaulaton
- URL: http://iot-modeling.gforge.inria.fr

TEA Project-Team

6. New Software and Platforms

6.1. ADFG

Affine data-flow graphs schedule synthesizer
KEYWORDS: Code generation - Scheduling - Static program analysis
FUNCTIONAL DESCRIPTION: ADFG is a synthesis tool of real-time system scheduling parameters: ADFG computes task periods and buffer sizes of systems resulting in a trade-off between throughput maximization and buffer size minimization. ADFG synthesizes systems modeled by ultimately cyclo-static dataflow (UCSDF) graphs, an extension of the standard CSDF model.

Knowing the WCET (Worst Case Execute Time) of the actors and their exchanges on the channels, ADFG tries to synthezise the scheduler of the application. ADFG offers several scheduling policies and can detect unschedulable systems. It ensures that the real scheduling does not cause overflows or underflows and tries to maximize the throughput (the processors utilization) while minimizing the storage space needed between the actors (i.e. the buffer sizes).

Abstract affine scheduling is first applied on the dataflow graph, that consists only of periodic actors, to compute timeless scheduling constraints (e.g. relation between the speeds of two actors) and buffering parameters. Then, symbolic schedulability policies analysis (i.e., synthesis of timing and scheduling parameters of actors) is applied to produce the scheduller for the actors.

ADFG, initially defined to synthesize real-time schedulers for SCJ/L1 applications, may be used for scheduling analysis of AADL programs.

- Authors: Thierry Gautier, Jean-Pierre Talpin, Adnan Bouakaz, Alexandre Honorat and Loïc Besnard
- Contact: Loïc Besnard

6.2. POLYCHRONY

KEYWORDS: Code generation - AADL - Proof - Optimization - Multi-clock - GALS - Architecture - Cosimulation - Real time - Synchronous Language
FUNCTIONAL DESCRIPTION: Polychrony is an Open Source development environment for critical/embedded systems. It is based on Signal, a real-time polychronous data-flow language. It provides a unified model-driven environment to perform design exploration by using top-down and bottom-up design methodologies formally supported by design model transformations from specification to implementation and from synchrony to asynchrony. It can be included in heterogeneous design systems with various input formalisms and output languages. The Polychrony tool-set provides a formal framework to: validate a design at different levels, by the way of formal verification and/or simulation, refine descriptions in a top-down approach, abstract properties needed for black-box composition, compose heterogeneous components (bottom-up with COTS), generate executable code for various architectures. The Polychrony tool-set contains three main components and an experimental interface to GNU Compiler Collection (GCC):

* The Signal toolbox, a batch compiler for the Signal language, and a structured API that provides a set of program transformations. Itcan be installed without other components and is distributed under GPL V2 license.

* The Signal GUI, a Graphical User Interface to the Signal toolbox (editor + interactive access to compiling functionalities). It can be used either as a specific tool or as a graphical view under Eclipse. It has been transformed and restructured, in order to get a more up-to-date interface allowing multi-window manipulation of programs. It is distributed under GPL V2 license.

* The POP Eclipse platform, a front-end to the Signal toolbox in the Eclipse environment. It is distributed under EPL license.

- Participants: Loïc Besnard, Paul Le Guernic and Thierry Gautier
- Partners: CNRS - Inria
- Contact: Loïc Besnard
- URL: https://www.polarsys.org/projects/polarsys.pop

6.3. Polychrony AADL2SIGNAL

KEYWORDS: Real-time application - Polychrone - Synchronous model - Polarsys - Polychrony - Signal - AADL - Eclipse - Meta model
FUNCTIONAL DESCRIPTION: This polychronous MoC has been used previously as semantic model for systems described in the core AADL standard. The core AADL is extended with annexes, such as the Behavior Annex, which allows to specify more precisely architectural behaviors. The translation from AADL specifications into the polychronous model should take into account these behavior specifications, which are based on description of automata.

For that purpose, the AADL state transition systems are translated as Signal automata (a slight extension of the Signal language has been defined to support the model of polychronous automata).

Once the AADL model of a system transformed into a Signal program, one can analyze the program using the Polychrony framework in order to check if timing, scheduling and logical requirements over the whole system are met.

We have implemented the translation and experimented it using a concrete case study, which is the AADL modeling of an Adaptive Cruise Control (ACC) system, a highly safety-critical system embedded in recent cars.

- Participants: Huafeng Yu, Loïc Besnard, Paul Le Guernic, Thierry Gautier and Yue Ma
- Partner: CNRS
- Contact: Loïc Besnard
- URL: http://www.inria.fr/equipes/tea

6.4. POP

Polychrony on Polarsys
KEYWORDS: Synchronous model - Model-driven engineering
FUNCTIONAL DESCRIPTION: The Eclipse project POP is a model-driven engineering front-end to our open-source toolset Polychrony. a major achievement of the ESPRESSO (and now TEA) project-team. The Eclipse project POP is a model-driven engineering front-end to our open-source toolset Polychrony. It was finalised in the frame of project OPEES, as a case study: by passing the POLARSYS qualification kit as a computer aided simulation and verification tool. This qualification was implemented by CS Toulouse in conformance with relevant generic (platform independent) qualification documents. Polychrony is now distributed by the Eclipse project POP on the platform of the POLARSYS industrial working group. Team TEA aims at continuing its dissemination to academic partners, as to its principles and features, and industrial partners, as to the services it can offer.

Project POP is composed of the Polychrony tool set, under GPL license, and its Eclipse framework, under EPL license. SSME (Syntactic Signal-Meta under Eclipse), is the meta-model of the Signal language implemented with Eclipse/Ecore. It describes all syntactic elements specified in Signal Reference Manual [0]: all Signal operators (e.g. arithmetic, clock synchronization), model (e.g. process frame, module), and construction (e.g. iteration, type declaration). The meta-model primarily aims at making the language and services of the Polychrony environment available to inter-operation and composition with other components (e.g. AADL, Simulink, GeneAuto, P) within an Eclipse-based development tool-chain. Polychrony now comprises the capability to directly import and export Ecore models instead of textual Signal programs, in order to facilitate interaction between components within such a tool-chain. The download site for project POP has opened in 2015 at https://www.polarsys.org/projects/polarsys.pop. It should be noted that the Eclipse Foundation does not host code under GPL license. So, the Signal toolbox useful to compile Signal code from Eclipse is hosted on our web server.

- Participants: Jean-Pierre Talpin, Loïc Besnard, Paul Le Guernic and Thierry Gautier
- Contact: Loïc Besnard
- URL: https://www.polarsys.org/projects/polarsys.pop

6.5. Sigali

FUNCTIONAL DESCRIPTION: Sigali is a model-checking tool that operates on ILTS (Implicit Labeled Transition Systems, an equational representation of an automaton), an intermediate model for discrete event systems. It offers functionalities for verification of reactive systems and discrete controller synthesis. The techniques used consist in manipulating the system of equations instead of the set of solutions, which avoids the enumeration of the state space. Each set of states is uniquely characterized by a predicate and the operations on sets can be equivalently performed on the associated predicates. Therefore, a wide spectrum of properties, such as liveness, invariance, reachability and attractivity, can be checked. Algorithms for the computation of predicates on states are also available. Sigali is connected with the Polychrony environment (Tea project-team) as well as the Matou environment (VERIMAG), thus allowing the modeling of reactive systems by means of Signal Specification or Mode Automata and the visualization of the synthesized controller by an interactive simulation of the controlled system.

- Contact: Hervé Marchand

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SIGNAL V4-Inria version: Reference Manual. Besnard, L., Gautier, T. and Le Guernic, P. http://www.irisa.fr/espresso/Polychrony, 2010

TOCCATA Project-Team

6. New Software and Platforms

6.1. Alt-Ergo

Automated theorem prover for software verification
KEYWORDS: Software Verification - Automated theorem proving
FUNCTIONAL DESCRIPTION: Alt-Ergo is an automatic solver of formulas based on SMT technology. It is especially designed to prove mathematical formulas generated by program verification tools, such as Frama-C for C programs, or SPARK for Ada code. Initially developed in Toccata research team, Alt-Ergo's distribution and support are provided by OCamlPro since September 2013.

RELEASE FUNCTIONAL DESCRIPTION: the "SAT solving" part can now be delegated to an external plugin, new experimental SAT solver based on mini-SAT, provided as a plugin. This solver is, in general, more efficient on ground problems, heuristics simplification in the default SAT solver and in the matching (instantiation) module, re-implementation of internal literals representation, improvement of theories combination architecture, rewriting some parts of the formulas module, bugfixes in records and numbers modules, new option "-no-Ematching" to perform matching without equality reasoning (i.e. without considering "equivalence classes"). This option is very useful for benchmarks coming from Atelier-B, two new experimental options: "-save-used-context" and "-replay-used-context". When the goal is proved valid, the first option allows to save the names of useful axioms into a ".used" file. The second one is used to replay the proof using only the axioms listed in the corresponding ".used" file. Note that the replay may fail because of the absence of necessary ground terms generated by useless axioms (that are not included in .used file) during the initial run.

- Participants: Alain Mebsout, Évelyne Contejean, Mohamed Iguernelala, Stéphane Lescuyer and Sylvain Conchon
- Partner: OCamlPro
- Contact: Sylvain Conchon
- URL: http://alt-ergo.lri.fr

6.2. CoqInterval

Interval package for Coq
KEYWORDS: Interval arithmetic - Coq
FUNCTIONAL DESCRIPTION: CoqInterval is a library for the proof assistant Coq.

It provides several tactics for proving theorems on enclosures of real-valued expressions. The proofs are performed by an interval kernel which relies on a computable formalization of floating-point arithmetic in Coq.

The Marelle team developed a formalization of rigorous polynomial approximation using Taylor models in Coq. In 2014, this library has been included in CoqInterval.

- Participants: Assia Mahboubi, Érik Martin-Dorel, Guillaume Melquiond, Jean-Michel Muller, Laurence Rideau, Laurent Théry, Micaela Mayero, Mioara Joldes, Nicolas Brisebarre and Thomas Sibut-Pinote
- Contact: Guillaume Melquiond
- Publications: Proving bounds on real-valued functions with computations - Floating-point arithmetic in the Coq system - Proving Tight Bounds on Univariate Expressions with Elementary Functions in Coq - Formally Verified Approximations of Definite Integrals - Formally Verified Approximations of Definite Integrals
- URL: http://coq-interval.gforge.inria.fr/

6.3. Coquelicot

The Coquelicot library for real analysis in Coq
KEYWORDS: Coq - Real analysis
FUNCTIONAL DESCRIPTION: Coquelicot is library aimed for supporting real analysis in the Coq proof assistant. It is designed with three principles in mind. The first is the user-friendliness, achieved by implementing methods of automation, but also by avoiding dependent types in order to ease the stating and readability of theorems. This latter part was achieved by defining total function for basic operators, such as limits or integrals. The second principle is the comprehensiveness of the library. By experimenting on several applications, we ensured that the available theorems are enough to cover most cases. We also wanted to be able to extend our library towards more generic settings, such as complex analysis or Euclidean spaces. The third principle is for the Coquelicot library to be a conservative extension of the Coq standard library, so that it can be easily combined with existing developments based on the standard library.

- Participants: Catherine Lelay, Guillaume Melquiond and Sylvie Boldo
- Contact: Sylvie Boldo
- URL: http://coquelicot.saclay.inria.fr/

6.4. Cubicle

The Cubicle model checker modulo theories
KEYWORDS: Model Checking - Software Verification
FUNCTIONAL DESCRIPTION: Cubicle is an open source model checker for verifying safety properties of array-based systems, which corresponds to a syntactically restricted class of parametrized transition systems with states represented as arrays indexed by an arbitrary number of processes. Cache coherence protocols and mutual exclusion algorithms are typical examples of such systems.

- Participants: Alain Mebsout and Sylvain Conchon
- Contact: Sylvain Conchon
- URL: http://cubicle.lri.fr/

6.5. Flocq

The Flocq library for formalizing floating-point arithmetic in Coq
KEYWORDS: Floating-point - Arithmetic code - Coq
FUNCTIONAL DESCRIPTION: The Flocq library for the Coq proof assistant is a comprehensive formalization of floating-point arithmetic: core definitions, axiomatic and computational rounding operations, high-level properties. It provides a framework for developers to formally verify numerical applications.

Flocq is currently used by the CompCert verified compiler to support floating-point computations.

- Participants: Guillaume Melquiond, Pierre Roux and Sylvie Boldo
- Contact: Sylvie Boldo
- Publications: Flocq: A Unified Library for Proving Floating-point Algorithms in Coq - A Formally-Verified C Compiler Supporting Floating-Point Arithmetic - Verified Compilation of Floating-Point Computations - Innocuous Double Rounding of Basic Arithmetic Operations - Formal Proofs of Rounding Error Bounds - Computer Arithmetic and Formal Proofs
- URL: http://flocq.gforge.inria.fr/

6.6. Gappa

The Gappa tool for automated proofs of arithmetic properties
KEYWORDS: Floating-point - Arithmetic code - Software Verification - Constraint solving

FUNCTIONAL DESCRIPTION: Gappa is a tool intended to help formally verifying numerical programs dealing with floating-point or fixed-point arithmetic. It has been used to write robust floating-point filters for CGAL and it is used to verify elementary functions in CRlibm. While Gappa is intended to be used directly, it can also act as a backend prover for the Why3 software verification plateform or as an automatic tactic for the Coq proof assistant.

- Participant: Guillaume Melquiond
- Contact: Guillaume Melquiond
- Publications: Generating formally certified bounds on values and round-off errors - Formal certification of arithmetic filters for geometric predicates - Assisted verification of elementary functions - From interval arithmetic to program verification - Formally Certified Floating-Point Filters For Homogeneous Geometric Predicates - Combining Coq and Gappa for Certifying Floating-Point Programs - Handbook of Floating-Point Arithmetic - Certifying the floating-point implementation of an elementary function using Gappa - Automations for verifying floating-point algorithms - Automating the verification of floating-point algorithms - Computer Arithmetic and Formal Proofs
- URL: http://gappa.gforge.inria.fr/

6.7. Why3

The Why3 environment for deductive verification

KEYWORDS: Formal methods - Trusted software - Software Verification - Deductive program verification

FUNCTIONAL DESCRIPTION: Why3 is an environment for deductive program verification. It provides a rich language for specification and programming, called WhyML, and relies on external theorem provers, both automated and interactive, to discharge verification conditions. Why3 comes with a standard library of logical theories (integer and real arithmetic, Boolean operations, sets and maps, etc.) and basic programming data structures (arrays, queues, hash tables, etc.). A user can write WhyML programs directly and get correct-by-construction OCaml programs through an automated extraction mechanism. WhyML is also used as an intermediate language for the verification of C, Java, or Ada programs.

- Participants: Andriy Paskevych, Claude Marché, François Bobot, Guillaume Melquiond, Jean-Christophe Filliâtre, Levs Gondelmans and Martin Clochard
- Partners: CNRS - Université Paris-Sud
- Contact: Claude Marché
- URL: http://why3.lri.fr/

6.8. Coq

The Coq Proof Assistant

KEYWORDS: Proof - Certification - Formalisation

SCIENTIFIC DESCRIPTION: Coq is an interactive proof assistant based on the Calculus of (Co-)Inductive Constructions, extended with universe polymorphism. This type theory features inductive and co-inductive families, an impredicative sort and a hierarchy of predicative universes, making it a very expressive logic. The calculus allows to formalize both general mathematics and computer programs, ranging from theories of finite structures to abstract algebra and categories to programming language metatheory and compiler verification. Coq is organised as a (relatively small) kernel including efficient conversion tests on which are built a set of higher-level layers: a powerful proof engine and unification algorithm, various tactics/decision procedures, a transactional document model and, at the very top an IDE.

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

RELEASE FUNCTIONAL DESCRIPTION: Coq version 8.8.2 contains the result of refinements and stabilization of features and deprecations, cleanups of the internals of the system along with a few new features.

Summary of changes:

Kernel: fix a subject reduction failure due to allowing fixpoints on non-recursive values (#407), by Matthieu Sozeau. Handling of evars in the VM (#935) by Pierre-Marie Pédrot.

Notations: many improvements on recursive notations and support for destructuring patterns in the syntax of notations by Hugo Herbelin.

Proof language: tacticals for profiling, timing and checking success or failure of tactics by Jason Gross. The focusing bracket { supports single-numbered goal selectors, e.g. 2:{, (#6551) by Théo Zimmermann.

Vernacular: cleanup of definition commands (#6653) by Vincent Laporte and more uniform handling of the Local flag (#1049), by Maxime Dénès. Experimental Show Extraction command (#6926) by Pierre Letouzey. Coercion now accepts Prop or Type as a source (#6480) by Arthur Charguéraud. Export modifier for options allowing to export the option to modules that Import and not only Require a module (#6923), by Pierre-Marie Pédrot.

Universes: many user-level and API level enhancements: qualified naming and printing, variance annotations for cumulative inductive types, more general constraints and enhancements of the minimization heuristics, interaction with modules by Gaëtan Gilbert, Pierre-Marie Pédrot and Matthieu Sozeau.

Library: Decimal Numbers library (#6599) by Pierre Letouzey and various small improvements.

Documentation: a large community effort resulted in the migration of the reference manual to the Sphinx documentation tool. The new documentation infrastructure (based on Sphinx) is by Clément Pit-Claudel. The migration was coordinated by Maxime Dénès and Paul Steckler, with some help of Théo Zimmermann during the final integration phase. The 14 people who ported the manual are Calvin Beck, Heiko Becker, Yves Bertot, Maxime Dénès, Richard Ford, Pierre Letouzey, Assia Mahboubi, Clément Pit-Claudel, Laurence Rideau, Matthieu Sozeau, Paul Steckler, Enrico Tassi, Laurent Théry, Nikita Zyuzin.

Tools: experimental -mangle-names option to coqtop/coqc for linting proof scripts (#6582), by Jasper Hugunin. Main changes:

Critical soundness bugs were fixed between versions 8.8.0 and 8.8.2, and a PDF version of the reference manual was made available. The Windows installer also includes many more external packages that can be individually selected for installation.

On the implementation side, the dev/doc/changes.md file documents the numerous changes to the implementation and improvements of interfaces. The file provides guidelines on porting a plugin to the new version.

More information can be found in the CHANGES file. Feedback and bug reports are extremely welcome.

Distribution Installers for Windows 32 bits (i686), Windows 64 bits (x8_64) and macOS are available. They come bundled with CoqIDE. Windows binaries now include the Bignums library.

Complete sources of the files installed by the Windows installers are made available, to comply with license requirements.

NEWS OF THE YEAR: Version 8.8.0 was released in April 2018 and version 8.8.2 in September 2018. This is the third release of Coq developed on a time-based development cycle. Its development spanned 6 months from the release of Coq 8.7 and was based on a public road-map. It attracted many external contributions. Code reviews and continuous integration testing were systematically used before integration of new features, with an important focus given to compatibility and performance issues.

The main advances in this version are cleanups and fixes in the many different components of the system, ranging from low level kernel fixes to advances in the support of notations and tacticals for selecting goals. A large community effort was made to move the documentation to the Sphinx format, providing a more accessible online ressource to users.

- Participants: Abhishek Anand, C. J. Bell, Yves Bertot, Frédéric Besson, Tej Chajed, Pierre Courtieu, Maxime Denes, Julien Forest, Emilio Jesús Gallego Arias, Gaëtan Gilbert, Benjamin Grégoire, Jason Gross, Hugo Herbelin, Ralf Jung, Matej Kosik, Sam Pablo Kuper, Xavier Leroy, Pierre Letouzey, Assia Mahboubi, Cyprien Mangin, Érik Martin-Dorel, Olivier Marty, Guillaume Melquiond, Pierre-Marie Pédrot, Benjamin C. Pierce, Lars Rasmusson, Yann Régis-Gianas, Lionel Rieg, Valentin Robert, Thomas Sibut-Pinote, Michael Soegtrop, Matthieu Sozeau, Arnaud Spiwack, Paul Steckler, George Stelle, Pierre-Yves Strub, Enrico Tassi, Hendrik Tews, Laurent Théry, Amin Timany, Vadim Zaliva and Théo Zimmermann
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Matthieu Sozeau
- Publication: The Coq Proof Assistant, version 8.8.0
- URL: http://coq.inria.fr/

VERIDIS Project-Team

6. New Software and Platforms

6.1. Redlog

Reduce Logic System
KEYWORDS: Computer algebra system (CAS) - First-order logic - Constraint solving
SCIENTIFIC DESCRIPTION: Redlog is an integral part of the interactive computer algebra system Reduce. It supplements Reduce's comprehensive collection of powerful methods from symbolic computation by supplying more than 100 functions on first-order formulas.

Redlog generally works with interpreted first-order logic in contrast to free first-order logic. Each first-order formula in Redlog must exclusively contain atoms from one particular Redlog-supported theory, which corresponds to a choice of admissible functions and relations with fixed semantics. Redlog-supported theories include Nonlinear Real Arithmetic (Real Closed Fields), Presburger Arithmetic, Parametric QSAT, and many more.
NEWS OF THE YEAR: Parts of the Redlog code are 25 years old now. Version 1 of the underlying computer algebra system Reduce has been published even 50 years ago. In 2018 we therefore decided to go for major revisions and improvements of Redlog's software architecture.

Redlog is, as well as the underlying Reduce, implemented in a language called RLISP, which technically parses an Algol-style procedural notation into a quite minimalistic Lisp 1 dialect called Standard Lisp. RLISP and Reduce and, subsequently, Redlog are bootstrapped on the basis of an existing Standard Lisp. Today, there are two independent implementations of Standard Lisp left, which are supported only on the basis of private commitment of essentially one individual per Lisp. With the large code base of Redlog plus the necessary algebraic algorithms from Reduce a migration to a different language or computer algebra system is not feasible. We are therefore experimenting with the realization of a Standard Lisp on the basis of ANSI Common Lisp, which could allow an RLISP-Reduce-Redlog bootstrap. Given that Common Lisp is a Lisp 2, this is feasible but not at all straightforward. Also, it naturally comes with a loss of efficiency, which requires careful programming. We are grateful that Inria supports this project with an engineer's position for limited time (ADT-135 Fast Track).

We are furthermore working on an improved design of Redlog's black-box and service schedulers [Dolzmann and Sturm, ACM SIGSAM Bull. 31, 1997] and a revision of global Boolean switches in favor of named optional arguments. In that course we store related information more explicitly, which will allow automatic consistency checks of the schedulers and automated interface generation with named arguments. In addition, this supports an interactive help system inside Reduce, which is also under construction.

- Participant: Thomas Sturm
- Contact: Thomas Sturm
- URL: http://www.redlog.eu/

6.2. SPASS

KEYWORD: First-order logic
SCIENTIFIC DESCRIPTION: The classic SPASS is an automated theorem prover based on superposition that handles first-order logic with equality and several extensions for particular classes of theories. With version SPASS 3.9 we have stopped the development of the classic prover and have started the bottom-up development of SPASS 4.0 that will actually be a workbench of automated reasoning tools. Furthermore, we use SPASS 3.9 as a test bed for the development of new calculi.

SPASS 3.9 has been used as the basis for SPASS-AR, a new approximation refinement theorem proving approach.
FUNCTIONAL DESCRIPTION: SPASS is an automated theorem prover based on superposition that handles first-order logic with equality and several extensions for particular classes of theories.
NEWS OF THE YEAR: We released the second version of SPASS-IQ, our solver for linear integer arithmetic that we are currently extending to real and mixed real-integer arithmetic.

- Contact: Christoph Weidenbach
- URL: http://www.spass-prover.org/

6.3. SPASS-SATT

KEYWORDS: Automated deduction - Decision
SCIENTIFIC DESCRIPTION: SPASS -SATT is an SMT solver for the theories of linear integer arithmetic, linear rational arithmetic and mixed linear arithmetic. It features new tests for the satisfiability of unbounded systems, as well as new algorithms for the detection of integer solutions.

We further investigated the use of redundancy elimination in SAT solving and underlying implementation techniques. Our aim is a new approach to SAT solving that needs fewer conflicts (on average) *and* is faster than the current state-of-the art solvers. Furthermore, we have developed a new calculus and first prototypical implementation of a SAT solver with mixed OR/XOR clauses.
FUNCTIONAL DESCRIPTION: SPASS-SATT is an SMT solver for linear integer arithmetic, mixed linear arithmetic and rational linear arithmetic.
NEWS OF THE YEAR: The first version of SPASS-SATT was released in June 2018. It participated in SMTCOMP-2018 in the quantifier free integer and rational linear arithmetic categories. In both categories it solved more problems in a shorter period of time than any other SMT solver. With respect to the weighted bucket ranking it scored first in the linear integer category and second in the linear rational category.

- Participants: Martin Bromberger, Mathias Fleury and Christoph Weidenbach
- Contact: Martin Bromberger
- URL: https://www.mpi-inf.mpg.de/departments/automation-of-logic/software/spass-workbench/spass-satt/

6.4. SPIKE

KEYWORDS: Proof - Automated deduction - Automated theorem proving - Term Rewriting Systems - Formal methods
SCIENTIFIC DESCRIPTION: SPIKE, an automatic induction-based theorem prover built to reason on conditional theories with equality, is one of the few formal tools able to perform automatically mutual and lazy induction. Designed in the 1990s, it has been successfully used in many non-trivial applications and served as a prototype for different proof experiments and extensions.
FUNCTIONAL DESCRIPTION: Automated induction-based theorem prover

RELEASE FUNCTIONAL DESCRIPTION: Proof certification with Coq, cyclic induction, decision procedures

- Participant: Sorin Stratulat
- Contact: Sorin Stratulat

6.5. veriT

KEYWORDS: Automated deduction - Formula solving - Verification
SCIENTIFIC DESCRIPTION: veriT comprises a SAT solver, a decision procedure for uninterpreted symbols based on congruence closure, a simplex-based decision procedure for linear arithmetic, and instantiation-based quantifier handling.

FUNCTIONAL DESCRIPTION: VeriT is an open, trustable and efficient SMT (Satisfiability Modulo Theories) solver, featuring efficient decision procedure for uninterpreted symbols and linear arithmetic, and quantifier reasoning.
NEWS OF THE YEAR: Efforts in 2018 have been focused on non-linear arithmetic reasoning, quantifier handling and proof production.

The veriT solver participated in the SMT competition SMT-COMP 2018 with good results.

We target applications where validation of formulas is crucial, such as the validation of TLA$^+$ and B specifications, and work together with the developers of the respective verification platforms to make veriT even more useful in practice. The solver is available as a plugin for the Rodin platform, it is integrated within the Atelier B.

veriT is also a prototype platform for ideas developed within the Matryoshka project, aiming at greater availability of automated reasoning for proof assistants.

- Participants: Haniel Barbosa, Daniel El Ouraoui, Pascal Fontaine and Hans-Jörg Schurr
- Partner: Université de Lorraine
- Contact: Pascal Fontaine
- URL: http://www.veriT-solver.org

6.6. Nunchaku

The Nunchaku Higher-Order Model Finder
KEYWORDS: Proof - Higher-order logic
SCIENTIFIC DESCRIPTION: Nunchaku is a model finder for higher-order logic, with dedicated support for various definitional principles. It is designed to work as a backend for various proof assistants (notably Isabelle/HOL and Coq) and to use state-of-the-art model finders and other solvers as backends.
FUNCTIONAL DESCRIPTION: Nunchaku is a model finder (counterexample generator) for higher-order logic.
NEWS OF THE YEAR: A noteworthy development this year is a preliminary integration of Nunchaku in the Lean proof assistant. This work was performed by Pablo Le Hénaff during an internship at Vrije Universiteit Amsterdam. See his internship report at http://matryoshka.gforge.inria.fr/pubs/lehenaff_report.pdf for details.

- Participants: Jasmin Christian Blanchette and Simon Cruanes
- Partner: Vrije Universiteit Amsterdam
- Contact: Jasmin Christian Blanchette
- Publications: Extending Nunchaku to Dependent Type Theory - Model Finding for Recursive Functions in SMT
- URL: https://github.com/nunchaku-inria

6.7. TLAPS

TLA+ proof system
KEYWORD: Proof assistant
FUNCTIONAL DESCRIPTION: TLAPS is a platform for developing and mechanically verifying proofs about TLA+ specifications. The TLA+ proof language is hierarchical and explicit, allowing a user to decompose the overall proof into proof steps that can be checked independently. TLAPS consists of a proof manager that interprets the proof language and generates a collection of proof obligations that are sent to backend verifiers. The current backends include the tableau-based prover Zenon for first-order logic, Isabelle/TLA+, an encoding of TLA+ set theory as an object logic in the logical framework Isabelle, an SMT backend designed for use with any SMT-lib compatible solver, and an interface to a decision procedure for propositional temporal logic.

NEWS OF THE YEAR: Ioannis Filippidis joined the development team in November 2018 and started designing and implementing support for reasoning about TLA+'s ENABLED construct.

- Participants: Damien Doligez, Stephan Merz and IOANNIS FILIPPIDIS
- Contact: Stephan Merz
- URL: https://tla.msr-inria.inria.fr/tlaps/content/Home.html

6.8. Apalache

Abstraction-based Parameterized TLA+ Checker
KEYWORD: Model Checker
FUNCTIONAL DESCRIPTION: The first version implements a symbolic bounded model checker for TLA$^+$ that runs under the same assumptions as the explicit-state model checker TLC. It checks whether a TLA$^+$ specification satisfies an invariant candidate by checking satisfiability of an SMT formula that encodes: (1) an execution of bounded length, and (2) preservation of the invariant candidate in every state of the execution. Our tool is still in the experimental phase, due to a number of challenges posed by the semantics of TLA$^+$ to SMT solvers.

- Partner: Technische Universität Wien
- Contact: Igor Konnov
- Publications: BmcMT: Bounded Model Checking of TLA + Specifications with SMT - Extracting Symbolic Transitions from $TLA+$ Specifications
- URL: https://forsyte.at/research/apalache/

6.9. ByMC

Byzantine Model Checker
KEYWORDS: Model Checker - Distributed computing - Verification
SCIENTIFIC DESCRIPTION: In recent work, we have introduced a series of techniques for automatic verification of threshold-guarded distributed algorithms that have the following features: (1) up to t of n processes may exhibit crash or Byzantine failures, (2) the correct processes count messages and progress when they receive sufficiently many messages, e.g., at least $t+1$, (3) the number n of processes in the system is a parameter, as well as t, (4) and the parameters are restricted by a resilience condition, e.g., $n > 3t$.
FUNCTIONAL DESCRIPTION: ByMC implements several techniques for the parameterized verification of threshold-guarded distributed algorithms such as reliable broadcast, one-step Byzantine consensus, non-blocking atomic commit, condition-based consensus, and randomized consensus. The tool accepts two kinds of inputs: (i) threshold automata (the framework of our verification techniques) and (ii) Parametric Promela (which is similar to the way in which the distributed algorithms are presented in the distributed computing literature). Internally, the tool analyzes representative executions by querying an SMT solver. Apart from verification, ByMC also implements a technique for the automatic synthesis of threshold guards.

The tool can run on a single computer as well as in an MPI cluster, e.g., Grid5000 or Vienna Scientific Cluster.
NEWS OF THE YEAR: We have introduced a parallel extension of the tool, which allows one to run verification experiments in an MPI cluster. The parallel version of the tool demonstrated a good speed-up on large benchmarks run in Vienna Scientific Cluster and Grid 5000.

- Partner: Technische Universität Wien
- Contact: Igor Konnov
- Publications: ByMC: Byzantine Model Checker - Reachability in Parameterized Systems: All Flavors of Threshold Automata - Model Checking of Fault-Tolerant Distributed Algorithms: from Classics towards Contemporary - Verification of Randomized Distributed Algorithms under Round-Rigid Adversaries
- URL: https://forsyte.at/software/bymc/

ACUMES Project-Team

6. New Software and Platforms

6.1. MGDA

Multiple Gradient Descent Algorithm
KEYWORDS: Descent direction - Multiple gradients - Multi-objective differentiable optimization
SCIENTIFIC DESCRIPTION: The software provides a vector d whose scalar product with each of the given gradients (or directional derivative) is positive provided a solution exists. When the gradients are linearly independent, the algorithm is direct following a Gram-Schmidt orthogonalization. Otherwise, a sub-family of the gradients is identified according to a hierarchical criterion as a basis of the spanned subspace associated with a cone that contains almost all the gradient directions. Then, one solves a quadratic programming problem formulated in this basis.

https://hal.inria.fr/hal-01139994 https://hal.inria.fr/hal-01414741
FUNCTIONAL DESCRIPTION: Concerning Chapter 1, the utilization of the platform can be made via two modes : – the interactive mode, through a web interface that facilitates the data exchange between the user and an Inria dedicated machine, – the iterative mode, in which the user downloads the object library to be included in a personal optimization software. Concerning Chapters 2 and 3, the utilizer specifies cost and constraint functions by providing procedures compatible with Fortran 90. Chapter 3 does not require the specification of gradients, but only the functions themselves that are approximated by the software by quadratic meta-models.

- Participant: Jean-Antoine Désidéri
- Contact: Jean-Antoine Désidéri
- URL: http://mgda.inria.fr

6.2. Igloo

Iso-Geometric anaLysis using discOntinuOus galerkin methods
KEYWORDS: Numerical simulations - Isogeometric analysis
SCIENTIFIC DESCRIPTION: Igloo contains numerical methods to solve partial differential equations of hyperbolic type, or convection-dominant type, using an isogeometric formulation (NURBS bases) with a discontinuous Galerkin method.
FUNCTIONAL DESCRIPTION: Igloo is composed of a set of C++ libraries and applications, which allow to simulate time-dependent physical phenomena using natively CAD-based geometry descriptions.

- Author: Régis Duvigneau
- Contact: Régis Duvigneau

6.3. BuildingSmart

BuildingSmart interactive visualization
KEYWORDS: Physical simulation - 3D rendering - 3D interaction
SCIENTIFIC DESCRIPTION: The aim of the BuildingSmart project is to develop a software environment for the simulation and interactive visualisation for the design of buildings (structural safety, thermal confort).
FUNCTIONAL DESCRIPTION: The main task of the project is to study and develop solutions dedicated to interactive visualisation of building performances (heat, structural) in relation to the Building Information Modeling BIM framework, using Occulus Rift immersion.
NEWS OF THE YEAR: Demo movies are available from Youtube (see web site)

- Participants: Régis Duvigneau, Jean-Luc Szpyrka, David Rey, Clement Welsch and Abderrahmane Habbal
- Contact: Abderrahmane Habbal
- URL: http://youtu.be/MW_gIF8hUdk

BONUS Team

6. New Software and Platforms

6.1. Platforms

6.1.1. Grid'5000 testbed: extension with GPUs at Lille

KEYWORDS: Experimental testbed, large-scale computing, high-performance computing, GPU computing, cloud computing, big data

FUNCTIONAL DESCRIPTION: Grid'5000 is a project initiated in 2003 by the French government to promote scientific research on large scale distributed systems. The project is later supported different research organizations including Inria, CNRS, the french universities, Renater which provides the wide-area network, etc. The overall objective of Grid'5000 was to build by 2007 a nation-wide experimental testbed composed of at least 5000 processing units and distributed over several sites in France. From a scientific point of view, the aim was to promote scientific research on large-scale distributed systems.

Grid'5000 was installed at the center of IT resources including supercomputing resources of Université de Lille 1 and opened to users in 2005. Since March 2017, the Grid'5000 site has moved to the premises on Inria Lille within the context of the phase 1 of the CPER data program (see Section 9.1) with a completely new hardware equipment. As a scientific leader of the testbed for the Lille's site, N. Melab has been strongly involved in the extension (phase 2 of CPER data) of the platform with 16 computing serveurs, 16 Nvidia GPUs (12 P100 and 4V100), 2 storage serveurs 200TB and 2 administration servers. Grid'5000 at Lille is used by more than 150 users including 100 external ones. The testbed is used for research as well as for teaching allowing a high scientific production (publications, PhD theses, etc.) and over 30 master students to get started with parallel and distributed programming.

- Participants: N. Melab, external collaborators: D. Delabroy, T. Peltier, L. Nussbaum.
- Contact: Nouredine Melab.
- URL: https://www.grid5000.fr/mediawiki/index.php/Grid5000:Home

CAGE Project-Team (section vide)

CAGIRE Project-Team

6. New Software and Platforms

6.1. AeroSol

KEYWORD: Finite element modelling
FUNCTIONAL DESCRIPTION: The AeroSol software is a high order finite element library written in C++. The code has been designed so as to allow for efficient computations, with continuous and discontinuous finite elements methods on hybrid and possibly curvilinear meshes. The work of the team CARDAMOM (previously Bacchus) is focused on continuous finite elements methods, while the team Cagire is focused on discontinuous Galerkin methods. However, everything is done for sharing the largest part of code we can. More precisely, classes concerning IO, finite elements, quadrature, geometry, time iteration, linear solver, models and interface with PaMPA are used by both of the teams. This modularity is achieved by mean of template abstraction for keeping good performances. The distribution of the unknowns is made with the software PaMPA , developed within the team TADAAM (and previously in Bacchus) and the team Castor.
NEWS OF THE YEAR: In 2018, the following points were addressed in AeroSol

* A 6 month CNRS contract, led by Vincent Perrier was obtained in the team Cagire, concentrated on the quality of the code. A two-year Inria Hub, led by Héloïse Beaugendre was obtained in the team Cardamom. On both of these contracts, Benjamin Lux was hired (January-June in Cagire team, and since October in Cardamom team). The library has kept on benefiting from the work of Florent Pruvost (Inria Hub HPCLib), on the continuous integration and packaging aspects.

* The CNRS contract, aiming at improving the code resulted in the successful porting from the inria gforge to the inria gitlab, with a functional pipeline of code assessment (based on Jenkins) and code quality assessment (based on sonarqube).

* Installation was simplified. A fully automatic installation script based on spack was developed.

* Development of a true documentation policy, based on a wiki. About half of the functional tests were documented and updated. Doxygen documentation was improved.

* An API was developed for the AeroSol library. The mesh reading, and parallel distribution was refactored.

* Update of the test case interface was updated by using this APIfor being more convenient. About half of the functional tests are now using this interface.

* Refactoring of the xml parameter file.

* Hyperbolized models, based on the hyperbolization of advection-diffusion models were added.

* Handling of nonconservative hyperbolic models.

* Improvement of mesh adaptation

* Beginning of implementation of droplet model for icing.

* Add the possibility of using several matrices, with a different number of variables

- Participants: Benjamin Lux, Damien Genet, Dragan Amenga Mbengoue, Hamza Belkhayat Zougari, Mario Ricchiuto, Maxime Mogé, Simon Delmas and Vincent Perrier
- Contact: Vincent Perrier

CARDAMOM Project-Team

6. New Software and Platforms

6.1. AeroSol

KEYWORD: Finite element modelling

FUNCTIONAL DESCRIPTION: The AeroSol software is a high order finite element library written in C++. The code has been designed so as to allow for efficient computations, with continuous and discontinuous finite elements methods on hybrid and possibly curvilinear meshes. The work of the team CARDAMOM (previously Bacchus) is focused on continuous finite elements methods, while the team Cagire is focused on discontinuous Galerkin methods. However, everything is done for sharing the largest part of code we can. More precisely, classes concerning IO, finite elements, quadrature, geometry, time iteration, linear solver, models and interface with PaMPA are used by both of the teams. This modularity is achieved by mean of template abstraction for keeping good performances. The distribution of the unknowns is made with the software PaMPA , developed within the team TADAAM (and previously in Bacchus) and the team Castor.

NEWS OF THE YEAR: In 2018, the following points were addressed in AeroSol

* A 6 month CNRS contract, led by Vincent Perrier was obtained in the team Cagire, concentrated on the quality of the code. A two-year Inria Hub, led by Héloïse Beaugendre was obtained in the team Cardamom. On both of these contracts, Benjamin Lux was hired (January-June in Cagire team, and since October in Cardamom team). The library has kept on benefiting from the work of Florent Pruvost (Inria Hub HPCLib), on the continuous integration and packaging aspects.

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- Participants: Benjamin Lux, Damien Genet, Dragan Amenga Mbengoue, Hamza Belkhayat Zougari, Mario Ricchiuto, Maxime Mogé, Simon Delmas and Vincent Perrier
- Contact: Vincent Perrier

6.2. Crysa

KEYWORDS: Image analysis - 2D

FUNCTIONAL DESCRIPTION: Analyzes the organization of objects placed in a hexagonal grid in an image and the crystalline structure induced in this image.

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

6.3. Cut-ANOVA

Cut-ANOVA Global Sensitivity Analysis
KEYWORDS: Stochastic models - Uncertainty quantification
SCIENTIFIC DESCRIPTION: An anchored analysis of variance (ANOVA) method is proposed to decompose the statistical moments. Compared to the standard ANOVA with mutually orthogonal component functions, the anchored ANOVA, with an arbitrary choice of the anchor point, loses the orthogonality if employing the same measure. However, an advantage of the anchored ANOVA consists in the considerably reduced number of deterministic solver's computations, which renders the uncertainty quantification of real engineering problems much easier. Different from existing methods, the covariance decomposition of the output variance is used in this work to take account of the interactions between non-orthogonal components, yielding an exact variance expansion and thus, with a suitable numerical integration method, provides a strategy that converges. This convergence is verified by studying academic tests. In particular, the sensitivity problem of existing methods to the choice of anchor point is analyzed via the Ishigami case, and we point out that covariance decomposition survives from this issue. Also, with a truncated anchored ANOVA expansion, numerical results prove that the proposed approach is less sensitive to the anchor point. The covariance-based sensitivity indices (SI) are also used, compared to the variance-based SI. Furthermore, we emphasize that the covariance decomposition can be generalized in a straightforward way to decompose higher-order moments. For academic problems, results show the method converges to exact solution regarding both the skewness and kurtosis. The proposed method can indeed be applied to a large number of engineering problems.
FUNCTIONAL DESCRIPTION: The Cut-ANOVA code (Fortran 90, MPI + OpenMP) is devoted to the stochastic analysis of numerical simulations. The method implemented is based on the spectral expansion of "anchored ANOVA", allowing the covariance-based sensitivity analysis. Compared to the conventional Sobol method, "Cut-ANOVA" provides three sensitivity indices instead of one, which allows a better analysis of the reliability of the numerical prediction. On the other hand, "Cut-ANOVA" is able to compute the higher order statistical moments such as the Skewness (3-rd order moment) and Kurtosis (4-th order moment). Several dimension reduction techniques have also been implemented to reduce the computational cost. Finally, thanks to the innovative method implemented into the Code Cut-ANOVA, one can obtain a similar accuracy for stochastic quantities by using a considerably less number of deterministic model evaluations, compared with the classical Monte Carlo method.

- Participants: Kunkun Tang and Pietro-Marco Congedo
- Contact: Kunkun Tang

6.4. Fmg

KEYWORD: Mesh adaptation
FUNCTIONAL DESCRIPTION: FMG is a library deforming an input/reference simplicial mesh w.r.t. a given smoothness error monitor (function gradient or Hessian), metric field, or given mesh size distribution. Displacements are computed by solving an elliptic Laplacian type equation with a continuous finite element method. The library returns an adapted mesh with a corresponding projected solution, obtained by either a second order projection, or by an ALE finite element remap. The addiction of a new mass conservative approach developed ad-hoc for shallow water flows is under way.

NEWS OF THE YEAR: - Development of the Elasticity model to compute the nodes displacement. - Development of a new model to compute the nodes displacement. This mixed model takes the advantages of the Laplacian model and the Elasticity model: a refined mesh where the solution varies a lot and a smooth gradation of the edges size elsewhere. - Extension in three dimension

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

6.5. Mmg

Mmg Platform
KEYWORDS: Mesh adaptation - Anisotropic - Mesh generation - Mesh - Isovalue discretization
SCIENTIFIC DESCRIPTION: The Mmg plateform gathers open source software for two-dimensional, surface and volume remeshing. The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescriptions satisfaction.

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

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

Inside the volume, the software perform local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).
FUNCTIONAL DESCRIPTION: The Mmg plateform gathers open source software for two-dimensional, surface and volume remeshing. It provides three applications : 1) mmg2d: generation of a triangular mesh , adaptation and optimization of a triangular mesh 2) mmgs: adaptation and optimization of a surface triangulation representing a piecewise linear approximation of an underlying surface geometry 3) mmg3d: adaptation and optimization of a tetrahedral mesh and isovalue discretization

The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescription satisfaction.
NEWS OF THE YEAR: Release 5.3.0 improves: - the mmg3d algorithm for mesh adaptation (better convergency and edge lengths closest to 1) - the software behaviour in case of failure (warnings/error messages are printed only 1 time and there is no more exits in the code) - the mmg2d software that now uses the same structure than mmgs and mmg3d

It adds: - the -hsiz option for mmg2d/s/3d (that allows to generate a uniform mesh of size) - the -nosurf option for mmg2d (that allows to not modify the mesh boundaries) - the -opnbdy option for mmg3d (that allow to preserve an open boundary inside a volume mesh) - the possibility to provide meshes containing prisms to mmg3d (the prisms entities are preserved while the tetra ones are modified)

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

6.6. MMG3D

Mmg3d
KEYWORDS: Mesh - Anisotropic - Mesh adaptation

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

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

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

Inside the volume, the software perform local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).
FUNCTIONAL DESCRIPTION: Mmg3d is one of the software of the Mmg platform. Is is dedicated to the modification of 3D volume meshes. It perform the adaptation and the optimization of a tetrahedral mesh and allow to discretize an isovalue.

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

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

6.7. NOMESH

KEYWORDS: Mesh - Curved mesh - Tetrahedral mesh
FUNCTIONAL DESCRIPTION: NOMESH is a software allowing the generation of three order curved simplicial meshes. Starting from a "classical" mesh with straight elements composed by triangles and/or tetrahedra, we are able to curve the boundary mesh. Starting from a mesh with some curved elements, we can verify if the mesh is valid, that means there is no crossing elements and only positive jacobian. If the curved mesh is non valid, we modify it using linear elasticity equations until having a valid curved mesh.

- Participants: Algiane Froehly, Ghina El Jannoun and Cécile Dobrzynski
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: Cécile Dobrzynski

6.8. ORComp

FUNCTIONAL DESCRIPTION: The ORComp platform is a simulation tool permitting to design an ORC cycle. Starting from the solar radiation, this plateform computes the cycle providing the best performance with optimal choices of the fluid and the operating conditions. It includes RobUQ , a simulation block of the ORC cycles, the RealfluiDS code for the simulation of the turbine and of the heat exchanger, the software FluidProp (developed at the University of Delft) for computing the fluid thermodynamic properties.

- Participants: Maria-Giovanna Rodio and Pietro-Marco Congedo
- Contact: Maria-Giovanna Rodio
- URL: https://github.com/Orcomp/Orcomp

6.9. RealfluiDS

KEYWORDS: Compressible flows - Finite element modelling - Residual distribution - Aeronautics

FUNCTIONAL DESCRIPTION: RealfluiDS is a software dedicated to the simulation of inert or reactive flows. It is also able to simulate multiphase, multimaterial, MHD flows and turbulent flows (using the SA model). There exist 2D and 3D dimensional versions. The 2D version is used to test new ideas that are later implemented in the 3D one. This software implements the more recent residual distribution schemes. The code has been parallelized with and without overlap of the domains. The uncertainty quantification library RobUQ has been coupled to the software. A partitioning tool exists in the package, which uses Scotch . Recently, the code has been developed for taking into account real-gas effects, in order to use arbitrarily complex equations of state. Further developments concerning multiphase effects are under way.

- Participants: Cécile Dobrzynski, Héloïse Beaugendre, Leo Nouveau, Pietro-Marco Congedo and Quentin Viville
- Contact: Héloïse Beaugendre

6.10. SH-COMP

KEYWORDS: Finite element modelling - Multi-physics simulation - Chemistry - Incompressible flows - 2D
FUNCTIONAL DESCRIPTION: Numerical modelling of the healing process in ceramic matrix composites

- Participants: Gérard Vignoles, Gregory Perrot, Guillaume Couegnat, Mario Ricchiuto and Virginie Drean
- Partner: LCTS (UMR 5801)
- Contact: Guillaume Couegnat

6.11. SLOWS

Shallow-water fLOWS
KEYWORDS: Simulation - Free surface flows - Unstructured meshes
SCIENTIFIC DESCRIPTION: Three different approaches are available, based on conditionally depth-positivity preserving implicit schemes, or on conditionally depth-positivity preserving genuinely explicit discretizations, or on an unconditionally depth-positivity preserving space-time approach. Newton and frozen Newton loops are used to solve the implicit nonlinear equations. The linear algebraic systems arising in the discretization are solved with the MUMPS library. This year implicit and explicit (extrapolated) multistep higher order time integration methods have been implemented, and a mesh adaptation technique based on simple mesh deformation has been also included.
FUNCTIONAL DESCRIPTION: SLOWS is a C-platform allowing the simulation of free surface shallow water flows with friction. It can be used to simulate near shore hydrodynamics, wave transformations processes, etc.

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

6.12. Sparse-PDD

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

SCIENTIFIC DESCRIPTION: The polynomial dimensional decomposition (PDD) is employed in this code for the global sensitivity analysis and uncertainty quantification (UQ) of stochastic systems subject to a moderate to large number of input random variables. Due to the intimate structure between the PDD and the Analysis of Variance (ANOVA) approach, PDD is able to provide a simpler and more direct evaluation of the Sobol' sensitivity indices, when compared to the Polynomial Chaos expansion (PC). Unfortunately, the number of PDD terms grows exponentially with respect to the size of the input random vector, which makes the computational cost of standard methods unaffordable for real engineering applications. In order to address the problem of the curse of dimensionality, this code proposes essentially variance-based adaptive strategies aiming to build a cheap meta-model (i.e. surrogate model) by employing the sparse PDD approach with its coefficients computed by regression. Three levels of adaptivity are carried out in this code: 1) the truncated dimensionality for ANOVA component functions, 2) the active dimension technique especially for second- and higher-order parameter interactions, and 3) the stepwise regression approach designed to retain only the most influential polynomials in the PDD expansion. During this adaptive procedure featuring stepwise regressions, the surrogate model representation keeps containing few terms, so that the cost to resolve repeatedly the linear systems of the least-square regression problem is negligible. The size of the finally obtained sparse PDD representation is much smaller than the one of the full expansion, since only significant terms are eventually retained. Consequently, a much less number of calls to the deterministic model is required to compute the final PDD coefficients.

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

- Participants: Kunkun Tang and Pietro-Marco Congedo
- Contact: Kunkun Tang

6.13. TUCWave

KEYWORD: Physical simulation

SCIENTIFIC DESCRIPTION: A novel work that advances a step ahead the methodology of the solution of dispersive models. TUCWave uses a high-order well-balanced unstructured finite volume (FV) scheme on triangular meshes for modeling weakly nonlinear and weakly dispersive water waves over varying bathymetries, as described by the 2D depth-integrated extended Boussinesq equations of Nwogu (1993), rewritten in conservation law form. The FV scheme numerically solves the conservative form of the equations following the median dual node-centered approach, for both the advective and dispersive part of the equations. The code developed follows an efficient edge based structured technique. For the advective fluxes, the scheme utilizes an approximate Riemann solver along with a well-balanced topography source term up-winding. Higher order accuracy in space and time is achieved through a MUSCL-type reconstruction technique and through a strong stability preserving explicit Runge-Kutta time stepping. Special attention is given to the accurate numerical treatment of moving wet/dry fronts and boundary conditions. Furthermore, the model is applied to several examples of wave propagation over variable topographies and the computed solutions are compared to experimental data.

FUNCTIONAL DESCRIPTION: Fortran Planform which accounts for the study of near shore processes

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

COMMANDS Project-Team

6. New Software and Platforms

6.1. BOCOP

Boite à Outils pour le Contrôle OPtimal
KEYWORDS: Dynamic Optimization - Identification - Biology - Numerical optimization - Energy management - Transportation
FUNCTIONAL DESCRIPTION: Bocop is an open-source toolbox for solving optimal control problems, with collaborations with industrial and academic partners. Optimal control (optimization of dynamical systems governed by differential equations) has numerous applications in transportation, energy, process optimization, energy and biology. Bocop includes a module for parameter identification and a graphical interface, and runs under Linux / Windows / Mac.

RELEASE FUNCTIONAL DESCRIPTION: Handling of delay systems Alternate automatic differentiation tool: CppAD Update for CMake and MinGW (windows version)

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

6.2. Bocop HJB

KEYWORDS: Optimal control - Stochastic optimization - Global optimization
FUNCTIONAL DESCRIPTION: Toolbox for stochastic or deterministic optimal control, dynamic programming / HJB approach.

RELEASE FUNCTIONAL DESCRIPTION: User interface State jumps for switched systems Explicit handling of final conditions Computation of state probability density (fiste step to mean field games)

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

6.3. Bocop Avion

KEYWORDS: Optimization - Aeronautics
FUNCTIONAL DESCRIPTION: Optimize the climb speeds and associated fuel consumption for the flight planning of civil airplanes.
NEWS OF THE YEAR: Improved atmosphere model 2D interpolations for temperature and wind data

- Participants: Gregorutti Baptiste, Cindie Andrieu, Anamaria Lupu, Joseph Frédéric Bonnans, Karim Tekkal, Pierre Jouniaux and Pierre Martinon
- Partner: Safety Line
- Contact: Pierre Martinon
- URL: http://www.safety-line.fr

6.4. Bocop HJB Avion

KEYWORDS: Optimization - Aeronautics
FUNCTIONAL DESCRIPTION: Optimize the climb and cruising trajectory of flight by a HJB approach.
NEWS OF THE YEAR: First demonstrator for cruise flight deployed at Safety Line

- Participants: Pierre Martinon, Joseph Frédéric Bonnans, Jinyan Liu, Gregorutti Baptiste and Anamaria Lupu
- Partner: Safety Line
- Contact: Pierre Martinon
- URL: http://www.safety-line.fr

CQFD Project-Team

5. New Software and Platforms

5.1. biips

Bayesian Inference with Interacting Particle Systems

FUNCTIONAL DESCRIPTION: Biips is a software platform for automatic Bayesian inference with interacting particle systems. Biips allows users to define their statistical model in the probabilistic programming BUGS language, as well as to add custom functions or samplers within this language. Then it runs sequential Monte Carlo based algorithms (particle filters, particle independent Metropolis-Hastings, particle marginal Metropolis-Hastings) in a black-box manner so that to approximate the posterior distribution of interest as well as the marginal likelihood. The software is developed in C++ with interfaces with the softwares R, Matlab and Octave.

- Participants: Adrien Todeschini and François Caron
- Contact: Adrien Todeschini
- URL: http://biips.gforge.inria.fr

5.2. PCAmixdata

KEYWORD: Statistic analysis

FUNCTIONAL DESCRIPTION: Mixed data type arise when observations are described by a mixture of numerical and categorical variables. The R package PCAmixdata extends standard multivariate analysis methods to incorporate this type of data. The key techniques included in the package are PCAmix (PCA of a mixture of numerical and categorical variables), PCArot (rotation in PCAmix) and MFAmix (multiple factor analysis with mixed data within a dataset). The MFAmix procedure handles a mixture of numerical and categorical variables within a group - something which was not possible in the standard MFA procedure. We also included techniques to project new observations onto the principal components of the three methods in the new version of the package.

- Contact: Marie Chavent
- URL: https://cran.r-project.org/web/packages/PCAmixdata/index.html

5.3. QuantifQuantile

KEYWORD: Regression

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

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

DEFI Project-Team

6. New Software and Platforms

6.1. samplings-2d

This software solves forward and inverse problems for the Helmholtz equation in 2-D.
FUNCTIONAL DESCRIPTION: This software is written in Fortran 90 and is related to forward and inverse problems for the Helmholtz equation in 2-D. It includes three independent components. * The first one solves to scattering problem using integral equation approach and supports piecewise-constant dielectrics and obstacles with impedance boundary conditions. * The second one contains various samplings methods to solve the inverse scattering problem (LSM, RGLSM(s), Factorization, MuSiC) for near-field or far-field setting. * The third component is a set of post processing functionalities to visualize the results

- Participant: Houssem Haddar
- Contact: Houssem Haddar
- URL: http://sourceforge.net/projects/samplings-2d/

6.2. SAXS-LMA-HSPY

SAXS inversion using LMA and HSPY models
KEYWORD: SAXS measurements
FUNCTIONAL DESCRIPTION: This software determines nanoparticles size distribution from SAXS measurements (Small Angle X-ray Scattering). It contains two different approaches. The first one is based on a linear LMA model with automatic search for model parameters. The second approach uses a non-linear inversion of the HSPY model.

- Authors: Marc Bakry and Houssem Haddar
- Contact: Marc Bakry

6.3. FVforBlochTorrey

KEYWORDS: Simulation - PDE - Diffusion imaging - MRI
FUNCTIONAL DESCRIPTION: We developed a Matlab toolbox for solving the multiple-compartments Bloch-Torrey partial differential equation in 3D to simulate the water proton magnetization of a sample under the influence of diffusion-encoing magnetic field gradient pulses. We coupled the finite element spatial discretization with several ODE solvers in time that are available inside Matlab.

Result: the code will be made available on GitHub in 2019.

- Participant: Jing Rebecca Li
- Contact: Jing Rebecca Li

DISCO Project-Team

5. New Software and Platforms

5.1. FEMMES

KEYWORD: Linear system
FUNCTIONAL DESCRIPTION: The Software FEMMES makes it possible to perform simulations for observers which converge to the exact value of the solutions of a studied system in finite time. The considered systems are linear continuous-time time-invariant systems.

- Partner: Inria
- Contact: Frédéric Mazenc

ECUADOR Project-Team

5. New Software and Platforms

5.1. AIRONUM

KEYWORDS: Computational Fluid Dynamics - Turbulence
FUNCTIONAL DESCRIPTION: Aironum is an experimental software that solves the unsteady compressible Navier-Stokes equations with k-epsilon, LES-VMS and hybrid turbulence modelling on parallel platforms, using MPI. The mesh model is unstructured tetrahedrization, with possible mesh motion.

- Participant: Alain Dervieux
- Contact: Alain Dervieux
- URL: http://www-sop.inria.fr/tropics/aironum

5.2. TAPENADE

KEYWORDS: Static analysis - Optimization - Compilation - Gradients
SCIENTIFIC DESCRIPTION: Tapenade implements the results of our research about models and static analyses for AD. Tapenade can be downloaded and installed on most architectures. Alternatively, it can be used as a web server. Higher-order derivatives can be obtained through repeated application.

Tapenade performs sophisticated data-flow analysis, flow-sensitive and context-sensitive, on the complete source program to produce an efficient differentiated code. Analyses include Type-Checking, Read-Write analysis, and Pointer analysis. AD-specific analyses include:

Activity analysis: Detects variables whose derivative is either null or useless, to reduce the number of derivative instructions.

Adjoint Liveness analysis: Detects the source statements that are dead code for the computation of derivatives.

TBR analysis: In adjoint-mode AD, reduces the set of source variables that need to be recovered.
FUNCTIONAL DESCRIPTION: Tapenade is an Algorithmic Differentiation tool that transforms an original program into a new program that computes derivatives of the original program. Algorithmic Differentiation produces analytical derivatives, that are exact up to machine precision. Adjoint-mode AD can compute gradients at a cost which is independent from the number of input variables. Tapenade accepts source programs written in Fortran77, Fortran90, or C. It provides differentiation in the following modes: tangent, vector tangent, adjoint, and vector adjoint.
NEWS OF THE YEAR: - Continued development of multi-language capacity: AD of codes mixing Fortran and C - Continued front-end for C++ based on Clang - Experimental support for building Abs-Normal Form tangent of non-smooth codes

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

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/~lixx4611/contact_friction.html

FACTAS Team

5. New Software and Platforms

5.1. pisa

KEYWORDS: Electrical circuit - Stability
FUNCTIONAL DESCRIPTION: To minimise prototyping costs, the design of analog circuits is performed using computer-aided design tools which simulate the circuit's response as accurately as possible.

Some commonly used simulation tools do not impose stability, which can result in costly errors when the prototype turns out to be unstable. A thorough stability analysis is therefore a very important step in circuit design. This is where pisa is used.

pisa is a Matlab toolbox that allows designers of analog electronic circuits to determine the stability of their circuits in the simulator. It analyses the impedance presented by a circuit to determine the circuit's stability. When an instability is detected, pisa can estimate location of the unstable poles to help designers fix their stability issue.

RELEASE FUNCTIONAL DESCRIPTION: First version

- Authors: Adam Cooman, David Martinez Martinez, Fabien Seyfert and Martine Olivi
- Contact: Fabien Seyfert
- Publications: Model-Free Closed-Loop Stability Analysis: A Linear Functional Approach - On Transfer Functions Realizable with Active Electronic Components
- URL: https://project.inria.fr/pisa

5.2. PUMA-HF

PUMA-HF: Passive Uniform Matching
KEYWORD: Transfer functions
FUNCTIONAL DESCRIPTION: PUMA computes a passive rational 2-port filtering function presenting a reference impedance (i.e. 50 Ohm) at the first port, and the conjugate of the given load impedance within a frequency band at the second port.

- Authors: David Martinez Martinez, Adam Cooman, Martine Olivi and Fabien Seyfert
- Partners: Xlim - DGA-MI - CNES
- Contact: Fabien Seyfert
- Publication: Synthesis Method for Matching Filters
- URL: https://project.inria.fr/puma/

GAMMA3 Project-Team

4. New Software and Platforms

4.1. ABL4FLO

Adaptive Boundary Layer 4 FLOw

KEYWORDS: Boundary layers - Hybrid meshes

FUNCTIONAL DESCRIPTION: ABL4FLO is a module used to perform adaptive boundary layer mesh adaptation as required in RANS solutions. It is included in Feflo.a/AMG-Lib software. It is based on a constrained version of the cavity operators in order to generate automatically hybrid elements. If a metric surface is provided, the normal and tangential direction are simultaneously adapted.

- Participant: Adrien Loseille
- Contact: Adrien Loseille
- Publications: Recent Improvements on Cavity-Based Operators for RANS Mesh Adaptation - Unstructured Mesh Generation and Adaptation - Robust Boundary Layer Mesh Generation
- URL: https://pyamg.saclay.inria.fr/

4.2. AMA4FLO

Anisotropic Mesh Adaptation 4 FLOw

KEYWORDS: 3D - Mesh adaptation

FUNCTIONAL DESCRIPTION: AMA4Flo is part of Feflo.a which is a robust anisotropic local remeshing software. It is intended for scientific computing with primary applications in aerodynamics and spatial studies. Surface and volume mesh adaptation are handled in a coupled-way. It also includes : - Boundary layers mesh generation for RANS simulations, - CAD re-projection and discrete surface remeshing, with - Hybrid mesh generation for boundary-layers - High-quality quasi-structured grids for complex geometries and complex corners: multi-normals, normals deactivation, ... - Highly anisotropic mesh adaptation, ratios up to 1 million are handled - Anisotropic/Boundary-layer coupling for supersonic shock/boundary layer interaction

The boundary layer module alone (abl4flo) is registered with the APP under nbr. IDDN. FR.001. 080032. 00.S.P.2012. 000.10000

initially, AMA4FLO was mainly focused on Computational Fluid Dynamics (4 FLOw), but it is now sed in many applications areas: seismic, reservoir engineering, spatial, hydrodynamics, hemodynamics, ...

- Participant: Adrien Loseille
- Contact: Adrien Loseille
- Publications: Very High Order Anisotropic Metric-Based Mesh Adaptation in 3D - Computational and Experimental Assessment of Models for the First AIAA Sonic Boom Prediction Workshop Using Adaptive High Fidelity CFD methods - Unique cavity-based operator and hierarchical domain partitioning for fast parallel generation of anisotropic meshes - Unstructured Mesh Generation and Adaptation - A Decade of Progress on Anisotropic Mesh Adaptation for Computational Fluid Dynamics - Metric-orthogonal Anisotropic Mesh Generation - Sonic Boom Assessment of a Hypersonic Transport Vehicle with Advanced Numerical Methods
- URL: https://pyamg.saclay.inria.fr/

4.3. BL2D

KEYWORDS: Abstraction - Meshing - Isotropic - Anisotropic - Delaunay - Mesher - Mesh

FUNCTIONAL DESCRIPTION: This software package stems from a former one called BL2D-V1. The meshing method is of controled Delaunay type, isotropic or anisotropic. The internal point generation follows a frontal logic, and their connection is realised as in a classical Delaunay approach. Quadrilaterals are obtained by a pairing process. The direct construction of degree 2 element has been made possible via the control of the domain boundary mesh, in order to ensure the desired compatibility. The boundary middle nodes are located according to the curvilinear abscissa. The internal middle nodes are, by default, at the middle of the corresponding edges.

RELEASE FUNCTIONAL DESCRIPTION: Par rapport à la version V1, il offre de nombreuses possibilités nouvelles : méthode frontale, triangles quadratiques courbes, quadrilatères de degré 1ou 2, frontières déformables, allocation dynamique de mémoire, etc

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: http://pages.saclay.inria.fr/patrick.laug/logiciels/logiciels.html

4.4. BL2D-ABAQ

KEYWORDS: Anisotropic - Delaunay - Automatic mesher - Meshing - Mesher - Mesh

FUNCTIONAL DESCRIPTION: The meshing method is the same as BL2D in an adaptive process. An a posteriori error estimation of a solution at the nodes of the current mesh results in a size map. A new mesh staisfying these size specifications (made continuous is built, and the solution is interpolated on the new mesh.

- Participants: Abel Cherouat, Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: http://pages.saclay.inria.fr/patrick.laug/logiciels/logiciels.html

4.5. BLGEOL

KEYWORDS: Automatic mesher - Geologic structure - Meshing - Mesher - Mesh

FUNCTIONAL DESCRIPTION: BLGEOL-V1 software can generate hex-dominant meshes of geologic structures complying with different geometric constraints: surface topography (valleys, reliefs, rivers), geologic layers and underground workings. First, a reference 2D domain is obtained by projecting all the line constraints into a horizontal plane. Different size specifications are given for rivers, outcrop lines and workings. Using an adaptive methodology, the size variation is bounded by a specified threshold in order to obtain a high quality quad-dominant mesh. Secondly, a hex-dominant mesh of the geological medium is generated by a vertical extrusion, taking into account the surfaces found (interfaces between two layers, top or bottom faces of underground workings). The generation of volume elements follows a global order established on the whole set of surfaces to ensure the conformity of the resulting mesh.

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: http://pages.saclay.inria.fr/patrick.laug/logiciels/logiciels.html

4.6. BLMOL

KEYWORDS: Mesher - Molecular surface - Meshing - Mesh

SCIENTIFIC DESCRIPTION: An increasingly important part of quantum chemistry is devoted to molecular surfaces. To model such a surface, each constituting atom is idealized by a simple sphere. Surface mesh generation techniques are then used either for visualization or for simulation, where mesh quality has a strong influence on solution accuracy. First, a boundary representation (B-rep) of the surface is obtained, i.e. a set of patches and the topological relations between them. Second, an appropriate parameterization and a metric map are computed for each patch. Third, meshes of the parametric domains are generated with respect to an induced metric map, using a combined advancing-front generalized-Delaunay approach. Finally these meshes are mapped onto the entire surface. Several application examples illustrate various capabilities of our method.

FUNCTIONAL DESCRIPTION: BLMOL is a molecular surface mesher.

- Participants: Houman Borouchaki and Patrick Laug
- Contact: Patrick Laug
- URL: http://pages.saclay.inria.fr/patrick.laug/logiciels/logiciels.html

4.7. BLSURF

KEYWORDS: Automatic mesher - Meshing - Mesher - Mesh
FUNCTIONAL DESCRIPTION: An indirect method for meshing parametric surfaces conforming to a user-specifiable size map is used. First, from this size specification, a Riemannian metric is defined so that the desired mesh is one with unit length edges with respect to the related Riemannian space (the so-called

- Participants: Houman Borouchaki and Patrick Laug
- Partner: Université de Technologie de Troyes
- Contact: Patrick Laug
- URL: http://pages.saclay.inria.fr/patrick.laug/logiciels/logiciels.html

4.8. FEFLOA-REMESH

KEYWORDS: Scientific calculation - Anisotropic - Mesh adaptation
FUNCTIONAL DESCRIPTION: FEFLOA-REMESH is intended to generate adapted 2D, surface and volume meshes by using a unique cavity-based operator. The metric-aligned or metric-orthogonal approach is used to generate high quality surface and volume meshes independently of the anisotropy involved.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Adrien Loseille
- URL: https://www.rocq.inria.fr/gamma/Adrien.Loseille/index.php?page=softwares

4.9. GAMANIC 3D

KEYWORDS: Tetrahedral mesh - Delaunay - Anisotropic size and direction control - Automatic mesher
FUNCTIONAL DESCRIPTION: GAMANIC3D is a volume mesher governed by a (anisotropic) size and directional specification metric field.

- Participants: Adrien Loseille, Éric Saltel, Frédéric Alauzet, Frederic Hecht, Houman Borouchaki and Paul Louis George
- Contact: Paul Louis Georges
- URL: http://www.meshgems.com/volume-meshing.html

4.10. GAMHIC 3D

KEYWORDS: Tetrahedral mesh - Delaunay - Isotropic - Automatic mesher
FUNCTIONAL DESCRIPTION: GAMHIC3D is a volume mesher governed by a (isotropic) size specification metric field.

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

4.11. GHS3D

KEYWORDS: Tetrahedral mesh - Delaunay - Automatic mesher

FUNCTIONAL DESCRIPTION: GHS3D is an automatic volume mesher

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

4.12. HEXOTIC

KEYWORDS: 3D - Mesh generation - Meshing - Unstructured meshes - Octree/Quadtree - Multi-threading - GPGPU - GPU
FUNCTIONAL DESCRIPTION: Input: a triangulated surface mesh and an optional size map to control the size of inner elements.

Output: a fully hexahedral mesh (no hybrid elements), valid (no negative jacobian) and conformal (no dangling nodes) whose surface matches the input geometry.

The software is a simple command line that requires no knowledge on meshing. Its arguments are an input mesh and some optional parameters to control elements sizing, curvature and subdomains as well as some features like boundary layers generation.

- Participant: Loïc Maréchal
- Partner: Distene
- Contact: Loïc Maréchal
- URL: https://team.inria.fr/gamma3/project-presentation/gamma-software/hexotic/

4.13. Nimbus 3D

KEYWORDS: Surface reconstruction - Point cloud
FUNCTIONAL DESCRIPTION: Nimbus3D is a surface reconstruction method piece of software

- Participants: Houman Borouchaki and Paul Louis George
- Contact: Paul Louis George
- URL: http://www.meshgems.com/volume-meshing.html

4.14. VIZIR

Interactive visualization of hybrid, curbed and high-order mesh and solution
KEYWORD: Mesh
FUNCTIONAL DESCRIPTION: Vizir is a light, simple and interactive mesh visualization software, including : (i) A curved meshes visualizator: it handles high order elements and solutions, (ii) Hybrid elements mesh visualization (pyramids, prisms, hexahedra), (iii) Solutions visualization : clip planes, capping, iso-lines, iso-surfaces.

- Participants: Adrien Loseille and Rémi Feuillet
- Contact: Adrien Loseille
- Publication: Vizir: High-order mesh and solution visualization using OpenGL 4.0 graphic pipeline
- URL: http://vizir.inria.fr

4.15. Wolf

KEYWORD: Scientific calculation

FUNCTIONAL DESCRIPTION: Numerical solver for the Euler and compressible Navier-Stokes equations with turbulence modelling. ALE formulation for moving domains. Modules of interpolation, mesh optimisation and moving meshes. Wolf is written in C++, and may be later released as an opensource library. FELiScE was registered in July 2014 at the Agence pour la Protection des Programmes under the Inter Deposit Digital Number IDDN.FR.001.340034.000.S.P.2014.000.10000.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html#Wolf-Nsc

4.16. Wolf-Bloom

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-Bloom is a structured boundary layer mesh generator using a pushing approach. It start from an existing volume mesh and insert a structured boundary layer by pushing the volume mesh. The volume mesh deformation is solved with an elasticity analogy. Mesh-connectivity optimizations are performed to control volume mesh element quality.

- Participants: Adrien Loseille, David Marcum and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

4.17. Wolf-Elast

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-Elast is a linear elasticity solver using the P1 to P3 Finite-Element method. The Young and Poisson coefficient can be parametrized. The linear system is solved using the Conjugate Gradient method with the LUSGS preconditioner.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

4.18. Wolf-Interpol

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-Interpol is a tool to transfer scalar, vector and tensor fields from one mesh to another one. Polynomial interpolation (from order 2 to 4) or conservative interpolation operators can be used. Wolf-Interpol also extract solutions along lines or surfaces.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

4.19. Wolf-MovMsh

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-MovMsh is a moving mesh algorithm coupled with mesh-connectivity optimization. Mesh deformation is computed by means of a linear elasticity solver or a RBF interpolation. Smoothing and swapping mesh optimization are performed to maintain good mesh quality. It handles rigid bodies or deformable bodies, and also rigid or deformable regions of the domain. High-order meshes are also handled

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Paul Louis George
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

4.20. Wolf-Nsc

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-Nsc is numerical flow solver solving steady or unsteady turbulent compressible Euler and Navier-Stokes equations. The available turbulent models are the Spalart-Almaras and the Menter SST k-omega. A mixed finite volume - finite element numerical method is used for the discretization. Second order spatial accuracy is reached thanks to MUSCL type methods. Explicit or implicit time integration are available. It also resolved dual (adjoint) problem and compute error estimate for mesh adaptation.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

4.21. Wolf-Spyder

KEYWORD: Scientific calculation
FUNCTIONAL DESCRIPTION: Wolf-Spyder is a metric-based high-order mesh quality optimizer using vertex smoothing and edge/face swapping.

- Participants: Adrien Loseille and Frédéric Alauzet
- Contact: Frédéric Alauzet
- URL: http://pages.saclay.inria.fr/frederic.alauzet/code_eng.html

GEOSTAT Project-Team

6. New Software and Platforms

6.1. Fluex

KEYWORDS: Signal - Signal processing
SCIENTIFIC DESCRIPTION: Fluex is a package consisting of the Microcanonical Multiscale Formalism for 1D, 2D 3D and 3D+t general signals.
FUNCTIONAL DESCRIPTION: Fluex is a C++ library developed under Gforge. Fluex is a library in nonlinear signal processing. Fluex is able to analyze turbulent and natural complex signals, Fluex is able to determine low level features in these signals that cannot be determined using standard linear techniques.

- Participants: Hussein Yahia and Rémi Paties
- Contact: Hussein Yahia
- URL: http://fluex.gforge.inria.fr/

6.2. FluidExponents

KEYWORDS: Signal processing - Wavelets - Fractal - Spectral method - Complexity
FUNCTIONAL DESCRIPTION: FluidExponents is a signal processing software dedicated to the analysis of complex signals displaying multiscale properties. It analyzes complex natural signals by use of nonlinear methods. It implements the multifractal formalism and allows various kinds of signal decomposition and reconstruction. One key aspect of the software lies in its ability to evaluate key concepts such as the degree of impredictability around a point in a signal, and provides different kinds of applications. The software can be used for times series or multidimensional signals.

- Participants: Antonio Turiel and Hussein Yahia
- Contact: Hussein Yahia
- URL: svn+ssh://fluidexponents@scm.gforge.inria.fr/svn/fluidexponents/FluidExponents

6.3. classifemo

KEYWORDS: Classification - Audio
FUNCTIONAL DESCRIPTION: Classifies vocal audio signals. Classifemo extracts characteristics from vocal audio signals. These characteristics are extracted from signals of different type: initially these were emotion databases, but it can also process signals recorded from patients with motor speach disorders. The software can train usual classifiers (SVM, random forests, etc) on these databases as well as classify new signals.

- Participants: Khalid Daoudi and Nicolas Brodu
- Contact: Khalid Daoudi
- URL: https://allgo.inria.fr/app/emotionclassifierprototype

6.4. superres

Super-Resolution of multi-spectral and multi-resolution images
KEYWORD: Multiscale
SCIENTIFIC DESCRIPTION: This resolution enhancement method is designed for multispectral and multiresolution images, such as these provided by the Sentinel-2 satellites (but not only). Starting from the highest resolution bands, band-dependent information (reflectance) is separated from information that is common to all bands (geometry of scene elements). This model is then applied to unmix low-resolution bands, preserving their reflectance, while propagating band-independent information to preserve the sub-pixel details.

FUNCTIONAL DESCRIPTION: This super-resolution software for multi-spectral images consists of: - A core C++ library, which can be used directly - A Python module interface to this library - A Java JNI interface to the library - An end-user Python script for super-resolving Sentinel-2 images - An end-user plugin for the widely used SNAP software of the ESA.

- Participant: Nicolas Brodu
- Contact: Nicolas Brodu
- URL: http://nicolas.brodu.net/recherche/superres/index.html

6.5. EdgeReconstruct

Edge Reconstruction With UPM Manifold
KEYWORDS: 2D - Fractal - Signal processing
FUNCTIONAL DESCRIPTION: EdgeReconstruct is a software that reconstructs a complex signal from the computation of most unpredictible points in the framework of the Microcanonical Multifractal Formalism. The quality of the reconstruction is also evaluated. The software is a companion of a paper published in 2013: https://hal.inria.fr/hal-00924137.

- Contact: Suman Kumar Maji
- URL: https://geostat.bordeaux.inria.fr/index.php/downloads.html

6.6. ProximalDenoising

KEYWORDS: 2D - Image filter - Filtering - Minimizing overall energy - Noise - Signal processing - Image reconstruction - Image processing
SCIENTIFIC DESCRIPTION: Image filtering is contemplated in the form of a sparse minimization problem in a non-convex setting. Given an input image I, one seeks to compute a denoised output image u such that u is close to I in the L2 norm. To do so, a minimization term is added which favors sparse gradients for output image u. Imposing sparse gradients lead to a non-convex minimization term: for instance a pseudo-norm Lp with $0 < p < 1$ or a Cauchy or Welsh function. Half-quadratic algorithm is used by adding a new variable in the minimization functionnal which leads to two sub-problems, the first sub-problem is non-convex and solved by use of proximal operators. The second sub-problem can be written in variational form, and is best solved in Fourier space: it takes the form of a deconvolution operator whose kernel can be approximated by a finite sum of separable filters. This solution method produces excellent computation times even on big images.
FUNCTIONAL DESCRIPTION: Use of proximal and non quadratic minimization. GPU implementation.

RELEASE FUNCTIONAL DESCRIPTION: This software implements H. Badri PhD thesis results.

- Authors: Marie Martin, Chiheb Sakka, Hussein Yahia, Nicolas Brodu, Gabriel Augusto Zebadua Garcia and Khalid Daoudi
- Partner: Innovative Imaging Solutions I2S
- Contact: Hussein Yahia
- URL: https://gitlab.inria.fr/marmarti/i2s_geostat_C

I4S Project-Team (section vide)

INOCS Project-Team

6. New Software and Platforms

6.1. HappyChic-ApproPick

KEYWORDS: Operational research - Optimization - Java
FUNCTIONAL DESCRIPTION: This software is a prototype developed for the bilateral contract with the company HappyChic. This software is a solver for an integrated warehouse order picking problem with manual picking operations. More precisely, the following problems are solved: (1) the assignment of references to storage positions, based on the iterative solving of minimum cost flow problems, (2) the division of clients orders into several parcels, respecting weight and size constraints, using a dynamic programming algorithm based on the split algorithm, (3) the batching of parcels into trolleys to perform picking tours, using a dynamic programming algorithm based on the split algorithm. The objective function is to minimize the total walking distance. This software is designed to deal with the large-sized industrial instances of HappyChic (considering hundreds of clients, thousands of positions and product references) in a short computation time (few minutes).

- Contact: Maxime Ogier

6.2. KEOLIS-MEDIATOUR

KEYWORDS: Operational research - Mathematical Optimization - Staff scheduling
FUNCTIONAL DESCRIPTION: This software is a prototype developed under a bilateral contract with the company Keolis. This software is a solver which aims to optimize the scheduling of mediation staff More precisely, for each member of the mediation staff working in a public transportation network, MEDIATOUR determines his/her schedule along the day, i.e. when and where he/she is present. Various operational constraints must be taken into account such as the coverage of the network. This software is designed to solve large-scale industrial instances (the subway network of Lille) in short computation times (less than 1 minute).

- Contact: Frédéric Semet

6.3. PARROT

Planning Adapter Performing ReRouting and Optimization of Timing
KEYWORDS: Decision aid - Railway - Scheduling
FUNCTIONAL DESCRIPTION: This is a decision support system addressing the problem of the rescheduling railway schedules on the Belgian network when maintenance operations are planned in the short term (2-3 weeks in advance). The deliverable is a software tool that will take as input: (1) the schedules initially planned for the different trains, (2) the initial routes of the trains, (3) maintenance operations / changes of elements in the form of constraints (unavailable routes etc.). He then provides in output: (1) the new train schedule, (2) the new routing of the fleet. The modifications must respect the constraints corresponding to the operations of maintenance. For example, in some cases it is common to leave at least a few minutes interval between two trains using the same track in the station. This constraint must then be propagated if a maintenance operation delays the arrival of a train. New schedules and routings have to be created following a specific goal. Changes made to schedules and routings must minimize: (1) variations on the time spent at the station, (2) the number of partially canceled trains (additional correspondence (s) or stations that are no longer served), (2) the number of fully canceled trains (no stations served).

- Contact: Martine Labbe

MATHERIALS Project-Team

5. New Software and Platforms

5.1. simol

KEYWORDS: Molecular simulation - Quantum chemistry - Statistical physics - C++ - OpenMP
FUNCTIONAL DESCRIPTION: Molecular simulation software written in C++

- Contact: Gabriel Stoltz

MATHRISK Project-Team

6. New Software and Platforms

6.1. PREMIA

KEYWORDS: Financial products - Computational finance - Option pricing
SCIENTIFIC DESCRIPTION: The Premia project keeps track of the most recent advances in the field of computational finance in a well-documented way. It focuses on the implementation of numerical analysis techniques for both probabilistic and deterministic numerical methods. An important feature of the platform Premia is the detailed documentation which provides extended references in option pricing.

Premia is thus a powerful tool to assist Research and Development professional teams in their day-to-day duty. It is also a useful support for academics who wish to perform tests on new algorithms or pricing methods without starting from scratch.

Besides being a single entry point for accessible overviews and basic implementations of various numerical methods, the aim of the Premia project is: 1 - to be a powerful testing platform for comparing different numerical methods between each other, 2 - to build a link between professional financial teams and academic researchers, 3 - to provide a useful teaching support for Master and PhD students in mathematical finance.
FUNCTIONAL DESCRIPTION: Premia is a software designed for option pricing, hedging and financial model calibration.

- Participants: Agnes Sulem, Antonino Zanette, Aurélien Alfonsi, Benjamin Jourdain, Jérôme Lelong and Bernard Lapeyre
- Partners: Inria - Ecole des Ponts ParisTech - Université Paris-Est
- Contact: Agnes Sulem
- URL: http://www.premia.fr

6.2. Platforms

6.2.1. Development of the quantitative platform Premia in 2018

Premia 20 has been delivered to the Consortium Premia on March 12th. It contains the following new algorithms :

6.2.1.1. Optimal Trade Execution, Risk Management, Insurance

- Optimal Execution Under Jump Models For Uncertain Price Impact. S.Moazeni, T.F.Coleman, Y.Li
The Journal of Computational Finance. Vol. 18, Issue 3, 2015.
- Nested Monte Carlo for Risk Margin computation. L.A. Abbas-Turki, S.Crepey, B.Diallo.
- Efficient Estimation of Sensitivities for Counterparty Credit Risk with the Finite Difference Monte-Carlo Method. C. S.L. de Graaf, D.Kandhai, P.M.A.Sloot.
The Journal of Computational Finance, Volume 21, Issue 1, 2017.
- Nested Simulation in Portfolio Risk Measurement. M.B.Gordy, S.Juneja
Management Science, Vol 56, Issue 10, 2010
- Spectral methods for the calculation of risk measures for variable annuity guaranteed benefits. R. Feng, H.W. Volkmer
ASTIN Bull., 44(3), 2014
- Fast computation of risk measures for variable annuities with additional earnings by conditional moment matching. N. Privault X.Wei
ASTIN Bull., 48(1):171–196, 2018.

6.2.1.2. Equity Derivatives

- Pricing under Rough volatility. C. Bayer, P.Friz, J. Gatheral
  Quantitative Finance, Vol. 16, No. 6, 887-904, 2016.
- Hybrid scheme for Brownian semistationary processes. M. Bennedsen, A. Lunde, M.S.Pakkanen
  Finance and Stochastics 21(4), 931–965, 2017.
- Antithetic multilevel Monte Carlo estimation for multi-dimensional SDEs without Lévy area simulation. M. B. Giles and L. Szpruch
  The Annals of Applied Probability, Vol. 24, No. 4, 2014
- Fourier transform algorithms for pricing and hedging discretely sampled exotic variance products and volatility derivatives under additive processes. W. Zheng and Y. K. Kwok
  The Journal of Computational Finance, Volume 18, Issue 2, 2014.
- Efficient Solution of Backward Jump-Diffusion PIDEs with Splitting and Matrix Exponentials. A.Iktin
  The Journal of Computational Finance, Volume 19, Issue 3, 2016
- High-Order Splitting Methods for Forward PDEs and PIDEs. A.Iktin
  International Journal of Theoretical and Applied Finance, 18(5), 2015
- Pricing Bullet option on local volatility model using GPU L.A. Abbas-Turki
- Pricing Bermudan Options via Multilevel Approximation Methods. D. Belomestny, F. Dickmann, T.Nagapetyan.
  Siam J. Financial Math., Volume 6, 2015.
- Pricing CIR yield options by conditional moment matching. A. Prayoga N. Privault
  Asia-Pacific Financial Markets, 24:19–38, 2017

We benefit from the help of the engineer Pierre-Guillaume Raverdy.

MCTAO Project-Team

6. New Software and Platforms

6.1. Hampath

KEYWORDS: Optimal control - Second order conditions - Differential homotopy - Ordinary differential equations

FUNCTIONAL DESCRIPTION: Hampath is a software developped to solve optimal control problems by a combination of Hamiltonian et path following methods. Hampath includes shooting and computation of conjugate points. It is an evolution of the software cotcot (apo.enseeiht.fr/cotcot). It has a Fortran kernel, uses Tapenade (www-sop.inria.fr/tropics/tapenade.html) for automatic differentiation and has a Matlab interface.

- Participants: Jean-Baptiste Caillau, Joseph Gergaud and Olivier Cots
- Contact: Jean-Baptiste Caillau
- URL: http://www.hampath.org

MEMPHIS Project-Team

6. New Software and Platforms

6.1. COCOFLOW

KEYWORDS: 3D - Elasticity - MPI - Compressible multimaterial flows
FUNCTIONAL DESCRIPTION: The code is written in fortran 95 with a MPI parallelization. It solves equations of conservation modeling 3D compressible flows with elastic models as equation of state.

- Contact: Florian Bernard
- URL: https://gforge.inria.fr/projects/cocoflow

6.2. KOPPA

Kinetic Octree Parallel PolyAtomic
FUNCTIONAL DESCRIPTION: KOPPA is a C++/MPI numerical code solving a large range of rarefied flows from external to internal flows in 1D, 2D or 3D. Different kind of geometries can be treated such as moving geometries coming from CAO files or analytical geometries. The models can be solved on Octree grids with dynamic refinement.

- Participant: Florian Bernard
- Contact: Florian Bernard
- URL: https://git.math.cnrs.fr/gitweb/?p=plm/fbernard/KOPPA.git;a=summary

6.3. NaSCar

Navier-Stokes Cartesian
KEYWORDS: HPC - Numerical analyse - Fluid mechanics - Langage C - PETSc
SCIENTIFIC DESCRIPTION: NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.
FUNCTIONAL DESCRIPTION: This code is devoted to solve 3D-flows in around moving and deformable bodies. The incompressible Navier-Stokes equations are solved on fixed grids, and the bodies are taken into account thanks to penalization and/or immersed boundary methods. The interface between the fluid and the bodies is tracked with a level set function or in a Lagrangian way. The numerical code is fully second order (time and space). The numerical method is based on projection schemes of Chorin-Temam's type. The code is written in C language and use Petsc library for the resolution of large linear systems in parallel.

NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.

- Participant: Michel Bergmann
- Contact: Michel Bergmann
- URL: https://gforge.inria.fr/projects/nascar/

6.4. NS-penal

Navier-Stokes-penalization
KEYWORDS: 3D - Incompressible flows - 2D
FUNCTIONAL DESCRIPTION: The software can be used as a black box with the help of a data file if the obstacle is already proposed. For new geometries the user has to define them. It can be used with several boundary conditions (Dirichlet, Neumann, periodic) and for a wide range of Reynolds numbers.

- Partner: Université de Bordeaux
- Contact: Charles-Henri Bruneau

MEPHYSTO-POST Team (section vide)

MINGUS Project-Team

6. New Software and Platforms

6.1. Selalib

SEmi-LAgrangian LIBrary
KEYWORDS: Plasma physics - Semilagrangian method - Parallel computing - Plasma turbulence
SCIENTIFIC DESCRIPTION: The objective of the Selalib project (SEmi-LAgrangian LIBrary) is to develop a well-designed, organized and documented library implementing several numerical methods for kinetic models of plasma physics. Its ultimate goal is to produce gyrokinetic simulations.

Another objective of the library is to provide to physicists easy-to-use gyrokinetic solvers, based on the semi-lagrangian techniques developed by Eric Sonnendrücker and his collaborators in the past CALVI project. The new models and schemes from TONUS are also intended to be incorporated into Selalib.
FUNCTIONAL DESCRIPTION: Selalib is a collection of modules conceived to aid in the development of plasma physics simulations, particularly in the study of turbulence in fusion plasmas. Selalib offers basic capabilities from general and mathematical utilities and modules to aid in parallelization, up to pre-packaged simulations.

- Partners: Max Planck Insitute - Garching - Université de Strasbourg
- Contact: Philippe Helluy
- URL: http://selalib.gforge.inria.fr/

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/

MODAL Project-Team

6. New Software and Platforms

6.1. MixtComp

Mixture Computation

KEYWORDS: Clustering - Statistics - Missing data

FUNCTIONAL DESCRIPTION: MixtComp (Mixture Computation) is a model-based clustering package for mixed data originating from the Modal team (Inria Lille). It has been engineered around the idea of easy and quick integration of all new univariate models, under the conditional independence assumption. New models will eventually be available from researches, carried out by the Modal team or by other teams. Currently, central architecture of MixtComp is built and functionality has been field-tested through industry partnerships. Three basic models (Gaussian, multinomial, Poisson) are implemented, as well as two advanced models (Ordinal and Rank). MixtComp has the ability to natively manage missing data (completely or by interval). MixtComp is used as an R package, but its internals are coded in C++ using state of the art libraries for faster computation.

- Participants: Christophe Biernacki, Étienne Goffinet, Matthieu Marbac-Lourdelle, Quentin Grimonprez, Serge Iovleff and Vincent Kubicki
- Contact: Christophe Biernacki
- URL: https://modal-research.lille.inria.fr/BigStat

6.2. BlockCluster

Block Clustering

KEYWORDS: Statistic analysis - Clustering package

SCIENTIFIC DESCRIPTION: Simultaneous clustering of rows and columns, usually designated by biclustering, co-clustering or block clustering, is an important technique in two way data analysis. It consists of estimating a mixture model which takes into account the block clustering problem on both the individual and variables sets. The blockcluster package provides a bridge between the C++ core library and the R statistical computing environment. This package allows to co-cluster binary, contingency, continuous and categorical data-sets. It also provides utility functions to visualize the results. This package may be useful for various applications in fields of Data mining, Information retrieval, Biology, computer vision and many more.

FUNCTIONAL DESCRIPTION: BlockCluster is an R package for co-clustering of binary, contingency and continuous data based on mixture models.

- Participants: Christophe Biernacki, Gilles Celeux, Parmeet Bhatia, Serge Iovleff, Vincent Brault and Vincent Kubicki
- Partner: Université de Technologie de Compiègne
- Contact: Serge Iovleff
- URL: http://cran.r-project.org/web/packages/blockcluster/index.html

6.3. CloHe

Clustering of Mixed data

KEYWORDS: Classification - Clustering - Missing data

FUNCTIONAL DESCRIPTION: Software of classification for mixed data with missing values with application to multispectral satellite image time-series

- Partners: CNRS - INRA
- Contact: Serge Iovleff
- URL: https://modal.lille.inria.fr/CloHe/

6.4. PACBayesianNMF

KEYWORDS: Statistics - Machine learning
FUNCTIONAL DESCRIPTION: Implementing NMF with a PAC-Bayesian approach relying upon block gradient descent

- Participants: Benjamin Guedj and Astha Gupta
- Contact: Benjamin Guedj
- URL: https://github.com/astha736/PACbayesianNMF

6.5. pycobra

KEYWORDS: Statistics - Data visualization - Machine learning
SCIENTIFIC DESCRIPTION: pycobra is a python library for ensemble learning, which serves as a toolkit for regression, classification, and visualisation. It is scikit-learn compatible and fits into the existing scikit-learn ecosystem.

pycobra offers a python implementation of the COBRA algorithm introduced by Biau et al. (2016) for regression.

Another algorithm implemented is the EWA (Exponentially Weighted Aggregate) aggregation technique (among several other references, you can check the paper by Dalalyan and Tsybakov (2007).

Apart from these two regression aggregation algorithms, pycobra implements a version of COBRA for classification. This procedure has been introduced by Mojirsheibani (1999).

pycobra also offers various visualisation and diagnostic methods built on top of matplotlib which lets the user analyse and compare different regression machines with COBRA. The Visualisation class also lets you use some of the tools (such as Voronoi Tesselations) on other visualisation problems, such as clustering.

- Participants: Bhargav Srinivasa Desikan and Benjamin Guedj
- Contact: Benjamin Guedj
- Publication: Pycobra: A Python Toolbox for Ensemble Learning and Visualisation
- URL: https://github.com/bhargavvader/pycobra

6.6. STK++

Statistical ToolKit
KEYWORDS: Statistics - Linear algebra - Framework - Learning - Statistical learning
FUNCTIONAL DESCRIPTION: STK++ (Statistical ToolKit in C++) is a versatile, fast, reliable and elegant collection of C++ classes for statistics, clustering, linear algebra, arrays (with an API Eigen-like), regression, dimension reduction, etc. The library is interfaced with lapack for many linear algebra usual methods. Some functionalities provided by the library are available in the R environment using rtkpp and rtkore.

STK++ is suitable for projects ranging from small one-off projects to complete data mining application suites.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: http://www.stkpp.org

6.7. rtkore

STK++ core library integration to R using Rcpp
KEYWORDS: C++ - Data mining - Clustering - Statistics - Regression
FUNCTIONAL DESCRIPTION: STK++ (http://www.stkpp.org) is a collection of C++ classes for statistics, clustering, linear algebra, arrays (with an Eigen-like API), regression, dimension reduction, etc. The integration of the library to R is using Rcpp. The rtkore package includes the header files from the STK++ core library. All files contain only templated classes or inlined functions. STK++ is licensed under the GNU LGPL version 2 or later. rtkore (the stkpp integration into R) is licensed under the GNU GPL version 2 or later. See file LICENSE.note for details.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/rtkore/index.html

6.8. MixAll

Clustering using Mixture Models
KEYWORDS: Clustering - Clustering package - Generative Models
FUNCTIONAL DESCRIPTION: MixAll is a model-based clustering package for modelling mixed data sets. It has been engineered around the idea of easy and quick integration of any kind of mixture models for any kind of data, under the conditional independence assumption. Currently five models (Gaussian mixtures, categorical mixtures, Poisson mixtures, Gamma mixtures and kernel mixtures) are implemented. MixAll has the ability to natively manage completely missing values when assumed as random. MixAll is used as an R package, but its internals are coded in C++ as part of the STK++ library (www.stkpp.org) for faster computation.

- Participant: Serge Iovleff
- Partner: Université Lille 1
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/MixAll/

6.9. simerge

Statistical Inference for the Management of Extrem Risks, Genetics and Global epidemiology
KEYWORD: Biclustering
FUNCTIONAL DESCRIPTION: Allows to perform Co-Clustering on binary (Bernoulli) and counting variables (Poisson) using co-variables.

- Partner: Inria
- Contact: Serge Iovleff

6.10. Platforms

6.10.1. MASSICCC Platform

MASSICCC is a demonstration platform giving access through a SaaS (service as a software) concept to data analysis libraries developed at Inria. It allows to obtain results either directly through a website specific display (specific and interactive visual outputs) or through an R data object download. It started in October 2015 for two years and is common to the Modal team (Inria Lille) and the Select team (Inria Saclay). In 2016, two packages have been integrated: Mixmod and MixtComp (see the specific section about MixtComp). In 2017, the BlockCluster package has been integrated and also a particular attention to provide meaningful graphical outputs (for Mixmod, MixtComp and BlockCluster) directly in the web platform itself has led to some specific developments.

MOKAPLAN Project-Team

5. New Software and Platforms

5.1. ALG2

FUNCTIONAL DESCRIPTION: ALG2 for Monge Mean-Field Games, Monge problem and Variational problems under divergence constraint. A generalisation of the ALG2 algorithm has been implemented in FreeFem++.

- Contact: Jean-David Benamou
- URL: https://team.inria.fr/mokaplan/augmented-lagrangian-simulations/

5.2. Mokabajour

FUNCTIONAL DESCRIPTION: We design a software resolving the following inverse problem: define the shape of a mirror which reflects the light from a source to a defined target, distribution and support of densities being prescribed. Classical applications include the conception of solar oven, public lightning, car headlights… Mathematical modeling of this problem, related to the optimal transport theory, takes the form of a nonlinear Monge-Ampere type PDE. The numerical resolution of these models remained until recently a largely open problem. MOKABAJOUR project aims to develop, using algorithms invented especially at Inria and LJK, a reflector design software more efficient than geometrical methods used so far. The final step is to realize and physically test prototype reflectors.

- Participants: Boris Thibert, Jean-David Benamou and Quentin Mérigot
- Contact: Jean-David Benamou
- URL: https://project.inria.fr/mokabajour/

NACHOS Project-Team

5. New Software and Platforms

5.1. DIOGENeS

DIscOntinuous GalErkin Nanoscale Solvers
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin - Computational nanophotonics
FUNCTIONAL DESCRIPTION: The DIOGENeS software suite provides several tools and solvers for the numerical resolution of light-matter interactions at nanometer scales. A choice can be made between time-domain (DGTD solver) and frequency-domain (HDGFD solver) depending on the problem. The available sources, material laws and observables are very well suited to nano-optics and nano-plasmonics (interaction with metals). A parallel implementation allows to consider large problems on dedicated cluster-like architectures.

- Authors: Stéphane Lanteri, Nikolai Schmitt, Alexis Gobe and Jonathan Viquerat
- Contact: Stéphane Lanteri
- URL: https://diogenes.inria.fr/

5.2. GERShWIN

discontinuous GalERkin Solver for microWave INteraction with biological tissues
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin - Computational bioelectromagnetics
FUNCTIONAL DESCRIPTION: GERShWIN is based on a high order DG method formulated on unstructured tetrahedral meshes for solving the 3D system of time-domain Maxwell equations coupled to a Debye dispersion model.

- Contact: Stéphane Lanteri
- URL: http://www-sop.inria.fr/nachos/index.php/Software/GERShWIN

5.3. HORSE

High Order solver for Radar cross Section Evaluation
KEYWORDS: High-Performance Computing - Computational electromagnetics - Discontinuous Galerkin
FUNCTIONAL DESCRIPTION: HORSE is based on a high order HDG (Hybridizable Discontinuous Galerkin) method formulated on unstructured tetrahedral and hybrid structured/unstructured (cubic/tetrahedral) meshes for the discretization of the 3D system of frequency-domain Maxwell equations, coupled to domain decomposition solvers.

- Contact: Stéphane Lanteri
- URL: http://www-sop.inria.fr/nachos/index.php/Software/HORSE

NANO-D Project-Team

5. New Software and Platforms

5.1. SAMSON

Software for Adaptive Modeling and Simulation Of Nanosystems
KEYWORDS: Bioinformatics - Simulation - Nanosystems - Structural Biology - Chemistry
SCIENTIFIC DESCRIPTION: Please refer to https://www.samson-connect.net
FUNCTIONAL DESCRIPTION: SAMSON is a software platform for real-time modelling and simulation of natural or artificial nanosystems. The objective is to make SAMSON a generic application for computer-aided design of nanosystems, similar to existing applications for macrosystem prototyping (CATIA, SolidWorks, etc.).

- Contact: Stéphane Redon
- URL: http://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 thedimensions 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 interction 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 Piuzzi 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 'exprtk' by Arash Partow (https://github.com/ArashPartow/exprtk)

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 'exprtk' by Arash Partow (https://github.com/ArashPartow/exprtk)

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 crystalic 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 avalaible 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 functionnalities. 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 alignes on xyz axes. The margen 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 margen 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 mojica2010modelisation. 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 Grudinin, 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 SAStbx 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. Ornate 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 Grudinin
- Contact: Sergey Grudinin
- 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 Edorh, 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/

NON-A POST Team

5. New Software and Platforms

5.1. ADHOMFI

Adaptive Homogeneous Filtering
KEYWORDS: Automatic differentiation - Filtering
FUNCTIONAL DESCRIPTION: allows to reconstruct a signal based on derivatives estimation and to filter high amplitude and wide frequencies spectrum perturbations.

- Contact: Denis Efimov

QUANTIC Project-Team (section vide)

RANDOPT Team

6. New Software and Platforms

6.1. COCO

COmparing Continuous Optimizers
KEYWORDS: Benchmarking - Numerical optimization - Black-box optimization - Stochastic optimization
SCIENTIFIC DESCRIPTION: COmparing Continuous Optimisers (COCO) is a tool for benchmarking algorithms for black-box optimisation. COCO facilitates systematic experimentation in the field of continuous optimization. COCO provides: (1) an experimental framework for testing the algorithms, (2) post-processing facilities for generating publication quality figures and tables, (3) LaTeX templates for scientific articles and HTML overview pages which present the figures and tables.

The COCO software is composed of two parts: (i) an interface available in different programming languages (C/C++, Java, Matlab/Octave, Python, external support for R) which allows to run and log experiments on several function test suites (unbounded noisy and noiseless single-objective functions, unbounded noiseless multiobjective problems, constrained problems) are provided (ii) a Python tool for generating figures and tables that can be looked at in every web browser and that can be used in the provided LaTeX templates to write scientific papers.
FUNCTIONAL DESCRIPTION: The Coco platform aims at supporting the numerical benchmarking of blackbox optimization algorithms in continuous domains. Benchmarking is a vital part of algorithm engineering and a necessary path to recommend algorithms for practical applications. The Coco platform releases algorithm developers and practitioners alike from (re-)writing test functions, logging, and plotting facilities by providing an easy-to-handle interface in several programming languages. The Coco platform has been developed since 2007 and has been used extensively within the “Blackbox Optimization Benchmarking (BBOB)” workshop series since 2009. Overall, 160+ algorithms and algorithm variants by contributors from all over the world have been benchmarked on the platform’s three supported test suites so far. The most recent extension towards bi-objective problems has been used for the BBOB-2016 workshop at GECCO and we are currently developing new test suites around large-scale and constrained optimization.

- Participants: Anne Auger, Asma Atamna, Dejan Tusar, Dimo Brockhoff, Marc Schoenauer, Nikolaus Hansen, Ouassim Ait Elhara, Raymond Ros, Tea Tusar, Thanh-Do Tran and Umut Batu
- Partners: TU Dortmund University - Charles University Prague - Jozef Stefan Institute (JSI)
- Contact: Dimo Brockhoff
- URL: https://github.com/numbbo/coco

6.2. CMA-ES

Covariance Matrix Adaptation Evolution Strategy
KEYWORDS: Numerical optimization - Black-box optimization - Stochastic optimization
SCIENTIFIC DESCRIPTION: The CMA-ES is considered as state-of-the-art in evolutionary computation and has been adopted as one of the standard tools for continuous optimisation in many (probably hundreds of) research labs and industrial environments around the world. The CMA-ES is typically applied to unconstrained or bounded constraint optimization problems, and search space dimensions between three and a hundred. The method should be applied, if derivative based methods, e.g. quasi-Newton BFGS or conjugate gradient, (supposedly) fail due to a rugged search landscape (e.g. discontinuities, sharp bends or ridges, noise, local optima, outliers). If second order derivative based methods are successful, they are usually faster than the CMA-ES: on purely convex-quadratic functions, f(x)=xTHx, BFGS (Matlabs function fminunc) is typically faster by a factor of about ten (in terms of number of objective function evaluations needed to reach a target function value, assuming that gradients are not available). On the most simple quadratic function f(x)=||x||2=xTx BFGS is faster by a factor of about 30.

FUNCTIONAL DESCRIPTION: The CMA-ES is an evolutionary algorithm for difficult non-linear non-convex black-box optimisation problems in continuous domain.

- Participant: Nikolaus Hansen
- Contact: Nikolaus Hansen
- URL: http://cma.gforge.inria.fr/cmaes_sourcecode_page.html

6.3. Platforms

6.3.1. New developments around COCO

There were two public releases of the COCO software this year including quite some new features that have also been used for the Blackbox Optimization Benchmarking workshop (BBOB) which was held in Kyoto, Japan during GECCO-2019.

The most important new features are updated, streamlined plots, a Python 3 compatible postprocessing module with a corresponding restructuring of the postprocessing code, the support for zip files in the postprocessing, a simplified example experiment script for beginners and a non-anytime example experiment for benchmarking budget-dependent algorithms, improved coverage of the continuous integration testing via CircleCI and AppVeyor, and finally and most-important from a practical perspective an archive with automatized download from all 200+ algorithm data sets available in the COCO data archive. Of these, 17 algorithm data sets have been made newly available in 2018 with four scientific papers being presented at the BBOB-2019 workshop.

In the background, there have been additional (preparational) activities, in particular due to the two Inria ADT projects “COCOpysuites” and “COCOpost”. The “COCOpysuites” project aimed at a rewriting of the experimental part of COCO in python to allow for an easier development, testing, and implementation of new test suites. The “COCOpost” project aimed at a complete rewrite of the python postprocessing with a focus on new, interactive plots and a clearer structure for improved maintenance. In addition, new test suites have been developed and implemented for large-scale, constrained, multiobjective, and mixed-integer optimization. All those extensions will be made available step-by-step to the scientific community after proper alpha- and beta-testing in the coming planned releases.

6.3.2. Developments within the CMA-ES library

The `pycma` library has not seen major changes, but overall 39 commits pushed for maintenance, bug-fixes and smaller improvements (roughly 1000 lines of code). An as of yet unpublished development has been the modularization of the data logger. A surrogate fitness model module with 969 lines of code has been developed and is already operative but has also not yet been released.

RAPSODI Project-Team

6. New Software and Platforms

6.1. Platform NS2DDV-M

`NS2DDV-M` is a Matlab code, developed by C. Calgaro Zotto, E. Creusé, and A. Mouton (CNRS research engineer at Université de Lille), for the simulation of homogeneous and inhomogeneous fluid flows by a combined Finite Volume-Finite Element method. The code is freely distributed, to allow for easy comparisons with concurrent codes on benchmark test-cases, and to promote new collaborations in the domain.

In 2018, a new version (v. 2.0) has been released, which contains a detailed documentation as well as some new functionalities, such as some post-processing tools and parallel computation capabilities.

REALOPT Project-Team

6. New Software and Platforms

6.1. BaPCod

A generic Branch-And-Price-And-Cut Code

KEYWORDS: Column Generation - Branch-and-Price - Branch-and-Cut - Mixed Integer Programming - Mathematical Optimization - Benders Decomposition - Dantzig-Wolfe Decomposition - Extended Formulation

FUNCTIONAL DESCRIPTION: BaPCod is a prototype code that solves Mixed Integer Programs (MIP) by application of reformulation and decomposition techniques. The reformulated problem is solved using a branch-and-price-and-cut (column generation) algorithms, Benders approaches, network flow and dynamic programming algorithms. These methods can be combined in several hybrid algorithms to produce exact or approximate solutions (primal solutions with a bound on the deviation to the optimum).

- Participants: Artur Alves Pessoa, Boris Detienne, Eduardo Uchoa Barboza, Franck Labat, François Clautiaux, Francois Vanderbeck, Halil Sen, Issam Tahiri, Michael Poss, Pierre Pesneau, Romain Leguay and Ruslan Sadykov
- Partners: Université de Bordeaux - CNRS - IPB - Universidade Federal Fluminense
- Contact: Francois Vanderbeck
- URL: https://wiki.bordeaux.inria.fr/realopt/pmwiki.php/Project/BaPCod

6.2. WineryPlanning

- Participants: Agnes Le Roux, Alexis Toullat, Francois Vanderbeck, Issam Tahiri and Ruslan Sadykov
- Contact: Francois Vanderbeck

6.3. ORTOJ

Operation Research Tools Under Julia

KEYWORDS: Modeling - Processing - Dashboard

FUNCTIONAL DESCRIPTION: This set of tools currently includes : 1) BlockJuMP.jl: extension of JuMP to model decomposable mathematical programs (using either Benders or Dantzig-Wolfe decomposition paradign) 2) Scanner.jl: a default data parser to ease the reading of the input data in the form that they are often encountered in operational research. 3) BenchmarkUtils.jl: Tools to ease the setup of numerical experiments to benchmark algorithmic feature performances. The test automation permits to quickly calibrate the parameters of an arbitrary algorithm control function.

- Participants: Francois Vanderbeck, Guillaume Marques, Issam Tahiri and Ruslan Sadykov
- Contact: Issam Tahiri

6.4. pmtool

KEYWORDS: Scheduling - Task scheduling - StarPU - Heterogeneity - GPGPU - Performance analysis

FUNCTIONAL DESCRIPTION: Analyse post-mortem the behavior of StarPU applications. Provide lower bounds on makespan. Study the performance of different schedulers in a simple context. Provide implementations of many scheduling algorithms from the literature

NEWS OF THE YEAR: Included many new algorithms, in particular online algorithms Better integration with StarPU by accepting .rec files as input

- Participant: Lionel Eyraud-Dubois
- Contact: Lionel Eyraud-Dubois
- Publications: Approximation Proofs of a Fast and Efficient List Scheduling Algorithm for Task-Based Runtime Systems on Multicores and GPUs - Fast Approximation Algorithms for Task-Based Runtime Systems
- URL: https://gitlab.inria.fr/eyrauddu/pmtool

6.5. Platforms

6.5.1. Bapcod

We have developed a stabilized Benders' decomposition in our generic library BapCod. This allowed to produce state-of-the-art results for an energy production planning.

SELECT Project-Team

5. New Software and Platforms

5.1. BlockCluster

Block Clustering
KEYWORDS: Statistic analysis - Clustering package
SCIENTIFIC DESCRIPTION: Simultaneous clustering of rows and columns, usually designated by biclustering, co-clustering or block clustering, is an important technique in two way data analysis. It consists of estimating a mixture model which takes into account the block clustering problem on both the individual and variables sets. The blockcluster package provides a bridge between the C++ core library and the R statistical computing environment. This package allows to co-cluster binary, contingency, continuous and categorical data-sets. It also provides utility functions to visualize the results. This package may be useful for various applications in fields of Data mining, Information retrieval, Biology, computer vision and many more.
FUNCTIONAL DESCRIPTION: BlockCluster is an R package for co-clustering of binary, contingency and continuous data based on mixture models.

- Participants: Christophe Biernacki, Gilles Celeux, Parmeet Bhatia, Serge Iovleff, Vincent Brault and Vincent Kubicki
- Partner: Université de Technologie de Compiègne
- Contact: Serge Iovleff
- URL: http://cran.r-project.org/web/packages/blockcluster/index.html

5.2. MASSICCC

Massive Clustering with Cloud Computing
KEYWORDS: Statistic analysis - Big data - Machine learning - Web Application
SCIENTIFIC DESCRIPTION: The web application let users use several software packages developed by Inria directly in a web browser. Mixmod is a classification library for continuous and categorical data. MixtComp allows for missing data and a larger choice of data types. BlockCluster is a library for co-clustering of data. When using the web application, the user can first upload a data set, then configure a job using one of the libraries mentioned and start the execution of the job on a cluster. The results are then displayed directly in the browser allowing for rapid understanding and interactive visualisation.
FUNCTIONAL DESCRIPTION: The MASSICCC web application offers a simple and dynamic interface for analysing heterogeneous data with a web browser. Various software packages for statistical analysis are available (Mixmod, MixtComp, BlockCluster) which allow for supervised and supervised classification of large data sets.

- Contact: Christophe Biernacki
- URL: https://massiccc.lille.inria.fr

5.3. Mixmod

Many-purpose software for data mining and statistical learning
KEYWORDS: Data mining - Classification - Mixed data - Data modeling - Big data
FUNCTIONAL DESCRIPTION: Mixmod is a free toolbox for data mining and statistical learning designed for large and highdimensional data sets. Mixmod provides reliable estimation algorithms and relevant model selection criteria.

It has been successfully applied to marketing, credit scoring, epidemiology, genomics and reliability among other domains. Its particularity is to propose a model-based approach leading to a lot of methods for classification and clustering.

Mixmod allows to assess the stability of the results with simple and thorough scores. It provides an easy-to-use graphical user interface (mixmodGUI) and functions for the R (Rmixmod) and Matlab (mixmodForMatlab) environments.

- Participants: Benjamin Auder, Christophe Biernacki, Florent Langrognet, Gérard Govaert, Gilles Celeux, Remi Lebret and Serge Iovleff
- Partners: CNRS - Université Lille 1 - LIFL - Laboratoire Paul Painlevé - HEUDIASYC - LMB
- Contact: Gilles Celeux
- URL: http://www.mixmod.org

SEQUEL Project-Team

6. New Software and Platforms

6.1. BAC

Bayesian Policy Gradient and Actor-Critic Algorithms
KEYWORDS: Machine learning - Incremental learning - Policy Learning
FUNCTIONAL DESCRIPTION: To address this issue, we proceed to supplement our Bayesian policy gradient framework with a new actor-critic learning model in which a Bayesian class of non-parametric critics, based on Gaussian process temporal difference learning, is used. Such critics model the action-value function as a Gaussian process, allowing Bayes' rule to be used in computing the posterior distribution over action-value functions, conditioned on the observed data. Appropriate choices of the policy parameterization and of the prior covariance (kernel) between action-values allow us to obtain closed-form expressions for the posterior distribution of the gradient of the expected return with respect to the policy parameters. We perform detailed experimental comparisons of the proposed Bayesian policy gradient and actor-critic algorithms with classic Monte-Carlo based policy gradient methods, as well as with each other, on a number of reinforcement learning problems.

- Contact: Michal Valko
- URL: https://team.inria.fr/sequel/Software/BAC/

6.2. GuessWhat?!

GuessWhat?! Visual object discovery through multi-modal dialogue
KEYWORDS: Deep learning - Dialogue System
FUNCTIONAL DESCRIPTION: This project train a AI to play the GuessWhat?! game. Thus, you can train an AI to ask questions, to answer questions about images. You can also perform basic visual reasoning. This project is a testbed for future interactive dialogue system.

- Partner: Universite de Montreal
- Contact: Florian Strub
- Publications: GuessWhat?! Visual object discovery through multi-modal dialogue - End-to-end optimization of goal-driven and visually grounded dialogue systems Harm de Vries

6.3. Squeak

Sequential sampling for kernel matrix approximation
KEYWORD: Machine learning

- Contact: Daniele Calandriello
- URL: http://researchers.lille.inria.fr/~valko/hp/serve.php?what=publications/squeak.py

6.4. OOR

Optimistic Optimization in R
KEYWORDS: Black-box optimization - Machine learning

- Contact: Mickael Binois
- URL: https://cran.r-project.org/web/packages/OOR/index.html

6.5. DPPy

Sampling Determinantal Point Processes with Python
KEYWORD: Determinantal point processes
FUNCTIONAL DESCRIPTION: Determinantal point processes (DPPs) are specific probability distributions over clouds of points that are used as models and computational tools across physics, probability, statistics, and more recently machine learning. Sampling from DPPs is nontrivial and therefore we present. DPPy, a Python toolbox that gathers known exact and approximate sampling algorithms. The project is hosted on GitHub and equipped with an extensive documentation.

- Contact: Guillaume Gautier
- URL: https://github.com/guilgautier/DPPy/

6.6. SMPyBandits

Open-Source Python package for Single- and Multi-Players multi-armed Bandits algorithms.
KEYWORD: Machine learning
FUNCTIONAL DESCRIPTION: The library contains the implementation of many single-player mutli-armed bandit algorithms as well as the implementation of all the state-of-the-art multi-player algorithms.

- Contact: Lilian Besson

SIERRA Project-Team

6. New Software and Platforms

6.1. ProxASAGA

KEYWORD: Optimization
FUNCTIONAL DESCRIPTION: A C++/Python code implementing the methods in the paper "Breaking the Nonsmooth Barrier: A Scalable Parallel Method for Composite Optimization", F. Pedregosa, R. Leblond and S. Lacoste-Julien, Advances in Neural Information Processing Systems (NIPS) 2017. Due to their simplicity and excellent performance, parallel asynchronous variants of stochastic gradient descent have become popular methods to solve a wide range of large-scale optimization problems on multi-core architectures. Yet, despite their practical success, support for nonsmooth objectives is still lacking, making them unsuitable for many problems of interest in machine learning, such as the Lasso, group Lasso or empirical risk minimization with convex constraints. In this work, we propose and analyze ProxASAGA, a fully asynchronous sparse method inspired by SAGA, a variance reduced incremental gradient algorithm. The proposed method is easy to implement and significantly outperforms the state of the art on several nonsmooth, large-scale problems. We prove that our method achieves a theoretical linear speedup with respect to the sequential version under assumptions on the sparsity of gradients and block-separability of the proximal term. Empirical benchmarks on a multi-core architecture illustrate practical speedups of up to 12x on a 20-core machine.

- Contact: Fabian Pedregosa
- URL: https://github.com/fabianp/ProxASAGA

6.2. object-states-action

KEYWORD: Computer vision
FUNCTIONAL DESCRIPTION: Code for the paper Joint Discovery of Object States and Manipulation Actions, ICCV 2017: Many human activities involve object manipulations aiming to modify the object state. Examples of common state changes include full/empty bottle, open/closed door, and attached/detached car wheel. In this work, we seek to automatically discover the states of objects and the associated manipulation actions. Given a set of videos for a particular task, we propose a joint model that learns to identify object states and to localize state-modifying actions. Our model is formulated as a discriminative clustering cost with constraints. We assume a consistent temporal order for the changes in object states and manipulation actions, and introduce new optimization techniques to learn model parameters without additional supervision. We demonstrate successful discovery of seven manipulation actions and corresponding object states on a new dataset of videos depicting real-life object manipulations. We show that our joint formulation results in an improvement of object state discovery by action recognition and vice versa.

- Participants: Jean-Baptiste Alayrac, Josef Sivic, Ivan Laptev and Simon Lacoste-Julien
- Contact: Jean-Baptiste Alayrac
- Publication: Joint Discovery of Object States and Manipulation Actions
- URL: https://github.com/jalayrac/object-states-action

SIMSMART Team (section vide)

SPHINX Project-Team

5. New Software and Platforms

5.1. GetDDM

KEYWORDS: Large scale - 3D - Domain decomposition - Numerical solver
FUNCTIONAL DESCRIPTION: GetDDM combines GetDP and Gmsh to solve large scale finite element problems using optimized Schwarz domain decomposition methods.

- Contact: Xavier Antoine
- URL: http://onelab.info/wiki/GetDDM

5.2. GPELab

Gross-Pitaevskii equations Matlab toolbox
KEYWORDS: 3D - Quantum chemistry - 2D
FUNCTIONAL DESCRIPTION: GPELab is a Matlab toolbox developed to help physicists for computing ground states or dynamics of quantum systems modeled by Gross-Pitaevskii equations. This toolbox allows the user to define a large range of physical problems (1d-2d-3d equations, general nonlinearities, rotation term, multi-components problems...) and proposes numerical methods that are robust and efficient.

- Contact: Xavier Antoine
- URL: http://gpelab.math.cnrs.fr/

TAU Team

6. New Software and Platforms

6.1. io.datascience

Input Output Data Science

KEYWORDS: Open data - Semantic Web - FAIR (Findable, Accessible, Interoperable, and Reusable)

FUNCTIONAL DESCRIPTION: io.datascience (Input Output Data Science) is the instance of the Linked Wiki platform developed specifically in Paris-Saclay University as part of its Center for Data Science.

The goal of io.datascience: to facilitate the sharing and use of scientific data. The technological concept of io.datascience: the exploitation of semantic web advances, and in particular wiki technologies.

(Findable, Accessible, Interoperable, and Reusable) (Wilkinson, M., and The FAIR Guiding Principles for Scientific Data Management and Stewardship, Nature Scientific Data 2016)

io.datascience is both a data sharing platform and a framework for further development. It realizes a practical implementation of FAIR (Findable, Accessible, Interoperable, and Reusable - Wilkinson, M., Nature Scientific Data 2016) principles through a user-centric approach.

- Partners: Border Cloud - Paris Saclay Center for Data Science - Université Paris-Sud
- Contact: Cécile Germain-Renaud
- Publications: Data acquisition for analytical platforms: Automating scientific workflows and building an open database platform for chemical anlysis metadata - A platform for scientific data sharing - TFT, Tests For Triplestores - Une autocomplétion générique de SPARQL dans un contexte multi-services - Certifying the interoperability of RDF database systems - Transforming Wikipedia into an Ontology-based Information Retrieval Search Engine for Local Experts using a Third-Party Taxonomy - The Grid Observatory 3.0 - Towards reproducible research and open collaborations using semantic technologies
- URL: https://io.datascience-paris-saclay.fr/

6.2. Codalab

KEYWORDS: Benchmarking - Competition

FUNCTIONAL DESCRIPTION: Challenges in machine learning and data science are competitions running over several weeks or months to resolve problems using provided datasets or simulated environments. Challenges can be thought of as crowdsourcing, benchmarking, and communication tools. They have been used for decades to test and compare competing solutions in machine learning in a fair and controlled way, to eliminate “inventor-evaluator" bias, and to stimulate the scientific community while promoting reproducible science. See our slide presentation.

As of december 2017 there are 145 public competitions on Codalab and over 10000 users. Some of the areas in which Codalab is used include Computer vision and medical image analysis, natural language processing, time series prediction, causality, and automatic machine learning. Codalab was selected for the million Euro challenge See.4C that was awarded a H2020 EU grant for its organization.

TAU is going to continue expanding Codalab to accommodate new needs. One of our current focus is to support use of challenges for teaching (i.e. include a grading system as part of Codalab) and support for hooking up data simulation engines in the backend of Codalab to enable Reinforcement Learning challenges and simulate interactions of machines with an environment. For the third year, we are using Codalab for student projects. M2 AIC students create mini data science challenges in teams of 6 students. L2 math and informatics students then solve them as part of their mini projects. We are collaborating with RPI (New York, USA) to use this platform as part of a curriculum of medical students. Our PhD. students are involved in co-organizing challenges to expose the research community at large with the topic of their PhD. This helps them formalizing a task with rigor and allows them to disseminate their research.

- Partner: Microsoft
- Contact: Isabelle Guyon
- URL: http://competitions.codalab.org

6.3. Cartolabe

KEYWORD: Information visualization

FUNCTIONAL DESCRIPTION: The goal of Cartolabe is to build a visual map representing the scientific activity of an institution/university/domain from published articles and reports. Using the HAL Database, Cartolabe provides the user with a map of the thematics, authors and articles . ML techniques are used for dimensionality reduction, cluster and topics identification, visualisation techniques are used for a scalable 2D representation of the results.

NEWS OF THE YEAR: Improvement of the graphical interface

- Partners: LRI - Laboratoire de Recherche en Informatique - CNRS
- Contact: Philippe Caillou
- URL: http://www.cartolabe.fr/

TOSCA Project-Team (section vide)

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, intercations, nonsmooth laws, ...) and to perform a numerical time integration and solving.
3. SICONOS/FRONT-END. This module is mainly an auto-generated wrapper in Python which provides a user-friendly interface to the Siconos libraries. A scilab interface is also provided in the Front-End module.
4. SICONOS/CONTROL This part is devoted to the implementation of control strategies of non smooth dynamical systems.
5. SICONOS/MECHANICS. This part is dedicated to the modeling and the simulation of multi-body systems with 3D contacts, impacts and Coulomb's friction. It uses the Siconos/Kernel as simulation engine but relies on a industrial CAD library (OpenCascade and pythonOCC) to deal with complex body geometries and to compute the contact locations and distances between B-Rep description and on Bullet for contact detection between meshes.

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

TROPICAL Project-Team

6. New Software and Platforms

6.1. Coq-Polyhedra

KEYWORDS: Coq - Polyhedra - Automated theorem proving - Linear optimization
SCIENTIFIC DESCRIPTION: Coq-Polyhedra is a library providing a formalization of convex polyhedra in the Coq proof assistant. While still in active development, it provides an implementation of the simplex method, and already handles the basic properties of polyhedra such as emptiness, boundedness, membership. Several fundamental results in the theory of convex polyhedra, such as Farkas Lemma, duality theorem of linear programming, and Minkowski Theorem, are also formally proved.

The formalization is based on the Mathematical Components library, and makes an extensive use of the boolean reflection methodology.
FUNCTIONAL DESCRIPTION: Coq-Polyhedra is a library which aims at formalizing convex polyhedra in Coq

- Participants: Xavier Allamigeon, Vasileios Charisopoulos and Ricardo Katz
- Partner: CIFASIS
- Contact: Xavier Allamigeon
- Publications: A Formalization of Convex Polyhedra Based on the Simplex Method - A Formalization of Convex Polyhedra Based on the Simplex Method - First steps in the formalization of convex polyhedra in Coq
- URL: https://github.com/nhojem/Coq-Polyhedra

ABS Project-Team

4. New Software and Platforms

4.1. SBL

Structural Bioinformatics Library
KEYWORDS: Structural Biology - Biophysics - Software architecture
FUNCTIONAL DESCRIPTION: The SBL is a generic C++/python cross-platform software library targeting complex problems in structural bioinformatics. Its tenet is based on a modular design offering a rich and versatile framework allowing the development of novel applications requiring well specified complex operations, without compromising robustness and performances.

More specifically, the SBL involves four software components (1-4 thereafter). For end-users, the SBL provides ready to use, state-of-the-art (1) applications to handle molecular models defined by unions of balls, to deal with molecular flexibility, to model macro-molecular assemblies. These applications can also be combined to tackle integrated analysis problems. For developers, the SBL provides a broad C++ toolbox with modular design, involving core (2) algorithms, (3) biophysical models, and (4) modules, the latter being especially suited to develop novel applications. The SBL comes with a thorough documentation consisting of user and reference manuals, and a bugzilla platform to handle community feedback.

RELEASE FUNCTIONAL DESCRIPTION: In 2018, major efforts targeted two points. First, the simplification of installation procedures – now possible with conda/python. Second, the development of packages revolving on molecular flexibility at large: representations in internal and Cartesian coordinates, generic representation of molecular mechanics force fields (and computation of gradients), exploration algorithms for conformational spaces.

- Contact: Frédéric Cazals
- Publication: The Structural Bioinformatics Library: modeling in biomolecular science and beyond
- URL: https://sbl.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

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

- Contact: 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

ANGE Project-Team

6. New Software and Platforms

6.1. Freshkiss

FREe Surface Hydrodynamics using KInetic SchemeS
KEYWORDS: Finite volume methods - Hydrostatic Navier-Stokes equations - Free surface flows
FUNCTIONAL DESCRIPTION: Freshkiss3D is a numerical code solving the 3D hydrostatic and incompressible Navier-Stokes equations with variable density.

- Participants: Fabien Souille, Emmanuel Audusse, Jacques Sainte Marie and Marie-Odile Bristeau
- Partners: UPMC - CEREMA
- Contact: Jacques Sainte Marie

6.2. TSUNAMATHS

KEYWORDS: Modeling - Tsunamis
FUNCTIONAL DESCRIPTION: Tsunamaths is an educational platform aiming at simulating historical tsunamis. Real data and mathematical explanations are provided to enable people to better understand the overall process of tsunamis.

- Participants: Emmanuel Audusse, Jacques Sainte Marie and Raouf Hamouda
- Contact: Jacques Sainte Marie
- URL: http://tsunamath.paris.inria.fr/

6.3. Verdandi

KEYWORDS: HPC - Model - Software Components - Partial differential equation
FUNCTIONAL DESCRIPTION: Verdandi is a free and open-source (LGPL) library for data assimilation. It includes various such methods for coupling one or several numerical models and observational data. Mainly targeted at large systems arising from the discretization of partial differential equations, the library is devised as generic, which allows for applications in a wide range of problems (biology and medicine, environment, image processing, etc.). Verdandi also includes tools to ease the application of data assimilation, in particular in the management of observations or for a priori uncertainty quantification. Implemented in C++, the library may be used with models implemented in Fortran, C, C++ or Python.

- Participants: Dominique Chapelle, Gautier Bureau, Nicolas Claude, Philippe Moireau and Vivien Mallet
- Contact: Vivien Mallet
- URL: http://verdandi.gforge.inria.fr/

6.4. Polyphemus

KEYWORD: Simulation
FUNCTIONAL DESCRIPTION: Polyphemus is a modeling system for air quality. As such, it is designed to yield up-to-date simulations in a reliable framework: data assimilation, ensemble forecast and daily forecasts. Its completeness makes it suitable for use in many applications: photochemistry, aerosols, radionuclides, etc. It is able to handle simulations from local to continental scales, with several physical models. It is divided into three main parts:

libraries that gather data processing tools (SeldonData), physical parameterizations (AtmoData) and post-processing abilities (AtmoPy), programs for physical pre-processing and chemistry-transport models (Polair3D, Castor, two Gaussian models, a Lagrangian model),

model drivers and observation modules for model coupling, ensemble forecasting and data assimilation.

- Participants: Sylvain Doré and Vivien Mallet
- Contact: Vivien Mallet
- URL: http://cerea.enpc.fr/polyphemus/

6.5. Urban noise analysis

KEYWORD: Environment perception
FUNCTIONAL DESCRIPTION: This software processes mobile observations collected by the application Ambiciti (previously known as SoundCity). It can merge simulated noise maps with the mobile observations.

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

6.6. Freshkiss3D

- Authors: Jacques Sainte Marie, Marie-Odile Bristeau, Anne-Céline Boulanger, Raouf Hamouda, Emmanuel Audusse, Alain Dervieux, Bijan Mohammadi and David Froger
- Partner: UPMC
- Contact: Jacques Sainte Marie

ARAMIS Project-Team

6. New Software and Platforms

6.1. Brain Networks Toolbox

KEYWORDS: Neuroimaging - Medical imaging
FUNCTIONAL DESCRIPTION: Brain Networks Toolbox is an open-source package of documented routines implementing new graph algorithms for brain network analysis. It mainly contains Matlab code of new methods developed by the team and associated to publications (e.g., brain network thresholding, extraction of the information redundancy, node accessibility, etc). It requires, as input, adjacency matrices representing brain connectivity networks. Thus, it is independent on the specific approach used to construct brain networks and it can be used to extract network properties from any neuroimaging modality in healthy and diseased subjects.

- Participants: Fabrizio De Vico Fallani, Jeremy Guillon and Mario Chavez
- Contact: Fabrizio De Vico Fallani
- URL: https://github.com/brain-network/bnt

6.2. Deformetrica

KEYWORDS: 3D modeling - C++ - Automatic Learning - Mesh - Anatomy - Image analysis
SCIENTIFIC DESCRIPTION: Deformetrica is a software for the statistical analysis of 2D and 3D shape data. It essentially computes deformations of the 2D or 3D ambient space, which, in turn, warp any object embedded in this space, whether this object is a curve, a surface, a structured or unstructured set of points, or any combination of them.

Deformetrica comes with two applications:

registration, which computes the best possible deformation between two sets of objects, atlas construction, which computes an average object configuration from a collection of object sets, and the deformations from this average to each sample in the collection.

Deformetrica has very little requirements about the data it can deal with. In particular, it does not require point correspondence between objects!
FUNCTIONAL DESCRIPTION: Deformetrica is a software for the statistical analysis of 2D and 3D shape data. It essentially computes deformations of the 2D or 3D ambient space, which, in turn, warp any object embedded in this space, whether this object is a curve, a surface, a structured or unstructured set of points, or any combination of them.

Deformetrica comes with two applications:

- Registration, which computes the optimal deformation between two sets of objects,

- Atlas construction, which computes an average object configuration from a collection of object sets, and the deformations from this average to each sample in the collection.

Deformetrica has very little requirements about the data it can deal with. In particular, it does not require point correspondence between objects!

- Participants: Alexandre Routier, Ana Fouquier, Barbara Gris, Benjamin Charlier, Cédric Doucet, Joan Alexis Glaunès, Marcel Prastawa, Michael Bacci, Pietro Gori and Stanley Durrleman
- Partners: University of Utah - Université de Montpellier 2 - Université Paris-Descartes
- Contact: Stanley Durrleman
- URL: http://www.deformetrica.org/

6.3. Clinica

KEYWORDS: Neuroimaging - Brain MRI - MRI - Clinical analysis - Image analysis - Machine learning
SCIENTIFIC DESCRIPTION: Clinica is a software platform for multimodal brain image analysis in clinical research studies. It makes it easy to apply advanced analysis tools to large scale clinical studies. For that purpose, it integrates a comprehensive set of processing tools for the main neuroimaging modalities: currently MRI (anatomical, functional, diffusion) and PET, in the future, EEG/MEG. For each modality, Clinica allows to easily extract various types of features (regional measures, parametric maps, surfaces, curves, networks). Such features are then subsequently used as input of machine learning, statistical modeling, morphometry or network analysis methods. Processing pipelines are based on combinations of freely available tools developed by the community. It provides an integrated data management specification to store raw and processing data. Clinica is written in Python. It uses the Nipype system for pipelining. It combines widely-used software for neuroimaging data analysis (SPM, Freesurfer, FSL, MRtrix...), morphometry (Deformetrica), machine learning (Scikit-learn) and the BIDS standard for data organization.
FUNCTIONAL DESCRIPTION: Clinica is a software platform for multimodal brain image analysis in clinical research studies. It makes it easy to apply advanced analysis tools to large scale clinical studies. For that purpose, it integrates a comprehensive set of processing tools for the main neuroimaging modalities: currently MRI (anatomical, functional, diffusion) and PET, in the future, EEG/MEG. For each modality, Clinica allows to easily extract various types of features (regional measures, parametric maps, surfaces, curves, networks). Such features are then subsequently used as input of machine learning, statistical modeling, morphometry or network analysis methods. Clinica also provides an integrated data management specification to store raw and processing data. Overall, Clinica helps to: i) apply advanced analysis tools to clinical research studies, ii) easily share data and results, iii) make research more reproducible.
NEWS OF THE YEAR: - Three clinical studies made with Clinica Clinica : Bertrand et al, JAMA Neurology, 2018 , Jacquemont et al, Neurobiol Aging, 2017, Wen et al, JNNP, 2018 - Clinica presented at OHBM 2018 conference - Clinica was the support for the tutorial "Pattern Recognition for Neuroimaging" at OHBM 2018

- Participants: Jeremy Guillon, Thomas Jacquemont, Pascal Lu, Arnaud Marcoux, Tristan Moreau, Alexandre Routier, Jorge Samper Gonzalez, Junhao Wen, Olivier Colliot, Stanley Durrleman, Michael Bacci, Simona Bottani, Ninon Burgos, Sabrina Fontanella, Pietro Gori, Mauricio Diaz Melo and Elina Thibeau-Sutre
- Partners: Institut du Cerveau et de la Moelle épinière (ICM) - CNRS - INSERM - UPMC
- Contact: Olivier Colliot
- Publications: Amyloidosis and neurodegeneration result in distinct structural connectivity patterns in mild cognitive impairment - Yet Another ADNI Machine Learning Paper? Paving The Way Towards Fully-reproducible Research on Classification of Alzheimer's Disease - Reproducible evaluation of classification methods in Alzheimer's disease: Framework and application to MRI and PET data - Neurite density is reduced in the presymptomatic phase of C9orf72 disease - Early cognitive, structural and microstructural changes in c9orf72 presymptomatic carriers before 40 years of age
- URL: http://www.clinica.run

6.4. Platforms

6.4.1. Platform Brain-computer interface

Our team coordinates the developments of the Brain-Computer Interface (BCI) platform at the Centre EEG/MEG of the neuroimaging core facility of the ICM. Several projects, including our NETBCI NSF/NIH/ANR and ATTACK Big-brain theory funded projects, as well as experiments by different researchers of the Institute, are currently being run. To reinforce the impact of the platform we have recently recruited an engineer (J. Gonzalez-Astudillo) for the software and technical development.

ATHENA Project-Team

5. New Software and Platforms

5.1. BCI-VIZAPP

BCI visual applications
KEYWORDS: Health - Brain-Computer Interface - GUI (Graphical User Interface)
SCIENTIFIC DESCRIPTION: Bci-Vizapp is a library that allows (in interaction with OpenViBE) to build BCI (Brain Computer Interfaces) applications based on the P300 speller principle. Bci-Vizapp provides a library that allows you to create the BCI's stimulation part as part of the Qt toolkit. Being able to use a standard toolkit to make BCI applications is a strong Bci-Vizapp originality. Indeed, in general the use of such toolkits is prohibited by the need for a very precise control of the display timings, which generally eliminates high-level graphic toolkits such as Qt.
FUNCTIONAL DESCRIPTION: BCI-VIZAPP includes a virtual keyboard for typing text, a photodiode monitoring application for checking timing issues. It communicates with the OpenViBE acquisition server for signal acquisition and with the OpenViBE designer for signal processing. The configuration is performed through a wizard.

This software is a new version following the CoAdapt P300 stimulator software.
NEWS OF THE YEAR: Bci-Vizapp is undergoing a profound transmutation with the help of CRISAM's SED in ADT BciBrowser (part of the AMDT). This change aims at integrating the functionality of Bci-Vizapp in third-party applications such as a web browsers.

- Participants: Nathanaël Foy, Romain Lacroix, Maureen Clerc and Théodore Papadopoulo
- Contact: Maureen Clerc

5.2. DIPY

Diffusion Imaging in Python
KEYWORDS: MRI - Medical imaging
FUNCTIONAL DESCRIPTION: Diffusion Imaging in Python (Dipy) is a free and open source software project for computational neuroanatomy, focusing mainly on diffusion magnetic resonance imaging (dMRI) analysis. E. Garyfallidis (now Indiana University) is the founder and lead engineer of this open source project in the development of diffusion MRI methods. We continuously collaborate with this global effort and our effort is combined with Université de Sherbrooke, in Canada and Stanford University among others. See for example our registration, denoising, tractography and microstructures tutorials.

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

5.3. High Performance Diffusion MRI

KEYWORDS: Health - Neuroimaging - Medical imaging

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

- Participants: Aurobrata Ghosh, Rachid Deriche and Théodore Papadopoulo
- Partner: Olea Medical
- Contact: Rachid Deriche

5.4. OpenMEEG

KEYWORDS: Health - Neuroimaging - Medical imaging
SCIENTIFIC DESCRIPTION: OpenMEEG provides a symmetric boundary element method (BEM) implementation for solving the forward problem of electromagnetic propagation over heterogeneous media made of several domains of homogeneous and isotropic conductivities. OpenMEEG works for the quasistatic regime (frequencies < 100Hz and medium diameter < 1m).
FUNCTIONAL DESCRIPTION: OpenMEEG provides state-of-the art tools for modelling bio-electromagnetic propagation in the quasi-static regime. It is based on the symmetric BEM for the EEG/MEG forward problem, with a distributed source model. OpenMEEG has also been used to model the forward problem of ECoG, for modelling nerves or the cochlea. OpenMEEG is a free, open software written in C++ with python bindings. OpenMEEG is used through a command line interface, but is also interfaced in graphical interfaces such as BrainStorm, FieldTrip or SPM.

RELEASE FUNCTIONAL DESCRIPTION: OpenMEEG has had a large update including notably the parallelisation of some operators and bug corrections. The new version allows in addition the use of non-nested domains.
NEWS OF THE YEAR: OpenMEEG has had a large update including notably the parallelisation of some operators and bug corrections. The new version allows in addition the use of non-nested domains. These improvements have been ditributed with the two new releases (2.4.0 and 2.4.1) made in 2018.

- Participants: Alexandre Gramfort, Emmanuel Olivi, Geoffray Adde, Jan Kybic, Kai Dang, Maureen Clerc, Perrine Landreau, Renaud Keriven and Théodore Papadopoulo
- Contact: Théodore Papadopoulo
- Publications: OpenMEEG: opensource software for quasistatic bioelectromagnetics - Forward Field Computation with OpenMEEG. - Source modeling of ElectroCorticoGraphy (ECoG) data: Stability analysis and spatial filtering
- URL: http://openmeeg.github.io/

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
- 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 developped 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 agregate logfile contents. The second one is a subspace clustering module, based on an evolutionary algorithm, to identify similar wifi activity contexts. This similarity is defined on signal strength of wifi devices and the clusters can change over time. The third module is a visualisation tool to display the cluster modifications over time.

- Participants: 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 segementation 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://fluobactracker.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

BIGS Project-Team (section vide)

BIOCORE Project-Team

6. New Software and Platforms

6.1. In@lgae

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

RELEASE FUNCTIONAL DESCRIPTION: The In@lgae platform has been optimised to make it faster. Some of the key models have been rewritten in C++ to allow a faster computation. Models have been improved to include, in the growth rate computation, the composition of the light spectrum. The graphical user interface has been enhanced and several sets of parameters describing different microalgal species have been stored.

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

6.2. Odin

Platform for advanced monitoring, control and optimisation of bioprocesses
KEYWORDS: Bioinformatics - Biotechnology - Monitoring - Automatic control
SCIENTIFIC DESCRIPTION: This C++ application enables researchers and industrials to easily develop and deploy advanced control algorithms through the use of a Scilab interpreter. It also contains a Scilab-based process simulator which can be harnessed for experimentation and training purposes. ODIN is primarily developed in the C++ programming language and uses CORBA to define component interfaces and provide component isolation. ODIN is a distributed platform, enabling remote monitoring of the controlled processes as well as remote data acquisition.It is very modular in order to adapt to any plant and to run most of the algorithms, and it can handle the high level of uncertainties that characterises the biological processes through explicit management of confidence indexes.
FUNCTIONAL DESCRIPTION: ODIN is a software framework for bioprocess control and supervision. ODIN is a distributed platform, where algorithms are described with a common structure easy to implement. Finally, ODIN can perform remote data acquisition and process these data to compute the signals to be applied to the actuators, together with estimates of state variables or process state. ODIN can handle the high level of uncertainties that characterises the biological processes through explicit management of confidence indexes.

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

BIOVISION Project-Team

5. New Software and Platforms

5.1. Virtual Retina

A biological retina model with contrast gain control for large scale simulations
KEYWORDS: Neurosciences - Simulation - Biology - Health
SCIENTIFIC DESCRIPTION: Virtual Retina has a variety of biological features implemented such as (i) spatio-temporal linear filter implementing the basic center/surround organization of retinal filtering, (ii) non-linear contrast gain control mechanism providing instantaneous adaptation to the local level of contrast, (iii) spike generation by one or several layers of ganglion cells paving the visual field.
FUNCTIONAL DESCRIPTION: Virtual Retina is a simulation software that allows large-scale simulations of biologically-plausible retinas.

- Participants: Adrien Wohrer, Pierre Kornprobst, Bruno Cessac, Maria-Jose Escobar and Thierry Viéville
- Contact: Pierre Kornprobst
- Publication: Virtual Retina: A biological retina model and simulator, with contrast gain control
- URL: https://team.inria.fr/biovision/virtualretina/

5.2. PRANAS

Platform for Retinal ANalysis And Simulation
KEYWORDS: Retina - Neural Code - Data management - Statistics - Modeling - Vision
SCIENTIFIC DESCRIPTION: PRANAS was designed as a user-friendly tool dedicated to neuroscientist community in a large sense, i.e., not only experienced computational neuroscientists. It has two main goals : (i) to analyze retina data, especially spatio-temporal correlations, at single cell but also population levels, (ii) to simulate the spike response of the retina to a visual flow with a customizable retina simulator which evolves in synergy with experimental data analysis. In general, PRANAS allows to explore several aspects of retinal image processing such as understanding how to reproduce accurately the statistics of the spiking activity at the population level, or reconciling connectomics and simple computational rules for visual motion detection. This makes this tool a unique platform to better understand how the retina works.
FUNCTIONAL DESCRIPTION: The retina encodes a visual scene by trains of action potentials sent to the brain via the optic nerve. PRANAS brings to neuroscientists and modelers tools to better understand this coding. It integrates a retina simulator allowing large scale simulations while keeping a strong biological plausibility and a toolbox for the analysis of spike trains population statistics. The statistical method (entropy maximization under constraints) takes into account both spatial and temporal correlations as constraints, allowing to analyze the effects of memory on statistics. PRANAS also integrates a tool computing and representing in 3D (time-space) receptive fields. All these tools are accessible through a friendly graphical user interface. The most CPU-costly of them has been implemented to run in parallel. The actual version simulates healty retinas but the long term goal is to study retinas with a pathology (DMLA, Retinitis Pigmentosa, Glaucoma).

- Authors: Bruno Cessac, Pierre Kornprobst, Sélim Kraria, Hassan Nasser, Daniela Pamplona, Geoffrey Portelli and Adrien Wohrer
- Contact: Bruno Cessac
- Publication: PRANAS: A New Platform for Retinal Analysis and Simulation
- URL: https://team.inria.fr/biovision/pranas-software/

5.3. Platforms

5.3.1. VRead

We are currently developing the VRead platform, a reading platform for digital content. We are now in the phase of building and testing prototypes with low-vision patients. We have started to conduct a qualitative Market research with patients to get a continuous feedback from them, discover their needs and thus better drive the developments. A special care is taken for ergonomics to optimize user experience in virtual reality. This is a crucial aspect in this project, especially because we primarily target a more fragile population so that we have to take into account their vision loss and cognitive skills. As for the technical aspect, we are using the Unity game engine along with the Oculus SDK, allowing us to deploy and test early on the Samsung GearVR mobile platform. For scripting the engine we code in C# using the proprietary directives of Unity. We ship the VRead Viewer with an operator application which allows for supervision and tuning of parameters of the reader in realtime. This application is written using the Unity SDK and is deployable under macOS, Windows and Linux.

This project received financial support from Université Côte d'Azur (France) (duration: 18 months, period: Aug. 2017– Jan. 2019 and Inria (via InriaHUB programme). It is done in collaboration with Aix-Marseille Université (CNRS, Laboratoire de Psychologie Cognitive, Marseille, France), Centre hospitalier Pasteur 2 (service d'ophtalmologie, Nice, France) and University of Genoa (DIBRIS, Genoa, Italy).

5.3.2. Macular

We are currently developing the platform Macular, a large-scale simulations platform of impaired retinas, allowing to mimic specific degeneracies or pharmacologically induced impairments, as well as to emulate electric stimulation by prostheses. With this tool scientists will be able to design a simulation gui adapted to their need, so as to test hypotheses, make in-silico experiments prior to real experiments, test models, change the equations of a model and look at the impact of the dynamics. We hope it will become a standard for the community of modelers, experimentalists in the academic word, as well as for companies doing research and development. Macular will also help to better understand how to design algorithms to help visually impaired individuals. Especially, the Biovision team wants to develop computer algorithms for retinal prostheses that reproduce the functions performed by the bypassed parts of the eye: these algorithms can then be used as a "camera to eye translator" in retinal prosthetics.

BONSAI Project-Team

5. New Software and Platforms

5.1. BCALM 2

KEYWORDS: Bioinformatics - NGS - Genomics - Metagenomics - De Bruijn graphs
SCIENTIFIC DESCRIPTION: BCALM 2 is a bioinformatics tool for constructing the compacted de Bruijn graph from sequencing data. It is a parallel algorithm that distributes the input based on a minimizer hashing technique, allowing for good balance of memory usage throughout its execution. It is able to compact very large datasets, such as spruce or pine genome raw reads in less than 2 days and 40 GB of memory on a single machine.
FUNCTIONAL DESCRIPTION: BCALM 2 is an open-source tool for dealing with DNA sequencing data. It constructs a compacted representation of the de Bruijn graph. Such a graph is useful for many types of analyses, i.e. de novo assembly, de novo variant detection, transcriptomics, etc. The software is written in C++ and makes extensive use of the GATB library.

- Participants: Antoine Limasset, Paul Medvedev and Rayan Chikhi
- Contact: Rayan Chikhi
- Publication: Compacting de Bruijn graphs from sequencing data quickly and in low memory
- URL: https://github.com/GATB/bcalm

5.2. NORINE

Nonribosomal peptides resource
KEYWORDS: Drug development - Knowledge database - Chemistry - Graph algorithmics - Genomics - Biology - Biotechnology - Bioinformatics - Computational biology
SCIENTIFIC DESCRIPTION: Since its creation in 2006, Norine remains the unique knowledgebase dedicated to non-ribosomal peptides (NRPs). These secondary metabolites, produced by bacteria and fungi, harbor diverse interesting biological activities (such as antibiotic, antitumor, siderophore or surfactant) directly related to the diversity of their structures. The Norine team goal is to collect the NRPs and provide tools to analyze them efficiently. We have developed a user-friendly interface and dedicated tools to provide a complete bioinformatics platform. The knowledgebase gathers abundant and valuable annotations on more than 1100 NRPs. To increase the quantity of described NRPs and improve the quality of associated annotations, we are now opening Norine to crowdsourcing. We believe that contributors from the scientific community are the best experts to annotate the NRPs they work on. We have developed MyNorine to facilitate the submission of new NRPs or modifications of stored ones.
FUNCTIONAL DESCRIPTION: Norine is a public computational resource with a web interface and REST access to a knowledge-base of nonribosomal peptides. It also contains dedicated tools : 2D graph viewer and editor, comparison of NRPs, MyNorine, a tool allowing anybody to easily submit new nonribosomal peptides, Smiles2monomers (s2m), a tool that deciphers the monomeric structure of polymers from their chemical structure.

- Participants: Areski Flissi, Juraj Michalik, Laurent Noé, Maude Pupin, Stéphane Janot, Valerie Leclère and Yoann Dufresne
- Partners: CNRS - Université Lille 1 - Institut Charles Viollette
- Contact: Maude Pupin
- Publications: Norine, the knowledgebase dedicated to non-ribosomal peptides, is now open to crowdsourcing - Smiles2Monomers: a link between chemical and biological structures for polymers - Norine: a powerful resource for novel nonribosomal peptide discovery - NORINE: a database of nonribosomal peptides. - Bioinformatics Tools for the Discovery of New Nonribosomal Peptides
- URL: http://bioinfo.lille.inria.fr/NRP

5.3. Vidjil

High-Throughput Analysis of V(D)J Immune Repertoire
KEYWORDS: Cancer - Indexation - NGS - Bioinformatics - Drug development
SCIENTIFIC DESCRIPTION: Vidjil is made of three components: an algorithm, a visualization browser and a server that allow an analysis of lymphocyte populations containing V(D)J recombinations.

Vidjil high-throughput algorithm extracts V(D)J junctions and gathers them into clones. This analysis is based on a spaced seed heuristics and is fast and scalable, as, in the first phase, no alignment is performed with database germline sequences. Each sequence is put in a cluster depending on its V(D)J junction. Then a representative sequence of each cluster is computed in time linear in the size of the cluster. Finally, we perform a full alignment using dynamic programming of that representative sequence against the germline sequences.

Vidjil also contains a dynamic browser (with D3JS) for visualization and analysis of clones and their tracking along the time in a MRD setup or in an immunological study.
FUNCTIONAL DESCRIPTION: Vidjil is an open-source platform for the analysis of high-throughput sequencing data from lymphocytes. V(D)J recombinations in lymphocytes are essential for immunological diversity. They are also useful markers of pathologies, and in leukemia, are used to quantify the minimal residual disease during patient follow-up. High-throughput sequencing (NGS/HTS) now enables the deep sequencing of a lymphoid population with dedicated Rep-Seq methods and software.

- Participants: Florian Thonier, Marc Duez, Mathieu Giraud, Mikaël Salson, Ryan Herbert and Tatiana Rocher
- Partners: CNRS - Inria - Université de Lille - CHRU Lille
- Contact: Mathieu Giraud
- Publications: High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges. - High-throughput sequencing in acute lymphoblastic leukemia: Follow-up of minimal residual disease and emergence of new clones - Diagnostic et suivi des leucémies aiguës lymphoblastiques (LAL) par séquençage haut-débit (HTS) - Multiclonal Diagnosis and MRD Follow-up in ALL with HTS Coupled with a Bioinformatic Analysis - A dataset of sequences with manually curated V(D)J designations - Vidjil: A Web Platform for Analysis of High-Throughput Repertoire Sequencing - Multi-loci diagnosis of acute lymphoblastic leukaemia with high-throughput sequencing and bioinformatics analysis - Fast multiclonal clusterization of V(D)J recombinations from high-throughput sequencing - The predictive strength of next-generation sequencing MRD detection for relapse compared with current methods in childhood ALL.
- URL: http://www.vidjil.org

5.4. MATAM

Mapping-Assisted Targeted-Assembly for Metagenomics
KEYWORDS: Metagenomics - Genome assembling - Graph algorithmics
SCIENTIFIC DESCRIPTION: MATAM relies on the construction of a read overlap graph. Overlaps are computed using SortMeRNA. The overlap graph is simplified into relevant components related to specific and conserved regions. Components are assembled into contigs using SGA and contigs are finally assembled into scaffolds. The process yields nearly full length marker sequences with a very low error rate compared to the state of the art approaches. Taxonomic assignation of the obtained scaffolds is performed using the RDP classifier and is represented using Krona.

FUNCTIONAL DESCRIPTION: MATAM provides targeted genes assembly from the short metagenomic reads issued from environmental samples sequencing. Its default application focuses on the gold standard for species identification, 16S / 18S ribosomal RNA SSU genes. The produced gene scaffolds are highly accurate and suitable for precise taxonomic assignation. The software also provides a RDP classification for the reconstructed scaffolds as well as an estimation of the relative population sizes.

- Participants: Hélène Touzet, Pierre Pericard, Yoann Dufresne, Samuel Blanquart and Loïc Couderc
- Contact: Hélène Touzet
- Publication: MATAM: reconstruction of phylogenetic marker genes from short sequencing reads in metagenomes
- URL: https://github.com/bonsai-team/matam

CAMIN Team

5. New Software and Platforms

5.1. RT_Stim

Real-Time simulation for functional electrical Stimulation
KEYWORDS: Real time - Biomechanics - Control - Co-simulation
FUNCTIONAL DESCRIPTION: Hybrid simulation architecture gathering in a single framework and consistent time scales both the numerical integration of the continuous model of a bio-mechanical system (bones, joints and muscles) and a model of the hardware and software control architecture, including control tasks, communication protocols and real-time schedulers. Simulation run in real-time when possible, and otherwise consistent time scales are generated. The framework is intended to seamlessly evolve from purely software models to hardware-in-the-loop simulation.

- Contact: Daniel Simon

5.2. Platforms

5.2.1. Modular embedded architecture for real time control of a FES system

Participants: Christine Azevedo Coste, Benoît Sijobert, Ronan Le Guillou.

The results presented in section 6.2 and 6.3 have led to the development of a new hardware and software architecture embedding a network of sensors and actuators interfaced to a controller, as part of Benoît Sijobert's PhD work and ADT STIMBIO (Ronan Le Guillou). In order to solve numerous issues and constraints observed during experiments, a new hardware and software architecture has been elaborated. The decision was made to decentralize the controller (i.e. the computer) directly on the participant, thereby relocating the essential wireless links around the user. For this purpose, a mini low-cost single board computer (Raspberry Pi3) was embedded in a 3D-printed case strapped around the waist of the subject. Using wireless inertial sensors connected as a WBAN, the sink node gets the data from all the IMUs, therefore highly decreasing the data flow when multiple IMUs were transmitting inside the network. To get rid of this limitation and guarantee an overall 100 Hz sampling rate no matter the number of IMUs, the wireless inertial sensors can be replaced by wired ones, low-cost with a high speed ARM Cortex-M0 based processor and a Kalman Filter directly providing quaternion estimation at 100 Hz for each IMU. The use of a multiplexer connected through an I2C interface (Inter Integrated Circuit) enabled to keep a 100 Hz rate using 4 IMUs.

The stimulator used in the experiments was a wireless programmable and controllable device. Latency issues and communication losses were observed when the computer sending the command to the stimulator was too far or if an obstacle was present between the computer and the participant wearing the stimulator. Taking advantage of the FES controller located on the subject to control the stimulator nearby has enabled us to solve this issue.

In this configuration, this autonomous FES controller is able to acquire the data, process them, execute control algorithms and send the appropriate stimulation command to the stimulator. For safety reasons, in order to access to the FES controller and to enable a remote access to the stimulation from a computer, an ad-hoc Wi-Fi network is automatically provided by the Raspberry on start-up. The ad-hoc network enables to be independent of a network infrastructure where the connection is not always possible (e.g. Wi-Fi network from the hospital).

This scalable architecture (Figure 3), developed as a modular system, now allows us to implement various new commands laws for Real Time closed loop control as well as giving us the ability to switch sensors and stimulators to meet the needs of specific applications. As part of making this system available for future projects in the team, the ability to easily change stimulators depending of the requirements was needed. To achieve this and in order for the FES architecture to directly control them, Application Programming Interfaces (APIs) were developed for 3 main commercial stimulators in the team. They each corresponds to a specific need and use case. The Vivaltis Phoenix Stimulator allows for low-weight embedding, wireless network control, but only 2 stimulation channels by pod, while being scalable. The BerkelBike Stimulator v2.0 presents a cumbersome but extended control compromise with 8 independent stimulation channels, which is an ideal solution for recumbent FES-assisted cycling. And finally the Hasomed Rehastim v1.0 allowing fine control but isn't battery powered in its commercial version and is not produced anymore.

This new architecture is currently used in clinical experiments and will continue to evolve with a goal of being easy to use, even by untrained clinicians. A funding (EDF Foundation) has been obtained by our clinical partner "CRF La Châtaigneraie" to perform a clinical protocol including 6 patients from which one will participate in the Cybathlon 2020 using this hardware and software architecture. The inclusions will begin in January 2019.

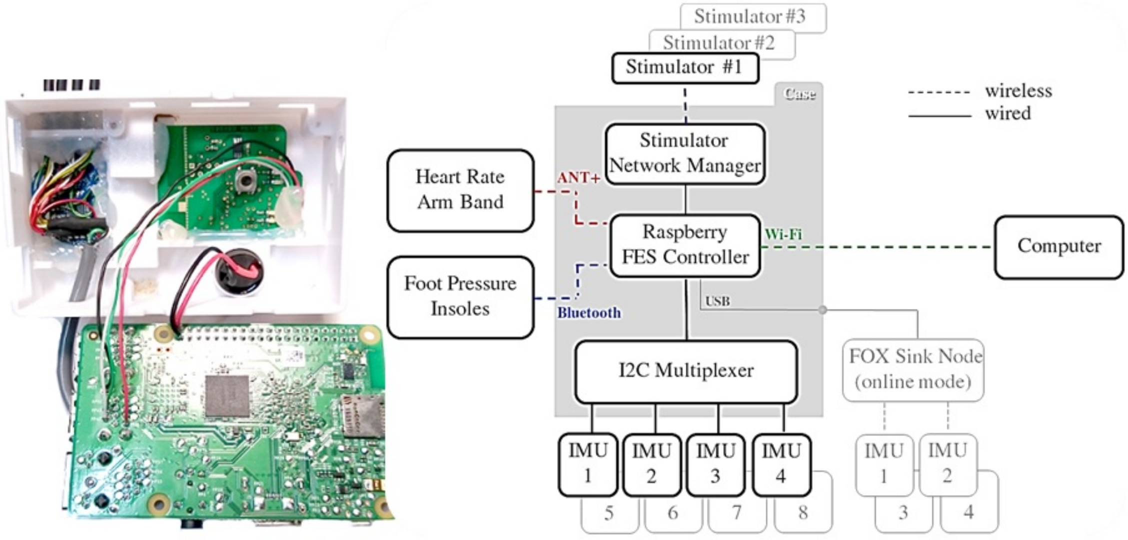
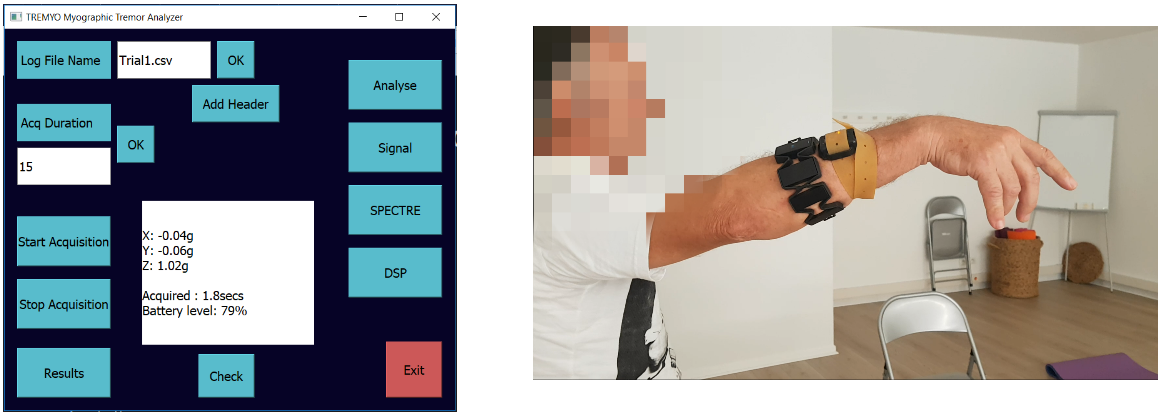


Figure 3. Experimental protocols have led to the development of a scalable hardware architecture decentralized on the subject.

5.2.2. Tremor monitoring system based on acceleration detection in Parkinson's Disease

Participants: Christine Azevedo Coste, Ronan Le Guillou.

As part of a preliminary study on the effects of Mindfulness meditation for patients with Parkinson's Disease (PD), an application was developed to monitor the accelerometer of a wrist worn device. The hypothesis being that reducing the cognitive load of a PD patient might reduce the severity of the tremors. We investigated a few devices that might correspond to our requirements : smartwatches, Myo armbands, Inertial Measurement Units,...Having already a Thalmic Myo Armband (Figure 4) we developed a program acquiring the accelerometer data in Real Time and logging it, as well as doing pre-processing and displaying it on the screen of the clinician to allow him to monitor the session. While this system was ready and already tested, we had to search for another solution due to the termination of the commercial product. We then selected the smartwatch Samsung Gear S3 as a possible alternative and the dedicated application is currently under development.



Trial1.csv

15

X: -0.04g
Y: -0.06g
Z: 1.02g

Acquired : 1.8secs
Battery level: 79%

Figure 4. i) Graphical User Interface of the TREMYO Armband monitoring application during acquisition ii) Baseline test with straight extended arm for temporal comparison of the tremors severity.

CAPSID Project-Team

6. New Software and Platforms

6.1. Hex

KEYWORDS: 3D rendering - Bioinformatics - 3D interaction - Structural Biology
SCIENTIFIC DESCRIPTION: Hex is an interactive protein docking and molecular superposition program for Linux Mac-OS and Windows-XP. Hex understands protein and DNA structures in PDB format, and it can also read small-molecule SDF files. The recent versions now include CUDA support for Nvidia GPUs. On a modern workstation, docking times range from a few minutes or less when the search is constrained to known binding sites, to about half an hour for a blind global search (or just a few seconds with CUDA).
FUNCTIONAL DESCRIPTION: The underlying algorithm uses a novel polar Fourier correlation technique to accelerate the search for close-fitting orientations of the two molecules.

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

6.2. Kbdock

KEYWORD: 3D interaction
SCIENTIFIC DESCRIPTION: Kbdock is a database of 3D protein domain-domain interactions with a web interface.
FUNCTIONAL DESCRIPTION: The Kbdock database is built from a snapshot of the Protein Databank (PDB) in which all 3D structures are cut into domains according to the Pfam domain description. A web interface allows 3D domain-domain interactions to be compared by Pfam family.

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

6.3. Kpax

KEYWORDS: Bioinformatics - Structural Biology
SCIENTIFIC DESCRIPTION: Kpax is a program for aligning and superposing the 3D structures of protein molecules.
FUNCTIONAL DESCRIPTION: The algorithm uses a Gaussian representation of the protein backbone in order to construct a similarity score based on the 3D overlap of the Gaussians of the proteins to be superposed. Multiple proteins may be aligned together (multiple structural alignment) and databases of protein structures may be searched rapidly.

- Participant: David Ritchie
- Contact: David Ritchie

6.4. Sam

Protein Symmetry Assembler
KEYWORDS: Proteins - Structural Biology
SCIENTIFIC DESCRIPTION: Sam is a program for making symmetrical protein complexes, starting from a single monomer.

FUNCTIONAL DESCRIPTION: The algorithm searches for good docking solutions between protein monomers using a spherical polar Fast Fourier transform correlation in which symmetry restraints are built into the calculation. Thus every candidate solution is guaranteed to have the desired symmetry.

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

6.5. gEMfitter

KEYWORDS: 3D reconstruction - Cryo-electron microscopy - Fitting

SCIENTIFIC DESCRIPTION: A program for fitting high resolution 3D protein structures into low resolution cryo-EM density maps.

FUNCTIONAL DESCRIPTION: A highly parallel fast Fourier transform (FFT) EM density fitting program which can exploit the special hardware properties of modern graphics processor units (GPUs) to accelerate both the translational and rotational parts of the correlation search.

- Authors: Van-Thai Hoang and David Ritchie
- Contact: David Ritchie
- URL: http://gem.loria.fr/gEMfitter/

6.6. ECDM

ECDomainMiner

KEYWORD: Functional annotation

SCIENTIFIC DESCRIPTION: EC-DomainMiner uses a recommender-based approach for associating EC (Enzyme Commission) numbers with protein Pfam domains from EC-sequence relationships that have been annotated previously in the SIFTS and Uniprot databases.

FUNCTIONAL DESCRIPTION: A program to associate protein Enzyme Commission numbers with Pfam domains

- Contact: David Ritchie
- URL: http://ecdm.loria.fr

6.7. GODM

GO-DomainMiner

KEYWORD: Functional annotation

FUNCTIONAL DESCRIPTION: GO-DomainMiner is is a graph-based approach for associating GO (gene ontology) terms with protein Pfam domains.

- Contact: David Ritchie
- URL: http://godm.loria.fr

6.8. BLADYG

A Block-centric graph processing framework for LArge Dynamic Graphs

KEYWORDS: Distributed computing - Dynamic graph processing

FUNCTIONAL DESCRIPTION: BLADYG is a block-centric framework that addresses the issue of dynamism in large-scale graphs. BLADYG starts its computation by collecting the graph data from various data sources. After collecting the graph data, BLADYG partitions the input graph into multiple partitions. Each BLADYG worker loads its block/partition and performs both local and remote computations, after which the status of the blocks is updated. The BLADYG coordinator orchestrates the execution of the considered graph operation in order to deal with graph updates.

- Partner: University of Trento
- Contact: Sabeur Aridhi

6.9. CGC

Clebsch-Gordan Coefficients

KEYWORDS: Clebsch-Gordan coupling coefficient - 3j symbol

FUNCTIONAL DESCRIPTION: Clebsch-Gordan coupling coefficients appear in many areas of physics and chemistry. CGC is a small library of functions and a demo driver program for calculating Clebsch-Gordan coupling coefficients up to very high principal quantum numbers.

- Contact: David Ritchie
- URL: http://cgc.loria.fr

6.10. GrAPFI

GrAPFI: Graph-based Automatic Protein Function Inference

KEYWORD: Proteins

FUNCTIONAL DESCRIPTION: GrAPFI is a Graph-based Automatic Protein Function Inference tool that aims to annotate protein sequences with EC numbers. The underlying philosophy of GrAPFI assumes that proteins can be linked through the domains, families, and superfamilies that they share. Several domain databases exist such as e.g. Pfam, SMART, CDD, Gene3D, and Prosite. Furthermore, InterPro aims to integrate information from all such databases by assigning them unique InterPro signatures. GrAPFI tool also shares Interpro signatures, as it includes information from several major family and domain databases. Our computational analysis and cross-validation show that GrAPFI achieves state-of-the-art performance in EC number prediction.

- Contact: Sabeur Aridhi
- URL: http://grapfi.loria.fr/

6.11. Platforms

6.11.1. The MBI Platform

The MBI (Modeling Biomolecular Interactions) platform (http://bioinfo.loria.fr) was established to support collaborations between Inria Nancy – Grand Est and other research teams associated with the University of Lorraine. The platform is a research node of the Institut Français de Bioinformatique (IFB), which is the French national network of bioinformatics platforms (http://www.france-bioinformatique.fr). **In 2018, funding for an engineer was awarded to Marie-Dominique Devignes for a project on bioinformatics service integration.**

- Contact: Marie-Dominique Devignes

CARMEN Project-Team

5. New Software and Platforms

5.1. CEPS

Cardiac ElectroPhysiology Simulation
KEYWORDS: Simulation - Health - Mesh - Cardiac - 3D - Cardiac Electrophysiology
SCIENTIFIC DESCRIPTION: As compared to other existing softwares, CEPS aims at providing a more general framework of integration for new methods or models and a better efficiency in parallel. CEPS is designed to run on massively parallel architectures, and to make use of state-of-the-art and well known computing libraries to achieve realistic and complex heart simulations. CEPS also includes software engineering and validation tools.
FUNCTIONAL DESCRIPTION: CEPS is a numerical simulation tool focused on the modeling of cardiac electrophysiology. The goal of CEPS is to easily allow the development of new numerical methods and new physical models.

- Participants: Mehdi Juhoor, Nejib Zemzemi, Antoine Gerard, Charlie Douanla Lontsi, Pierre-Elliott Bécue, Marc Fuentes and Yves Coudière
- Partners: Université de Bordeaux - Fondation Bordeaux Université - CHU de Bordeaux - Inria
- Contact: Yves Coudière
- URL: https://gforge.inria.fr/projects/ceps/

5.2. Platforms

5.2.1. CEMPACK

CEMPACK is a new collection of software that was previously archived in different places. It includes the high-performance simulation code Propag and a suite of software for the creation of geometric models, preparing inputs for Propag, and analysing its outputs. In 2017 the code was collected in an archive on Inria's GitLab platform, and a public website was created for documentation (http://cempack.gforge.inria.fr). The main components of CEMPACK are the following.

Propag-5.1 Applied modeling studies performed by the Carmen team in collaboration with IHU Liryc and foreign partners [7] [65], [56], [55], [53] rely on high-performance computations on the national supercomputers Irene, Occigen, and Turing. The Propag-5 code is optimized for these systems. It is the result of a decades-long development first at the *Université de Montréal* in Canada, then at Maastricht University in the Netherlands, and finally at the Institute of Computational Science of the *Università della Svizzera italiana* in Lugano, Switzerland. Since 2016 most of the development on Propag has been done by M. Potse at the Carmen team [27]. The code scales excellently to large core counts and, as it is controlled completely with command-line flags and configuration files, it can be used by non-programmers. It also features

- a plugin system for membrane models,
- a completely parallel workflow, including the initial anatomy input and mesh partitioning, which allows it to work with meshes of more than 10^9 nodes,
- a flexible output scheme allowing hundreds of different state variables and transient variables to be output to file, when desired, using any spatial and temporal subsampling,
- a configurable, LUSTRE-aware parallel output system in which groups of processes write HDF5/netCDF files, and
- CWEB documentation of the entire code base.

The code has been stable and reliable for several years. It can be considered the workhorse for our HPC work until CEPS takes over.

Gepetto The Gepetto suite, named after a famous model maker, transforms a surface mesh of the heart into a set of (semi-)structured meshes for use by the Propag software or others. It creates the different fiber orientations in the model, including the transmurally rotating ventricular fibers and the various bundle structures in the atria (figure 2), and creates layers with possibly different electrophysiological properties across the wall. A practically important function is that it automatically builds the matching heart and torso meshes that Propag uses to simulate potentials in the torso (at a resolution of 1 mm) after projecting simulation results from the heart model (at 0.1 to 0.2 mm) on the coarser torso mesh [64]. Like Propag, the Gepetto software results from a long-term development that started in Montreal, Canada, around 2002. The code for atrial fiber structure was developed by our team.

Blender plugins Blender (https://www.blender.org) is a free software package for the production of 3-D models, renderings, and animations, comparable to commercial software such as Cinema4D. CEMPACK includes a set of plugins for Blender that facilitate the production of anatomical models and the visualization of measured and simulated data. It uses the MMG remeshing library, which is developed by the CARDAMOM team at Inria Bordeaux.

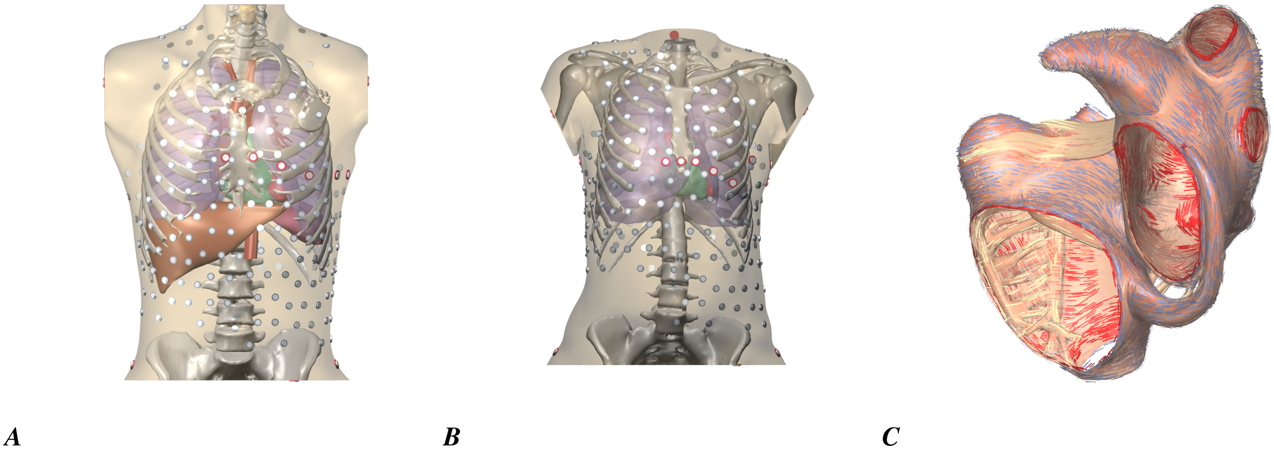


*Figure 2. **A and B:** Complete heart-torso geometries created with CEMPACK tools. **C:** Bundle structures and different layers of fiber orientation created by the Gepetto software.*

5.2.2. MUSIC

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

Several members of the Carmen team use MUSIC for their work, and the team contributes to the software through the IDAM project.

CASTOR Project-Team

6. New Software and Platforms

6.1. CEDRES++

KEYWORDS: 2D - Magnetic fusion - Plasma physics
FUNCTIONAL DESCRIPTION: In Tokamaks, at the slow resistive diffusion time scale, the magnetic configuration in the plasma can be described by the MHD equilibirum equations inside the plasma and the Maxwell equations outside. Moreover, the magnetic field is often supposed not to depend on the azimutal angle.

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

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

6.2. Equinox

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

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

6.3. FBGKI

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

- Contact: Sebastian Minjeaud

6.4. FEEQS.M

Finite Element Equilibrium Solver in MATLAB

KEYWORDS: Finite element modelling - Optimal control - Plasma physics

FUNCTIONAL DESCRIPTION: FEEQS.M (Finite Element Equilibrium Solver in Matlab) is a MATLAB implementation of the numerical methods in [Heumann2015] to solve equilibrium problems for toroidal plasmas. Direct and inverse problems for both the static and transient formulations of plasma equilibrium can be solved. FEEQS.M exploits MATLAB's evolved sparse matrix methods and uses heavily the vectorization programming paradigm, which results in running times comparable to C/C++ implementations. FEEQS.M complements the production code CEDRES++ in being considered as fast prototyping test bed for computational methods for equilibrium problems. This includes aspects of numerics such as improved robustness of the Newton iterations or optimization algorithms for inverse problems. The latest developments aim at incorporating the resistive diffusion equation.

[Heumann2015]: Heumann, H., Blum, J., Boulbe, C., Faugeras, B., Selig, G., Ané, J.-M., Brémond, S., Grandgirard, V., Hertout, P., Nardon, E.: Quasi-static free-boundary equilibrium of toroidal plasma with CEDRES++: Computational methods and applications. In: Journal of Plasma Physics 81 (2015)

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

6.5. Fluidbox

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

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

6.6. Jorek-Inria

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

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

- Participants: Ahmed Ratnani, Boniface Nkonga, Emmanuel Franck and Hervé Guillard
- Contact: Hervé Guillard
- URL: https://gforge.inria.fr/projects/jorek/

6.7. Plato

A platform for Tokamak simulation

FUNCTIONAL DESCRIPTION: PlaTo (A platform for Tokamak simulation) is a suite of data and softwares dedicated to the geometry and physics of Tokamaks. Plato offers interfaces for reading and handling distributed unstructured meshes, numerical templates for parallel discretizations, interfaces for distributed matrices and linear and non-linear equation solvers. Plato provides meshes and solutions corresponding to equilibrium solutions that can be used as initial data for more complex computations as well as tools for visualization using Visit or Paraview.

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

6.8. VacTH

KEYWORD: Problem inverse
FUNCTIONAL DESCRIPTION: VacTH implements a method based on the use of toroidal harmonics and on a modelization of the poloidal field coils and divertor coils to perform the 2D interpolation and extrapolation of discrete magnetic measurements in a tokamak and the identification of the plasma boundary. The method is generic and can be used to provide the Cauchy boundary conditions needed as input by a fixed domain equilibrium reconstruction code like EQUINOX. It can also be used to extrapolate the magnetic measurements in order to compute the plasma boundary itself. The method is foreseen to be used in the real-time plasma control loop on the WEST tokamak.

- Contact: Blaise Faugeras

6.9. NICE

Newton direct and Inverse Computation for Equilibrium
KEYWORDS: 2D - C++ - Scientific computing - Finite element modelling - Plasma physics - Optimal control - Optimization - Identification
FUNCTIONAL DESCRIPTION: The NICE code is under development. Its goal is to gather in a single modern, modular and evolutionary C++ code, the different numerical methods and algorithms from VACTH, EQUINOX and CEDRES++ which share many common features. It also integrates new methods as for example the possibility to use the Stokes model for equilibrium reconstruction using polarimetry measurements.

- Contact: Blaise Faugeras

COFFEE Project-Team

6. New Software and Platforms

6.1. AP_PartFlow

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

- Contact: Thierry Goudon

6.2. Mka3d

KEYWORDS: Scientific computing - Elasticity - Elastodynamic equations
FUNCTIONAL DESCRIPTION: The Mka3d method simulates an elastic solid by discretizing the solid into rigid particles. An adequate choice of forces and torques between particles allows to recover the equations of elastodynamics.

- Partners: Ecole des Ponts ParisTech - CEA
- Contact: Laurent Monasse
- URL: http://cermics.enpc.fr/~monassel/Mka3D/

6.3. Compass

Computing Architecture to Speed up Simulation
KEYWORDS: Finite volume methods - Porous media - High performance computing
FUNCTIONAL DESCRIPTION: Compass is a parallel code initiated in 2012 and co-developed by LJAD-Inria Coffee and BRGM since 2015. It is devoted to the simulation of multiphase flows in porous media, it accounts for non isothermal and compositional flows and includes complex network of fractures or faults represented as interfaces of co-dimension one coupled to the surrounding matrix. The discretization is based on vertex and cell unknowns and is adapted to polyhedral meshes and heterogeneous media. The ComPASS code is co-developed since december 2016 by the partners of the ANR CHARMS project including BGRM, LJAD-Inria Coffee, Storengy, MdS and LJLL with the objective to develop a new generation simulator for geothermal systems focusing on fluids and accounting for complex fault networks and wells.

- Participants: Simon Lopez, Farid Smai, Michel Kern, Yacine Ould Rouis, Nabil Birgle, Laurence Beaude, Konstantin Brenner and Roland Masson
- Partners: Université de Nice Sophia Antipolis (UNS) - BRGM
- Contact: Roland Masson
- URL: http://www.anr-charms.org/page/compass-code

6.4. NS2DDV-M

2D Navier-Stokes equations with variable density
KEYWORDS: Partial differential equation - Finite volume methods - Finite element modelling

FUNCTIONAL DESCRIPTION: The NS2DDV Matlab toolbox is an open-source program written in Matlab for simulating 2D viscous, incompressible and inhomogeneous flows. The computation kernel of the code is based on Finite Elements - Finite Volumes hybrid methods applied on the 2D Navier-Stokes equations. It works on unstructured meshes and can include mesh refinements strategies. We develop and freely distribute a new version of the Matlab code NS2DDV-M (equipped with a graphic interface and an accurate documentation) to promote new collaborations in the domain, allow some easy comparisons with concurrent codes on the same benchmark cases, and compare alternative numerical solution methods.

- Partner: Laboratoire Paul Painlevé
- Contact: Caterina Calgaro-Zotto
- URL: https://wikis.univ-lille1.fr/painleve/ns2ddv

6.5. SimBiof

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

- Contact: Thierry Goudon

6.6. CELIA3D

KEYWORDS: Fluid mechanics - Multi-physics simulation
FUNCTIONAL DESCRIPTION: The CELIA3D code simulates the coupling between a compressible fluid flow and a deformable structure. The fluid is handled by a Finite Volume method on a structured Cartesian grid. The solid is handled by a Discrete Element method (Mka3d scheme). The solid overlaps the fluid grid and the coupling is carried out with immersed boundaries (cut cells) in a conservative way.

- Partners: Ecole des Ponts ParisTech - CEA
- Contact: Laurent Monasse
- URL: http://cermics.enpc.fr/~monassel/CELIA3D/

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

DYLISS Project-Team

6. New Software and Platforms

6.1. AskOmics

Convert tabulated data into RDF and create SPARQL queries intuitively and "on the fly".
KEYWORDS: RDF - SPARQL - Querying - Graph - LOD - Linked open data
FUNCTIONAL DESCRIPTION: AskOmics aims at bridging the gap between end user data and the Linked (Open) Data cloud. It allows heterogeneous bioinformatics data (formatted as tabular files) to be loaded in a RDF triplestore and then be transparently and interactively queried. AskOmics is made of three software blocks: (1) a web interface for data import, allowing the creation of a local triplestore from user's datasheets and standard data, (2) an interactive web interface allowing "à la carte" query-building, (3) a server performing interactions with local and distant triplestores (queries execution, management of users parameters).
NEWS OF THE YEAR: (1) Improvements: Bugfixes and ui improvements in response to user feedback. (2) Versionning: Regular development cycle: a new version of AskOmics will be available every 3 months (currently 18.10, next 19.01) (3) Deployment: Deployment has been improved with docker and docker-compose. Virtual machine images are available on genostack to easy deploy AskOmics and Virtuoso (4) Federation: AskOmics can perform federated queries on mutliple triplestores, including other AskOmics endpoints, but also external endpoints like uniprot or dbpedia. (still in development)

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

6.2. CADBIOM

Computer Aided Design of Biological Models
KEYWORDS: Health - Biology - Biotechnology - Bioinformatics - Systems Biology
FUNCTIONAL DESCRIPTION: The Cadbiom software provides a formal framework to help the modeling of biological systems such as cell signaling network with Guarder Transition Semantics. It allows synchronization events to be investigated in biological networks among large-scale network in order to extract signature of controllers of a phenotype. Three modules are composing Cadbiom. 1) The Cadbiom graphical interface is useful to build and study moderate size models. It provides exploration, simulation and checking. For large-scale models, Cadbiom also allows to focus on specific nodes of interest. 2) The Cadbiom API allows a model to be loaded, performing static analysis and checking temporal properties on a finite horizon in the future or in the past. 3) Exploring large-scale knowledge repositories, since the translations of the large-scale PID repository (about 10,000 curated interactions) have been translated into the Cadbiom formalism.
NEWS OF THE YEAR: - Comprehensive command line to run the calculations and analyze the generated results. - Module designed to produce models through the interpretation of various databases or ontologies, formalized according to the BioPAX standard. - Update of the site and the documentation.

- Participants: Geoffroy Andrieux, Michel Le Borgne, Nathalie Theret, Nolwenn Le Meur, Pierre Vignet and Anne Siegel
- Contact: Anne Siegel
- URL: http://cadbiom.genouest.org

6.3. MiSCoTo

Microbiota Screening and COmmunity Selection with TOpology
KEYWORDS: Metabolic networks - ASP - Answer Set Programming - Logic programming
SCIENTIFIC DESCRIPTION: MiSCoTo solves combinatorial problems using Answer Set Programming. It aims at minimizing either the number of selected species or both the number of selected species and the cost of the interaction between them, characterized by the number of metabolic exchanges. In the first case, the level of modeling is called lumped or mixed-bag, in the latter, it is compartmentalized.
FUNCTIONAL DESCRIPTION: Metabolic networks are composed of biochemical reactions and gather the expected metabolic capabilities of species. For organisms that live in interaction altogether (microbiotas), complementarity between these networks can be exploited to predict cooperation events. This software takes as inputs metabolic networks for various species (host, symbionts of the microbiota), components of the growth medium and a metabolic objective (metabolites to be produced), and aims at selecting a minimal set of symbionts to ensure the metabolic objective can be achieved. The software can use two types of modelings: a simplified one and another that takes into account the cost of metabolic exchanges and aims at minimizing it.
NEWS OF THE YEAR: Release of the first version of the software

- Participants: Clémence Frioux, Anne Siegel, Enora Fremy and Camille Trottier
- Contact: Anne Siegel
- Publication: Scalable and exhaustive screening of metabolic functions carried out by microbial consortia
- URL: https://github.com/cfrioux/miscoto

6.4. Pathmodel

KEYWORDS: ASP - Answer Set Programming - Metabolic networks - Metabolic Pathway Drift - Bioinformatics - Systems Biology - Metabolomics
SCIENTIFIC DESCRIPTION: This tool is a prototype of the Metabolic Pathway Drift concept. This concept states that metabolic pathways undergo substantial turnover. The reactions involved in a pathway can change between species (change in reaction order or replacement of an enzyme by another one). Another goal of this tool is to linked genomics and metabolomics data. To implement this concept, Pathmodel uses the Answer Set Programming language. The input are the reactants and products involved in the pathway, known reactions occurring between these molecules, known m/z ratio, known domains shard by these molecules, an initial molecule and a goal molecule. Using these data, Pathmodel will infer reactions between molecules to reach the goal molecule using the known reactions. The result consist of potential alternative pathways for the studied organism.
FUNCTIONAL DESCRIPTION: A metabolic pathway is a series of biochemical reactions. These reactions modify metabolites in order to synthesize a new metabolite or to produce energy. One difficulties when dealing with pathways in non-model organism is their incomplete conservation during evolution. To deal with this problem, we developed a prototype inferring new biochemical reactions using reactions and metabolites from known metabolic pathways and metabolomics data. This method produce alternative pathway that could occurred in the species of interest.

RELEASE FUNCTIONAL DESCRIPTION: First version.
NEWS OF THE YEAR: Development of the tool. First release.

- Participants: Arnaud Belcour, Jacques Nicolas, Gabriel Markov and Anne Siegel
- Partner: Station Biologique de Roscoff
- Contact: Anne Siegel
- Publication: Inferring biochemical reactions and metabolite structures to cope with metabolic pathway drift
- URL: https://gitlab.inria.fr/DYLISS/PathModel

6.5. AuReMe

Automatic Reconstruction of Metabolic networks
KEYWORDS: Workflow - Bioinformatics - Metabolic networks - Omic data - Toolbox - Data management
FUNCTIONAL DESCRIPTION: AuReMe enables the reconstruction of metabolic networks from different sources based on sequence annotation, orthology, gap-filling and manual curation. The metabolic network is exported as a local wiki allowing to trace back all the steps and sources of the reconstruction. It is highly relevant for the study of non-model organisms, or the comparison of metabolic networks for different strains or a single organism.

Five modules are composing AuReMe: 1) The Model-management PADmet module allows manipulating and traceing all metabolic data via a local database. 2) The meneco python package allows the gaps of a metabolic network to be filled by using a topological approach that implements a logical programming approach to solve a combinatorial problem 3) The shogen python package allows genome and metabolic network to be aligned in order to identify genome units which contain a large density of genes coding for enzymes, it also implements a logical programming approach. 4) The manual curation assistance PADmet module allows the reported metabolic networks and their metadata to be curated. 5) The Wiki-export PADmet module enables the export of the metabolic network and its functional genomic unit as a local wiki platform allowing a user-friendly investigation.
NEWS OF THE YEAR: (1) Creation of a python package for the multiprocessing of Pathway-Tools. (2) Moving from Python 2 to Python 3. (3) Application of AuReMe to microbiome reconstructions and wikis.

- Participants: Marie Chevallier, Meziane Aite, Guillaume Collet, Nicolas Loira, Sylvain Prigent, Jeanne Got, Anne Siegel and Alejandro Maass
- Partner: University of Chile
- Contact: Meziane Aite
- Publication: Traceability, reproducibility and wiki-exploration for ”à-la-carte” reconstructions of genome-scale metabolic models
- URL: http://aureme.genouest.org/

6.6. biseau

KEYWORDS: ASP - Answer Set Programming - Graph - Formal concept analysis
SCIENTIFIC DESCRIPTION: Use ASP as a Domain Specific Language to specify dot-based visualizations.
NEWS OF THE YEAR: First release.

- Contact: Lucas Bourneuf
- Publication: An Answer Set Programming Environment for High-Level Specification and Visualization of FCA
- URL: https://gitlab.inria.fr/lbourneu/biseau

EPIONE Project-Team

5. New Software and Platforms

5.1. CardiacSegmentationPropagation

KEYWORDS: 3D - Segmentation - Cardiac - MRI - Deep learning
FUNCTIONAL DESCRIPTION: Training of a deep learning model which is used for cardiac segmentation in short-axis MRI image stacks.

- Authors: Qiao Zheng, Hervé Delingette, Nicolas Duchateau and Nicholas Ayache
- Contact: Qiao Zheng
- Publication: hal-01753086, version 1

5.2. CardiacMotionFlow

KEYWORDS: 3D - Deep learning - Cardiac - Classification
FUNCTIONAL DESCRIPTION: Creation of a deep learning model for the motion tracking of the heart, extraction of characteristic quantities of the movement and shape of the heart to classify a sequence of cine-MRI cardiac images in terms of the types of pathologies (infarcted heart, dilated , hypertrophied, abnormality of the right ventricle).

- Contact: Qiao Zheng

5.3. MedInria

KEYWORDS: Visualization - DWI - Health - Segmentation - Medical imaging
SCIENTIFIC DESCRIPTION: medInria aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010, renewed in 2012. A fast-track ADT was awarded in 2017 to transition the software core to more recent dependencies and study the possibility of a consortium creation.The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.
FUNCTIONAL DESCRIPTION: MedInria is a free software platform dedicated to medical data visualization and processing.

- Participants: Maxime Sermesant, Olivier Commowick and Théodore Papadopoulo
- Partners: HARVARD Medical School - IHU - LIRYC - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

5.4. GP-ProgressionModel

GP progression model
KEYWORDS: Data modeling - Data visualization - Data integration - Machine learning - Biostatistics - Statistical modeling - Medical applications - Evolution - Brain - Uncertainly - Uncertainty quantification - Alzheimer's disease - Probability - Stochastic models - Stochastic process - Trajectory Modeling - Marker selection - Health - Statistic analysis - Statistics - Bayesian estimation
FUNCTIONAL DESCRIPTION: Disease progression modeling (DPM) of Alzheimer's disease (AD) aims at revealing long term pathological trajectories from short term clinical data. Along with the ability of providing a data-driven description of the natural evolution of the pathology, DPM has the potential of representing a valuable clinical instrument for automatic diagnosis, by explicitly describing the biomarker transition from normal to pathological stages along the disease time axis.

In this software we reformulate DPM within a probabilistic setting to quantify the diagnostic uncertainty of individual disease severity in an hypothetical clinical scenario, with respect to missing measurements, biomarkers, and follow-up information. The proposed formulation of DPM provides a statistical reference for the accurate probabilistic assessment of the pathological stage of de-novo individuals, and represents a valuable instrument for quantifying the variability and the diagnostic value of biomarkers across disease stages.

This software is based on the publication:

Probabilistic disease progression modeling to characterize diagnostic uncertainty: Application to staging and prediction in Alzheimer's disease. Marco Lorenzi, Maurizio Filippone, Daniel C. Alexander, Sebastien Ourselin Neuroimage. 2017 Oct 24. pii: S1053-8119(17)30706-1. doi: 10.1016/j.neuroimage.2017.08.059. HAL Id : hal-01617750 https://hal.archives-ouvertes.fr/hal-01617750/

- Authors: Marco Lorenzi and Maurizio Filippone
- Contact: Marco Lorenzi
- URL: http://gpprogressionmodel.inria.fr

5.5. Music

Multi-modality Platform for Specific Imaging in Cardiology
KEYWORDS: Medical imaging - Cardiac Electrophysiology - Computer-assisted surgery - Cardiac - Health
FUNCTIONAL DESCRIPTION: MUSIC is a software developed by the Asclepios research project in close collaboration with the IHU LIRYC in order to propose functionalities dedicated to cardiac interventional planning and guidance. This includes specific tools (algorithms of segmentation, registration, etc.) as well as pipelines. The software is based on the MedInria platform.

- Participants: Florent Collot, Mathilde Merle and Maxime Sermesant
- Partner: IHU- Bordeau
- Contact: Maxime Sermesant
- URL: https://team.inria.fr/asclepios/software/music/

5.6. SOFA

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

- Participants: Christian Duriez, François Faure, Hervé Delingette and Stéphane Cotin
- Partner: IGG
- Contact: Stéphane Cotin
- URL: http://www.sofa-framework.org

5.7. geomstats

Computations and statistics on manifolds with geometric structures

KEYWORD: Geometry
FUNCTIONAL DESCRIPTION: Geomstats is a python package that performs computations on manifolds such as hyperspheres, hyperbolic spaces, spaces of symmetric positive definite matrices and Lie groups of transformations. It provides efficient and extensively unit-tested implementations of these manifolds, together with useful Riemannian metrics and associated Exponential and Logarithm maps. The corresponding geodesic distances provide a range of intuitive choices of Machine Learning loss functions. We also give the corresponding Riemannian gradients. The operations implemented in geomstats are available with different computing backends such as numpy, tensorflow and keras. Geomstats manifold computations have are integrated into keras deep learning framework thanks to GPU-enabled implementations.

- Partner: Stanford Department of Statistics
- Contact: Nina Miolane
- URL: https://github.com/geomstats/

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 Deniélou
- 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 Sinaimeri, Catherine Matias, Christian Baudet, Christian Gautier, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinaimeri
- 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/leoisl/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 Sinaimeri, Christian Baudet, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinaimeri
- 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://kissplice.prabi.fr/tools/kissDE/

5.13. KisSplice

KEYWORDS: Bioinformatics - Bioinfirmatics 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://kissplice.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://kissplice.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://kissplice.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 synthetise 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 / PAPAPITUFO) 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/whatshap/whatshap

FLUMINANCE Project-Team

5. New Software and Platforms

5.1. 2DLayeredMotion

Estimation of 2D independent mesoscale layered atmospheric motion fields

FUNCTIONAL DESCRIPTION: This software enables to estimate a stack of 2D horizontal wind fields corresponding to a mesoscale dynamics of atmospheric pressure layers. This estimator is formulated as the minimization of a global energy function. It relies on a vertical decomposition of the atmosphere into pressure layers. This estimator uses pressure data and classification clouds maps and top of clouds pressure maps (or infra-red images). All these images are routinely supplied by the EUMETSAT consortium which handles the Meteosat and MSG satellite data distribution. The energy function relies on a data model built from the integration of the mass conservation on each layer. The estimator also includes a simplified and filtered shallow water dynamical model as temporal smoother and second-order div-curl spatial regularizer. The estimator may also incorporate correlation-based vector fields as additional observations. These correlation vectors are also routinely provided by the Eumetsat consortium.

- Participant: Étienne Mémin
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr/index.html

5.2. 3DLayeredMotion

Estimation of 3D interconnected layered atmospheric motion fields

FUNCTIONAL DESCRIPTION: This software extends the previous 2D version. It allows (for the first time to our knowledge) the recovery of 3D wind fields from satellite image sequences. As with the previous techniques, the atmosphere is decomposed into a stack of pressure layers. The estimation relies also on pressure data and classification clouds maps and top of clouds pressure maps. In order to recover the 3D missing velocity information, physical knowledge on 3D mass exchanges between layers has been introduced in the data model. The corresponding data model appears to be a generalization of the previous data model constructed from a vertical integration of the continuity equation.

- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.3. DenseMotion

Estimation of 2D dense motion fields

FUNCTIONAL DESCRIPTION: This code allows the computation from two consecutive images of a dense motion field. The estimator is expressed as a global energy function minimization. The code enables the choice of different data models and different regularization functionals depending on the targeted application. Generic motion estimators for video sequences or fluid flows dedicated estimators can be set up. This software allows in addition the users to specify additional correlation based matching measurements. It enables also the inclusion of a temporal smoothing prior relying on a velocity vorticity formulation of the Navier-Stoke equation for Fluid motion analysis applications.

- Participant: Étienne Mémin
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr/index.html

5.4. Low-Order-Motion

Estimation of low order representation of fluid motion

FUNCTIONAL DESCRIPTION: This code enables the estimation of a low order representation of a fluid motion field from two consecutive images.The fluid motion representation is obtained using a discretization of the vorticity and divergence maps through regularized Dirac measure. The irrotational and solenoidal components of the motion fields are expressed as linear combinations of basis functions obtained through the Biot-Savart law. The coefficient values and the basis function parameters are formalized as the minimizer of a functional relying on an intensity variation model obtained from an integrated version of the mass conservation principle of fluid mechanics.

- Participants: Anne Cuzol and Étienne Mémin
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.5. TYPHOON

- Participants: Christopher Mauzey, Étienne Mémin and Pierre Dérian
- Partner: CSU Chico
- Contact: Étienne Mémin
- URL: http://phys.csuchico.edu/lidar/typhoon/

5.6. H2OLab

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

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

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

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

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

5.7. PALMTREE

KEYWORD: Monte-Clarlo

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

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

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

- Authors: Lionel Lenôtre, Géraldine Pichot, Lionel Lenôtre and Lionel Lenôtre
- Contact: Géraldine Pichot

5.8. GRT3D

Global Reactive Transport in 3D
KEYWORDS: Geochemistry - Dispersion - Scientific calculation - Simulation - Advection
SCIENTIFIC DESCRIPTION: Participants : Édouard Canot, Jocelyne Erhel [correspondant] .

Version: version 2.0, April 2014

APP: registered

Programming language: C

Abstract: Reactive transport modeling has become an essential tool for understanding complex environmental problems. It is an important issue for MoMaS and C2S@EXA partners (see sections 8.2.5 , 8.2.3), in particular Andra. We have developed a method coupling transport and chemistry, based on a method of lines such that spatial discretization leads to a semi-discrete system of algebraic differential equations (DAE system). The main advantage is to use a complex DAE solver, which controls simultaneously the timestep and the convergence of Newton algorithm. The approach SIA uses a fixed-point method to solve the nonlinear system at each timestep, whereas the approach SNIA uses an explicit scheme.

The software suite GRT3D has four executable modules:

SIA1D: Sequential Iterative Approach for 1D domains,

GDAE1D: Global DAE approach for 1D domains,

SNIA3D: Sequential Non Iterative Approach for 1D, 2D or 3D domains.

GDAE3D: Global DAE approach for 1D, 2D or 3D domains. This module has three variants: the original one with logarithms, an optimized one still with logarithms, an optimized one which does not use logarithms.

Current work: extension of the chemistry module and parallelization.
FUNCTIONAL DESCRIPTION: Reactive transport modeling has become an essential tool for understanding complex environmental problems. It is an important issue for MoMaS and C2S@EXA partners, in particular Andra. We have developed a method coupling transport and chemistry, based on a method of lines such that spatial discretization leads to a semi-discrete system of algebraic differential equations (DAE system). The main advantage is to use a complex DAE solver, which controls simultaneously the timestep and the convergence of Newton algorithm. The approach SIA uses a fixed-point method to solve the nonlinear system at each timestep, whereas the approach SNIA uses an explicit scheme.

The software suite GRT3D has four executable modules:

SIA1D: Sequential Iterative Approach for 1D domains,

GDAE1D: Global DAE approach for 1D domains,

SNIA3D: Sequential Non Iterative Approach for 1D, 2D or 3D domains.

GDAE3D: Global DAE approach for 1D, 2D or 3D domains. This module has three variants: the original one with logarithms, an optimized one still with logarithms, an optimized one which does not use logarithms.

- Participants: Caroline De Dieuleveult, Édouard Canot, Jocelyne Erhel, Nadir Soualem and Souhila Sabit
- Partner: ANDRA
- Contact: Jocelyne Erhel

GALEN-POST Team

6. New Software and Platforms

6.1. Platforms

6.1.1. The Proximity Operator Repository

Participants: Emilie Chouzenoux and Jean-Christophe Pesquet (in collaboration with Giovanni Chierchia, Univ. Paris Est, and Patrick Combettes, North Carolina State University).
link: http://proximity-operator.net/
Proximity operators have become increasingly important tools as basic building blocks of proximal splitting algorithms, a class of algorithms that decompose complex composite convex optimization methods into simple steps involving one of the functions present in the model. This website provides formulas for efficiently computing the proximity operator of various functions, along with the associated codes.

6.1.2. Kymatio

Participant: Edouard Oyallon.
link: http://www.kymat.io
The website shares the software `Kymatio` for Scattering Transform, that computes cascade of wavelets and modulus non-linearity. The codes have been optimized for GPUs and work on the open-source framework *PyTorch*.

6.1.3. Topical Node Embeddings

Participant: Abdulkadir Çelikkanat
link: https://abdcelikkanat.github.io/projects/TNE/
TNE learns node representations on graphs combining node and topic information, as described in [45]. The framework has been implemented in Python and has been built upon widely used modules, including `networkx`, `scipy`, `gensim` and `scikit-learn`.

6.1.4. BiasedWalk: Learning latent node features with biased random walks

Participants: Fragkiskos Malliaros and Duong Nguyen (UC San Diego)
link: https://github.com/duong18/BiasedWalk/
The BiasedWalk network representation learning algorithm, computes latent node features on graphs based on biased random walks [33]. The framework has been implemented in Python and has been built upon widely used modules, including `networkx`, `numpy`, `gensim` and `scikit-learn`.

6.1.5. DiffuGreedy: Influence maximization in complex networks based on diffusion cascades

Participants: Fragkiskos Malliaros, Georgios Panagopoulos and Michalis Vazirgiannis (École Polytechnique)
link: https://goo.gl/GpfCVZ
The DiffuGreedy is an algorithm for influence maximization in complex networks, that is based on diffusion cascades. The algorithm implements the methodology described in [35]. It has been implemented in Python and has been built upon widely used modules, including `networkx`, `igraph`, `numpy` and `pandas`.

6.1.6. Graph-based text categorization

Participants: Fragkiskos Malliaros, Konstantinos Skianis and Michalis Vazirgiannis (École Polytechnique)
link: https://github.com/y3nk0/Graph-Based-TC/

Graph-based TC is a framework for text categorization that relies on a graph representation of documents. The framework uses various graph centrality criteria to determine the importance of a term within a document. It also makes use of word embeddings to further boost the performance of graph-based methods. The algorithm implements the methodology described in [39]. It has been implemented in Python and has been built upon widely used modules, including `networkx`, `igraph`, `numpy` and `scikit-learn`.

6.1.7. The PINK image library

Participant: Hugues Talbot
link: http://ibipio.hu/joomla/
The PINK image library is a general-purpose, open-source, portable image processing library specializing in discrete geometry and mathematical morphology. It is the result of several decades of research in these domains and features state-of-the art algorithmic implementation of both classical and leading edge DG and MM operators. These include nD parallel thinning and skeletonization methods and efficient hierarchical morphological transforms.

6.1.8. The Vivabrain AngioTK toolkit

Participant: Hugues Talbot
link: https://github.com/vivabrain/angiotk
AngioTK is a toolkit supported by Kitware (the authors of VTK) for the filtering, segmentation, generation and simulation of blood vessels. It was started in the context of the Vivabrain ANR project in 2012, but continues with the same as well as new partners. Applications are numerous, from the simulation and understanding of perfusion (see associated theme) to the simulation of realistic blood flow MRI images with associated ground truth, via the generation of blood vessel atlases.

GENSCALE Project-Team

6. New Software and Platforms

6.1. GATB-Core

Genome Assembly and Analysis Tool Box
KEYWORDS: Bioinformatics - NGS - Genomics - Genome assembling
FUNCTIONAL DESCRIPTION: The GATB-Core library aims to lighten the design of NGS algorithms. It offers a panel of high-level optimized building blocks to speed-up the development of NGS tools related to genome assembly and/or genome analysis. The underlying data structure is the de Bruijn graph, and the general parallelism model is multithreading. The GATB library targets standard computing resources such as current multicore processor (laptop computer, small server) with a few GB of memory. From high-level API, NGS programming designers can rapidly elaborate their own software based on domain state-of-the-art algorithms and data structures. The GATB-Core library is written in C++.

- Participants: Charles Deltel, Rayan Chikhi, Erwan Drezen, Antoine Limasset, Gaëtan Benoit, Uricaru Raluca, Claire Lemaitre, Dominique Lavenier, Guillaume Rizk, Patrick Durand and Pierre Peterlongo
- Contact: Dominique Lavenier
- URL: http://gatb.inria.fr/

6.2. CARNAC-LR

Clustering coefficient-based Acquisition of RNA Communities in Long Reads
KEYWORDS: Transcriptomics - Clustering - Bioinformatics
FUNCTIONAL DESCRIPTION: Carnac-LR is a clustering method for third generation sequencing data. Used on RNA sequences it retrieves all sequences that relate to a same gene and put them in a cluster. CARNAC-LR is an efficient implementation of a novel clustering algorithm for detecting communities in a graph of reads from Third Generation Sequencing. It is a part of a pipeline that allows to retrieve expressed variants from each gene de novo (without reference genome/transcriptome), for transcriptomic sequencing data.

- Participants: Camille Marchet, Pierre Peterlongo and Jacques Nicolas
- Contact: Camille Marchet
- Publication: De Novo Clustering of Long Reads by Gene from Transcriptomics Data
- URL: https://github.com/kamimrcht/CARNAC

6.3. MindTheGap

KEYWORDS: Bioinformatics - NGS - Genome assembly
FUNCTIONAL DESCRIPTION: MindTheGap is a NGS software that performs local assembly of short reads. It is a structural variant detection tool as well as a genome assembly finishing tool. As a variant caller, it performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It is designed to call insertions of any size, whether they are novel or duplicated, homozygous or heterozygous in the donor genome. Local assembly is performed to recover the inserted sequences from the whole read dataset. The local assembly module can also be used to fill the gaps between a set of input contigs without any a priori on their relative order and orientation, in order to improve a draft genome assembly.

RELEASE FUNCTIONAL DESCRIPTION: Since version 2.1.0, MindTheGap can also be used as a genome assembly finishing tool: it can fill the gaps between a set of input contigs without any a priori on their relative order and orientation. This new feature is available in the Fill module with option -contig.

- Participants: Claire Lemaitre, Guillaume Rizk, Pierre Marijon, Rayan Chikhi, Wesley Delage and Cervin Guyomar
- Contact: Claire Lemaitre
- Publication: MindTheGap: integrated detection and assembly of short and long insertions
- URL: https://gatb.inria.fr/software/mind-the-gap/

6.4. bcool

de Bruijn graph cOrrectiOn from graph aLignment

KEYWORDS: De Bruijn graphs - Reads correction - Short reads - Read mapping

FUNCTIONAL DESCRIPTION: BCool is a method to correct short reads using de Bruijn graphs. BCool includes two steps. As a first step, Bcool constructs a corrected compacted de Bruijn graph from the reads. This graph is then used as a reference and the reads are corrected according to their mapping on the graph.This approach yields a better correction than kmer-spectrum techniques, while being scalable, making it possible to apply it to human-size genomic datasets and beyond. The implementation is open source and available at github.com/Malfoy/BCOOL

- Participants: Antoine Limasset and Pierre Peterlongo
- Partner: Université libre de Bruxelles
- Contact: Pierre Peterlongo
- Publication: Toward perfect reads: self-correction of short reads via mapping on de Bruijn graphs
- URL: http://github.com/Malfoy/BCOOL

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/wellfare

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 segementation 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://fluobactracker.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

LEMON Team

6. New Software and Platforms

6.1. SW2D

Shallow Water 2 Dimensions
KEYWORDS: Numerical simulations - Shallow water equations
FUNCTIONAL DESCRIPTION: Urban floods are usually simulated using two-dimensional shallow water models. A correct representation of the urban geometry and hydraulics would require that the average computational cell size be between 0.1 m and 1 m. The meshing and computation costs make the simulation of entire districts/conurbations impracticable in the current state of computer technology.

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

- specific momentum/energy dissipation models that are active only under transient conditions. Such models, that are not present in classical shallow water models, stem from the upscaling of the shallow water equations and prove essential in modeling the features of fast urban flow transients accurately

- modified HLLC solvers for an improved discretization of the momentum source terms stemming from porosity gradients

- higher-order reconstruction techniques that allow for faster and more stable calculations in the presence of wetting/drying fronts.

- Participant: Vincent Guinot
- Contact: Vincent Guinot

6.2. WindPoS-SDM-LAM

KEYWORDS: Numerical simulations - 3D - Fluid mechanics
FUNCTIONAL DESCRIPTION: Software platform for wind modeling.

- Authors: Antoine Rousseau, Cristian Paris Ibarra, Jacques Morice, Mireille Bossy and Sélim Kraria
- Contact: Mireille Bossy
- URL: https://windpos.inria.fr

6.3. SDM

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

- Participants: Antoine Rousseau, Antoine Rousseau, Claire Chauvin, Frederic Bernardin and Mireille Bossy
- Contact: Mireille Bossy

6.4. OceaPoS-SDM

KEYWORDS: 3D - Turbulence - Oceanography - Numerical simulations - Stochastic models - Marine Energies
FUNCTIONAL DESCRIPTION: Simulation platform for ocean turbulence and interaction with hydroturbines

- Partner: MERIC
- Contact: Mireille Bossy

LIFEWARE Project-Team

6. New Software and Platforms

6.1. BIOCHAM

The Biochemical Abstract Machine

KEYWORDS: Systems Biology - Bioinformatics

FUNCTIONAL DESCRIPTION: The Biochemical Abstract Machine (BIOCHAM) is a software environment for modeling, analyzing and synthesizing biochemical reaction networks (CRNs) with respect to a formal specification of the observed or desired behavior of a biochemical system. BIOCHAM is compatible with the Systems Biology Markup Language (SBML) and contains some unique features about formal specifications in quantitative temporal logic, sensitivity and robustness analyses and parameter search in high dimension w.r.t. behavioral specifications, static analyses, and synthesis of CRNs.

RELEASE FUNCTIONAL DESCRIPTION: influence networks with forces – PAC learning of influence networks from time series data – synthesis of continuous reaction networks for mathematical functions defined by polynomial differential equations – complete modular rewriting of Biocham in SWI-Prolog

- Participants: François Fages, David Coudrin, Sylvain Soliman and Thierry Martinez
- Contact: François Fages
- URL: http://lifeware.inria.fr/biocham4/

6.2. Platforms

6.2.1. Smart experimental platforms to automate microbiology experiments

Models play a central role in our work, either to test our understanding or to guide the design of novel systems. Model development and parameter calibration necessitate informative experiments. We develop methods to assist with the optimal design of experiments. In consequence, we have to perform, in sequence or in parallel, experiments with possibly complex input profiles. This led us to develop experimental platforms that allow for flexible and automated stimulations and measurements. Three platforms are being developed, based on (i) a microplate photometer, (ii) a bioreactor platform coupled with a flow cytometer, and (iii) a microscope equipped with microfluidic systems, respectively. In all cases, the real-time measurement and actuation capabilities allow for making reactive experiments, notably including real-time control experiments.

M3DISIM Project-Team

6. New Software and Platforms

6.1. HeartLab

KEYWORDS: Computational geometry - Image analysis - Cardiac - Health - Simulation
FUNCTIONAL DESCRIPTION: The heartLab software is a library designed to perform both simulation and estimation of the heart mechanical behavior (based on various types of measurements, e.g. images).

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

- Participants: Radomir Chabiniok, Gautier Bureau, Martin Genet, Federica Caforio, Ustim Khristenko, Dominique Chapelle and Philippe Moireau
- Contact: Philippe Moireau
- URL: https://raweb.inria.fr/rapportsactivite/RA2013/m3disim/uid14.html

6.2. Verdandi

KEYWORDS: HPC - Model - Software Components - Partial differential equation
FUNCTIONAL DESCRIPTION: Verdandi is a free and open-source (LGPL) library for data assimilation. It includes various such methods for coupling one or several numerical models and observational data. Mainly targeted at large systems arising from the discretization of partial differential equations, the library is devised as generic, which allows for applications in a wide range of problems (biology and medicine, environment, image processing, etc.). Verdandi also includes tools to ease the application of data assimilation, in particular in the management of observations or for a priori uncertainty quantification. Implemented in C++, the library may be used with models implemented in Fortran, C, C++ or Python.

- Participants: Dominique Chapelle, Gautier Bureau, Nicolas Claude, Philippe Moireau and Vivien Mallet
- Contact: Vivien Mallet
- URL: http://verdandi.gforge.inria.fr/

6.3. CardiacLab

KEYWORDS: Cardiovascular and respiratory systems - Matlab - Real time
FUNCTIONAL DESCRIPTION: CardiacLab is a MATLAB toolbox allowing to perform “real-time” cardiac simulations using 0D models of the cardiovascular systems. Its modular development includes (1) a module integrating the mechanical dynamics of the cavity taking into account its particular geometry, (2) a module allowing to choose a micro-model of the cardiac contraction, (3) a module of phase management, (4) a circulation module based on Windkessel models or more advanced 1D flows models, and (5) a perfusion module. The objective of this code is threefold: (1) demonstrate to students, engineers, medical doctors, the interest of modeling in cardiac applications, (2) unify our original modeling developments with the possibility to evaluate them with previous team developments before integrating them into 3D complex formulations, and (3) explore some avenues pertaining to real-time simulat

- Participants: Sebastien Impériale, Martin Genet, Federica Caforio, Ustim Khristenko, Peter Baumgartner, Radomir Chabiniok, François Kimmig and Arthur Le Gall
- Contact: Philippe Moireau
- URL: https://gitlab.inria.fr/M3DISIM/CardiacLab

6.4. MoReFEM

Modeling Research with the Finite Element Method

KEYWORDS: HPC - Multiphysics modelling - Data assimilation

FUNCTIONAL DESCRIPTION: MoReFEM is a HPC finite element library for simulating multiphysics evolution problems like the ones encounter in cardiac modeling (electrophysiology, structure and fluid mechanics, transport-diffusion, wave equations)

- Participants: Philippe Moireau, Patrick Le Tallec, Antoine Olivier, Dominique Chapelle, Ustim Khristenko, François Kimmig, Gautier Bureau and Sébastien Gilles
- Contact: Sébastien Gilles
- URL: https://gitlab.inria.fr/MoReFEM

MAGIQUE-3D Project-Team

5. New Software and Platforms

5.1. Elasticus

KEYWORDS: Discontinuous Galerkin - Acoustic equation - Elastodynamic equations - Elastoacoustic - 2D - 3D - Time Domain

SCIENTIFIC DESCRIPTION: Elasticus simulate acoustic and elastic wave propagation in 2D and in 3D, using Discontinuous Galerkin Methods. The space discretization is based on two kind of basis functions, using Lagrange or Jacobi polynomials. Different kinds of fluxes (upwind and centered) are implemented, coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION: Elasticus is a sequential library, independent of Total plateform and developped in Fortran, to simulate wave propagation in geophysical environment, based on a DG method. It is meant to help PhD students and post-doctoral fellows to easily implement their algorithms in the library. Thus, readability of the code is privileged to optimization of its performances. Developped features should be easily transferred in the computing platform of Total. Elasticus manages arbitrary orders for the spatial discretization with DG method.

NEWS OF THE YEAR: In 2018, we implemented the coupling between hexahedra and tetrahedra and the coupling between Discontinuous Galerkin methods and Spectral Element methods in 2D and in 3D. We also introduced Perfectly Matched layers in the Spectral Element kernel.

- Participants: Julien Diaz, Lionel Boillot and Simon Ettouati
- Contact: Julien Diaz
- Publications: Spectral Element Method and Discontinuous Galerkin approximation for elasto-acoustic problems - Hybrid space discretization to solve elasto-acoustic coupling - On the coupling of Spectral Element Method with Discontinuous Galerkin approximation for elasto-acoustic problems - SEM-DG Approximation for elasto-acoustics

5.2. Hou10ni

KEYWORDS: 2D - 3D - Elastodynamic equations - Acoustic equation - Elastoacoustic - Frequency Domain - Time Domain - Discontinuous Galerkin

SCIENTIFIC DESCRIPTION: Hou10ni simulates acoustic and elastic wave propagation in time domain and in harmonic domain, in 2D and in 3D. It is also able to model elasto acoustic coupling. It is based on the second order formulation of the wave equation and the space discretization is achieved using Interior Penalty Discontinuous Galerkin Method. Recently, the harmonic domain solver has been extended to handle Hybridizable Discontinuous Galerkin Methods.

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

NEWS OF THE YEAR: In 2018, we have finished scalablity tests and performance comparison of Hou10ni/Mumps vs Hou10ni/Maphys on Plafrim, in the framework of the european project HPC4E. The code is now being ported on Turing, in order to extend the scability tests to the time-domain problem.

- Participants: Conrad Hillairet, Elodie Estecahandy, Julien Diaz, Lionel Boillot and Marie Bonnasse Gahot
- Contact: Julien Diaz
- Publications: Hybridizable discontinuous Galerkin method for the two-dimensional frequency-domain elastic wave equations - Convergence of seismic full waveform inversion and extension to Cauchy data - Convergence Analysis for Seismic Full Waveform Inversion - Stability and convergence analysis for seismic depth imaging using FWI - On the use of a laser ablation as a laboratory seismic source - Towards Energy-Efficient Storage Servers - Equivalent Robin Boundary Conditions for Acoustic and Elastic Media - Comparison of solvers performance when solving the 3D Helmholtz elastic wave equations over the Hybridizable Discontinuous Galerkin method - Comparison of solvers performance when solving the 3D Helmholtz elastic wave equations using the Hybridizable Discontinuous Galerkin method - Resolution strategy for the Hybridizable Discontinuous Galerkin system for solving Helmholtz elastic wave equations - Seismic imaging in laboratory trough laser Doppler vibrometry - Absorbing Boundary Conditions for 3D Elastic TTI Modeling, Application to Time-Based and Time-Harmonic Simulations - Shape and material parameter reconstruction of an isotropic or anisotropic solid immersed in a fluid - Modelling and advanced simulation of wave propagation phenomena in 3D geophysical media. - Multi-level explicit local time-stepping methods for second-order wave equations - Absorbing Boundary Conditions for 3D elastic TTI modeling - Modeling of elastic Helmholtz equations by hybridizable discontinuous Galerkin method (HDG) for geophysical applications - Performance Assessment on Hybridizable Dg Approximations for the Elastic Wave Equation in Frequency Domain - High-Order IPDG Approximations for Elasto-Acoustic Problems - High-order Discontinuous Galerkin approximations for elasto-acoustic scattering problems - Modelling of seismic waves propagation in harmonic domain by hybridizable discontinuous Galerkin method (HDG) - Absorbing Boundary Conditions for 3D Tilted Transverse Isotropic media - Performance comparison between hybridizable DG and classical DG methods for elastic waves simulation in harmonic domain - Polynomial speeds in a Discontinuous Galerkin code - Hybridizable Discontinuous Galerkin method for the simulation of the propagation of the elastic wave equations in the frequency domain - Discontinuous Galerkin methods for the simulation of the propagation of the elastic wave equations in the frequency domain - High order discontinuous Galerkin methods for time-harmonic elastodynamics - Hybridizable discontinuous Galerkin method for the two-dimensional frequency-domain elastic wave equations - Efficient DG-like formulation equipped with curved boundary edges for solving elasto-acoustic scattering problems - Numerical schemes for the simulation of seismic wave propagation in frequency domain - Performance analysis of DG and HDG methods for the simulation of seismic wave propagation in harmonic domain - Hybridizable Discontinuous Galerkin method for solving Helmholtz elastic wave equations - Discontinuous Galerkin methods for solving Helmholtz elastic wave equations for seismic imaging - Performance comparison of HDG and classical DG method for the simulation of seismic wave propagation in harmonic domain - Contributions to the mathematical modeling and to the parallel algorithmic for the optimization of an elastic wave propagator in anisotropic media - Contribution to the mathematical analysis and to the numerical solution of an inverse elasto-acoustic scattering problem
- URL: https://team.inria.fr/magique3d/software/hou10ni/

5.3. MONTJOIE

KEYWORDS: High order finite elements - Edge elements - Aeroacoustics - High order time schemes

SCIENTIFIC DESCRIPTION: Montjoie is designed for the efficient solution of time-domain and time-harmonic linear partial differential equations using high-order finite element methods. This code is mainly written for quadrilateral/hexahedral finite elements, partial implementations of triangular/tetrahedral elements are provided. The equations solved by this code, come from the ”wave propagation” problems, particularly acoustic, electromagnetic, aeroacoustic, elastodynamic problems.

FUNCTIONAL DESCRIPTION: Montjoie is a code that provides a C++ framework for solving partial differential equations on unstructured meshes with finite element-like methods (continuous finite element, discontinuous Galerkin formulation, edge elements and facet elements). The handling of mixed elements (tetrahedra, prisms, pyramids and hexahedra) has been implemented for these different types of finite elements methods. Several applications are currently available : wave equation, elastodynamics, aeroacoustics, Maxwell’s equations.

- Participants: Gary Cohen, Juliette Chabassier, Marc Duruflé and Morgane Bergot
- Contact: Marc Duruflé
- URL: http://montjoie.gforge.inria.fr/

5.4. tmodeling-DG

Time-domain Wave-equation Modeling App

KEYWORDS: 2D - 3D - Elastoacoustic - Elastodynamic equations - Discontinuous Galerkin - Time Domain

SCIENTIFIC DESCRIPTION: tmodeling-DG simulate acoustic and elastic wave propagation in 2D and in 3D, using Discontinuous Galerkin Methods. The space discretization is based on two kind of basis functions, using Lagrange or Jacobi polynomials. Different kinds of fluxes (upwind and centered) are implemented, coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION: tmodelling-DG is the follow up to DIVA-DG that we develop in collaboration with our partner Total. Its purpose is more general than DIVA-DG and should contains various DG schemes, basis functions and time schemes. It models wave propagation in acoustic media, elastic (isotropic and TTI) media and elasto-acoustic media, in two and three dimensions.

NEWS OF THE YEAR: In 2018, we have coupled the code with a Reverse Time Migration algorithm.

- Participants: Julien Diaz, Lionel Boillot, Simon Ettouati and Hélène Barucq
- Partner: TOTAL
- Contact: Julien Diaz

5.5. OpenWind

Open Wind Instrument Design

KEYWORDS: Wave propagation - Inverse problem - Experimental mechanics - Image processing

FUNCTIONAL DESCRIPTION: -Computes resonating pipes’ impedance using one-dimensional nite element method and the transfer matrix method -sound synthesis in the time domain (FDTD and FEM in space) -informatic interface for the usage of an input impedance measurement setup. -instrument bore extraction using tomographical image processing -inverse problem solving

- Contact: Juliette Chabassier

5.6. ffwi

Frequency-domain Full Waveform Inversion

KEYWORDS: 2D - 3D - Discontinuous Galerkin - Inverse problem - Frequency Domain - Acoustic equation - Elasticity

FUNCTIONAL DESCRIPTION: ffwi is developed in partnership with Total in the context of the Depth Imaging Partnership (DIP). It is devoted to perform seismic imaging using the Full Waveform Inversion method, in the frequency domain. It is based upon the software Fmodeling, which is itself dedicated to the forward problem. In FWI, the forward problem is solved using Hybridizable Discontinuous Galerkin Methods. The reconstruction of medium parameter is conducted with an iterative minimization scheme, which uses gradient descent techniques. The software can work with acoustic and elastic media, in two and three dimensions.

- Partner: TOTAL
- Contact: Florian Faucher

MAMBA Project-Team

6. New Software and Platforms

6.1. TiQuant

Tissue Quantifier

KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology

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

- Author: Dirk Drasdo
- Contact: Dirk Drasdo

6.2. TiSim

Tissue Simulator

KEYWORDS: Systems Biology - Bioinformatics - Biology - Physiology

SCIENTIFIC DESCRIPTION: TiSim (Tissue Simulator) is a versatile and efficient simulation environment for tissue models. TiSim is a software for agent-based models of multicellular systems. It permits model development with center-based models and deformable cell models, it contains modules for monolayer and multicellular spheroid simulations as well as for simulations of liver lobules. Besides agent-based simulations, the flow of blood and the transport of molecules can be modelled in the extracellular space, intracellular processes such as signal transduction and metabolism can be simulated, for example over an interface permitting integration of SBML-formulated ODE models. TiSim is written in modern C++ , keeping central model constituents in modules to be able to reuse them as building blocks for new models. For user interaction, the GUI Framework Qt is used in combination with OpenGL for visualisation. The simulation code is in the process of being published. The modeling strategy and approaches slowly reach systems medicine and toxicology. The diffusion of software is a fundamental component as it provides the models that are complex and difficult to implement (implementing a liver lobule model from scratch takes about 2-2.5yrs) in form of a software to the developer and users who like to build upon them. This increases significantly the speed of implementing new models. Moreover, standardization is indispensible as it permits coupling different software tools that may have implemented models at different scales / levels.

FUNCTIONAL DESCRIPTION: TiSim is a software that permits agent-based simulations of multicellular systems. - center-based lattice-free agent-based model - modular - C++, Qt, OpenGL, GUI, batch mode - permits multiscale simulations by integration of molecular pathways (for signaling, metabolisms, drug) into each individual cell - applications so far: monolayer growth, multicellular spheroids - Boolean networks (development time = coding time (60 MMs) + model development time (264 MMs)) - in follow-up version 1: - liver lobule regeneration - SBML interface - in follow-up version 2: - deformable cell model (by triangulation of cell surface) - deformable rod models - extracellular matrix - vascular flow and transport TiSim can be directly fed by processed image data from TiQuant.

- Participants: Andreas Buttenschoen, Dirk Drasdo, Eugenio Lella, Géraldine Cellière, Johannes Neitsch, Margaretha Palm, Nick Jagiella, Noémie Boissier, Paul Van Liedekerke, Stefan Hoehme and Tim Johann
- Partner: IZBI, Université de Leipzig
- Contact: Dirk Drasdo

6.3. Platforms

6.3.1. TiSim

New side branches have been developed that integrate the deformable cell model and extracellular matrix model in the TiSim software.

6.3.2. TiQuant

The software has been further extended for machine learning components.

MATHNEURO Team (section vide)

MIMESIS Team

6. New Software and Platforms

6.1. SOFA

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

- Participants: Christian Duriez, François Faure, Hervé Delingette and Stéphane Cotin
- Partner: IGG
- Contact: Stéphane Cotin
- URL: http://www.sofa-framework.org

6.2. SofaCV Plugin

Keywords: Simulation - Visualization - Image processing
Functional Description: SofaCV is a plugin for the simulation framework SOFA. Its purpose is to provide computer vision tools to SOFA. More specifically, its goal is to enable the use of SOFA simulations in augmented reality, and virtual reality applications. The SofaCV plugin is not a standalone plugin by itself. Instead it provides an API for submodules (mainly Sofa's ImageProcessing and DataAcquisition plugin) such as base datatypes, Python bindings, SofaQtQuick widgets etc, along with some utility SOFA Components to read, write or display an image in the scene view.

The ImageProcessing plugin is a plugin for the simulation framework SOFA. Its purpose is to provide general purpose Computer vision features to Sofa. More specifically, its goal is to enable the use of SOFA simulations in augmented reality, and virtual reality applications. The ImageProcessing plugin depends on the SofaCV Base plugin. The ImageProcessing plugin doesn't have the ambition to provide cutting-edge computer vision algorithms, but instead, wraps OpenCV's features while taking advantage of SOFA's Component-based API. This plugin also provides useful Camera components, providing on-the-fly conversions from/to OpenGL & OpenCV's camera calibration parameters. (calibrating cameras, modifying both intrinsic and extrinsic camera parameters in OpenGL)

- Author: Bruno Marques
- Contact bruno.josue.marques@inria.fr

6.3. Needle Insertion Plugin

Keywords: Simulation - Needle insertion - Haptic feedback

Functional Description: This plugin contains needle/tissue interaction models for real time simulations of needle insertion in deformable objects using the open-source sofa framework. This allows for modeling the different forces playing a role during the insertion process (penetration forces, friction along the shaft...) using a constrained-based formulation. This formulation provides a fast and stable solution for the simulation of complex insertions (and reinsertion) of the needle in deformable Finite Element models.

- Authors: Hadrien Courtecuisse
- Contact: hcourtecuisse@unistra.fr

6.4. Optimus Plugin

Keywords: Simulation - Stochastic Filtering - Data Assimilation - State Estimation - Medical applications
Functional Description:

The goal of the plugin is to implement a real integration of Verdandi in SOFA in order to provide a complex and efficient tool for data-assimilation and state-estimation based on filtering prediction-correction scheme.

- Main Author: Igor Peterlik
- Collaborators: Sergei Nikolaev, Nava Schulmann, Raffaella Trivisonne
- Contact:
  - igor.peterlik@inria.fr
  - sergei.nikolaev@inria.fr
  - nava.schulmann@inria.fr
  - raffaella.trivisonne@inria.fr

6.5. RGBDTracking Plugin

Keywords: Simulation - RGBD data Processing - Object tracking - data fusion - Numerical simulations
Functional Description: RGBDTracking is a SOFA plugin to register and track deformable objects in real-time using an RGB-D sensor. This frame-by-frame system relies on a prior visual segmentation of the object in the RGB image. The resulting segmented point cloud is then used to register the object, first in a rigid manner, and then by non-rigidly fitting the known mesh, based on the Finite Element Method to model elasticity, and on vision-based external forces exerted on the mesh.

- Author: Antoine Petit
- Contact: antoine.a.petit@inria.fr

MNEMOSYNE Project-Team

6. New Software and Platforms

6.1. DANA

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

- Participant: Nicolas Rougier
- Contact: Nicolas Rougier
- URL: http://dana.loria.fr/

6.2. Virtual Enaction

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

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

- Participants: André Garenne, Frédéric Alexandre, Nicolas Rougier and Thierry Viéville
- Contact: Frédéric Alexandre

6.3. Mnemonas

KEYWORDS: Recurrent network - Manifold

FUNCTIONAL DESCRIPTION: This source bundle provides source files of the: - Manifold representation of ontology for machine learning (in progress). - Recurrent neural network weight estimation though backward tuning publication.

- Contact: Thierry Viéville

6.4. ReservoirPy

KEYWORDS: Recurrent network - Artificial intelligence - Reservoir Computing - Multi-label classification - Timeseries Prediction - Time Series - Machine learning - Classification

FUNCTIONAL DESCRIPTION: This toolbox provides a class of Echo State Networks that can be used with Python and its scientific librairies like Numpy, Scipy and Matplolib. It includes useful expertise to train recurrent neural networks of ESN architecture kind.

ESN is a particular kind of recurrent neural network (RNN) with or without leaky neurons. The input stream is projected to a random recurrent layer and a linear output layer (called "read-out") is modified by learning (which can also be done in an online fashion).

Compared to other RNNs, the input layer and the recurrent layer (called "reservoir") do not need to be trained. For other RNNs, the structure of the recurrent layer evolves in most cases by gradient descent algorithms like Backpropagation-Through-Time, which is not biologically plausible and is adapted iteratively to be able to hold a representaion of the input sequence. In contrast, the random weights of the ESN's reservoir are not trained, but adapted to possess the "Echo State Property" (ESP) or at least suitable dynamics (e.g. 'edge of chaos') to generalize, which includes a non-linear transformation of the input that can be learned by a linear classifier. The weights are adapted by scaling the weights based on the maximum absolute eigenvalue (also called spectral radius), which is a hyperparameter specific to the task. The states of the reservoir are linearly separable and can be mapped to the output layer by a computationally cheap linear regression, as no gradient descent is necessary. The weights of the input layer can be scaled by the input scaling hyperparameter, which also depends on the nature of the inputs.

- Partners: Université de Hamburg - University of Hamburg
- Contact: Xavier Hinaut
- URL: https://github.com/neuronalX/reservoirpy

MONC Project-Team

6. New Software and Platforms

6.1. Nenuphar

KEYWORDS: Modeling - Oncologie - Cancer - Partial differential equation - Medical - Medical imaging
FUNCTIONAL DESCRIPTION: The goal of project is to evaluate the aggressiveness of a tumor or its response to therapy. For that purpose, we use a mathematical model based on a set of nonlinear partial differential equations. This model is calibrated on patient data using a longitudinal sequence of CT Scan or MRI of the patient. This approach has been validated on about 35 clinical cases of lung metastases from various primary tumors (kidney, bladder, thyroid). Using two initial images showing the targeted lesion, we recover the patient-specific parameters of the model. The evolution of the disease is then predicted by letting the model run for later times with these parameters.

- Partners: CNRS - INP Bordeaux - Université Bordeaux 1
- Contact: Olivier Saut
- URL: https://team.inria.fr/monc/software/

6.2. papriK

KEYWORDS: Medical imaging - DICOM - Image registration - Image segmentation - 2D - 3D - Image analysis - Image processing - Medical applications - Radiomics
SCIENTIFIC DESCRIPTION: PapriK is the team toolkit devoted to processing and analyzing medical images. It currently wraps VTK and ITK and contains our own algorithms as well : - images input/output (including DICOM) - filtering, rescaling, resampling - segmentation/registration - radiomics computation: histogram, texture, shape
NEWS OF THE YEAR: - add python3 support - work on registration - simplify the library - fix bugs

- Participants: Cynthia Perier, Olivier Saut and Erwan Le Masson
- Partners: Institut Bergonié - Université de Bordeaux
- Contact: Cynthia Perier
- Publications: T2-based MRI Delta-Radiomics Improve Response Prediction in Soft-Tissue Sarcomas Treated by Neoadjuvant Chemotherapy - Pre-treatment magnetic resonance-based texture features as potential imaging biomarkers for predicting event free survival in anal cancer treated by chemoradiotherapy
- URL: https://team.inria.fr/monc/software/

6.3. NENUCORE

KEYWORDS: Image segmentation - Biomedical imaging - Image processing - Real-time rendering
SCIENTIFIC DESCRIPTION: Standalone application for visualization, manipulation and segmentation of 2D and 3D images. The software has been developed for application to medical imaging. The visualization is done in real time and the segmentation can be manual or semi-automatic. The software contains a database including medical images of patients, the segmentation data of these images as well as the associated meta-data.

- Participants: Benjamin Taton, Boris Raymond, Jean Mercat and Vivien Pianet
- Contact: Boris Raymond

6.4. metamats_burden

KEYWORDS: Metastasis - Cancer - Data assimilation - Regression - Biostatistics - Mechanistic modeling - Simulation
SCIENTIFIC DESCRIPTION: This Matlab software is a minimal code for fitting simultaneously primary tumor growth and metastatic burden data using nonlinear mixed-effects modeling.
FUNCTIONAL DESCRIPTION: Set of functions for calibration of models of metastatic burden and primary tumor growth to empirical population data
NEWS OF THE YEAR: Submission to the French agency of software protection (APP). Inclusion of a new model for pre-operative anti-angiogenic treatment. Validation of the previous models on large databases (400+ animals)

- Participants: Sébastien Benzekry and Chiara Nicolo
- Partner: Roswell Park Comprehensive Cancer Center
- Contact: Sébastien Benzekry
- Publications: Modeling Spontaneous Metastasis following Surgery: An In Vivo-In Silico Approach - Computational Modelling of Metastasis Development in Renal Cell Carcinoma
- URL: http://metamats.bordeaux.inria.fr/

6.5. metamats_core

KEYWORDS: Metastasis - Cancer - Mechanistic modeling - Simulation - Modeling
SCIENTIFIC DESCRIPTION: This code is devoted to the simulation of partial differential equation (PDE) based models for the time development of a population of secondary tumors (metastases).
FUNCTIONAL DESCRIPTION: Metamats_core simulates a partial differential equation (PDE)-based model for the time development of a population of secondary tumors (metastases).
NEWS OF THE YEAR: Submission to the French agency of software protection (APP)

- Participant: Sébastien Benzekry
- Contact: Sébastien Benzekry
- Publications: Modeling Spontaneous Metastasis following Surgery: An In Vivo-In Silico Approach - Passing to the limit 2D-1D in a model for metastatic growth - Mathematical analysis of a two-dimensional population model of metastatic growth including angiogenesis - Modeling the impact of anticancer agents on metastatic spreading - Global Dormancy of Metastases due to Systemic Inhibition of Angiogenesis
- URL: http://benzekry.perso.math.cnrs.fr/

6.6. IRENA

Numerical Assessment of IRreversible Electroporation ablation
KEYWORDS: Cancer - Numerical electroporation
SCIENTIFIC DESCRIPTION: The C++ software IRENA developed by O. Gallinato and C. Poignard within the Inria team Monc enable sto compute the static electric field distribution in the clinical configuration of IRE ablation of liver tumors. The code is based on the finite volume method on Cartesian grid. The needles and the liver boundary are determined as the zero of a level-set function. Close to the boundaries, the first and second order derivatives are computed with the standard Ghost Fluid Method. The equivalent conductivities at half points are computed thanks to harmonic mean (additivity law of resistivity). In order to maintain a reasonable computation time, the refinement is low enough (1 mm3 grid voxels). As the mesh does not pick up the very fine needles, the Dirichlet conditions imposed on the active parts of the electrodes and the Neumann conditions imposed on the insulated parts are changed into Robin conditions on the first layer of points around the needles, thanks to a second order development. This results in a numerical scheme, which is computationally efficient and accurate enough.

FUNCTIONAL DESCRIPTION: Digital simulation tool for the assessment of irreversible electroporation clinical process

- Authors: Olivier Gallinato and Clair Poignard
- Contact: Clair Poignard

6.7. metamats_size

Fitting longitudinal data of size and number of metastases using mechanistic models
KEYWORDS: Cancer - Mechanistic modeling - Metastasis - Regression - Simulation - Data assimilation
SCIENTIFIC DESCRIPTION: This software fits models of metastatic development to longitudinal data of metastatic sizes and provides simulation and visualization tools for metastatic modeling.
NEWS OF THE YEAR: Establishment of a first clean and minimal version. Validation of the software on clinical data of brain metastases from non-small cell lung cancer. Submission to the French agency of software protection (APP).

- Participants: Sébastien Benzekry and Mariia Bilous
- Partners: Centre de Recherches en Cancérologie de Marseille - Institut Bergonié - Assistance Publique - Hôpitaux de Marseille
- Contact: Sébastien Benzekry
- Publication: Computational modeling reveals dynamics of brain metastasis in non-small cell lung cancer and provides a tool for personalized therapy
- URL: http://metamats.bordeaux.inria.fr/

6.8. Carcinom

Computer-Assisted Research about Cancer growth and INsights on Oncological Mechanisms
KEYWORDS: Cancer - Regression - Tumor growth
SCIENTIFIC DESCRIPTION: This software is primarily designed to perform a modeling analysis of tumor growth kinetics. Given a data set of longitudinal measurements of tumor size in a population, it fits multiple models of tumor growth (either user-defined or selected from a library of classical models), computes goodness-of-fit statistical metrics, identifies the parameters of the models and estimates associated standard errors. Fits of the data can be performed either individual per individual or using a population approach (nonlinear mixed-effects).
FUNCTIONAL DESCRIPTION: Software for modeling and fitting tumor growth kinetics. Given a data set of longitudinal measurements of tumor size in a population, it fits multiple models of tumor growth (either user-defined or selected from a library of classical models), computes goodness-of-fit statistical metrics, identifies the parameters of the models and estimates associated standard errors. Fits of the data can be performed either on an individual basis or using a population approach (nonlinear mixed-effects).

Graphical and statistical tools of use when analyzing growth curves are also included.
NEWS OF THE YEAR: Submission to the French agency of software protection (APP). Development of a python module for interaction with Monolix.

- Participants: Simon Evain, Vivien Pianet and Cristina Vaghi
- Partner: Roswell Park Comprehensive Cancer Center
- Contact: Sébastien Benzekry
- Publication: Classical Mathematical Models for Description and Forecast of Experimental Tumor Growth
- URL: https://team.inria.fr/monc/software/

6.9. Platforms

6.9.1. Transport Equation Solver v1

Submission to the French agency of software protection of the software "Transport Equation Solver v1".

Ce logiciel répond aux besoins liés à l’analyse fonctionnelle de la vascularisation d’un organe par imagerie dynamique et en particulier il concerne l’analyse de la vascularisation placentaire qui est destinée au diagnostic d’anomalies d’invasion placentaire par échographie dynamique de contraste. De manière plus précise, ce logiciel permet, à partir d’un modèle physique d’écoulement des fluides, d’estimer et de quantifier le transport du produit de contraste injecté lors d’une imagerie par échographie dynamique de contraste.

MORPHEME Project-Team

5. New Software and Platforms

5.1. Obj.MPP

KEYWORDS: Object detection - Marked Point Process - Parametric model
FUNCTIONAL DESCRIPTION: Obj.MPP implements the detection of parametric objects using a Marked Point Process (MPP). A parametric object is an n-dimensional piece of signal defined by a finite set of parameters. Detecting an object in a signal amounts to finding a position at which the signal can be described well enough by a specific set of parameters (unknowns of the detection problem). The detection task amounts to finding all such objects. Typically, the signal is a 2-dimensional grayscale image and the parametric objects are bright disks on a dark background. In this case, each object is defined by a single parameter: the disk radius. Note however that the core function of Obj.MPP is not tied to a particular context (2-dimensional imaging is just an example).

- Author: Eric Debreuve
- Contact: Eric Debreuve
- Publications: Stochastic geometry for image analysis - Multiple objects detection in biological images using a marked point process framework - An efficient optimizer for simple point process models - Multiple Birth and Cut Algorithm for Multiple Object Detection
- URL: https://team.inria.fr/morpheme/obj-mpp-object-detection-using-a-marked-point-process/

5.2. ATOLS

Adaptative Threshold Operator based on Level Sets
KEYWORDS: Object detection - Level Set
FUNCTIONAL DESCRIPTION: Atols is a Python script allowing to detect features on images using a contrast scoring. Thus, it's possible to detect features at different levels of intensity unlike a simple threshold which would only keep features above its value.

- Authors: Kevin Giulietti and Guillaume Lavisse
- Contact: Xavier Descombes
- URL: https://team.inria.fr/morpheme/software/

5.3. Small particle detection

KEYWORDS: Image processing - Image segmentation - Object detection - Computational biology - Fluorescence microscopy - Biomedical imaging
FUNCTIONAL DESCRIPTION: An algorithm primarily design to detect objects whose sizes aren't larger a few pixels (particles) on fluorescence microscopy images.

It is an simplified version of marked point process.

- Contact: Nicolas Cedilnik
- Publications: SPADE: A Small Particle Detection Method Using A Dictionary Of Shapes Within The Marked Point Process Framework - SPADE: A Small Particle Detection Method Using A Dictionary Of Shapes Within The Marked Point Process Framework
- URL: https://gitlab.inria.fr/ncedilni/spade

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 Developpement Tecnologique, 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 Developpement Tecnologique, 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 exit 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 algotithms. 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.

NEUROSYS Project-Team

6. New Software and Platforms

6.1. OpenVIBE

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

FUNCTIONAL DESCRIPTION: OpenViBE is a free and open-source software platform devoted to the design, test and use of Brain-Computer Interfaces (BCI). The platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. The key features of OpenViBE software are its modularity, its high-performance, its portability, its multiple-users facilities and its connection with high-end/VR displays. The designer of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge under the terms of the AGPL licence, and it was officially released in June 2009. Since then, the OpenViBE software has already been downloaded more than 60000 times, and it is used by numerous laboratories, projects, or individuals worldwide. More information, downloads, tutorials, videos, documentations are available on the OpenViBE website.

- Participants: Cédric Riou, Thierry Gaugry, Anatole Lécuyer, Fabien Lotte, Jussi Tapio Lindgren, Laurent Bougrain, Maureen Clerc and Théodore Papadopoulo
- Partners: INSERM - GIPSA-Lab
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

6.2. Platforms

6.2.1. EEG experimental room

A room at Inria Nancy - Grand Est is dedicated to electroencephalographic recordings. An umbrella agreement and several additional experiment descriptions have been approved by the Inria Operational Legal and Ethical Risk Assessment Committee (COERLE). A new 64 channels Biosemi EEG amplifier has been added this year to be able to record two experimental campaign in parallel (Regional initiative *Contrat de Projet État Région (CPER) IT2MP* see section 8.1). Specific experimentation have been done in interaction with Pepper, a semi-humanoid robot.

Figure 1. Electroencephalographic Experimental room at Inria Nancy-Grand Est

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

- Contact: 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

PARIETAL Project-Team

6. New Software and Platforms

6.1. Mayavi

FUNCTIONAL DESCRIPTION: Mayavi is the most used scientific 3D visualization Python software. Mayavi can be used as a visualization tool, through interactive command line or as a library. It is distributed under Linux through Ubuntu, Debian, Fedora and Mandriva, as well as in PythonXY and EPD Python scientific distributions. Mayavi is used by several software platforms, such as PDE solvers (fipy, sfepy), molecule visualization tools and brain connectivity analysis tools (connectomeViewer).

- Contact: Gaël Varoquaux
- URL: http://mayavi.sourceforge.net/

6.2. MedInria

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

SCIENTIFIC DESCRIPTION: medInria aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010, renewed in 2012. A fast-track ADT was awarded in 2017 to transition the software core to more recent dependencies and study the possibility of a consortium creation.The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.

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

- Participants: Maxime Sermesant, Olivier Commowick and Théodore Papadopoulo
- Partners: HARVARD Medical School - IHU - LIRYC - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

6.3. Nilearn

NeuroImaging with scikit learn

KEYWORDS: Health - Neuroimaging - Medical imaging

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

- Participants: Alexandre Abraham, Alexandre Gramfort, Bertrand Thirion, Elvis Dohmatob, Fabian Pedregosa Izquierdo, Gaël Varoquaux, Loïc Estève, Michael Eickenberg and Virgile Fritsch
- Contact: Bertrand Thirion
- URL: http://nilearn.github.io/

6.4. 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

6.5. Scikit-learn

KEYWORDS: Regession - Clustering - Learning - Classification - Medical imaging
SCIENTIFIC DESCRIPTION: Scikit-learn is a Python module integrating classic machine learning algorithms in the tightly-knit scientific Python world. It aims to provide simple and efficient solutions to learning problems, accessible to everybody and reusable in various contexts: machine-learning as a versatile tool for science and engineering.
FUNCTIONAL DESCRIPTION: Scikit-learn can be used as a middleware for prediction tasks. For example, many web startups adapt Scikitlearn to predict buying behavior of users, provide product recommendations, detect trends or abusive behavior (fraud, spam). Scikit-learn is used to extract the structure of complex data (text, images) and classify such data with techniques relevant to the state of the art.

Easy to use, efficient and accessible to non datascience experts, Scikit-learn is an increasingly popular machine learning library in Python. In a data exploration step, the user can enter a few lines on an interactive (but non-graphical) interface and immediately sees the results of his request. Scikitlearn is a prediction engine . Scikit-learn is developed in open source, and available under the BSD license.

- Participants: Alexandre Gramfort, Bertrand Thirion, Fabian Pedregosa Izquierdo, Gaël Varoquaux, Loïc Estève, Michael Eickenberg and Olivier Grisel
- Partners: CEA - Logilab - Nuxeo - Saint Gobain - Tinyclues - Telecom Paris
- Contact: Olivier Grisel
- URL: http://scikit-learn.org

6.6. MODL

Massive Online Dictionary Learning
KEYWORDS: Pattern discovery - Machine learning
FUNCTIONAL DESCRIPTION: Matrix factorization library, usable on very large datasets, with optional sparse and positive factors.

- Participants: Arthur Mensch, Gaël Varoquaux, Bertrand Thirion and Julien Mairal
- Contact: Arthur Mensch
- Publications: Subsampled online matrix factorization with convergence guarantees - Stochastic Subsampling for Factorizing Huge Matrices
- URL: http://github.com/arthurmensch/modl

6.7. MNE

MNE-Python
KEYWORDS: Neurosciences - EEG - MEG - Signal processing - Machine learning
FUNCTIONAL DESCRIPTION: Open-source Python software for exploring, visualizing, and analyzing human neurophysiological data: MEG, EEG, sEEG, ECoG, and more.

RELEASE FUNCTIONAL DESCRIPTION: http://martinos.org/mne/stable/what_new.html

- Partners: HARVARD Medical School - New York University - University of Washington - CEA - Aalto university - Telecom Paris - Boston University - UC Berkeley
- Contact: Alexandre Gramfort
- URL: http://martinos.org/mne/

PLEIADE Team

6. New Software and Platforms

6.1. Magus

KEYWORDS: Bioinformatics - Genomic sequence - Knowledge database
SCIENTIFIC DESCRIPTION: MAGUS can be used on small installations with a web server and a relational database on a single machine, or scaled out in clusters or elastic clouds using Apache Cassandra for NoSQL data storage and Apache Hadoop for Map-Reduce.
FUNCTIONAL DESCRIPTION: The MAGUS genome annotation system integrates genome sequences and sequences features, in silico analyses, and views of external data resources into a familiar user interface requiring only a Web navigator. MAGUS implements annotation workflows and enforces curation standards to guarantee consistency and integrity. As a novel feature the system provides a workflow for simultaneous annotation of related genomes through the use of protein families identified by in silico analyses this has resulted in a three-fold increase in curation speed, compared to one-at-a-time curation of individual genes. This allows us to maintain standards of high-quality manual annotation while efficiently using the time of volunteer curators.
NEWS OF THE YEAR: Magus is now available as a Docker image, and can be integrated with other containerized services using Pleiade's Alcyone system.

- Participants: David Sherman, Florian Lajus, Natalia Golenetskaya, Pascal Durrens and Xavier Calcas
- Partners: Université de Bordeaux - CNRS - INRA
- Contact: David James Sherman
- Publication: High-performance comparative annotation
- URL: http://magus.gforge.inria.fr

6.2. Mimoza

KEYWORDS: Systems Biology - Bioinformatics - Biotechnology
FUNCTIONAL DESCRIPTION: Mimoza uses metabolic model generalization and cartographic paradigms to allow human experts to explore a metabolic model in a hierarchical manner. Mimoza generalizes genome-scale metabolic models, by factoring equivalent reactions and metabolites while preserving reaction consistency. The software creates an zoomable representation of a model submitted by the user in SBML format. The most general view represents the compartments of the model, the next view shows the visualization of generalized versions of reactions and metabolites in each compartment , and the most detailed view visualizes the initial model with the generalization-based layout (where similar metabolites and reactions are placed next to each other). The resulting map can be explored on-line, or downloaded in a COMBINE archive. The zoomable representation is implemented using the Leaflet JavaScript library for mobile-friendly interactive maps. Users can click on reactions and compounds to see the information about their annotations.
NEWS OF THE YEAR: Mimoza is now available as a Docker image, and can be integrated with other containerized services using Pleiade's Alcyone system.

- Participants: Anna Zhukova and David James Sherman
- Contact: David James Sherman
- Publications: Knowledge-based generalization of metabolic models - Knowledge-based zooming for metabolic models - Knowledge-based generalization of metabolic networks: a practical study
- URL: http://mimoza.bordeaux.inria.fr/

6.3. Declic

FUNCTIONAL DESCRIPTION: Declic is a Python library that provides several tools for data analysis in the domains of multivariate data analysis, machine learning, and graph based methods. It can be used to study in-depth the accuracy of the dictionary between molecular based and morphological based taxonomy.

Declic includes an interpreter for a Domain Specific Language (DSL) to make its Python library easy to use for scientists familiar with environments such as R.

- Partner: INRA
- Contact: Alain Franc

6.4. Diagno-Syst

diagno-syst: a tool for accurate inventories in metabarcoding
KEYWORDS: Biodiversity - Clustering - Ecology
FUNCTIONAL DESCRIPTION: Diagno-syst builds accurate inventories for biodiversity. It performs supervised clustering of reads obtained from a next-generation sequencing experiment, mapping onto an existing reference database, and assignment of taxonomic annotations.

- Participants: Alain Franc, Jean-Marc Frigerio, Philippe Chaumeil and Franck Salin
- Partner: INRA
- Contact: Alain Franc
- Publication: diagno-syst: a tool for accurate inventories in metabarcoding

6.5. Alcyone

Alcyone instantiates bioinformatics environments from specifications committed to a Git repository
KEYWORDS: Docker - Orchestration - Bioinformatics - Microservices - Versioning
SCIENTIFIC DESCRIPTION: Alcyone conceives the user's computing environment as a microservices architecture, where each bioinformatics tool in the specification is a separate containerized Docker service. Alcyone builds a master container for the specified environment that is responsible for building, updating, deploying and stopping these containers, as well as recording and sharing the environment in a Git repository. The master container can be manipulated using a command-line interface.
FUNCTIONAL DESCRIPTION: Alcyone defines a file structure for the specifying bioinformatics analysis environments, including tool choice, interoperability, and sources of raw data. These specifications are recorded in a Git repository. Alcyone compiles a specification into a master Docker container that deploys and orchestrates containers for each of the component tools. Alcyone can restore any version of an environment recorded in the Git repository.
NEWS OF THE YEAR: Alcyone was designed and implemented this year.

- Participants: Louise-Amelie Schmitt and David Sherman
- Contact: David Sherman
- URL: https://team.inria.fr/pleiade/alcyone/

6.6. family-3d

KEYWORDS: Biodiversity - Point cloud - 3D modeling
SCIENTIFIC DESCRIPTION: The method statistically selects a subset of pairwise distances between proteins in the family, constructs a weighted graph, and lays it out using an adaptation of the three-dimensional extension of the Kamada-Kawai force-directed layout.
FUNCTIONAL DESCRIPTION: Family-3D lays out high-dimension protein family point clouds in 3D space. The resulting lower-dimension forms can be printed, so that they can be explored and compared manually. They can also be explored interactively or stereographically.

Comparison of the 3D forms reveals classes of structurally similar families, whose characteristic shapes correspond to different evolutionary scenarios. Some of these scenarios are: neofunctionalization, subfunctionalization, founder gene effect, ancestral family.

To facilitate curator training, Family-3D includes an interactive terminal containing a microcontroller, an RFID reader, and an LED ring. A set of shapes that fall in predetermined classes is printed, with a unique RFID tag in each shape. Trainees classify family shapes by manual inspection and submit their classes to the terminal, which evaluates the proposed class and provides visual feedback.

- Participant: David Sherman
- Contact: David Sherman
- URL: https://gitlab.inria.fr/pleiade/family-3d

6.7. magecal

KEYWORD: Genomics
SCIENTIFIC DESCRIPTION: Magecal independently runs training and prediction steps for Augustus, Conrad, GeneID, GeneMark, and Snap. The results are cleaned and integrated into a common format. Jigsaw is trained and used for model reconciliation. Consistency constraints are applied to ensure that phase and intron structure are biologically plausible.
FUNCTIONAL DESCRIPTION: Magecal predicts a set of protein coding genes in fungal genomic sequences, using different de novo prediction algorithms, and reconciling the predictions with the aid of comparative data. Magecal applies consistency constraints to guarantee that the predicted genes are biologically valid.

RELEASE FUNCTIONAL DESCRIPTION: Dockerization and compatibility with Alcyone

- Participants: Pascal Durrens and David Sherman
- Contact: David Sherman
- URL: https://gitlab.inria.fr/magecal/magecal

6.8. AsebaHub

Turn-key bridging of Aseba mobile robots to wifi networks
KEYWORD: Robotics
SCIENTIFIC DESCRIPTION: Aseba is an open-source modular architecture for event-based control of multi-microcontroller robots, used in the Thymio-II educational robot, and integrated into development environments for teaching robotics programming to 8-18 year old children. Since 2014 Inria has contributed several modules to Aseba, including mDNS-sd support for discovering TCP/IP connections, an HTTP bridge that allows Aseba robots to be used with the Scratch programming environment, and photo-realistic 2D simulation.

Thymio-II robots only communicate through USB connections from a host computer, so until now it has been necessary to install Aseba software on that computer. This is not always possible in schools.

AsebaHub is a firmware image for wifi routers that takes responsibility for USB communication with Aseba robots. Each robot is exposed as a TCP/IP target, advertised using mDNS-sd. AsebaHub can group robots together in ad hoc Aseba networks. It provides HTTP access to robots so that they can be used with Scratch or Snap!. These services work out of the box, without any host configuration or software installation.

AsebaHub can operate as a wifi Access Point, or as a network Bridge to an existing local-area network. A slide switch on the side of the router seamlessly switches between these configurations.

AsebaHub is implemented by compiling Aseba software for the OpenWrt/LEDE open source router platform, adding interfacing code that automatically associates new robots, starts and stops the corresponding network services, and provides a web-based administrative interface.

FUNCTIONAL DESCRIPTION: AsebaHub is a small device with a USB port for connecting Aseba robots, single or with a USB hub. Every robot is made available as a network target on the wifi and wired local-area networks, where they can be discovered using mDNS-sd (Zeroconf/Bonjour). No network or user configuration is necessary.

AsebaHub works out of the box with the Aseba Studio and VPL programming environments. AsebaHub can be configured to also provide an HTTP service that is compatible with Scratch or other environments.

AsebaHub acts as either a wireless Access Point to which users may connect, or as a Bridge to an existing local-area network. Either configuration can be chosen seamlessly with the flick of a switch.

- Participants: David Sherman and Louise-Amelie Schmitt
- Contact: David Sherman

REO Project-Team

6. New Software and Platforms

6.1. FELiScE

Finite Elements for Life SCiences and Engineering problems
KEYWORDS: Finite element modelling - Cardiac Electrophysiology - Cardiovascular and respiratory systems
FUNCTIONAL DESCRIPTION: FELiScE is a finite element code which the M3DISIM and REO project-teams have decided to jointly develop in order to build up on their respective experiences concerning finite element simulations. One specific objective of this code is to provide in a unified software environment all the state-of-the-art tools needed to perform simulations of the complex respiratory and cardiovascular models considered in the two teams – namely involving fluid and solid mechanics, electrophysiology, and the various associated coupling phenomena. FELISCE is written in C++, and may be later released as an opensource library. FELiScE was registered in July 2014 at the Agence pour la Protection des Programmes under the Inter Deposit Digital Number IDDN.FR.001.350015.000.S.P.2014.000.10000.

- Participants: Axel Fourmont, Benoit Fabreges, Damiano Lombardi, Dominique Chapelle, Irène Vignon-Clementel, Jean-Frédéric Gerbeau, Marina Vidrascu, Matteo Aletti, Miguel Angel Fernandez Varela, Mikel Landajuela Larma, Philippe Moireau and Sébastien Gilles
- Contact: Miguel Angel Fernandez Varela
- URL: http://felisce.gforge.inria.fr

6.2. SHELDDON

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

- Participants: Dominique Chapelle, Marina Vidrascu and Patrick Le Tallec
- Contact: Marina Vidrascu
- URL: https://gforge.inria.fr/projects/shelddon/

6.3. DCIMaL

KEYWORD: Cardiac Electrophysiology
FUNCTIONAL DESCRIPTION: DCIMaL is a Python and C++ software for safety pharmacology studies and particularly field potentials signals measured with micro-electrode array (MEA). The software includes a solver for field potential simulations and a dictionary of entries corresponding to features which can be extracted from real or simulated potential signals. It also includes an algorithm for drug classification (channel blockade or torsadogenic risk) and a tool for estimating ion channel activity (based on the CMAES library). DCIMaL was registered in 2018 at the Agence pour la Protection des Programmes Inter Deposit Digital Number IDDN.FR.001.270003.000.S.P.2018.000.31230

- Participants: Fabien Raphel, Jean-Frédéric Gerbeau and Damiano Lombardi
- Contact: Damiano Lombardi

6.4. FELiScE-NS

KEYWORDS: Incompressible flows - Thin-walled solids

FUNCTIONAL DESCRIPTION: FELiScE-NS is a set finite elements solvers for incompressible fluids (fractional-step schemes) and non-linear thin-walled structures (3D shells, and 2D curved beams) developed in the framework of the FELiScE library. FELiSCe-NS was registered in 2018 at the Agence pour la Protection des Programmes Inter Deposit Digital Number IDDN.FR.001.270015.000.S.A.2018.000.31200.

- Participants: Benoit Fabreges, Miguel Angel Fernandez Varela, Axel Fourmont, Jean-Frédéric Gerbeau and Marina Vidrascu
- Contact: Miguel Angel Fernandez Varela

SERENA Project-Team

6. New Software and Platforms

6.1. CELIA3D

KEYWORDS: Fluid mechanics - Multi-physics simulation
FUNCTIONAL DESCRIPTION: The CELIA3D code simulates the coupling between a compressible fluid flow and a deformable structure. The fluid is handled by a Finite Volume method on a structured Cartesian grid. The solid is handled by a Discrete Element method (Mka3d scheme). The solid overlaps the fluid grid and the coupling is carried out with immersed boundaries (cut cells) in a conservative way.

- Partners: Ecole des Ponts ParisTech - CEA
- Contact: Laurent Monasse
- URL: http://cermics.enpc.fr/~monassel/CELIA3D/

6.2. DiSk++

KEYWORDS: High order methods - Polyhedral meshes - C++
SCIENTIFIC DESCRIPTION: Discontinuous Skeletal methods approximate the solution of boundary-value problems by attaching discrete unknowns to mesh faces (hence the term skeletal) while allowing these discrete unknowns to be chosen independently on each mesh face (hence the term discontinuous). Cell-based unknowns, which can be eliminated locally by a Schur complement technique (also known as static condensation), are also used in the formulation. Salient examples of high-order Discontinuous Skeletal methods are Hybridizable Discontinuous Galerkin methods and the recently-devised Hybrid High-Order methods. Some major benefits of Discontinuous Skeletal methods are that their construction is dimension-independent and that they offer the possibility to use general meshes with polytopal cells and non-matching interfaces. The mathematical flexibility of Discontinuous Skeletal methods can be efficiently replicated in a numerical software: by using generic programming, the DiSk++ library offers an environment to allow a programmer to code mathematical problems in a way completely decoupled from the mesh dimension and the cell shape.
FUNCTIONAL DESCRIPTION: The software provides a numerical core to discretize partial differential equations arising from the engineering sciences (mechanical, thermal, diffusion). The discretization is based on the "Hybrid high-order" or "Discontinuous Skeletal" methods, which use as principal unknowns polynomials of arbitrary degree on each face of the mesh. An important feature of these methods is that they make it possible to treat general meshes composed of polyhedral cells. The DiSk ++ library, using generic programming techniques, makes it possible to write a code for a mathematical problem independently of the mesh. When a user writes the code for his problem using the basic operations offered by DiSk ++, that code can be executed without modifications on all types of mesh already supported by the library and those that will be added in the future.

- Author: Matteo Cicuttin
- Partner: CERMICS
- Contact: Matteo Cicuttin
- Publication: Implementation of Discontinuous Skeletal methods on arbitrary-dimensional, polytopal meshes using generic programming
- URL: https://github.com/wareHHOuse/diskpp

6.3. GENFIELD

KEYWORDS: Hydrogeology - Algorithm - Heterogeneity

SCIENTIFIC DESCRIPTION: GENFIELD implements a parallel version of the algorithm initially proposed by [E. Pardo-Iguzquiza and M. Chica-Olmo, Mathematical Geology, 25(2):177-217, 1993].
FUNCTIONAL DESCRIPTION: GENFIELD allows the generation of gaussian correlated fields. It is based on the circulant embedding method. Parallelism is implemented using MPI communications. GENFIELD is used in hydrogeology to model natural fields, like hydraulic conductivity or porosity fields.
NEWS OF THE YEAR: In 2018, we have performed scaling tests on ADA cluster. They have revealed that the symmetry of the phases required by this algorithm penalized a lot the parallel efficiency of GENFIELD (cf poster hal-01960444, version 1). We have decided to stop the development of GENFIELD. In 2018, we have developed a complete new software (cf BIL Inria ParaCIRCE) based on another algorithm initially proposed by [C. R. Dietrich and G. N. Newsam. A fast and exact method for multidimensional gaussian stochastic simulations. Water Resources Research, 29(8):2861-2869, 1993].

- Participants: Géraldine Pichot, Simon Legrand, Grégoire Lecourt, Jean-Raynald De Dreuzy and Jocelyne Erhel
- Contact: Géraldine Pichot
- Publications: GENFIELD: A parallel software for the generation of stationary Gaussian random fields - Algorithms for stationary Gaussian random field generation
- URL: https://gitlab.inria.fr/slegrand/Genfield_dev

6.4. Mka3d

KEYWORDS: Scientific computing - Elasticity - Elastodynamic equations
FUNCTIONAL DESCRIPTION: The Mka3d method simulates an elastic solid by discretizing the solid into rigid particles. An adequate choice of forces and torques between particles allows to recover the equations of elastodynamics.

- Partners: Ecole des Ponts ParisTech - CEA
- Contact: Laurent Monasse
- URL: http://cermics.enpc.fr/~monassel/Mka3D/

6.5. NEF-Draw

Numerical Experiments involving Fractures -Visualisation
KEYWORD: Fracture network
FUNCTIONAL DESCRIPTION: This software is a visualization tool of discrete fractured networks. It allows the visualization of the network geometry, the mesh of the network together with several quantities of interest (mesh quality, flow solution including wells) computed with the software NEF-Flow.
NEWS OF THE YEAR: This version includes Matlab vectorization of the operations which makes it possible to load flow solution on meshes with more than one million of fractures. It includes a text menu allowing the user to choose between different visualisation options (geometry, mesh together with the aspect ratio or together with the flow solution) A selective visualisation of fractures is also possible, loading only the fractures that carry most of the flow.

- Participant: Géraldine Pichot
- Contact: Géraldine Pichot
- URL: https://gitlab.inria.fr/gpichot/NEF

6.6. NEF-Flow

KEYWORDS: Hydrogeology - Numerical simulations - 3D
SCIENTIFIC DESCRIPTION: NEF-Flow is a Matlab software for the simulation of steady state single phase flow in Discrete Fracture Networks (DFNs) using the Mixed Hybrid Finite Element (MHFEM) method for conforming and non conforming discretizations.

FUNCTIONAL DESCRIPTION: The software NEF-Flow solves the problem of an incompressible fluid flowing through a network of fractures. The software is interfaced with different mesh generators, among which BLSURF from the GAMMA3 team. A mixed hybrid finite element method is implemented.
NEWS OF THE YEAR: The last version includes new feature: - wells, sink/source terms boundary conditions - Implementation of P1 non conforming finite elements - New data structures to save the information local to each fracture - New tests per fracture have been added to check the solution - Add wells and sink/sources boundary conditions in the function that check the solution.

- Participants: Géraldine Pichot, Jean-Raynald De Dreuzy and Jocelyne Erhel
- Contact: Géraldine Pichot
- Publication: A mixed hybrid Mortar method for solving flow in discrete fracture networks
- URL: https://gitlab.inria.fr/gpichot/NEF

6.7. ParaCirce

Parallel Circulant Embedding
KEYWORDS: 2D - 3D - Hydrogeology - Gaussian random fields - MPI
SCIENTIFIC DESCRIPTION: ParaCirce implements the algorithm proposed by [C. R. Dietrich and G. N. Newsam. A fast and exact method for multidimensional gaussian stochastic simulations. Water Resources Research, 29(8):2861-2869, 1993].
FUNCTIONAL DESCRIPTION: ParaCirce implements a parallel Circulant Embedding method for the generation in parallel of 2D or 3D Gaussian Random Fields (second order stationary).
NEWS OF THE YEAR: - MPI implementation - Dedicated C++ classes to allow a user-friendly and safe usage of the library - Efficient use of the external library RngStream (L'Ecuyer) for a guarantee of independent realizations and reproductibility. - Splitting of the domain along one direction. The repartition of the field is automatic or defined by the user. - Automatic computation of the padding

- Participants: Géraldine Pichot and Simon Legrand
- Contact: Géraldine Pichot
- URL: https://gitlab.inria.fr/slegrand/paracirce

6.8. PRune

ParserRUNnEr
KEYWORD: Test
FUNCTIONAL DESCRIPTION: Python tool to parse single or multi configurations parameters files and to automatically run a program and store the results in a predefined tree.

- Participants: Simon Legrand and Géraldine Pichot
- Contact: Simon Legrand

SERPICO Project-Team

6. New Software and Platforms

6.1. ATLAS

KEYWORDS: Image segmentation - Object detection - Photonic imaging - Image analysis - Fluorescence microscopy

FUNCTIONAL DESCRIPTION: The ATLAS software enables to detect spots in 2D fluorescence images. The spot size is automatically selected and the detection threshold adapts to the local image contrasts. ATLAS relies on the Laplacian of Gaussian (LoG) filter, which both reduces noise and enhances spots. A multiscale representation of the image is built to automatically select the optimal LoG variance. Local statistics of the LoG image are estimated in a Gaussian window, and the detection threshold is pointwise inferred from a probability of false alarm (PFA). The user only has to specify: i/ size of the Gaussian window, ii/ PFA value. The Gaussian window must be about the size of the background structures, increasing the PFA increases the number of detections.

- Participants: Antoine Basset, Patrick Bouthemy, Charles Kervrann, Jérôme Boulanger and Jean Salamero
- Partner: UMR 144 CNRS - Institut Curie
- Contact: Patrick Bouthemy
- Publication: Adaptive spot detection with optimal scale selection in fluorescence microscopy images
- URL: http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::ATLAS

6.2. C-CRAFT

KEYWORDS: Fluorescence microscopy - Photonic imaging - Image analysis - Detection - 3D - Health - Biology - Segmentation

FUNCTIONAL DESCRIPTION: The C-CRAFT software enables to jointly segment small particles and estimate background in 2D or 3D fluorescence microscopy image sequences. The vesicle segmentation and background estimation problem is formulated as a global energy minimization problem in the Conditional Random Field framework. A patch-based image representation is used to detect spatial irregularity in the image. An iterative scheme based on graph-cut algorithm is proposed for energy minimization.

- Participants: Thierry Pécot, Charles Kervrann, Patrick Bouthemy and Jean Salamero
- Partner: UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- Publication: Background Fluorescence Estimation and Vesicle Segmentation in Live Cell Imaging with Conditional Random Fields
- URL: http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::C-CRAFT

6.3. F2D-SAFIR

KEYWORDS: Biomedical imaging - Photonic imaging - Fluorescence microscopy - Image processing

FUNCTIONAL DESCRIPTION: The F2D-SAFIR software removes mixed Gaussian-Poisson noise in large 2D images, typically 10000 x 10000 pixels, in a few seconds. The method is unsupervised and is a simplified version of the method related to the ND-SAFIR software. The software is dedicated to microarrays image denoising for disease diagnosis and multiple applications (gene expression, genotyping, aCGH, ChIP-chip, microRNA, ...).

- Participant: Charles Kervrann
- Partner: INRA
- Contact: Charles Kervrann

6.4. GcoPS

KEYWORDS: Photonic imaging - Fluorescence microscopy - Image processing - Statistic analysis

FUNCTIONAL DESCRIPTION: The GCOPS (Geo-Co-Positioning System) software is dedicated to the co-localization of fluorescence image pairs for both conventional and super-resolution microscopy. The procedure is only controlled by a p-value and tests whether the Pearson correlation between two binary images is significantly positive. It amounts to quantifying the interaction strength by the area/volume of the intersection between the two binary images viewed as random distributions of geometrical objects. Under mild assumptions, it turns out that the appropriately normalized Pearson correlation follows a standard normal distribution under the null hypothesis if the number of image pixels is large. Unlike previous methods, GcoPS handles 2D and 3D images, variable SNRs and any kind of cell shapes. It is able to co-localize large regions with small dots, as it is the case in TIRF-PALM experiments and to detect negative co-localization. The typical processing time is two milliseconds per image pair in 2D and a few seconds in 3D, with no dependence on the number of objects per image. In addition, the method provides maps to geo-co-localize molecule interactions in specific image regions.

- Participants: Thierry Pécot, Frédéric Lavancier, Charles Kervrann and Liu Zengzhen
- Partners: Université de Nantes - UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- Publication: A Fast Automatic Colocalization Method for 3D Live Cell and Super-Resolution Microscopy
- URL: http://icy.bioimageanalysis.org/plugin/GcoPS

6.5. Hullkground

KEYWORDS: Biomedical imaging - Photonic imaging - Fluorescence microscopy - Image processing

FUNCTIONAL DESCRIPTION: The HullkGround software decomposes a fluorescence microscopy image sequence into two dynamic components: i) an image sequence showing mobile objects, ii) an image sequence showing the slightly moving background. Each temporal signal of the sequence is processed individually and analyzed with computational geometry tools. The convex hull is estimated automatically for each pixel and subtracted to the original signal. The method is unsupervised, requires no parameter tuning and is a simplified version of the shapes-based scale-space method.

- Participants: Anatole Chessel, Charles Kervrann and Jean Salamero
- Partner: UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- URL: http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Hullkground

6.6. Motion2D

KEYWORDS: Image sequence - Motion model - 2D

FUNCTIONAL DESCRIPTION: The Motion2D software is a multi-platform object-oriented library to estimate 2D parametric motion models in an image sequence. It can handle several types of motion models, namely, constant (translation), affine, and quadratic models. Moreover, it includes the possibility of accounting for a global variation of illumination and more recently for temporal image intensity decay (e.g. due to photobleaching decay in fluorescence microscopy). The use of such motion models has been proved adequate and efficient for solving problems such as optic flow computation, motion segmentation, detection of independent moving objects, object tracking, or camera motion estimation, and in numerous application domains (video surveillance, visual servoing for robots, video coding, video indexing), including biological imaging (image stack registration, motion compensation in videomicroscopy). Motion2D is an extended and optimized implementation of the robust, multi-resolution and incremental estimation method (exploiting only the spatio-temporal derivatives of the image intensity function). Real-time processing is achievable for motion models involving up to six parameters. Motion2D can be applied to the entire image or to any pre-defined window or region in the image.

RELEASE FUNCTIONAL DESCRIPTION: Modifications and improvements in the PNG image file support. Support RAW and Mpeg2 video format as input (see CReader). The available video format which can be handled by the motion estimator are given by CReader::EReaderFormat. For the results, video sequences can be writen using the format specified by CWriter::EWriterFormat. Support Fedora 3 (g++ 3.4.2).

- Participants: Patrick Bouthemy, Jean Marc Odobez, Fabien Spindler, Thierry Pécot and Charles Kervrann
- Contact: Patrick Bouthemy
- URL: http://www.irisa.fr/vista/Motion2D/

6.7. ND-SAFIR

KEYWORDS: Fluorescence microscopy - Photonic imaging - Image analysis - Health - Biomedical imaging

SCIENTIFIC DESCRIPTION: ND-SAFIR is a software for denoising n-dimentionnal images especially dedicated to microscopy image sequence analysis. It is able to deal with 2D, 3D, 2D+time, 3D+time images have one or more color channel. It is adapted to Gaussian and Poisson-Gaussian noise which are usually encountered in photonic imaging. Several papers describe the detail of the method used in ndsafir to recover noise free images (see references).

- Participants: Jérôme Boulanger, Charles Kervrann, Patrick Bouthemy and Jean Salamero
- Partners: INRA - PiCT - UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- URL: http://serpico.rennes.inria.fr/doku.php?id=software:nd-safir:index

6.8. OWF

KEYWORDS: Image filter - Image processing - Statistics

FUNCTIONAL DESCRIPTION: The OWF software enables to denoise images corrupted by additive white Gaussian noise. In the line of work of the Non-Local means and ND-SAFIR algorithms, this adaptive estimator is based on the weighted average of observations taken in a neighborhood with weights depending on the similarity of local patches. The idea is to compute adaptive weights that best minimize an upper bound of the pointwise L2 risk. The spatially varying smoothing parameter is automatically adjusted to the image context. The proposed algorithm is fast and easy to control and is competitive when compared to the more sophisticated NL-means filters.

- Participants: Qiyu Jin, Ion Grama, Quansheng Liu and Charles Kervrann
- Partner: University of Bretagne-Sud
- Contact: Charles Kervrann
- Publication: Non-local means and optimal weights for noise removal
- URL: http://serpico.rennes.inria.fr/doku.php?id=software:owf

6.9. QuantEv

KEYWORDS: Photonic imaging - Fluorescence microscopy - Biomedical imaging - Image analysis - Image sequence - Statistic analysis

FUNCTIONAL DESCRIPTION: The QUANTEV software analyzes the spatial distribution of intracellular events represented by any static or dynamical descriptor, provided that the descriptors are associated with spatial coordinates. QUANTEV first computes 3D histograms of descriptors in a cylindrical coordinate system with computational cell shape normalization, enabling comparisons between cells of different shape. Densities are obtained via adaptive kernel density estimation, and we use the Circular Earth Mover's Distance to measure the dissimilarity between densities associated to different experimental conditions. A statistical analysis on these distances reliably takes into account the biological variability over replicated experiments.

- Participants: Thierry Pécot, Charles Kervrann, Jérôme Boulanger, Liu Zengzhen and Jean Salamero
- Partner: UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- Publication: QuantEv: quantifying the spatial distribution of intracellular events
- URL: http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::QuantEv-Densities

6.10. TMA-Lib

KEYWORDS: Photonic imaging - Fluorescence microscopy - Biomedical imaging - Image processing

FUNCTIONAL DESCRIPTION: The TMA-LIB enables to jointly detect suing adaptive wavelet transform, segment with parametric active contours and restore (i.e., artifact correction and deconvolution) TMA (Tissue MicroArrays) images.

- Participants: Hoai Nam Nguyen, Charles Kervrann, Cyril Cauchois and Vincent Paveau
- Partner: Innopsys
- Contact: Charles Kervrann
- Publications: A variational method for dejittering large fluorescence line scanner images - Generalized Sparse Variation Regularization for Large Fluorescence Image Deconvolution - ATMAD : robust image analysis for Automatic Tissue MicroArray De-arraying

6.11. TOTH

KEYWORDS: Photonic imaging - Fluorescence microscopy - Biomedical imaging - Classification - Statistical categorisation techniques - Statistics - Image sequence - Visual tracking

FUNCTIONAL DESCRIPTION: The TOTH software classifies trajectories of biomolecules computed with tracking algorithms. Trajectories in living cells are generally modelled with three types of diffusion processes: (i) free diffusion, (ii) subdiffusion or (iii) superdiffusion. We used a test approach with the Brownian motion as the null hypothesis, and developed a non-parametric three-decision test whose alternatives are subdiffusion and superdiffusion. First, we built a single test procedure for testing a single trajectory. Second, we proposed a multiple test procedure for testing a collection of trajectories. These procedures control respectively the type I error and the false discovery rate. Our approach can be considered as an alternative to the Mean Square Displacement (MSD) method commonly used to address this issue. It gives more reliable results as confirmed by our Monte Carlo simulations and evaluations on real sequences of images depicting protein dynamics acquired with TIRF or SPT-PALM microscopy.

- Participants: Vincent Briane, Charles Kervrann and Myriam Vimond
- Partner: ENSAI
- Contact: Charles Kervrann
- Publication: A Statistical Analysis of Particle Trajectories in Living Cells
- URL: http://serpico.rennes.inria.fr/doku.php?id=software:thot:index

6.12. SparseVolution

Sparse Variation for 2D Image Decovolution

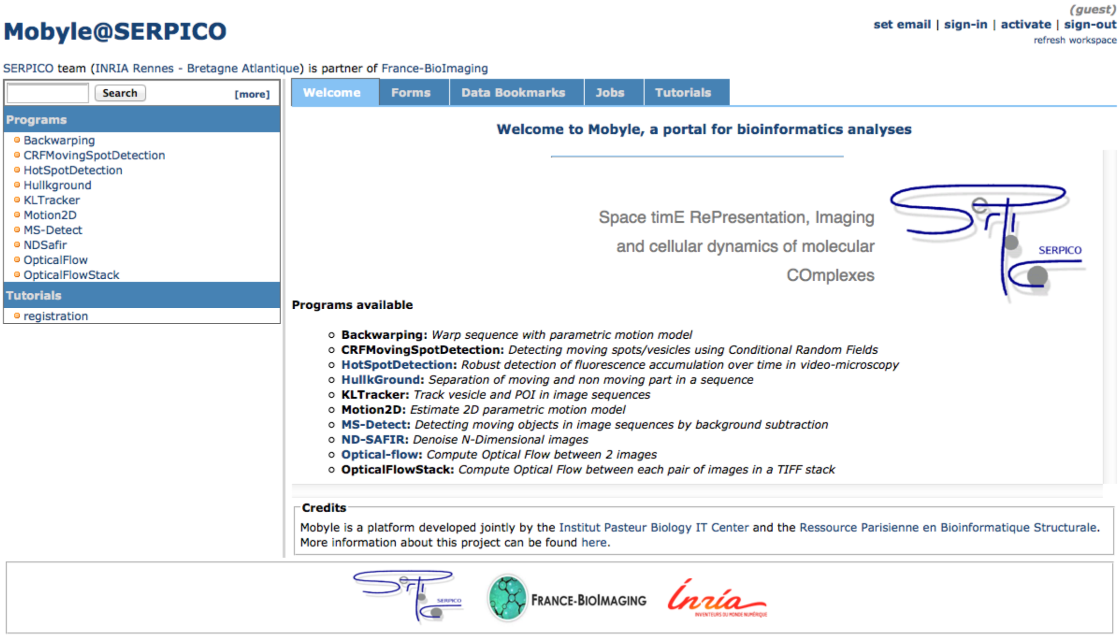
KEYWORDS: 2D - Fluorescence microscopy - Image processing - Problem inverse - Deconvolution

FUNCTIONAL DESCRIPTION: In order to improve the resolution of acquired fluorescence images, we introduced a method of image deconvolution by considering a family of convex regularizers. The considered regularizers are generalized from the concept of Sparse Variation which combines the L1 norm and Total Variation (TV) to favors the colocalization of high-intensity pixels and high-magnitude gradient. The experiments showed that the proposed regularization approach produces competitive deconvolution results on fluorescence images, compared to those obtained with other approaches such as TV or the Schatten norm of Hessian matrix. The final deconvolution algorithm has been dedicated to large 2D 20 000 x 20 000 images. The method is able to process a 512 x 512 image in 250 ms (Matlab) with a non optimized implementation.

- Participants: Hoai Nam Nguyen and Charles Kervrann
- Partner: Innopsys
- Contact: Charles Kervrann

6.13. Platforms

6.13.1. Mobyle@Serpico plateform and software distribution



SERPICO team (INRIA Rennes - Bretagne Atlantique) is partner of France-BioImaging

Welcome to Mobyle, a portal for bioinformatics analyses

Space timE RePresentation, Imaging and cellular dynamics of molecular COmplexes

Programs available

- **Backwarping:** *Warp sequence with parametric motion model*
- **CRFMovingSpotDetection:** *Detecting moving spots/vesicles using Conditional Random Fields*
- **HotSpotDetection:** *Robust detection of fluorescence accumulation over time in video-microscopy*
- **HullkGround:** *Separation of moving and non moving part in a sequence*
- **KLTracker:** *Track vesicle and POI in image sequences*
- **Motion2D:** *Estimate 2D parametric motion model*
- **MS-Detect:** *Detecting moving objects in image sequences by background subtraction*
- **ND-SAFIR:** *Denoise N-Dimensional images*
- **Optical-flow:** *Compute Optical Flow between 2 images*
- **OpticalFlowStack:** *Compute Optical Flow between each pair of images in a TIFF stack*

Credits

Mobyle is a platform developed jointly by the Institut Pasteur Biology IT Center and the Ressource Parisienne en Bioinformatique Structurale. More information about this project can be found here.

Figure 2. Mobyle@SERPICO web portal.

The objective is to disseminate the distribution of SERPICO image processing software in the community of cell biology and cell imaging.

Free binaries: software packages have been compiled for the main operating systems (Linux, MacOS, Windows) using CMake (see http://www.cmake.org/). They are freely available on the team website under a proprietary license (e.g. ND-SAFIR and HULLKGROUND are distributed this way at http://serpico.rennes.inria.fr/doku.php?id=software:index).

Mobyle@Serpico web portal: An on-line version (http://mobyle-serpico.rennes.inria.fr) of the image processing algorithms has been developped using the Mobyle framework (Institut Pasteur, see http://mobyle.pasteur.fr/). The main role of this web portal (see Fig. 2) is to demonstrate the performance of the programs developed by the team: QUANTEV, C-CRAFT[14], ATLAS[1], HULLKGROUND[38], KLTRACKER[44], MOTION2D[43], MS-DETECT[39], ND-SAFIR[6], OPTICALFLOW and FLUX ESTIMATION [14]. The web interface makes our image processing methods available for biologists at Mobyle@SERPICO (http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#welcome) without any installation or configuration on their own. The size of submitted images is limited to 200 MegaBytes per user and all the results are kept 15 days. The web portal and calculations run on a server with 2 CPU x 8 cores, 64 GigaBytes of RAM (500 MegaBytes for each user / Data is saved for 3 months).

ImageJ plugins: IMAGEJ (see http://rsb.info.nih.gov/ij/) is a widely used image visualization and analysis software for biologist users. We have developed IMAGEJ plug-in JAVA versions of the following software: ND-SAFIR [6], HULLKGROUND [38], MOTION2D [43], ATLAS [1]. The C-CRAFT algorithm [14] has been developped for the image processing ICY platform (http://icy.bioimageanalysis.org/).

- **Contact:** Charles Kervrann, Charles Deltel (Inria Rennes SED).
- **Partner:** UMR 144 CNRS-Institut Curie and France-BioImaging.

6.13.2. IGRIDA-Serpico cluster

The IGRIDA-Serpico cluster of 200 nodes is opened for end-users for large scale computing and data sets processing (200 TeraBytes).

- **Batch Scheduler:** OAR
- **File management:** Puppet / Git / Capistrano
- **OS:** Linux Debian 7
- **User connexion:** public ssh key
- **Contact:** Charles Kervrann, Charles Deltel (Inria Rennes SED).

SISTM Project-Team

6. New Software and Platforms

6.1. marqLevAlg

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

- Contact: Melanie Prague
- URL: https://cran.r-project.org/web/packages/marqLevAlg/index.html

6.2. VSURF

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

- Contact: Robin Genuer
- URL: https://github.com/robingenuer/VSURF

6.3. NPflow

Bayesian Nonparametrics for Automatic Gating of Flow-Cytometry Data
KEYWORDS: Bayesian estimation - Bioinformatics - Biostatistics
FUNCTIONAL DESCRIPTION: Dirichlet process mixture of multivariate normal, skew normal or skew t-distributions modeling oriented towards flow-cytometry data pre-processing applications.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/NPflow/

6.4. COVVSURF

Combination of Clustering Of Variables and Variable Selection Using Random Forests
KEYWORDS: Classification - Statistics - Cluster - Machine learning - Regression

- Contact: Robin Genuer
- URL: https://github.com/robingenuer/CoVVSURF

6.5. clogitLasso

KEYWORDS: Biostatistics - Bioinformatics - Machine learning - Regression
FUNCTIONAL DESCRIPTION: R package to fit a sequence of conditional logistic regression models with lasso, for small to large sized samples.

RELEASE FUNCTIONAL DESCRIPTION: Optimisation

- Partner: DRUGS-SAFE
- Contact: Marta Avalos Fernandez
- URL: https://cran.r-project.org/web/packages/clogitLasso/index.html

6.6. TcGSA

Time-course Gene Set Analysis
KEYWORDS: Bioinformatics - Genomics
FUNCTIONAL DESCRIPTION: An R package for the gene set analysis of longitudinal gene expression data sets. This package implements a Time-course Gene Set Analysis method and provides useful plotting functions facilitating the interpretation of the results.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/TcGSA/index.html

6.7. NIMROD

Normal approximation Inference in Models with Random effects based on Ordinary Differential equations
KEYWORDS: Ordinary differential equations - Statistical modeling
FUNCTIONAL DESCRIPTION: We have written a specific program called NIMROD for estimating parameter of ODE based population models.

- Contact: Melanie Prague
- URL: http://etudes.isped.u-bordeaux2.fr/BIOSTATISTIQUE/NIMROD/documentation/html/index.html

6.8. tcgsaseq

Time-Course Gene Set Analysis for RNA-Seq Data
KEYWORDS: Genomics - Biostatistics - Statistical modeling - RNA-seq - Gene Set Analysis
FUNCTIONAL DESCRIPTION: Gene set analysis of longitudinal RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/tcgsaseq/index.html

6.9. cytometree

KEYWORDS: Clustering - Biostatistics - Bioinformatics
FUNCTIONAL DESCRIPTION: Given the hypothesis of a bimodal distribution of cells for each marker, the algorithm constructs a binary tree, the nodes of which are subpopulations of cells. At each node, observed cells and markers are modeled by both a family of normal distributions and a family of bimodal normal mixture distributions. Splitting is done according to a normalized difference of AIC between the two families.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/cytometree/index.html

6.10. CRTgeeDR

KEYWORDS: Missing data - Statistics - Regression

FUNCTIONAL DESCRIPTION: The CRTgeeDR package allows you to estimates parameters in a regression model (with possibly a link function). It allows treatment augmentation and IPW for missing outcome. It is particularly of use when the goal is to estimate the intervention effect of a prevention strategy agains epidemics in cluster randomised trials.

- Contact: Melanie Prague
- URL: https://cran.r-project.org/web/packages/CRTgeeDR/index.html

6.11. ludic

KEYWORDS: Probability - Biostatistics
FUNCTIONAL DESCRIPTION: An R package to perform probabilistic record Linkage Using only DIagnosis Codes without direct identifiers, using C++ code to speed up computations. Available on CRAN, development version on github.

- Contact: Boris Hejblum
- URL: https://cran.r-project.org/web/packages/ludic/index.html

6.12. CoDaPCA

KEYWORDS: Unsupervised learning - PCA
FUNCTIONAL DESCRIPTION: R functions associated to the article Avalos et al. Representation Learning of Compositional Data. NeurIPS 2018 http://papers.nips.cc/paper/7902-representation-learning-of-compositional-data

- Contact: Marta Avalos Fernandez
- URL: https://github.com/sistm/CoDa-PCA

6.13. Left-censored Lasso

KEYWORDS: Biostatistics - Machine learning
FUNCTIONAL DESCRIPTION: R function associatied to the article Soret et al. Lasso regularization for left-censored Gaussian outcome and high-dimensional predictors. BMC Medical Research Methodology (2018) 18:159 https://doi.org/10.1186/s12874-018-0609-4

RELEASE FUNCTIONAL DESCRIPTION: https://github.com/psBiostat/left-censored-Lasso

- Contact: Marta Avalos Fernandez

6.14. dd-sPLS

Data-Driven Sparse PLS
KEYWORDS: Marker selection - Classification - Regression - Missing data - Multi-Block - High Dimensional Data - PLS - SVD
FUNCTIONAL DESCRIPTION: Allows to build Multi-Data-Driven Sparse PLS models. Multi-blocks with high-dimensional settings are particularly sensible to this. Whatsmore it deals with missing samples (entire lines missing per block) thanks to the Koh-Lanta algorithm. SVD decompositions permit to offer a fast and controlled method.

- Contact: Hadrien Lorenzo
- URL: https://hadrienlorenzo.netlify.com/projects/ddspls/

6.15. kernscr

KEYWORDS: Genomics - Biostatistics

FUNCTIONAL DESCRIPTION: An R package to perform KERNel machine score test for pathway analysis in the presence of Semi-Competing Risks

- Contact: Boris Hejblum
- URL: https://CRAN.R-project.org/package=kernscr

6.16. phenotypr

KEYWORDS: Phenotyping - Automatic labelling - Automatic Learning
FUNCTIONAL DESCRIPTION: Machine learning prediction algorithm for predicting a clinical phenotype from structured diagnostic data and CUI occurrence data collected from medical reports, previously processed by NLP approaches.

- Contact: Boris Hejblum
- URL: https://github.com/borishejblum/phenotypr

6.17. R2GUESS

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

- Contact: Rodolphe Thiebaut

STEEP 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 website). Databases include socio-economic and environmental datasets. Visualization tools include interactive piecharts, maps and Sankey diagrams.

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

TONUS Team

6. New Software and Platforms

6.1. CLAC

Conservation Laws Approximation on many Cores

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

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

Because of the envisaged applications of CLAC, which may be either academic or commercial, it is necessary to conceive a modular framework. The heart of the library is made of generic parallel algorithms for solving conservation laws. The parallelism can be both fine-grained (oriented towards GPUs and multicore processors) and coarse-grained (oriented towards GPU clusters). The separate modules allow managing the meshes and some specific applications. In this way, it is possible to isolate parts that should be protected for trade secret reasons.

FUNCTIONAL DESCRIPTION: CLAC is a generic Discontinuous Galerkin solver, written in C/C++, based on the OpenCL and MPI frameworks.

- Partner: AxesSim
- Contact: Philippe Helluy
- URL: http://clac.gforge.inria.fr/

6.2. Selalib

SEmi-LAgrangian LIBrary

KEYWORDS: Plasma physics - Semilagrangian method - Parallel computing - Plasma turbulence

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

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

FUNCTIONAL DESCRIPTION: Selalib is a collection of modules conceived to aid in the development of plasma physics simulations, particularly in the study of turbulence in fusion plasmas. Selalib offers basic capabilities from general and mathematical utilities and modules to aid in parallelization, up to pre-packaged simulations.

- Partners: Max Planck Insitute - Garching - Université de Strasbourg
- Contact: Philippe Helluy
- URL: http://selalib.gforge.inria.fr/

6.3. SCHNAPS

Solver for Conservative Hyperbolic Nonlinear Applications for PlasmaS
KEYWORDS: Discontinuous Galerkin - StarPU - Kinetic scheme
FUNCTIONAL DESCRIPTION: Generic systems of conservation laws. Specific models: fluids, Maxwell, Vlasov, acoustics (with kinetic representation). Multitasking with StarPU. Explicit solvers (RK2, RK3, RK4): accelerated with OpenCL Implicit solvers: through kinetic representations and palindromic time integration.

- Contact: Philippe Helluy
- URL: http://schnaps.gforge.inria.fr/

6.4. Slappy

KEYWORDS: Python - Opencl
FUNCTIONAL DESCRIPTION: The code Slappy solves the advection equations on multi-patch and non-conform complex geometries with the Semi-Lagrangian method. Using this we can also treat some hyperbolic/parabolic PDE with the Approximate BGK method which, allows to write a PDE as a transport plus a local relaxation step. The code is written in PyOpcenCL and can be used on CPU/GPU.

- Contact: Emmanuel Franck

6.5. Patapon

Parallel Task in Python
KEYWORDS: Python - Parallel computing - High order time schemes
FUNCTIONAL DESCRIPTION: Patapon is a code in PyOpenCL which allows to solve PDE like MHD using the vectorial Lattice Boltzmann method on Cartesian grids.

- Contact: Philippe Helluy

VISAGES Project-Team

6. New Software and Platforms

6.1. Anima

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

- Participants: Aymeric Stamm, Fang Cao, Florent Leray, Guillaume Pasquier, Laurence Catanese, Olivier Commowick, Renaud Hedouin and René-Paul Debroize
- Contact: Olivier Commowick
- URL: https://github.com/Inria-Visages/Anima-Public/wiki

6.2. autoMRI

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

- Participants: Camille Maumet, Cédric Meurée, Elise Bannier, Fang Cao, Isabelle Corouge, Pierre Maurel, Quentin Duche and Julie Coloigner
- Contact: Isabelle Corouge
- URL: https://team.inria.fr/visages/software/

6.3. MedInria

KEYWORDS: Visualization - DWI - Health - Segmentation - Medical imaging
SCIENTIFIC DESCRIPTION: medInria aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010, renewed in 2012. A fast-track ADT was awarded in 2017 to transition the software core to more recent dependencies and study the possibility of a consortium creation.The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.

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

- Participants: Maxime Sermesant, Olivier Commowick and Théodore Papadopoulo
- Partners: HARVARD Medical School - IHU - LIRYC - NIH
- Contact: Olivier Commowick
- URL: http://med.inria.fr

6.4. QtShanoir

KEYWORDS: Qt - Nifti - Medical imaging - Plug-in - DICOM - Health - C++ - Soap - Webservices - Shanoir
SCIENTIFIC DESCRIPTION: QtShanoir is based on Qt/C++ librairy. It interacts with the Shanoir server using SOAP web services provided. This application queries the server and displays hierarchical data extracted in tree view. Data could also be easily downloaded or uploaded on the server. In order to extend the Shanoir environment, QtShanoir is developed to contain two shared libraries: - « GUI » that represents all user interfaces. - « DAO » that takes in charge the data model. This library assures the connection to the server and provides all QtShanoir services : research, download and upload of Processed Dataset (NIfTI). QtShanoir dynamic libraries are already reused and integrated in other projects: in the software medInria and in an under development command line program.
FUNCTIONAL DESCRIPTION: QtShanoir is a graphical client application of the medical imaging database Shanoir. This application provides various functionalities to satisfy researchers' needs. It allows users to: - explore neuroimaging data derived from multicenter research trials. Through an intuitive user interface, users could easily visualize voluminous amount of structured data: studies, patients and datasets extracted from Shanoir - download and to upload data from the server. This application is available on Windows, UNIX, MacOs X. It is integrated as a plugin in medInria, a multi-plateform for medical image processing and visualization.

- Participants: Alexandre Abadie, Guillaume Renard, Nicolas Wiest Daessle, Olivier Commowick and Wefa Hakem
- Contact: Christian Barillot
- URL: http://qtshanoir.gforge.inria.fr

6.5. Shanoir

SHAring NeurOImaging Resources
KEYWORDS: Neuroimaging - Medical imaging - PACS - Nifti - Data Sharing - DICOM - Health - Shanoir - Webservices - Data base - Biology - Web Application
FUNCTIONAL DESCRIPTION: SHAring NeurOImaging Resources (Shanoir, Previously InriaNeuroTk) is an open source software platform designed to designed to share, archive, search and visualize neuroimaging data.

It provides a user-friendly secure web access and offers an intuitive workflow to facilitate the collecting and retrieving of neuroimaging data from multiple sources and a wizzard to make the completion of metadata easy. Shanoir comes along many features such as anonymization of data, support for multi-centric clinical studies on subjects or group of subjects.

Shanoir offers an ontology-based data organization (OntoNeuroLOG). Among other things, this facilitates the reuse of data and metadata, the integration of processed data and provides traceability trough an evolutionary approach. Shanoir allows researchers, clinicians, PhD students and engineers to undertake quality research projects with an emphasis on remote collaboration. As a secured J2EE web application, it therefore allows you safely storing and archiving, with no more requirements than a computer with an internet connection!

Furthermore, Shanoir is not only a web application: it is also a complete neuroinformatics platform in which you can easily integrate your existing processing tools or develop your own ones: see ShanoirTk.

The clinical scores resulting from instrument based assessments (e.g. neuropsychological tests) can also be entered and easily retrieved and exported in different formats (Excel, CSV, Xml). Scores and image acquisitions are bound together which makes relationship analysis possible. The instrument database is scalable an new measures can be added in order to meet specific project needs, by use of intuitive graphical interfaces.

Using cross-data navigation and advanced search criteria, the users can quickly point to a subset of data of data to be downloaded. Client side applications have as well been developed to illustrate how to locally access and exploit data through the available web services. With regards to security, the system requires authentication and user rights are tunable for each hosted studies. The person responsible for the study can define which users are allowed to see, download or import data.

Shanoir serves neuroimaging researchers in organizing efficiently their studies while cooperating with other laboratories. By managing patient privacy, Shanoir allows the exploitation of clinical data in a research context. It is finally a handy solution to publish and share data with a broader community.

- Participants: Adrien Férial, Anthony Baire, Bernard Gibaud, Christian Barillot, Guillaume Renard, Justine Guillaumont, Michael Kain and Yao Yao
- Partners: Université de Rennes 1 - CNRS - INSERM
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr

6.6. ShanoirUploader

KEYWORDS: Webservices - PACS - Medical imaging - Neuroimaging - DICOM - Health - Biology - Java - Shanoir

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

FUNCTIONAL DESCRIPTION: ShanoirUploader is a Java desktop application that transfers data securely between a PACS and a Shanoir server instance (e.g., within a hospital). It uses either a DICOM query/retrieve connection or a local CD/DVD access to search and access images from a local PACS or the local CD/DVD. After having retrieved the data, the DICOM files are locally anonymized and then uploaded to the Shanoir server. A possible integration of a hash creation application for patient identifiers is provided as well. The primary goals of that application are to enable mass data transfers between different remote server instances and therefore reduce the waiting time of the users, when importing data into Shanoir. Most of the time during import is spent with data transfers.

- Participants: Christian Barillot, Ines Fakhfakh, Justine Guillaumont, Michael Kain and Yao Yao
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr

6.7. Shanoir-NG

KEYWORDS: Neuroimaging - DICOM - Nifti

FUNCTIONAL DESCRIPTION: Shanoir-NG provides a user-friendly secure web access and offers an intuitive workflow to facilitate the collecting and retrieving of neuroimaging data from multiple sources and a wizzard to make the completion of metadata easy. Shanoir-NG comes along many features such as anonymization of data, support for multi-centric clinical studies on subjects or group of subjects.

Shanoir-NG offers an ontology-based data organization (OntoNeuroLOG). Among other things, this facilitates the reuse of data and metadata, the integration of processed data and provides traceability through an evolutionary approach. Shanoir allows researchers, clinicians, PhD students and engineers to undertake quality research projects with an emphasis on remote collaboration. As a secured Jakarta EE web application, it therefore allows you safely storing and archiving, with no more requirements than a computer with an internet connection!

RELEASE FUNCTIONAL DESCRIPTION: Shanoir-NG is a complete technological remake of the first version of the Shanoir application, but maintaining the key concepts of Shanoir.
NEWS OF THE YEAR: Shanoir-NG is a complete technological remake of the first version of the Shanoir application, but maintaining the key concepts of Shanoir.

- Participants: Christian Barillot, Mathieu Simon, Michael Kain, Yao Yao, Aneta Morawin, Arnaud Touboulic, Ines Fakhfakh and Anthony Baire
- Contact: Michael Kain

6.8. Platforms

6.8.1. The Neurinfo Platform

VisAGeS is the founding actor of an experimental research platform which was installed in August 2009 at the University Hospital of Rennes. The University of Rennes 1, Inria, Inserm for the academic side, and the University Hospital of Rennes and the Cancer Institute “Eugene Marquis” for the clinical side, are partners of this neuroinformatics platform called Neurinfo (http://www.neurinfo.org). This platform has been supported under the “Contrat de Projets Etat-Région” (Christian Barillot is the PI) and has received a total amount of 4.01 M€ for the period 2007–2014. European (FEDER), National (through Ministry of research, Inria, Inserm and ANR) and local councils (Brittany Region, Ille et Vilaine, and Rennes Metropole) have joined their effort to support this operation for a total amount of 4 010 k€ (600 k€ for the infrastructures, 2 850 k€ for the equipments and 560 k€ for the functioning). This application was set up through the Regional PIMATGI initiative coordinated by INSERM in Brittany (C. Roux). The PIMATGI initiative participated to the funding of three complementary platforms: Neurinfo, TheraFONC as a technical platform dedicated to therapy guided by functional imaging especially in the oncology domain (Inserm U650 - LaTIM, Dir. Ch. Roux, Brest), and TherA-Image as a platform dedicated to image guided mini-invasive surgery and therapy especially in the domain of cardio-vascular diseases (U642 -LTSI, Dir. L. Senhadji, Rennes).

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

In this context, a research 3T MRI system (Siemens Verio) was acquired in summer 2009 in order to develop the clinical research in the domain of morphological, functional, structural and cellular in-vivo imaging. In 2014 a new equipment for simultaneous recording of EEG and MRI images was acquired from Brain Product. In 2015, a mock scanner for experimental set-up was acquired as well as a new High Performance Computing environment made of one large computing cluster and a data center that is shared and operated by the Inria center at IRISA (UMR CNRS 6074). The computation cluster (240 cores) and the data center (up to 50 TB) are dedicated to host and process imaging data produced by the Neurinfo platform, but also by other research partners that share their protocols on the Neurinfo neuroinformatics system (currently more than 30 sites).

VisAGeS and its partners in the Neurinfo project are committed to use this new research platform for developing new regional, national and international collaborations around fundamental and applied clinical research projects dealing with in-vivo medical imaging.

In 2016, VisAGeS has been awarded by IBISA as a “Plateforme d’excellence”.

In 2017, funding was collected to replace the 3T Siemens Verio MRI that led to the installation of a new 3T Siemens Prisma in 2018.

In 2018, the INS2I institute of CNRS did awarded the neurinfo platform with a specific support for experimental platform that will be dedicated to the acquisition in 2019 of a EEG-compatible fNIRS system.

XPOP Project-Team

6. New Software and Platforms

6.1. mlxR

KEYWORDS: Simulation - Data visualization - Clinical trial simulator
FUNCTIONAL DESCRIPTION: The models are encoded using the model coding language ’Mlxtran’, automatically converted into C++ codes, compiled on the fly and linked to R using the ’Rcpp’ package. That allows one to implement very easily complex ODE-based models and complex statistical models, including mixed effects models, for continuous, count, categorical, and time-to-event data.

- Contact: Marc Lavielle
- URL: http://simulx.webpopix.org/

6.2. Rsmlx

R speaks Monolix
KEYWORDS: Data modeling - Nonlinear mixed effects models - Statistical modeling
FUNCTIONAL DESCRIPTION: Among other tasks, ’Rsmlx’ provides a powerful tool for automatic PK model building, performs statistical tests for model assessment, bootstrap simulation and likelihood profiling for computing confidence intervals. ’Rsmlx’ also proposes several automatic covariate search methods for mixed effects models.

- Partner: Lixoft
- Contact: Marc Lavielle

6.3. SPIX

KEYWORDS: Data modeling - Mass spectrometry - Chemistry
FUNCTIONAL DESCRIPTION: SPIX allows you to - To automatically identify, on the basis of statistical approaches, small but significant differences in spectra measured under different conditions, - Model the kinetics of entities that evolve over time

- Partner: Laboratoire de Chimie Moléculaire - Ecole Polytechnique
- Contact: Marc Lavielle

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 scalabiliy, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation. We still hope to find the proper resource to make WSNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem 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 leaded by Khaled Boussetta. The mutualization of the software tools will allows 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.

ALPINES Project-Team

6. New Software and Platforms

6.1. FreeFem++

FeeFrem++
SCIENTIFIC DESCRIPTION: FreeFem++ is a partial differential equation solver. It has its own language. freefem scripts can solve multiphysics non linear systems in 2D and 3D.

Problems involving PDE (2d, 3d) from several branches of physics such as fluid-structure interactions require interpolations of data on several meshes and their manipulation within one program. FreeFem++ includes a fast 2dˆ-tree-based interpolation algorithm and a language for the manipulation of data on multiple meshes (as a follow up of bamg (now a part of FreeFem++).

FreeFem++ is written in C++ and the FreeFem++ language is a C++ idiom. It runs on Macs, Windows, Unix machines. FreeFem++ replaces the older freefem and freefem+.
FUNCTIONAL DESCRIPTION: FreeFem++ is a PDE (partial differential equation) solver based on a flexible language that allows a large number of problems to be expressed (elasticity, fluids, etc) with different finite element approximations on different meshes.

- Partner: UPMC
- Contact: Frederic Hecht
- URL: http://www.freefem.org/ff++/

6.2. HPDDM

SCIENTIFIC DESCRIPTION: HPDDM is an efficient implementation of various domain decomposition methods (DDM) such as one- and two-level Restricted Additive Schwarz methods, the Finite Element Tearing and Interconnecting (FETI) method, and the Balancing Domain Decomposition (BDD) method. This code has been proven to be efficient for solving various elliptic problems such as scalar diffusion equations, the system of linear elasticity, but also frequency domain problems like the Helmholtz equation. A comparison with modern multigrid methods can be found in the thesis of Pierre Jolivet.
FUNCTIONAL DESCRIPTION: HPDDM is an efficient implementation of various domain decomposition methods (DDM) such as one- and two-level Restricted Additive Schwarz methods, the Finite Element Tearing and Interconnecting (FETI) method, and the Balancing Domain Decomposition (BDD) method.

- Participants: Frédéric Nataf and Pierre Jolivet
- Contact: Pierre Jolivet
- URL: https://github.com/hpddm

6.3. LORASC

LORASC preconditioner
KEYWORD: Preconditioner

- Participants: Laura Grigori and Rémi Lacroix
- Contact: Laura Grigori

6.4. Platforms

6.4.1. HTOOL

KEYWORD: Hierarchical Matrices

FUNCTIONAL DESCRIPTION: HTOOL is a C++ header-only library implementing compression techniques (e.g. Adaptive Cross Approximation) using hierarchical matrices. The library uses MPI and OpenMP for parallelism, and is interfaced with HPDDM for the solution of linear systems.

- Partners: CNRS - UPMC - ANR NonlocalDD
- Contact: Pierre Marchand
- URL: https://github.com/PierreMarchand20/htool

6.4.2. BemTool

KEYWORD: Boundary Element Method
FUNCTIONAL DESCRIPTION: BemTool is a C++ header-only library implementing the boundary element method for the discretisation of the Laplace, Helmholtz and Maxwell equations, in 2D and 3D. Its main purpose is the assembly of classic boundary element matrices, which can be compressed and inverted through its interface with HTOOL.

- Partners: UPMC - ANR NonlocalDD
- Contact: Xavier Claeys
- URL: https://github.com/xclaeys/BemTool

6.4.3. Geneo4PETSc

KEYWORD: Domain decomposition method
FUNCTIONAL DESCRIPTION: Implementation of the GenEO preconditioner with PETSc and SLEPc.

- Partners: CNRS - UPMC - European project NLAFET
- Contact: Frédéric Nataf
- URL: https://github.com/geneo4PETSc/geneo4PETSc

6.4.4. ffddm

KEYWORD: Domain decomposition method
FUNCTIONAL DESCRIPTION: In the acronym ffddm, ff stands for FreeFem++ and ddm for domain decomposition methods. The idea behind ffddm is to simplify the use of parallel solvers in FreeFem++: distributed direct methods and domain decomposition methods.

- Partners: CNRS - UPMC
- Contact: Pierre-Henri Tournier and Frédéric Nataf
- URL: https://doc.freefem.org/documentation/ffddm/ffddm

6.4.5. preAlps

KEYWORD: Preconditioned enlarged Krylov subspace methos
FUNCTIONAL DESCRIPTION: Contains enlarged Conjugate Gradient Krylov subspace method and Lorasc preconditioner.

- Partners: Inria
- Contact: Simplice Donfack, Laura Grigori, Olivier Tissot
- URL: https://github.com/NLAFET/preAlps

6.4.6. FreeFem++ v4

KEYWORD: New version of Freefem++, with new sparce matrix kernel, and with surface finite element.
FUNCTIONAL DESCRIPTION:

- Partners: UPMC - Inria
- Contact: Frederic Hecht
- URL: https://github.com/FreeFem/FreeFem-sources/tree/v4

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, Hélène Coullon and Maverick Chardet
- Partners: IMT Atlantique - LS2N - LIP
- Contact: Hélène 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, Aurélien Bouteiller, Benjamin Isnard, Daniel Balouek, Eddy Caron, Eric Bois, Frédéric Desprez, Frédéric Lombart, Gaël Le Mahec, Guillaume Verger, Huaxi Zhang, Jean-Marc Nicod, Jonathan Rouzaud-Cornabas, Lamiel Toch, Maurice Faye, Peter Frauenkron, Philippe Combes, Philippe Laurent, Raphaël 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/

Coast Project-Team

5. New Software and Platforms

5.1. BeGoood

FUNCTIONAL DESCRIPTION: BeGoood is a generic system for managing non-regression tests on knowledge bases. BeGoood allows to define test plans in order to monitor the evolution of knowledge-bases. Any system answering queries by providing results in the form of set of strings can be tested with BeGoood. BeGoood has been developed following a REST architecture and is independent of any application domain. BeGoood is a part of the Kolflow infrastructure.

- Participant: Gérôme Canals
- Contact: Gérôme Canals
- URL: https://github.com/kolflow/begoood

5.2. MUTE

Multi-User Text Editor

FUNCTIONAL DESCRIPTION: MUTE (Multi-User Text Editor) is a web-based text editing tool that allows to edit documents collaboratively in real-time. It implements our recent work on collaborative editing algorithms and more specifically the LogootSplit+ approach. Compared to existing web-based collaborative text editing tool this editor does not require a powerful central server since the server is not performing any computation and acts as a simple broadcast server. Our editor offers support for working offline while still being able to reconnect at a later time.

- Participants: Claudia-Lavinia Ignat, François Charoy, Gérald Oster and Luc André
- Contact: Gérald Oster
- URL: https://github.com/coast-team/mute-demo/

5.3. Replication Benchmarker

FUNCTIONAL DESCRIPTION: The Replication Benchmarker is a performance evaluation framework for optimistic replication mechanisms used in collaborative applications. It contains a library of implementation of several CRDT (Commutative Replicated Data Type) and OT (Operational Transformation) algorithms for different data types: text, set, trees. The framework is able to evaluate the performance of comparable algorithms on different corpus of events traces. These events traces can be produced randomly according to different parameters, can be extracted from real real-time editing session that have been recorded, or can be automatically extracted from distributed version control repositories such as the one produced with Git. Performances of the algorithms are measured in term of execution time, memory footprint and merge result quality (compared to manual merge history stored in git repositories).

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

5.4. Rivage

Real-tIme Vector grAphic Group Editor

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

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

COATI Project-Team

6. New Software and Platforms

6.1. GRPH

The high performance graph library for Java
KEYWORDS: Graph - Graph algorithmics - Java
FUNCTIONAL DESCRIPTION: Grph is an open-source Java library for the manipulation of graphs. Its design objectives are to make it portable, simple to use/extend, computationally/memory efficient, and, according to its initial motivation: useful in the context of graph experimentation and network simulation. Grph also has the particularity to come with tools like an evolutionary computation engine, a bridge to linear programming solvers, a framework for distributed computing, etc.

Grph offers a very general model of graphs. Unlike other graph libraries which impose the user to first decide if he wants to deal with directed, undirected, hyper (or not) graphs, the model offered by Grph is unified in a general class that supports mixed graphs made of undirected and directed simple and hyper edges. Grph achieves great efficiency through the use of multiple code optimization techniques such as multi-core parallelism, caching, adequate data structures, use of primitive objects, exploitation of low-level processor caches, on-the-fly compilation of specific C/C++ code, etc. Grph attempts to access the Internet in order to check if a new version is available and to report who is using it (login name and hostname). This has no impact whatsoever on performance and security.

- Participants: Aurélien Lancin, David Coudert, Issam Tahiri, Luc Hogie and Nathann Cohen
- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/grph/

6.2. BigGraphs

KEYWORDS: Graph algorithmics - Distributed computing - Java - Graph processing
FUNCTIONAL DESCRIPTION: The objective of BigGraphs is to provide a distributed platform for very large graphs processing. A typical data set for testing purpose is a sample of the Twitter graph : 240GB on disk, 398M vertices, 23G edges, average degree of 58 and max degree of 24635412.

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

This platform is based on the existing BIGGRPH library and we are now in the phasis where we focus on the quality and the improvement of the code. In particular we have designed strong test suites and some non trivial bugs have been fixed. We also have solved problems of scalability, in particular concerning the communication layer with billions of messages exchanged between BSP steps. We also have implemented specific data structures for BSP and support for distributed debugging. This comes along with the implementation of algorithms such as BFS or strongly connected components that are run on the NEF cluster.

In 2017 we have developed a multi-threaded shared-memory parallel version of the Bulk Synchronous Parallel framework. This new version uses advanced synchronization mechanisms and strategies to minimize the congestion of multiple threads working on the same graph. Using the NEF cluster (Inria Sophia Antipolis), this parallel version exhibits speed-ups up to 6.5 using 8 nodes (16 cores each) when computing a BFS on the 23 G edges Twitter graph sample.

- Participants: Luc Hogie, Michel Syska and Nicolas Chleq
- Partner: CNRS
- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/software/?name=biggrph

6.3. JMaxGraph

KEYWORDS: Java - HPC - Graph algorithmics

FUNCTIONAL DESCRIPTION: JMaxGraph is a collection of techniques for the computation of large graphs on one single computer. The motivation for such a centralized computing platform originates in the constantly increasing efficiency of computers which now come with hundred gigabytes of RAM, tens of cores and fast drives. JMaxGraph implements a compact adjacency-table for the representation of the graph in memory. This data structure is designed to 1) be fed page by page, à-la GraphChi, 2) enable fast iteration, avoiding memory jumps as much as possible in order to benefit from hardware caches, 3) be tackled in parallel by multiple-threads. Also, JMaxGraph comes with a flexible and resilient batch-oriented middleware, which is suited to executing long computations on shared clusters. The first use-case of JMaxGraph allowed F. Giroire, T. Trolliet and S. Pérennes to count K2,2s, and various types of directed triangles in the Twitter graph of users (23G arcs, 400M vertices). The computation campaign took 4 days, using up to 400 cores in the NEF Inria cluster.

- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/software/?name=jmaxgraph

6.4. Sagemath

SageMath

KEYWORDS: Graph algorithmics - Graph - Combinatorics - Probability - Matroids - Geometry - Numerical optimization

SCIENTIFIC DESCRIPTION: SageMath is a free open-source mathematics software system. It builds on top of many existing open-source packages: NumPy, SciPy, matplotlib, Sympy, Maxima, GAP, FLINT, R and many more. Access their combined power through a common, Python-based language or directly via interfaces or wrappers.

FUNCTIONAL DESCRIPTION: SageMath is an open-source mathematics software initially created by William Stein (Professor of mathematics at Washington University). We contribute the addition of new graph algorithms along with their documentations and the improvement of underlying data structures.

RELEASE FUNCTIONAL DESCRIPTION: See http://www.sagemath.org/changelogs/sage-8.4.txt

NEWS OF THE YEAR: 1) Implementation of a linear time algorithm for partitioning a graph into 3-connected components. Done in the context of Google Summer of Code 2018. 2) Main contributor for making the graph module (more than 100,000 lines of code) of SageMath compatible with Python3 (ongoing, already more than 100 patchs)

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

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 Synchrone, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

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 controler on a Turtlebot2 providing the IoT-LAB node mobility functionnality

- 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. WSNet

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

- Participants: Rodrigue Domga Komguem 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, instanciate 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 trow 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).

DELYS Team (section vide)

DIANA Project-Team

5. New Software and Platforms

5.1. ACQUAmobile

KEYWORDS: Android - Internet access - Performance measure - Quality of Experience
FUNCTIONAL DESCRIPTION: ACQUA is an Application for prediCting QUality of Experience (QoE) at Internet Access. It is developed by the Diana team at Inria Sophia Antipolis – Méditerranée and was supported by Inria under the ADT ACQUA grant. The scientific project around ACQUA is supported by Inria Project Lab BetterNet and the French National Project ANR BottleNet. The project also got the approval of Inria COERLE and French CNIL for the part on experimentation with real users. ACQUA presents a new way for the evaluation of the performance of Internet access. Starting from network-level measurements as the ones we often do today (bandwidth, delay, loss rates, jitter, etc), ACQUA targets the estimated Quality of Experience (QoE) related to the different applications of interest to the user without the need to run them (e.g., estimated Skype quality, estimated video streaming quality).

An application in ACQUA is a function, or a model, that links the network-level and device-level measurements to the expected Quality of Experience. Supervised machine learning techniques are used to establish such link between measurements both at the network level and the device level, and estimations of the Quality of Experience for different Internet applications. The required data for such learning can be obtained either by controlled experiments as we did in [22], [21] on YouTube Quality of Experience, or by soliciting the crowd (i.e. crowdsourcing) for combinations (i.e. tuples) of measurements and corresponding application-level Quality of Experience. Our current work is concentrating on using the ACQUA principle in the estimation and prediction of the Quality of Experience for main user's applications. We refer to the web site of the project for further details.

The ACQUA Android application is supposed to be on one hand the reference application for QoE forecasting and troubleshooting for end users at their Internet access, and on the other hand, the feedback channel that allows end users to report to us (if they are willing) on their experience together with the corresponding network measurements so as to help us calibrating better and more realistic models. For this calibration, we are currently performing extensive, efficient and automatic measurements in the laboratory, we will count on end users to help us completing this dataset with further applications and more realistic network and user conditions.

ACQUA is mainly meant for end users, but it is also of interest to (mobile) network operators and to content providers to estimate the QoE of their customers and their networks without each time having to run expensive application-level traffic and to involve real users.

- Authors: Thierry Spetebroot and Chadi Barakat
- Contact: Chadi Barakat
- URL: http://project.inria.fr/acqua/

5.2. ElectroSmart

KEYWORDS: Crowd-sourcing - UMTS - GSM - Bluetooth - Wi-Fi - 4G - 3G - 2G - Electromagnetic waves - Android - LTE

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

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

This project is supported by the UCN@Sophia Labex in 2016/2017/2018 (funding the engineer Mondi Ravi), by an Inria ADT (funding the engineer Abdelhakim Akodadi) 2017/2018, by and Inria ATT (funding the business developer David Migliacci) in 2017/2018, and by the academy 1 of UCAJedi (funding a Ph.D. student Yanis Boussad) 2017/2020.

In August 2016, we released the first stable public release of ElectroSmart. On the 13th July 2018 we have 84 000 downloads in Google Play, an average score of 4.4/5, 30 000 active users, 850 millions measured signals.

We are in a process of creating a startup to commercialize the exposition maps we can build with the data we are collecting.

- Participants: Arnaud Legout, Abdelhakim Akodadi, Hackob Melconian, Inderjeet Singh and Mondi Ravi
- Contact: Arnaud Legout
- URL: https://es.inria.fr/home/index?path_prefix=en

5.3. OpenLISP

KEYWORDS: LISP - Routing - Control-plane

FUNCTIONAL DESCRIPTION: Among many options tackling the scalability issues of the current Internet routing architecture, the Locator/Identifier Separation Protocol (LISP) appears as a viable solution. LISP improves a network's scalability, flexibility, and traffic engineering, enabling mobility with limited overhead. As for any new technology, implementation and deployment are essential to gather and master the real benefits that it provides. We propose a complete open source implementation of the LISP control plane. Our implementation is deployed in the worldwide LISP Beta Network and the French LISP-Lab testbed, and includes the key standardized control plane features. Our control plane software is the companion of the existing OpenLISP dataplane implementation, allowing the deployment of a fully functional open source LISP network compatible with any implementation respecting the standards.

- Contact: Damien Saucez
- URL: http://www.openlisp.org/downloads

5.4. nepi-ng

KEYWORDS: Wireless network - Experimentation

FUNCTIONAL DESCRIPTION: In the specific context of R2lab, we have created a tool suite for orchestrating network experiments, that for historical reasons we refer to collectively as `nepi-ng`, for NEPI new generation. An umbrella website is available at https://nepi-ng.inria.fr/.

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

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

`nepi-ng` is currently made of two separate python libraries:

- asynciojobs:
  - URL: http://asynciojobs.readthedocs.io/en/latest/
  - Version: asynciojobs v0.5.4
  - Keywords: networking experimentation, orchestration
  - License: CC BY-SA 4.0
  - Type of human computer interaction: python library
  - OS/Middleware: Linux
  - Required library or software: python-3.5 / asyncio
  - Programming language: python3
- apssh:
  - URL: http://apssh.readthedocs.io/en/latest/
  - Version: apssh v0.7.1
  - Keywords: networking experimentation, orchestration
  - License: CC BY-SA 4.0
  - Type of human computer interaction: python library
  - OS/Middleware: Linux
  - Required library or software: python-3.5 / asyncio
  - Programming language: python3
- Contact: Thierry Parmentelat
- URL: http://nepi-ng.inria.fr

5.5. Platforms

5.5.1. Reproducible research Lab - R2lab

Scientific evaluation of network protocols requires for experiments to be reproducible before they can be deemed valid. This is particularly difficult to obtain in the wireless networking area, where characteristics of wireless channels are known to be variable, unpredictable and hardly controllable.

The R2lab wireless testbed is built around an isolated and anechoic chamber, featuring RF absorbers preventing radio waves reflections and a Faraday cage blocking external interferences. This lab, named R2lab, represents an ideal environment for experiments reproducibility.

It represents a perfect facility for making wireless experiments reproducible. It has been operated for 3 years now, in the context of the FIT (Future Internet of Things) Equipment of Excellence project, and as such, it is now federated with the other testbeds that are part of the FIT initiative. This testbed is for the long-haul, and is scheduled to remain operational until at least 2020.

During 2018, our focus regarding R2lab has been set on enhancing the `nepi-ng` software toolkit, extending the set of tutorials and on deploying more network devices such as LoRa and Ettus USRP devices. The chamber now offers 19 USRP devices, as well as a couple of lime-sdr devices and a couple of E3372 LTE dongles. Moreover, two remotely controllable iphone are available. All these additions aim at widening even further the spectrum of experiments that the testbed can support.

Access to R2lab is open 24/7. We currently have around 150 active users from all over the world among them 45 new users registered in 2018. For more details see http://r2lab.inria.fr.

5.5.2. Network simulator for aircrafts

- Keywords: network, simulation, real-time
- Functional Description: In collaboration with Safran Electrical and Power we produced a network design tool for aircrafts. This tool simulates aircraft networks. The tool is about 10,000 lines of code, out of which we produced 2,000.
- Assessment: A-2up,SO-3,SM-2up,EM-4,SDL-3,OC-DA-CD-TPM
- Licence: confidential
- URL: confidential
- Contact: Damien Saucez

DIONYSOS Project-Team

6. New Software and Platforms

6.1. IPv6 Test Toolkit

FUNCTIONAL DESCRIPTION: These test suites are developed using the TTCN-3 environment.

The packages contains the full Abstract Test Suites written in TTCN-3 and the source files for building the codecs and adapters with the help of T3DevKit.

- Participants: Annie Floch, Anthony Baire, Ariel Sabiguero, Bruno Deniaud, César Viho and Frédéric Roudaut
- Contact: César Viho

6.2. Passive Test Tool

- Participants: Anthony Baire and César Viho
- Contact: Anthony Baire

6.3. T3DevKit

KEYWORDS: IPv6 - Conformance testing - TTCN-3
SCIENTIFIC DESCRIPTION: We have built a toolkit for easing executing tests written in the standardized TTCN-3 test specification language. This toolkit is made of a C++ library together with a highly customizable CoDec generator that allows fast development of external components (that are required to execute a test suite) such as CoDec (for message Coding/Decoding), System and Platform Adapters. It also provides a framework for representing and manipulating TTCN-3 events so as to ease the production of test reports. The toolkit addresses issues that are not yet covered by ETSI standards while being fully compatible with the existing standard interfaces: TRI (Test Runtime Interfaces) and TCI (Test Control Interfaces), it has been tested with four TTCN-3 environments (IBM, Elvior, Danet and Go4IT) and on three different platforms (Linux, Windows and Cygwin).
FUNCTIONAL DESCRIPTION: T3DevKit is a free open source toolkit to ease the development of test suites in the TTCN-3 environment. It provides:

a CoDec generator (t3cdgen) that automates the development process of the CoDec needed for coding TTCN-3 values into physically transmittable messages and decoding incoming messages a library (t3devlib) that provides an object oriented framework to manipulate TTCN-3 entities (values, ports, timers, external functions…) an implementation of the TRI and TCI standard interfaces default implementations for the system adapter (SA), platform adapter (PA), test management (TM), test logging (TL) and component handling (CH) modules default codecs build scripts for the generation of executable test suites, these are tool-independent and facilitate the distribution of test suite sources

- Participants: Annie Floch, Anthony Baire, Ariel Sabiguero, César Viho and Frédéric Roudaut
- Contact: Federico Sismondi

6.4. ttproto

Testing Tool Prototype
KEYWORDS: Interoperability - Conformance testing - TTCN-3
FUNCTIONAL DESCRIPTION: ttproto is an experimental tool for implementing testing tools, for conformance and interoperability testing.

It was first implemented to explore new features and concepts for the TTCN-3 standard, but we also used it to implement a passive interoperability test suite we provided for the CoAP interoperability event held in Paris in March 2012.

This tool is implemented in python3 and its design was influenced mainly by TTCN-3 (abstract model, templates, snapshots, behaviour trees, communication ports, logging) and by Scapy (syntax, flexibility, customisability)

Its purpose is to facilitate rapid prototyping rather than experimentations (rather than production use). We choosed to maximise its modularity and readability rather than performances and real-time considerations.

Now you should have a look at the Features page: https://www.irisa.fr/tipi/wiki/doku.php/testing_tool_prototype:features

- Contact: Federico Sismondi
- URL: https://www.irisa.fr/tipi/wiki/doku.php/testing_tool_prototype

6.5. CoAP Testing Tool

KEYWORDS: Test - Interoperability - Conformance testing - Plugtests
FUNCTIONAL DESCRIPTION: The software helps developers of the CoAP protocol assessing if their implementations (either CoAP clients or CoAP servers) are conformant to protocol specifications, and interoperable with other implementations. It encompasses:

- Coordination of CoAP interoperability tests
- Analysis of CoAP traces & issuing verdicts
- Automation of open source CoAP implementations for based reference interop testing
- Authors: Federico Sismondi and César Viho
- Contact: Federico Sismondi

6.6. ioppytest

Interoperability testing
KEYWORDS: Interoperability - Conformance testing - CoAP - 6LoWPAN - OneM2M
FUNCTIONAL DESCRIPTION: The software is a framework for developing interoperability tests. The interoperability tests help developers of network protocol assessing if their implementations are conformant to protocol specifications, and interoperable with other implementations.

The software already integrates interoperability tests for CoAP, OneM2M and 6LoWPAN The framework provides the following features to the users:

- Coordination of the interoperability tests (enabling remote testing)
- VPN-like connectivity between users' implementations (enabling remote testing)
- Analysis of exchanged network traces & issuing verdicts
- Automation of open source implementations for based reference interop testing

This framework is the evolution of the CoAP Testing Tool (https://bil.inria.fr/fr/software/view/2937/tab)

- Contact: Federico Sismondi
- URL: https://gitlab.f-interop.eu/f-interop-contributors/ioppytest

DIVERSE Project-Team

5. New Software and Platforms

5.1. amiunique

KEYWORDS: Privacy - Browser fingerprinting
SCIENTIFIC DESCRIPTION: The amiunique web site has been deployed in the context of the DiverSE's research activities on browser fingerprinting and how software diversity can be leveraged in order to mitigate the impact of fingerprinting on the privacy of users. The construction of a dataset of genuine fingerprints is essential to understand in details how browser fingerprints can serve as unique identifiers and hence what should be modified in order to mitigate its impact privacy. This dataset also supports the large-scale investigation of the impact of web technology advances on fingerprinting. For example, we can analyze in details the impact of the HTML5 canvas element or the behavior of fingerprinting on mobile devices.

The whole source code of amiunique is open source and is distributed under the terms of the MIT license.

Similar sites: Panopticlick https://panopticlick.eff.org/ BrowserSpy http://browserspy.dk/ http://noc.to/ Main innovative features: canvas fingerprinting WebGL fingerprinting advanced JS features (platform, DNT, etc.)

Impact: The website has been showcased in several professional forums in 2014 and 2015 (Open World Forum 2014, FOSSA'14, FIC'15, ICT'15) and it has been visited by more than 100000 unique visitors in one year.
FUNCTIONAL DESCRIPTION: This web site aims at informing visitors about browser fingerprinting and possible tools to mitigate its effect, as well as at collecting data about the fingerprints that can be found on the web. It collects browser fingerprints with the explicit agreement of the users (they have to click on a button on the home page). Fingerprints are composed of 17 attributes, which include regular HTTP headers as well as the most recent state of the art techniques (canvas fingerprinting, WebGL information).

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

5.2. FAMILIAR

KEYWORDS: Software line product - Configators - Customisation
SCIENTIFIC DESCRIPTION: FAMILIAR (for FeAture Model scrIpt Language for manIpulation and Automatic Reasoning) is a language for importing, exporting, composing, decomposing, editing, configuring, computing "diffs", refactoring, reverse engineering, testing, and reasoning about (multiple) feature models. All these operations can be combined to realize complex variability management tasks. A comprehensive environment is proposed as well as integration facilities with the Java ecosystem.
FUNCTIONAL DESCRIPTION: Familiar is an environment for large-scale product customisation. From a model of product features (options, parameters, etc.), Familiar can automatically generate several million variants. These variants can take many forms: software, a graphical interface, a video sequence or even a manufactured product (3D printing). Familiar is particularly well suited for developing web configurators (for ordering customised products online), for providing online comparison tools and also for engineering any family of embedded or software-based products.

- Participants: Aymeric Hervieu, Benoit Baudry, Didier Vojtisek, Edward Mauricio Alferez Salinas, Guillaume Bécan, Joao Bosco Ferreira-Filho, Julien Richard-Foy, Mathieu Acher, Olivier Barais and Sana Ben Nasr
- Contact: Mathieu Acher
- URL: http://familiar-project.github.com

5.3. GEMOC Studio

KEYWORDS: DSL - Language workbench - Model debugging
SCIENTIFIC DESCRIPTION: The language workbench put together the following tools seamlessly integrated to the Eclipse Modeling Framework (EMF):

- Melange, a tool-supported meta-language to modularly define executable modeling languages with execution functions and data, and to extend (EMF-based) existing modeling languages. - MoCCML, a tool-supported meta-language dedicated to the specification of a Model of Concurrency and Communication (MoCC) and its mapping to a specific abstract syntax and associated execution functions of a modeling language. - GEL, a tool-supported meta-language dedicated to the specification of the protocol between the execution functions and the MoCC to support the feedback of the data as well as the callback of other expected execution functions. - BCOoL, a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models. - Sirius Animator, an extension to the model editor designer Sirius to create graphical animators for executable modeling languages.
FUNCTIONAL DESCRIPTION: The GEMOC Studio is an eclipse package that contains components supporting the GEMOC methodology for building and composing executable Domain-Specific Modeling Languages (DSMLs). It includes the two workbenches: The GEMOC Language Workbench: intended to be used by language designers (aka domain experts), it allows to build and compose new executable DSMLs. The GEMOC Modeling Workbench: intended to be used by domain designersto create, execute and coordinate models conforming to executable DSMLs. The different concerns of a DSML, as defined with the tools of the language workbench, are automatically deployed into the modeling workbench. They parametrize a generic execution framework that provide various generic services such as graphical animation, debugging tools, trace and event managers, timeline, etc.

- Participants: Didier Vojtisek, Dorian Leroy, Erwan Bousse, Fabien Coulon and Julien Deantoni
- Partners: IRIT - ENSTA - I3S - OBEO - Thales TRT
- Contact: Benoît Combemale
- URL: http://gemoc.org/studio.html

5.4. Kevoree

Kevoree Core
KEYWORDS: M2M - Dynamic components - Iot - Heterogeneity - Smart home - Cloud - Software architecture - Dynamic deployment
SCIENTIFIC DESCRIPTION: Kevoree is an open-source models@runtime platform (http://www.kevoree.org) to properly support the dynamic adaptation of distributed systems. Models@runtime basically pushes the idea of reflection [132] one step further by considering the reflection layer as a real model that can be uncoupled from the running architecture (e.g. for reasoning, validation, and simulation purposes) and later automatically resynchronized with its running instance.

Kevoree has been influenced by previous work that we carried out in the DiVA project [132] and the Entimid project [135] . With Kevoree we push our vision of models@runtime [131] farther. In particular, Kevoree provides a proper support for distributed models@runtime. To this aim we introduced the Node concept to model the infrastructure topology and the Group concept to model semantics of inter node communication during synchronization of the reflection model among nodes. Kevoree includes a Channel concept to allow for multiple communication semantics between remoteComponents deployed on heterogeneous nodes. All Kevoree concepts (Component, Channel, Node, Group) obey the object type design pattern to separate deployment artifacts from running artifacts. Kevoree supports multiple kinds of very different execution node technology (e.g. Java, Android, MiniCloud, FreeBSD, Arduino, ...).

Kevoree is distributed under the terms of the LGPL open source license.

Main competitors:

- the Fractal/Frascati eco-system (http://frascati.ow2.org).
- SpringSource Dynamic Module (http://spring.io/)

GCM-Proactive (http://proactive.inria.fr/)

OSGi (http://www.osgi.org)

Chef

Vagran (http://vagrantup.com/)

Main innovative features:

distributed models@runtime platform (with a distributed reflection model and an extensible models@runtime dissemination set of strategies).

Support for heterogeneous node type (from Cyber Physical System with few resources until cloud computing infrastructure).

Fully automated provisioning model to correctly deploy software modules and their dependencies.

Communication and concurrency access between software modules expressed at the model level (not in the module implementation).

Impact:

Several tutorials and courses have been performed this year at EJCP for French PhD student, at ECNU summer school for 82 chineese PhD students. See also the web page http://www.kevoree.org .

In 2015, we mainly created a new implementation in C# and we created an implementation for system containers for driving resources using Kevoree. We also use Kevoree in the context of Mohammed's PhD to create testing infrastructure on-demand.

FUNCTIONAL DESCRIPTION: Kevoree is an open-source models@runtime platform to properly support the dynamic adaptation of distributed systems. Models@runtime basically pushes the idea of reflection one step further by considering the reflection layer as a real model that can be uncoupled from the running architecture (e.g. for reasoning, validation, and simulation purposes) and later automatically resynchronized with its running instance.

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

5.5. Melange

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

SCIENTIFIC DESCRIPTION: Melange is a follow-up of the executable metamodeling language Kermeta, which provides a tool-supported dedicated meta-language to safely assemble language modules, customize them and produce new DSMLs. Melange provides specific constructs to assemble together various abstract syntax and operational semantics artifacts into a DSML. DSMLs can then be used as first class entities to be reused, extended, restricted or adapted into other DSMLs. Melange relies on a particular model-oriented type system that provides model polymorphism and language substitutability, i.e. the possibility to manipulate a model through different interfaces and to define generic transformations that can be invoked on models written using different DSLs. Newly produced DSMLs are correct by construction, ready for production (i.e., the result can be deployed and used as-is), and reusable in a new assembly.

Melange is tightly integrated with the Eclipse Modeling Framework ecosystem and relies on the meta-language Ecore for the definition of the abstract syntax of DSLs. Executable meta-modeling is supported by weaving operational semantics defined with Xtend. Designers can thus easily design an interpreter for their DSL in a non-intrusive way. Melange is bundled as a set of Eclipse plug-ins.
FUNCTIONAL DESCRIPTION: Melange is a language workbench which helps language engineers to mashup their various language concerns as language design choices, to manage their variability, and support their reuse. It provides a modular and reusable approach for customizing, assembling and integrating DSMLs specifications and implementations.

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

5.6. Opencompare

KEYWORD: Software Product Line
FUNCTIONAL DESCRIPTION: Product comparison matrices (PCMs) are tabular data: supported and unsupported features are documented for both describing the product itself and for discriminating one product compared to another. PCMs abound – we are all using PCMs – and constitute a rich source of knowledge for easily comparing and choosing product. Yet the current practice is suboptimal both for humans and computers, mainly due to unclear semantics, heterogeneous forms of data, and lack of dedicated support.

OpenCompare.org is an ambitious project for the collaborative edition, the sharing, the standardisation, and the open exploitation of PCMs. The goal of OpenCompare.org is to provide an integrated set of tools (e.g., APIs, visualizations, configurators, editors) for democratizing their creation, import, maintenance, and exploitation.

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

5.7. DSpot

KEYWORDS: Software testing - Test amplification
FUNCTIONAL DESCRIPTION: DSpot is a tool that generates missing assertions in JUnit tests. DSpot takes as input a Java project with an existing test suite. As output, DSpot outputs new test cases on console. DSpot supports Java projects built with Maven and Gradle

- Participants: Benoit Baudry, Martin Monperrus and Benjamin Danglot
- Partner: KTH Royal Institute of Technology
- Contact: Benjamin Danglot
- URL: https://github.com/STAMP-project/dspot

5.8. ALE

Action Language for Ecore
KEYWORDS: Meta-modeling - Executable DSML
FUNCTIONAL DESCRIPTION: Main features of ALE include:

- Executable metamodeling: Re-open existing EClasses to insert new methods with their implementations - Metamodel extension: The very same mechanism can be used to extend existing Ecore metamodels and insert new features (eg. attributes) in a non-intrusive way - Interpreted: No need to deploy Eclipse plugins, just run the behavior on a model directly in your modeling environment - Extensible: If ALE doesn't fit your needs, register Java classes as services and invoke them inside your implementations of EOperations.

- Partner: OBEO
- Contact: Benoît Combemale
- URL: http://gemoc.org/ale-lang/

5.9. InspectorGuidget

KEYWORDS: Static analysis - Software testing - User Interfaces

FUNCTIONAL DESCRIPTION: InspectorGuidget is a static code analysing tool. InspectorGuidget analyses UI (user interface/interaction) code of a software system to extract high level information and metrics. InspectorGuidget also finds bad UI coding pratices, such as Blob listener instances. InspectorGuidget analyses Java code.

- Participants: Arnaud Blouin and Benoit Baudry
- Contact: Arnaud Blouin
- Publications: User Interface Design Smell: Automatic Detection and Refactoring of Blob Listeners - Automatic Detection of GUI Design Smells: The Case of Blob Listener
- URL: https://github.com/diverse-project/InspectorGuidget

DYOGENE Project-Team (section vide)

EASE Team

5. New Software and Platforms

5.1. THEGAME

KEYWORD: Contextual service

SCIENTIFIC DESCRIPTION: Context-aware applications have to sense the environment in order to adapt themselves and provide with contextual services. This is the case of Smart Homes equipped with sensors and augmented appliances. However, sensors can be numerous, heterogeneous and unreliable. Thus the data fusion is complex and requires a solid theory to handle those problems. The aim of the data fusion, in our case, is to compute small pieces of context we call context attributes. Those context attributes are diverse and could be for example the presence in a room, the number of people in a room or even that someone may be sleeping in a room. For this purpose, we developed an implementation of the belief functions theory (BFT). THE GAME (THeory of Evidence in a lanGuage Adapted for Many Embedded systems) is made of a set of C-Libraries. It provides the basics of belief functions theory, computations are optimized for an embedded environment (binary representation of sets, conditional compilation and diverse algorithmic optimizations).

THE GAME is published under apache licence (https://github.com/bpietropaoli/THEGAME/). It is maintained and experimented by Aurélien Richez within a sensor network platform developed by TACOMA since June 2013.

FUNCTIONAL DESCRIPTION: THEGAME is a set of software services for detecting different types of situation in a building (presence in a room, activity level, etc.) based on a set of raw data sourced from all sorts of sensors. Written in C or Java, it can be integrated in an embedded computer: tablet, smartphone, box, etc., and can be connected to different sensor networks. It can be used to implement context-aware services: for example, to alert the user if s/he forgets to close a window when leaving the building, or to turn off the heating in an empty room, etc.

- Participants: Aurélien Richez and Bastien Pietropaoli
- Contact: Frédéric Weis
- URL: https://github.com/bpietropaoli/THEGAME/

5.2. Platform Pervasive_RFID

SCIENTIFIC DESCRIPTION

The RFID experiment testbed has been designed and deployed in collaboration with IETR (see Figure 2). This system allows both interactive testing as well as long running experiments of RFID reading protocols. It comprises a software platform allowing fine control over all dynamic aspects influencing RFID readings: movements for target and antenna, RFID reader configuration, and smart antenna configuration (diversity and power control).

KEYWORDS: Composite objects - RFID

- Participants: Paul Couderc and Anthony Blair (Univ. Rennes 1)
- Partner: Univ. Rennes 1 (IETR - lab bringing together researchers in the electronics and telecommunications)
- Contact: Paul Couderc

5.3. ISO/IEC 15118-2 Open source Implementation

SCIENTIFIC DESCRIPTION

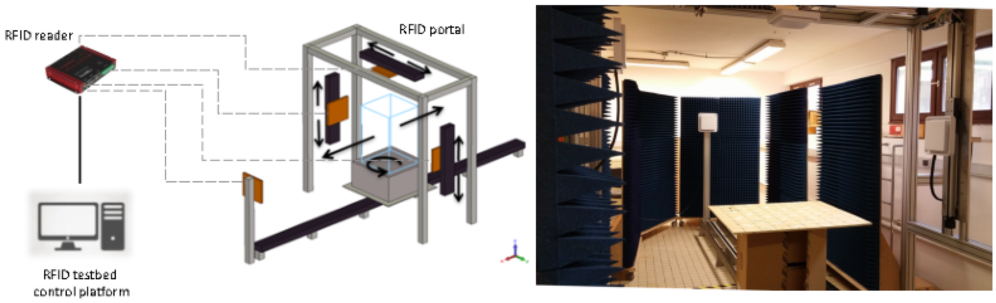


Figure 2. RFID testbed

The ISO/IEC 15118 standard, named "Road vehicles – Vehicle-to-Grid Communication Interface", defines how an electric vehicle and a charging station should communicate. It enables the Smart Charging of electric vehicles by allowing them to plan their charging sessions. As we want to be able to manage the charge of electric vehicles in our micro Smart Grid systems, we decided to implement the protocol defined by this standard. The goal is also to participate actively in the design of the new version of this protocol. During a charging session the charging station provides the vehicle with the status of the electric power grid. The vehicle is then able to plan its sharing session accordingly. It sends back its charge plan to the charging station, so that the Smart Grid is aware of it. The protocol also provides security and authentication features.

This software platform was implemented onto small PCs, and was used to control the charge in a small and portable demonstration platform, to demonstrate how it is possible to interconnect this high level decision and communication software with low level components, such as a Battery Management System (BMS), and a battery charger. In 2016, in the context of the Greenfeed project our software has been demonstrated to control the charge of the electric vehicle during the final demonstration of the project. The integration work has been done in collaboration with VeDeCom [0].

KEYWORDS: Smart Grid - Intelligent Transport System

- Partner: IMT Atlantique
- Participants: Guillaume Le Gall
- Contact: Jean-Marie Bonnin

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[0] http://www.vedecom.fr/

EVA Project-Team

6. New Software and Platforms

6.1. OpenWSN

KEYWORDS: Internet of things - 6TiSCH - 6LoWPAN - CoAP
FUNCTIONAL DESCRIPTION: OpenWSN is an open-source implementation of a fully standards-based protocol stack for the Internet of Things. It has become the de-facto implementation of the IEEE802.15.4e TSCH standard, has a vibrant community of academic and industrial users, and is the reference implementation of the work we do in the IETF 6TiSCH standardization working group.

- Partner: University of California Berkeley
- Contact: Thomas Watteyne
- URL: http://www.openwsn.org/

6.2. 6TiSCH Simulator

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

- Contact: Malisa Vucinic

6.3. Argus

KEYWORDS: Cloud - Low-Power WIreless - Sniffer
FUNCTIONAL DESCRIPTION: There are three piece to the Argus:

The Argus Probe is the program which attaches to your low-power wireless sniffer and forwards its traffic to the Argus Broker.

The Argus Broker sits somewhere in the cloud. Based on MQTT, it connect Argus Probes with Argus Clients based on a pub-sub architecture.

Several Argus Clients can the started at the same time. It is a program which subscribes to the Argus Broker and displays the frames in Wireshark.

- Contact: Rémy Leone

6.4. SolSystem

Sensor Object Library System
KEYWORDS: Low-Power WIreless - Back-End System - SmartMesh IP
FUNCTIONAL DESCRIPTION: The source code is composed of the definition of the SOL structure (https://github.com/realms-team/sol), the code that runs on the manager (https://github.com/realms-team/solmanager, written in Python) and the code that runs on the server receiving the data (https://github.com/realms-team/solserver, written in Python)

- Contact: Keoma Brun-Laguna
- URL: http://www.solsystem.io/

6.5. 6TiSCH Wireshark Dissector

KEYWORDS: 6TiSCH - Wireshark
FUNCTIONAL DESCRIPTION: Implementation on the dissectors is done through an open-source repository, stable code is regularly contributed back to the main Wireshark code base.

- Contact: Jonathan Munoz

6.6. F-Interop

Remote Conformance and Interoperability Tests for the Internet of Thing
KEYWORDS: Interoperability - Iot - Conformance testing - Standardization

- Partners: UPMC - IMEC - ETSI - EANTC - Mandat International - Digital Catapult - University of Luxembourg - Device Gateway
- Contact: Rémy Leone

6.7. Mercator

KEYWORDS: Deployment - Low-Power WIreless - Testbeds - Connectivity
FUNCTIONAL DESCRIPTION: The firmware is written as part of the OpenWSN project. Scripts and analysis tools are written in Python.

- Contact: Keoma Brun-Laguna

FOCUS Project-Team

5. New Software and Platforms

5.1. HoCA

Higher-Order Complexity Analysis

KEYWORDS: Ocaml - Verification - Runtime Complexity Analysis

SCIENTIFIC DESCRIPTION: Over the last decade, various tools for the static analysis of resource properties of programs have emerged. In particular, the rewriting community has recently developed several tools for the time complexity analysis of term rewrite systems. These tools have matured and are nowadays able to treat non-trivial programs, in a fully automatic setting. However, none of these automatic complexity analysers can deal with higher-order functions, a pervasive feature of functional programs. HoCA (Higher-Order Complexity Analyser) overcomes this limitation by translating higher-order programs – in the form of side-effect free OCaml programs - into equivalent first-order rewrite systems. At the heart of our tool lies Reynold's defunctionalization technique. Defunctionalization however is not enough. Resulting programs have a recursive structure too complicated to be analysed automatically in all but trivial cases. To overcome this issue, HoCA integrates a handful of well established program transformation techniques, noteworthy dead-code elimination, inlining, instantiation and uncurrying. A complexity bound on the resulting first-order program can be relayed back reliably to the higher-order program of interest. A detailed description of HoCA is available on http://arxiv.org/abs/1506.05043.

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

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

5.2. JOLIE

Java Orchestration Language Interpreter Engine

KEYWORD: Microservices

SCIENTIFIC DESCRIPTION: Jolie enforces a strict separation of concerns between behaviour, describing the logic of the application, and deployment, describing the communication capabilities. The behaviour is defined using the typical constructs of structured sequential programming, communication primitives, and operators to deal with concurrency (parallel composition and input choice). Jolie communication primitives comprise two modalities of interaction typical of Service-Oriented Architectures (SOAs), namely one-way (sends an asynchronous message) and request-response (sends a message and waits for an answer). A main feature of the Jolie language is that it allows one to switch among many communication media and data protocols in a simple, uniform way. Since it targets the field of SOAs, Jolie supports the main communication media (TCP/IP sockets, Bluetooth L2CAP, Java RMI, and Unix local sockets) and data protocols (HTTP, JSON-RPC, XML-RPC, SOAP and their respective SSL versions) from this area.

FUNCTIONAL DESCRIPTION: Jolie is a language for programming service-oriented and microservice applications. It directly supports service-oriented abstractions such as service, port, and session. Jolie allows to program a service behaviour, possibly obtained by composing existing services, and supports the main communication protocols and data formats used in service-oriented architectures. Differently from other service-oriented programming languages such as WS-BPEL, Jolie is based on a user-friendly Java-like syntax (more readable than the verbose XML syntax of WS-BPEL). Moreover, the kernel of Jolie is equipped with a formal operational semantics. Jolie is used to provide proof of concepts around Focus activities.

RELEASE FUNCTIONAL DESCRIPTION: There are many fixes to the HTTP extension, improvements to the embedding engine for Javascript programs, and improvements to the support tools jolie2java and wsdl2jolie.
NEWS OF THE YEAR: During 2018 Jolie was complemented by the creation of the JIoT project, aimed at integrating IoT-related technologies into the Jolie language. The final goal is to provide easy-to-use and flexible communication abstractions to interconnect and make interact disparate IoT islands. Jolie currently supports some of the main technologies used in SOAs (e.g., HTTP). However, only a limited amount of IoT devices uses the media and protocols already supported by Jolie. Indeed, protocols such as CoAP and MQTT, which are widely used in IoT scenarios, are not implemented in Jolie. Integrating these protocols, as we have done, is essential in order to allow Jolie programs to directly interact with the majority of IoT devices. We note that emerging frameworks for interoperability, such as the Web of Things, rely on the same protocols we mentioned for IoT, thus JIoT is also compliant with them. Concretely, work in 2018 comprised the inclusion of the CoAP/UDP and MQTT/TCP protocols among the communication technologies supported by the language. The Jolie implementation of MQTT and CoAP, as well as the UDP transport protocol used by CoAP, are based on the JAVA framework Netty.

- Participants: Claudio Guidi, Fabrizio Montesi, Maurizio Gabbrielli, Saverio Giallorenzo and Ivan Lanese
- Contact: Fabrizio Montesi
- URL: http://www.jolie-lang.org/

5.3. NightSplitter

KEYWORD: Constraint-based programming
FUNCTIONAL DESCRIPTION: Nightsplitter deals with the group preference optimization problem. We propose to split users into subgroups trying to optimize members' satisfaction as much as possible. In a large city with a huge volume of activity information, designing subgroup activities and avoiding time conflict is a challenging task. Currently, the Demo is available only for restaurant and movie activities in the city of Paris.

- Contact: Tong Liu
- URL: http://cs.unibo.it/t.liu/nightsplitter/

5.4. AIOCJ

Adaptive Interaction-Oriented Choreographies in Jolie
KEYWORD: Dynamic adaptation
SCIENTIFIC DESCRIPTION: AIOCJ is an open-source choreographic programming language for developing adaptive systems. It allows one to describe a distributed system as an AIOC, to generate code for each role avoiding by construction errors such as deadlocks. Furthermore, it supports dynamic adaptation of the distributed system via adaptation rules.

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

NEWS OF THE YEAR: In 2018 we did minor changes to AIOCJ, including the possibility of generating code only for a few roles, thus avoiding the need for deployment information for other roles.

- Participants: Ivan Lanese, Jacopo Mauro, Maurizio Gabbrielli, Mila Dalla Preda and Saverio Giallorenzo
- Contact: Saverio Giallorenzo
- URL: http://www.cs.unibo.it/projects/jolie/aiocj.html

5.5. CauDEr

Causal-consistent Debugger for Erlang

KEYWORDS: Debug - Reversible computing

SCIENTIFIC DESCRIPTION: The reversible debugger is based on the theory of causal-consistent reversibility, which states that any action can be undone provided that its consequences, if any, are undone beforehand. This theory relies on a causal semantic for the target language, and can be used even if different processes have different notions of time

FUNCTIONAL DESCRIPTION: CauDEr is a debugger allowing one to explore the execution of concurrent Erlang programs both forward and backward. Notably, when going backward, any action can be undone provided that its consequences, if any, are undone beforehand. The debugger also provides commands to automatically find and undo consequences of a given action. Forward computation can be driven by a log taken from a computation in the standard Erlang/OTP environment. An action in the log can be selected and replayed together with all and only its causes. The debugger enables one to find a bug by following the causality links from the visible misbehaviour to the bug. The debugger takes an Erlang program but debugging is done on its translation into Core Erlang.

- Partner: Universitat Politècnica de València
- Contact: Ivan Lanese
- URL: https://github.com/mistupv/cauder

5.6. SUNNY-AS

SUNNY FOR ALGORITHM SELECTION

KEYWORDS: Optimisation - Machine learning

FUNCTIONAL DESCRIPTION: SUNNY-AS is a portfolio solver derived from SUNNY-CP for Algorithm Selection Problems (ASLIB). The goal of SUNNY-AS is to provide a flexible, configurable, and usable portfolio solver that can be set up and executed just like a regular individual solver.

- Contact: Tong Liu
- URL: https://github.com/lteu/oasc

FUN Project-Team

6. New Software and Platforms

6.1. AspireRFID ALE

FUNCTIONAL DESCRIPTION: AspireRFID middleware is a modular OW2 open source RFID middleware. It is compliant with EPC Global standards. This new module integrates the modifications of the new standard release, including new RP and LLRP definitions and fixing bugs. This module has been implemented in the framework of the MIAOU project.

- Participants: Ibrahim Amadou, Julien Vandaële, Nathalie Mitton and Rim Driss
- Contact: Nathalie Mitton

6.2. ETINODE-CONTIKI-PORT

FUNCTIONAL DESCRIPTION: Contiki is an open source embedded OS for Internet of Things (IoT). It is light and portable to different hardware architectures. It embeds communication stacks for IoT Il embarque aussi des piles de communication pour l'internet des objets. This driver allows the running of Contiki OS over Etinode-MSP430. The code dalso allows the use of radio chip and embedded sensors. This module has been implemented in the framework of the ETIPOPS project.

- Participants: Nathalie Mitton, Roudy Dagher and Salvatore Guzzo Bonifacio
- Contact: Salvatore Guzzo Bonifacio

6.3. ETINODE-DRIVERS

FUNCTIONAL DESCRIPTION: These drivers for Etinode-MSP430 control the different embedded sensors and hardware components available on an Etinode-MSP430 node such as gyroscope, accelerometer and barometric sensor. This module has been implemented in the framework of the ETIPOPS project.

- Participants: Nathalie Mitton, Roudy Dagher and Salvatore Guzzo Bonifacio
- Contact: Salvatore Guzzo Bonifacio

6.4. EVe-TCF

Embedded Verifier for Transitive Control Flow

KEYWORDS: Control Flow - JavaCard - Embedded systems - Embedded - Security - Code analysis

FUNCTIONAL DESCRIPTION: Verification of transitive control flow policies on JavaCard 2.x bytecode. Control flow policies expressed using a DSL language are embedded in JavaCard packages (CAP files) using EVe-TCF convert tool. Control flow policies are then statically verified on-device at loading-time thanks to an embedded verifier (designed for smart cards in EVe-TCF). EVe-TCF (Embedded Verifier for Transitive Control Flow) also contains an off-device (i.e. PC tool) to simulate on-device loading process of JavaCard 2.x platforms with GlobalPlatform 2.x installed.

- Participants: Arnaud Fontaine and Isablle Simplot Ryl
- Contact: Nathalie Mitton

6.5. GOLIATH

Generic Optimized LIghtweight communication stack for Ambient TecHnologies

KEYWORDS: WSN - WSN430

FUNCTIONAL DESCRIPTION: GOLIATH (Generic Optimized LIghtweight communication stack for Ambient TecHnologies) is a full protocol stack for wireless sensor networks. This module has been implemented in the framework of the ETIPOPS project.

- Participants: David Simplot Ryl, Fadila Khadar, Nathalie Mitton and Salvatore Guzzo Bonifacio
- Contact: Nathalie Mitton
- URL: https://gforge.inria.fr/projects/goliath/

6.6. IoT-LAB robots

KEYWORDS: Internet of things - Robotics
FUNCTIONAL DESCRIPTION: IoT-LAB robots is an embedded robot controler on a Turtlebot2 providing the IoT-LAB node mobility functionnality

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

6.7. T-SCAN

KEYWORDS: Rfid - RFID Middleware
FUNCTIONAL DESCRIPTION: T-Scan is an interface ensuring the translation from a SGTIN tag format to an ONS hostname format according to the EPCGlobal standards. It allows the sending of a DNS request to look up the EPC-IS aides to which the product belongs in order to access the data relative to that product. This module has been implemented in the framework of the TRACAVERRE project.

- Participants: Gabriele Sabatino and Nathalie Mitton
- Contact: Gabriele Sabatino

6.8. FIT IoT-Lab

Participants: Nathalie Mitton [correspondant], Julien Vandaele, Matthieu Berthome.

FIT IoT-LAB is a very large scale open testbed that features over 2700 wireless sensor nodes and more than 200 robots spread across six different sites in France. Nodes are either fixed or mobile and can be allocated in various topologies throughout all sites. A variety of wireless sensors are available, with different processor architectures (MSP430, STM32 and Cortex-A8) and different wireless chips (802.15.4 PHY at 800 MHz or 2.4 GHz). In addition, “open nodes” can receive custom wireless sensors for inclusion in IoT-LAB testbed. This platform is completely open and can be used by any one wishing to run experiment on wireless sensors and robots.

The Lille site displays 3 subsets of the platforms:

- Euratechnologies: this site features 256 WSN430 sensor nodes operating in the 2.4GHz band. 64 nodes are mobile, embedded on mobile trains.
- Haute Borne: this site features 256 M3 sensor nodes operating in the 2.4GHz band and 64 mobile robots (32 turtlebots and 32 wifibots) completely remotely programmable.
- Opennodes: this site will feature (opening beginning 2015) 64 hardware open slots to allow any one to plug his own hardware and benefits from the platform debugging and monitoring tools.

GANG Project-Team

6. New Software and Platforms

6.1. big-graph-tools

KEYWORD: Graph algorithmics
FUNCTIONAL DESCRIPTION: Gang is developping a software for big graph manipulation. A preliminary library offering diameter and skeleton computation. This library was used to compute the diameters of the worldwide road network (200M edges) and the largest strongly connected component of the Twitter follower-followee graph (23G edges).

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

6.2. GRPH

The high performance graph library for Java
KEYWORDS: Graph - Graph algorithmics - Java
FUNCTIONAL DESCRIPTION: Grph is an open-source Java library for the manipulation of graphs. Its design objectives are to make it portable, simple to use/extend, computationally/memory efficient, and, according to its initial motivation: useful in the context of graph experimentation and network simulation. Grph also has the particularity to come with tools like an evolutionary computation engine, a bridge to linear programming solvers, a framework for distributed computing, etc.

Grph offers a very general model of graphs. Unlike other graph libraries which impose the user to first decide if he wants to deal with directed, undirected, hyper (or not) graphs, the model offered by Grph is unified in a general class that supports mixed graphs made of undirected and directed simple and hyper edges. Grph achieves great efficiency through the use of multiple code optimization techniques such as multi-core parallelism, caching, adequate data structures, use of primitive objects, exploitation of low-level processor caches, on-the-fly compilation of specific C/C++ code, etc. Grph attempts to access the Internet in order to check if a new version is available and to report who is using it (login name and hostname). This has no impact whatsoever on performance and security.

- Participants: Aurélien Lancin, David Coudert, Issam Tahiri, Luc Hogie and Nathann Cohen
- Contact: Luc Hogie
- URL: http://www.i3s.unice.fr/~hogie/grph/

HIEPACS Project-Team

6. New Software and Platforms

6.1. Chameleon

KEYWORDS: Runtime system - Task-based algorithm - Dense linear algebra - HPC - Task scheduling
SCIENTIFIC DESCRIPTION: Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

We expect advances in three directions based first on strong and closed interactions between the runtime and numerical linear algebra communities. This initial activity will then naturally expand to more focused but still joint research in both fields.

1. Fine interaction between linear algebra and runtime systems. On parallel machines, HPC applications need to take care of data movement and consistency, which can be either explicitly managed at the level of the application itself or delegated to a runtime system. We adopt the latter approach in order to better keep up with hardware trends whose complexity is growing exponentially. One major task in this project is to define a proper interface between HPC applications and runtime systems in order to maximize productivity and expressivity. As mentioned in the next section, a widely used approach consists in abstracting the application as a DAG that the runtime system is in charge of scheduling. Scheduling such a DAG over a set of heterogeneous processing units introduces a lot of new challenges, such as predicting accurately the execution time of each type of task over each kind of unit, minimizing data transfers between memory banks, performing data prefetching, etc. Expected advances: In a nutshell, a new runtime system API will be designed to allow applications to provide scheduling hints to the runtime system and to get real-time feedback about the consequences of scheduling decisions.

2. Runtime systems. A runtime environment is an intermediate layer between the system and the application. It provides low-level functionality not provided by the system (such as scheduling or management of the heterogeneity) and high-level features (such as performance portability). In the framework of this proposal, we will work on the scalability of runtime environment. To achieve scalability it is required to avoid all centralization. Here, the main problem is the scheduling of the tasks. In many task-based runtime environments the scheduler is centralized and becomes a bottleneck as soon as too many cores are involved. It is therefore required to distribute the scheduling decision or to compute a data distribution that impose the mapping of task using, for instance the so-called “owner-compute” rule. Expected advances: We will design runtime systems that enable an efficient and scalable use of thousands of distributed multicore nodes enhanced with accelerators.

3. Linear algebra. Because of its central position in HPC and of the well understood structure of its algorithms, dense linear algebra has often pioneered new challenges that HPC had to face. Again, dense linear algebra has been in the vanguard of the new era of petascale computing with the design of new algorithms that can efficiently run on a multicore node with GPU accelerators. These algorithms are called “communication-avoiding” since they have been redesigned to limit the amount of communication between processing units (and between the different levels of memory hierarchy). They are expressed through Direct Acyclic Graphs (DAG) of fine-grained tasks that are dynamically scheduled. Expected advances: First, we plan to investigate the impact of these principles in the case of sparse applications (whose algorithms are slightly more complicated but often rely on dense kernels). Furthermore, both in the dense and sparse cases, the scalability on thousands of nodes is still limited, new numerical approaches need to be found. We will specifically design sparse hybrid direct/iterative methods that represent a promising approach.

Overall end point. The overall goal of the MORSE associate team is to enable advanced numerical algorithms to be executed on a scalable unified runtime system for exploiting the full potential of future exascale machines.

FUNCTIONAL DESCRIPTION: Chameleon is a dense linear algebra software relying on sequential task-based algorithms where sub-tasks of the overall algorithms are submitted to a Runtime system. A Runtime system such as StarPU is able to manage automatically data transfers between not shared memory area (CPUs-GPUs, distributed nodes). This kind of implementation paradigm allows to design high performing linear algebra algorithms on very different type of architecture: laptop, many-core nodes, CPUs-GPUs, multiple nodes. For example, Chameleon is able to perform a Cholesky factorization (double-precision) at 80 TFlop/s on a dense matrix of order 400 000 (e.i. 4 min).

RELEASE FUNCTIONAL DESCRIPTION: Chameleon includes the following features:

- BLAS 3, LAPACK one-sided and LAPACK norms tile algorithms - Support QUARK and StarPU runtime systems and PaRSEC since 2018 - Exploitation of homogeneous and heterogeneous platforms through the use of BLAS/LAPACK CPU kernels and cuBLAS/MAGMA CUDA kernels - Exploitation of clusters of interconnected nodes with distributed memory (using OpenMPI)

- Participants: Cédric Castagnede, Samuel Thibault, Emmanuel Agullo, Florent Pruvost and Mathieu Faverge
- Partners: Innovative Computing Laboratory (ICL) - King Abdullha University of Science and Technology - University of Colorado Denver
- Contact: Emmanuel Agullo
- URL: https://gitlab.inria.fr/solverstack/chameleon

6.2. Fabulous

Fast Accurate Block Linear krylOv Solver
KEYWORDS: Numerical algorithm - Block Krylov solver
SCIENTIFIC DESCRIPTION: Versatile and flexible numerical library that implements Block Krylov iterative schemes for the solution of linear systems of equations with multiple right-hand sides
FUNCTIONAL DESCRIPTION: Versatile and flexible numerical library that implements Block Krylov iterative schemes for the solution of linear systems of equations with multiple right-hand sides. The library implements block variants of minimal norm residual variants with partial convergence management and spectral information recycling. The package already implements regular block-GMRES (BGMRES), Inexact Breakdown BGMRES (IB-BMGRES), Inexact Breakdown BGMRES with Deflated Restarting (IB-BGMRES-DR), Block Generalized Conjugate Residual with partial convergence management. The C++ library relies on callback mechanisms to implement the calculations (matrix-vector, dot-product, ...) that depend on the parallel data distribution selected by the user.

- Participants: Emmanuel Agullo, Luc Giraud and Cyrille Piacibello
- Contact: Luc Giraud
- Publication: Block GMRES method with inexact breakdowns and deflated restarting
- URL: https://gitlab.inria.fr/solverstack/fabulous/

6.3. HIPS

Hierarchical Iterative Parallel Solver
KEYWORDS: Simulation - HPC - Parallel calculation - Hybrid direct iterative method

SCIENTIFIC DESCRIPTION: The key point of the methods implemented in HIPS is to define an ordering and a partition of the unknowns that relies on a form of nested dissection ordering in which cross points in the separators play a special role (Hierarchical Interface Decomposition ordering). The subgraphs obtained by nested dissection correspond to the unknowns that are eliminated using a direct method and the Schur complement system on the remaining of the unknowns (that correspond to the interface between the subgraphs viewed as sub-domains) is solved using an iterative method (GMRES or Conjugate Gradient at the time being). This special ordering and partitioning allows for the use of dense block algorithms both in the direct and iterative part of the solver and provides a high degree of parallelism to these algorithms. The code provides a hybrid method which blends direct and iterative solvers. HIPS exploits the partitioning and multistage ILU techniques to enable a highly parallel scheme where several subdomains can be assigned to the same process. It also provides a scalar preconditioner based on the multistage ILUT factorization.

HIPS can be used as a standalone program that reads a sparse linear system from a file , it also provides an interface to be called from any C, C++ or Fortran code. It handles symmetric, unsymmetric, real or complex matrices. Thus, HIPS is a software library that provides several methods to build an efficient preconditioner in almost all situations.
FUNCTIONAL DESCRIPTION: HIPS (Hierarchical Iterative Parallel Solver) is a scientific library that provides an efficient parallel iterative solver for very large sparse linear systems.

- Participants: Jérémie Gaidamour, Pascal Hénon and Yousef Saad
- Contact: Pierre Ramet
- URL: https://gitlab.inria.fr/solverstack/hips

6.4. MAPHYS

Massively Parallel Hybrid Solver
KEYWORD: Parallel hybrid direct/iterative solution of large linear systems
FUNCTIONAL DESCRIPTION: MaPHyS is a software package that implements a parallel linear solver coupling direct and iterative approaches. The underlying idea is to apply to general unstructured linear systems domain decomposition ideas developed for the solution of linear systems arising from PDEs. The interface problem, associated with the so called Schur complement system, is solved using a block preconditioner with overlap between the blocks that is referred to as Algebraic Additive Schwarz. A fully algebraic coarse space is available for symmetric positive definite problems, that insures the numerical scalability of the preconditioner.

The parallel implementation is based on MPI+thread. Maphys relies on state-of-the art sparse and dense direct solvers.

MaPHyS is essentially a preconditioner that can be used to speed-up the convergence of any Krylov subspace method and is coupled with the ones implemented in the Fabulous package.

- Participants: Emmanuel Agullo, Luc Giraud, Matthieu Kuhn, Gilles Marait and Louis Poirel
- Contact: Emmanuel Agullo
- Publications: Hierarchical hybrid sparse linear solver for multicore platforms - Robust coarse spaces for Abstract Schwarz preconditioners via generalized eigenproblems
- URL: https://gitlab.inria.fr/solverstack/maphys

6.5. MetaPart

KEYWORDS: High performance computing - HPC - Parallel computing - Graph algorithmics - Graph - Hypergraph

FUNCTIONAL DESCRIPTION: MetaPart is a framework for graph or hypergraph manipulation that addresses different problems, like partitioning, repartitioning, or co-partitioning, ... MetaPart is made up of several projects, such as StarPart, LibGraph or CoPart. StarPart is the core of the MetaPart framework. It offers a wide variety of graph partitioning methods (Metis, Scotch, Zoltan, Patoh, ParMetis, Kahip, ...), which makes it easy to compare these different methods and to better adjust the parameters of these methods. It is built upon the LibGraph library, that provides basic graph and hypergraph routines. The Copart project is a library used on top of StarPart, that provides co-partitioning algorithms for the load-blancing of parallel coupled simulations.

- Participant: Aurélien Esnard
- Contact: Aurélien Esnard
- URL: https://gitlab.inria.fr/metapart

6.6. MPICPL

MPI CouPLing

KEYWORDS: MPI - Coupling software

FUNCTIONAL DESCRIPTION: MPICPL is a software library dedicated to the coupling of parallel legacy codes, that are based on the well-known MPI standard. It proposes a lightweight and comprehensive programing interface that simplifies the coupling of several MPI codes (2, 3 or more). MPICPL facilitates the deployment of these codes thanks to the mpicplrun tool and it interconnects them automatically through standard MPI intercommunicators. Moreover, it generates the universe communicator, that merges the world communicators of all coupled-codes. The coupling infrastructure is described by a simple XML file, that is just loaded by the mpicplrun tool.

- Participant: Aurélien Esnard
- Contact: Aurélien Esnard
- URL: https://gitlab.inria.fr/esnard/mpicpl

6.7. OptiDis

KEYWORDS: Dislocation dynamics simulation - Fast multipole method - Large scale - Collision

FUNCTIONAL DESCRIPTION: OptiDis is a new code for large scale dislocation dynamics simulations. Its purpose is to simulate real life dislocation densities (up to 5.1022 dislocations/m-2) in order to understand plastic deformation and study strain hardening. The main application is to observe and understand plastic deformation of irradiated zirconium. Zirconium alloys are the first containment barrier against the dissemination of radioactive elements. More precisely, with neutron irradiated zirconium alloys we are talking about channeling mechanism, which means to stick with the reality, more than tens of thousands of induced loops, i. e. 100 million degrees of freedom in the simulation. The code is based on Numodis code developed at CEA Saclay and the ScalFMM library developed in HiePACS project. The code is written in C++ language and using the last features of C++11/14. One of the main aspects is the hybrid parallelism MPI/OpenMP that gives the software the ability to scale on large cluster while the computation load rises. In order to achieve that, we use different levels of parallelism. First of all, the simulation box is distributed over MPI processes, then we use a thinner level for threads, dividing the domain by an Octree representation. All theses parts are controlled by the ScalFMM library. On the last level, our data are stored in an adaptive structure that absorbs the dynamics of this type of simulation and manages the parallelism of tasks..

- Participant: Olivier Coulaud
- Contact: Olivier Coulaud
- URL: http://optidis.gforge.inria.fr/

6.8. PaStiX

Parallel Sparse matriX package

KEYWORDS: Linear algebra - High-performance calculation - Factorisation - Sparse Matrices - Linear Systems Solver
SCIENTIFIC DESCRIPTION: PaStiX is based on an efficient static scheduling and memory manager, in order to solve 3D problems with more than 50 million of unknowns. The mapping and scheduling algorithm handle a combination of 1D and 2D block distributions. A dynamic scheduling can also be applied to take care of NUMA architectures while taking into account very precisely the computational costs of the BLAS 3 primitives, the communication costs and the cost of local aggregations.
FUNCTIONAL DESCRIPTION: PaStiX is a scientific library that provides a high performance parallel solver for very large sparse linear systems based on block direct and block ILU(k) methods. It can handle low-rank compression techniques to reduce the computation and the memory complexity. Numerical algorithms are implemented in single or double precision (real or complex) for LLt, LDLt and LU factorization with static pivoting (for non symmetric matrices having a symmetric pattern). The PaStiX library uses the graph partitioning and sparse matrix block ordering packages Scotch or Metis.

The PaStiX solver is suitable for any heterogeneous parallel/distributed architecture when its performance is predictable, such as clusters of multicore nodes with GPU accelerators or KNL processors. In particular, we provide a high-performance version with a low memory overhead for multicore node architectures, which fully exploits the advantage of shared memory by using an hybrid MPI-thread implementation.

The solver also provides some low-rank compression methods to reduce the memory footprint and/or the time-to-solution.

- Participants: Grégoire Pichon, Mathieu Faverge and Pierre Ramet
- Partners: Université Bordeaux 1 - INP Bordeaux
- Contact: Pierre Ramet
- URL: https://gitlab.inria.fr/solverstack/pastix

6.9. ScalFMM

Scalable Fast Multipole Method
KEYWORDS: N-body - Fast multipole method - Parallelism - MPI - OpenMP
SCIENTIFIC DESCRIPTION: ScalFMM is a software library to simulate N-body interactions using the Fast Multipole Method. The library offers two methods to compute interactions between bodies when the potential decays like 1/r. The first method is the classical FMM based on spherical harmonic expansions and the second is the Black-Box method which is an independent kernel formulation (introduced by E. Darve @ Stanford). With this method, we can now easily add new non oscillatory kernels in our library. For the classical method, two approaches are used to decrease the complexity of the operators. We consider either matrix formulation that allows us to use BLAS routines or rotation matrix to speed up the M2L operator.

ScalFMM intends to offer all the functionalities needed to perform large parallel simulations while enabling an easy customization of the simulation components: kernels, particles and cells. It works in parallel in a shared/distributed memory model using OpenMP and MPI. The software architecture has been designed with two major objectives: being easy to maintain and easy to understand. There is two main parts:

the management of the octree and the parallelization of the method the kernels. This new architecture allow us to easily add new FMM algorithm or kernels and new paradigm of parallelization.
FUNCTIONAL DESCRIPTION: Compute N-body interactions using the Fast Multipole Method for large number of objects

- Participants: Bramas Bérenger and Olivier Coulaud
- Contact: Olivier Coulaud
- URL: https://gitlab.inria.fr/solverstack/ScalFMM

6.10. VITE

Visual Trace Explorer

KEYWORDS: Visualization - Execution trace
FUNCTIONAL DESCRIPTION: ViTE is a trace explorer. It is a tool made to visualize execution traces of large parallel programs. It supports Pajé, a trace format created by Inria Grenoble, and OTF and OTF2 formats, developed by the University of Dresden and allows the programmer a simpler way to analyse, debug and/or profile large parallel applications.

- Participant: Mathieu Faverge
- Contact: Mathieu Faverge
- URL: http://vite.gforge.inria.fr/

6.11. PlaFRIM

Plateforme Fédérative pour la Recherche en Informatique et Mathématiques
KEYWORDS: High-Performance Computing - Hardware platform
FUNCTIONAL DESCRIPTION: PlaFRIM is an experimental platform for research in modeling, simulations and high performance computing. This platform has been set up from 2009 under the leadership of Inria Bordeaux Sud-Ouest in collaboration with computer science and mathematics laboratories, respectively Labri and IMB with a strong support in the region Aquitaine.

It aggregates different kinds of computational resources for research and development purposes. The latest technologies in terms of processors, memories and architecture are added when they are available on the market. It is now more than 1,000 cores (excluding GPU and Xeon Phi) that are available for all research teams of Inria Bordeaux, Labri and IMB. This computer is in particular used by all the engineers who work in HiePACS and are advised by F. Rue from the SED.

- Contact: Olivier Coulaud
- URL: https://www.plafrim.fr/en/home/

INDES Project-Team

4. New Software and Platforms

4.1. Bigloo

KEYWORD: Compilers
FUNCTIONAL DESCRIPTION: Bigloo is a Scheme implementation devoted to one goal: enabling Scheme based programming style where C(++) is usually required. Bigloo attempts to make Scheme practical by offering features usually presented by traditional programming languages but not offered by Scheme and functional programming. Bigloo compiles Scheme modules. It delivers small and fast stand alone binary executables. Bigloo enables full connections between Scheme and C programs, between Scheme and Java programs.

RELEASE FUNCTIONAL DESCRIPTION: modification of the object system (language design and implementation), new APIs (alsa, flac, mpg123, avahi, csv parsing), new library functions (UDP support), new regular expressions support, new garbage collector (Boehm's collection 7.3alpha1).

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

4.2. Hop

KEYWORDS: Programming language - Multimedia - Iot - Web 2.0 - Functional programming
SCIENTIFIC DESCRIPTION: The Hop programming environment consists in a web broker that intuitively combines in a single architecture a web server and a web proxy. The broker embeds a Hop interpreter for executing server-side code and a Hop client-side compiler for generating the code that will get executed by the client.

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

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

4.3. IFJS

Infomation Flow monitor inlining for JavaScript
KEYWORD: Cybersecurity
FUNCTIONAL DESCRIPTION: The IFJS compiler is applied to JavaScript code. The compiler generates JavaScript code instrumented with checks to secure code. The compiler takes into account special features of JavaScript such as implicit type coercions and programs that actively try to bypass the inlined enforcement mechanisms. The compiler guarantees that third-party programs cannot (1) access the compiler internal state by randomizing the names of the resources through which it is accessed and (2) change the behaviour of native functions that are used by the enforcement mechanisms inlined in the compiled code.

- Contact: Tamara Rezk
- URL: http://www-sop.inria.fr/indes/ifJS/

4.4. iflowsigs.js

KEYWORDS: Compilers - Monitoring
FUNCTIONAL DESCRIPTION: iflowsigs.js is a JavaScript library designed to inline an information flow monitor into JavaScript code. iflowsigs.js support is able to track information flow even in programs that interact with arbitrary Web APIs.

- Participants: José Fragoso Santos and Tamara Rezk
- Contact: Tamara Rezk
- URL: http://j3fsantos.github.io/PersonalPage/IFMonitor/

4.5. iflowTYPES.js

FUNCTIONAL DESCRIPTION: iflowtypes.js is a JavaScript library designed to type secure information flow in JavaScript. iflowtypes.js has two main modes of operation: fully static and hybrid. In the hybrid mode, the program to be typed is instrumented with runtime assertions that are verified at runtime. By deferring rejection to runtime, the hybrid type system is able to type more programs than fully static mechanisms.

- Contact: Tamara Rezk
- URL: http://j3fsantos.github.io/PersonalPage/TypeSystem/

4.6. Mashic

KEYWORD: Security
FUNCTIONAL DESCRIPTION: The Mashic compiler is applied to mashups with untrusted scripts. The compiler generates mashups with sandboxed scripts, secured by the same origin policy of the browsers. The compiler is written in Bigloo.

- Contact: Tamara Rezk
- URL: http://web.ist.utl.pt/~ana.matos/Mashic/mashic.html

4.7. Hiphop.js

KEYWORDS: Web 2.0 - Synchronous Language - Programming language
FUNCTIONAL DESCRIPTION: HipHop.js is an Hop.js DLS for orchestrating web applications. HipHop.js helps programming and maintaining Web applications where the orchestration of asynchronous tasks is complex.

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

4.8. Server-Side Protection against Third Party Web Tracking

KEYWORDS: Privacy - Web Application - Web - Architecture - Security by design - Program rewriting techniques
FUNCTIONAL DESCRIPTION: We present a new web application architecture that allows web developers to gain control over certain types of third party content. In the traditional web application architecture, a web application developer has no control over third party content. This allows the exchange of tracking information between the browser and the third party content provider.

To prevent this, our solution is based on the automatic rewriting of the web application in such a way that the third party requests are redirected to a trusted third party server, called the Middle Party Server. It may be either controlled by a trusted party, or by a main site owner and automatically eliminates third-party tracking cookies and other technologies that may be exchanged by the browser and third party server

- Contact: Doliere Some
- URL: http://www-sop.inria.fr/members/Doliere.Some/essos/

4.9. BELL

Browser fingerprinting via Extensions and Login-Leaks
KEYWORDS: Browser Extensions - Security and Privacy in Web Services - Social Networks Security and Privacy
FUNCTIONAL DESCRIPTION: Recent studies show that users can be tracked based on their web browser properties. This software is designed to conduct an experiment on such kinds of user tracking. In this experiment, we demonstrate that a Web user can also be tracked by

- her browser extensions (such as AdBlock, Pinterest, or Ghostery), and

- the websites she has logged in (such as Facebook, Gmail, or Twitter).

In the experiment, we collect user's browser fingerprint, together with the browser extensions installed and a list of websites she has logged in. We only collect anonymous data during the experiment (more details in our Privacy Policy [0]), we will securely store the data on an Inria server, use it only for research purposes and not share it with anyone outside of Inria.

- Contact: Gabor Gulyas
- URL: https://extensions.inrialpes.fr/

4.10. webstats

Webstats
KEYWORDS: Web Usage Mining - Statistic analysis - Security
FUNCTIONAL DESCRIPTION: The goal of this tool is to perform a large-scale monthly crawl of the top Alexa sites, collecting both inline scripts (written by web developers) and remote scripts, and establishing the popularity of remote scripts (such as Google Analytics and jQuery). With this data, we establish whether the collected scripts are actually written in a subset of JavaScript by analyzing the different constructs used in those scripts. Finally, we collect and analyze the HTTP headers of the different sites visited, and provide statistics about the usage of HTTPOnly and Secure cookies, and the Content Security Policy in top sites.

- Contact: Doliere Some
- URL: https://webstats.inria.fr

4.11. Platforms

4.11.1. Skini

Skini is a distributed system for composing and producing live performances with audience participation using HTML5 devices. Skini is developed in Hop and HipHop. It proposes a framework for composing music based on patterns and dynamic control of the orchestration for either synthesizers or musicians.

The system has two basic concepts, "Pattern" and "Orchestration" which can be modulated as much as the composer wants in terms of complexity, duration, etc. The platform is meant for interaction with the audience during the show. Each participant can interact with the platform as well as with other participants. According to our experience during the Golem show in MANCA 2017, we implemented five levels of interaction, which allowed theoretically 120 possible combinations.

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[0] https://extensions.inrialpes.fr/privacy.php

INFINE-POST Team (section vide)

KERDATA Project-Team

4. New Software and Platforms

4.1. Damaris

KEYWORDS: Visualization - I/O - HPC - Exascale - High performance computing
SCIENTIFIC DESCRIPTION: Damaris is a middleware for I/O and data management targeting large-scale, MPI-based HPC simulations. It initially proposed to dedicate cores for asynchronous I/O in multicore nodes of recent HPC platforms, with an emphasis on ease of integration in existing simulations, efficient resource usage (with the use of shared memory) and simplicity of extension through plug-ins. Over the years, Damaris has evolved into a more elaborate system, providing the possibility to use dedicated cores or dedicated nodes to in situ data processing and visualization. It proposes a seamless connection to the VisIt visualization framework to enable in situ visualization with minimum impact on run time. Damaris provides an extremely simple API and can be easily integrated into the existing large-scale simulations.

Damaris was at the core of the PhD thesis of Matthieu Dorier, who received an Accessit to the Gilles Kahn Ph.D. Thesis Award of the SIF and the Academy of Science in 2015. Developed in the framework of our collaboration with the JLESC – Joint Laboratory for Extreme-Scale Computing, Damaris was the first software resulted from this joint lab validated in 2011 for integration to the Blue Waters supercomputer project. It scaled up to 16,000 cores on Oak Ridge's leadership supercomputer Titan (first in the Top500 supercomputer list in 2013) before being validated on other top supercomputers. Active development is currently continuing within the KerData team at Inria, where it is at the center of several collaborations with industry as well as with national and international academic partners.
FUNCTIONAL DESCRIPTION: Damaris is a middleware for data management and in-situ visualization targeting large-scale HPC simulations: - In situ data analysis by some dedicated cores/nodes of the simulation platform - Asynchronous and fast data transfer from HPC simulations to Damaris - Semantic-aware dataset processing through Damaris plug-ins - Writing aggregated data (by hdf5 format) or visualizating them either by VisIt or ParaView

- Participants: Gabriel Antoniu, Lokman Rahmani, Luc Bougé, Matthieu Dorier, Orçun Yildiz and Hadi Salimi
- Partner: ENS Rennes
- Contact: Matthieu Dorier
- URL: https://project.inria.fr/damaris/

4.2. OverFlow

FUNCTIONAL DESCRIPTION: OverFlow is a uniform data management system for scientific workflows running across geographically distributed sites, aiming to reap economic benefits from this geo-diversity. The software is environment-aware, as it monitors and models the global cloud infrastructure, offering high and predictable data handling performance for transfer cost and time, within and across sites. OverFlow proposes a set of pluggable services, grouped in a data-scientist cloud kit. They provide the applications with the possibility to monitor the underlying infrastructure, to exploit smart data compression, deduplication and geo-replication, to evaluate data management costs, to set a tradeoff between money and time, and optimize the transfer strategy accordingly.

Currently, OverFlow is used for data transfers by the Microsoft Research ATLE Munich team as well as for synthetic benchmarks at the Politehnica University of Bucharest.

- Participants: Alexandru Costan, Gabriel Antoniu and Radu Marius Tudoran
- Contact: Alexandru Costan

4.3. Pufferbench

KEYWORDS: Distributed Storage Systems - Elasticity - Benchmarking
SCIENTIFIC DESCRIPTION: Pufferbench is a benchmark for evaluating how fast one can scale up and down a distributed storage system on a given infrastructure and, thereby, how viably can one implement storage malleability on it. Besides, it can serve to quickly prototype and evaluate mechanisms for malleability in existing distributed storage systems.
FUNCTIONAL DESCRIPTION: Pufferbench is a benchmark to designed to evaluate whether to use malleable distributed storage systems on a given platform. - It measures the duration of commission and decommission operations. - Its modularity allows to quickly change and adapt each component to the needs of the user. - It can serve as a baseline when implementing commission and decommission mechanisms in a distributed storage system.

RELEASE FUNCTIONAL DESCRIPTION: This is the first release of Pufferbench.

It includes default components for each of the customisable components: - storage: in memory, on drive with file system cache, and on drive without file system cache - network: MPI network - IODispatcher: basic, and with acknowledgements - DataTransferScheduler: basic - DataDistributionGenerator: uniform, and random - MetadataGenerator: Files of same size The diversity of available components enables Pufferbench to fit to multiple use cases.

- Participants: Nathanaël Cheriere, Matthieu Dorier and Gabriel Antoniu
- Partner: ENS Rennes
- Contact: Nathanaël Cheriere
- Publication: Pufferbench: Evaluating and Optimizing Malleability of Distributed Storage
- URL: https://gitlab.inria.fr/Puffertools/Pufferbench/wikis/home

4.4. Tyr

KEYWORDS: Cloud storage - Distributed Storage Systems - Big data
FUNCTIONAL DESCRIPTION: Tyr is the first blob storage system to provide built-in, multiblob transactions, while retaining sequential consistency and high throughput under heavy access concurrency. Tyr offers fine-grained random write access to data and in-place atomic operations.

- Partner: Universidad Politécnica de Madrid
- Contact: Gabriel Antoniu

4.5. Planner

KEYWORDS: Edge elements - Cloud computing - Scheduling
FUNCTIONAL DESCRIPTION: Planner is a middleware for uniform and transparent stream processing across Edge and Cloud. Planner automatically selects which parts of the executiongraph will be executed at the Edge in order to minimize thenetwork cost.

- Partner: ENS Cachan
- Contact: Gabriel Antoniu
- URL: https://team.inria.fr/kerdata/

4.6. KerA

KerAnalytics
KEYWORD: Distributed Storage Systems

FUNCTIONAL DESCRIPTION: A unified architecture for stream ingestion and storage which can lead to the optimization of the processing of Big Data applications. This approach minimizes data movement within the analytics architecture, finally leading to better utilized resources.

- Contact: Gabriel Antoniu

4.7. TailWind

KEYWORDS: Fault-tolerance - Data management. - Distributed Data Management

FUNCTIONAL DESCRIPTION: Replication is essential for fault-tolerance. However, in in-memory systems, it is a source of high overhead. Remote direct memory access (RDMA) is attractive to create redundant copies of data, since it is low-latency and has no CPU overhead at the target. However, existing approaches still result in redundant data copying and active receivers. To ensure atomic data transfers, receivers check and apply only fully received messages. Tailwind is a zero-copy recovery-log replication protocol for scale-out in-memory databases. Tailwind is the first replication protocol that eliminates *all* CPU-driven data copying and fully bypasses target server CPUs, thus leaving backups idle. Tailwind ensures all writes are atomic by leveraging a protocol that detects incomplete RDMA transfers. Tailwind substantially improves replication throughput and response latency compared with conventional RPC-based replication. In symmetric systems where servers both serve requests and act as replicas, Tailwind also improves normal-case throughput by freeing server CPU resources for request processing. We implemented and evaluated Tailwind on RAMCloud, a low-latency in-memory storage system. Experiments show Tailwind improves RAMCloud's normal-case request processing throughput by $1.7\times$. It also cuts down writes median and 99^{th} percentile latencies by 2x and 3x respectively.

- Contact: Gabriel Antoniu

MIMOVE Project-Team

6. New Software and Platforms

6.1. SocialBus

Universal Social Network Bus

KEYWORDS: Middleware - Interoperability - Social networks - Software Oriented Service (SOA)

FUNCTIONAL DESCRIPTION: Online social network services (OSNSs) have become an integral part of our daily lives. At the same time, the aggressive market competition has led to the emergence of multiple competing siloed OSNSs that cannot interoperate. As a consequence, people face the burden of creating and managing multiple OSNS accounts and learning how to use them, to stay connected. The goal of the Universal Social Network Bus (USNB) is to relieve users from such a burden, letting them use their favorite applications to communicate.

- Authors: Rafael Angarita Arocha, Nikolaos Georgantas and Valérie Issarny
- Contact: Valérie Issarny
- URL: https://gitlab.inria.fr/usnb/universal-social-network-bus

6.2. WeBrowse

KEYWORDS: Web Usage Mining - Content analysis - Recommendation systems

FUNCTIONAL DESCRIPTION: The amount of information available on the web today, and the fast rate with which new information appears, overwhelm most users. The goal of our research is to assist Web users in discovering content. One of the most powerful means today to help people discover new web content is sharing between members of online communities. In the case of communities of a place (e.g., people who live, study, or work together) people share common interests, but often fail to actively share content. To address this problem, we have developed WeBrowse, a passive crowdsourced content discovery system for communities of a place.

WeBrowse leverages the passive observation of web-clicks (i.e., the URLs users intentionally visit) as an indication of users' interest in a piece of content. Intuitively, the more users click on a URL, the higher the interest in the content on the corresponding page. Our approach is then to leverage the collective clicks in a community to automatically discover relevant content to promote to users of the community.

To implement passive crowdsourcing, one must be in a position to observe the aggregated web-clicks of the community. Luckily, in many communities of a place, users will connect to the Internet from the same network, such as, e.g., the campus/enterprise network or the network of a residential Internet Service Provider (ISP) in a neighborhood. WeBrowse (i) observes web packets flowing through a network link, (ii) passively extracts HTTP logs (i.e., streams recording the headers of HTTP requests), and (iii) detects and decides on-the-fly the set of URLs to show to users.

- Contact: Renata Cruz Teixeira
- URL: https://team.inria.fr/muse/webrowse-info-page/

6.3. EEE

Experiment Execution Engine

KEYWORD: Iot

FUNCTIONAL DESCRIPTION: Experiment Execution Engine (EEE) eases the development of IoT applications that perform analysis of recent or continuously increasing volumes of IoT data from various data stores. To this end, EEE provides APIs for scheduling queries on federated large-scale semantically-enabled IoT data stores. Queries are expressed in the FIESTA-IoT (http://fiesta-iot.eu) Experiment Description Specification (FEDSpec), which acts as a Domain Specific Language (DSL). EEE (in combination with Experiment Management Console - EMC) further provides features such as: (a) manage scheduled experiments, (b) (un)subscribe to already existing FEDSpec objects, (c) execute an on-demand query outside a described schedule, (d) monitor execution logs, (e) interact with third-party services such as Analytics and Result Storage, (e) handle dynamic attributes, and (f) API sandbox. EEE is integrated within the FIESTA-IoT Platform. It can be customised depending on needs.

- Authors: Rachit Agarwal and Nikolaos Georgantas
- Contact: Nikolaos Georgantas
- URL: https://github.com/fiesta-iot/ExperimentExecutionEngine

6.4. EMC

Experiment Management Console

KEYWORD: Iot

FUNCTIONAL DESCRIPTION: Experiment Management Console (EMC) is a simple easy-to-use user interface that enables experimenters to control their experiments/queries that execute using the Experiment Execution Engine (EEE). EMC provides features such as managing experiment execution, (un)subscribing an existing experiment, and monitoring execution logs.

- Authors: Nikolaos Georgantas and Rachit Agarwal
- Contact: Nikolaos Georgantas
- URL: https://github.com/fiesta-iot/ExperimentManagementConsole

6.5. VSB

eVolution Service Bus

KEYWORDS: Service and Thing choreographies - Middleware protocol interoperability - Enterprise service bus

FUNCTIONAL DESCRIPTION: VSB is a development and runtime environment dedicated to complex distributed applications of the Future Internet. Such applications are open, dynamic choreographies of extremely heterogeneous services and Things, including lightweight embedded systems (e.g., sensors, actuators and networks of them), mobile systems (e.g., smartphone applications), and resource-rich IT systems (e.g., systems hosted on enterprise servers and Cloud infrastructures). VSB's objective is to seamlessly interconnect, inside choreographies, services and Things that employ heterogeneous interaction protocols at the middleware level, e.g., SOAP Web services, REST Web services, Things using CoAP. This is based on runtime conversions between such protocols, with respect to their primitives and data type systems, while properly mapping between their semantics. This also includes mapping between the public interfaces of services/Things, regarding their operations and data, from the viewpoint of the middleware: the latter means that operations and data are converted based on their middleware-level semantics, while their business semantics remains transparent to the conversion. VSB follows the well-known Enterprise Service Bus (ESB) paradigm. We propose a generic interface description, which we call GIDL, for application components that employ VSB. Based on GIDL, we enable automated synthesis of binding components for connecting heterogeneous services and Things onto VSB.

- Participants: Georgios Bouloukakis, Nikolaos Georgantas and Patient Ntumba
- Contact: Nikolaos Georgantas
- URL: https://gitlab.ow2.org/chorevolution/evolution-service-bus

6.6. Service traceroute

KEYWORDS: Network monitoring - Network diagnosis
FUNCTIONAL DESCRIPTION: Traceroute is often used to help diagnose when users experience issues with Internet applications or services. Unfortunately, probes issued by classic traceroute tools differ from application traffic and hence can be treated differently by middleboxes within the network. We propose a new traceroute tool, called Service traceroute. Service traceroute leverages the idea from paratrace, which passively listens to application traffic to then issue traceroute probes that pretend to be part of the application flow. We extend this idea to work for modern Internet services with support for identifying the flows to probe automatically, for tracing of multiple concurrent flows, and for UDP flows. We implement command-line and library versions of Service traceroute, which we release as open source.

- Partner: Princeton University
- Contact: Renata Cruz Teixeira
- URL: https://github.com/wontoniii/service-traceroute

6.7. TA

TA - Traffic Analysis
KEYWORDS: Quality of Experience - Network monitoring - Video analysis
FUNCTIONAL DESCRIPTION: System running at the home getaway that analyzes traffic generated by DASH on-demand and live video streams. The system tracks traffic patterns to infer key video QoE metrics such as average bitrate and re-buffering events. Moreover, the system exploits novel algorithms that use probing techniques, i.e. lightweight pings and traceroutes, to detect possible congestion location.

- Participants: Francesco Bronzino and Renata Cruz Teixeira
- Contact: Francesco Bronzino

6.8. HostView Mobile

KEYWORDS: Quality of Experience - Network monitoring
FUNCTIONAL DESCRIPTION: HostView for mobile runs on Android devices to monitor user system and network performance together with user feedback on Internet experience.

- Contact: Giulio Grassi

MYRIADS Project-Team

6. New Software and Platforms

6.1. GinFlow

KEYWORDS: Workflow - Distributed computing - Distributed - Distributed Applications - Dynamic adaptation - Framework

FUNCTIONAL DESCRIPTION: GinFlow decentralizes the coordination of the execution of workflow-based applications. GinFlow relyies on an architecture where multiple service agents (SA) coordinate each others through a shared space containing the workflow description and current status. GinFlow allows the user to define several variants of a workflow and to switch from one to the other during run time.

- Participants: Cédric Tedeschi, Hector Fernandez, Javier Rojas Balderrama, Matthieu Simonin and Thierry Priol
- Partner: Université de Rennes 1
- Contact: Cédric Tedeschi
- URL: http://ginflow.inria.fr

6.2. PaaSage Adapter

KEYWORDS: Cloud computing - Dynamic adaptation - Cloud applications management

FUNCTIONAL DESCRIPTION: The purpose of the Adapter is to transform the current configuration of a cloud application into a target configuration in an efficient and safe way. The Adapter is part of PaaSage, an open-source platform for modeling, deploying and executing applications on different clouds in an optimal manner. The Adapter has the following responsibilities: (1) validating reconfiguration plans, (2) applying the plans to the running system, and (3) maintaining an up-to-date representation of the current system state.

- Contact: Nikolaos Parlavantzas
- URL: https://team.inria.fr/myriads/software-and-platforms/paasage-adapter/

6.3. SAIDS

self-adaptable intrusion detection system

KEYWORDS: Cloud - Security

FUNCTIONAL DESCRIPTION: SAIDS is a self-adaptable intrusion detection system for IaaS clouds. To maintain an effective level of intrusion detection, SAIDS monitors changes in the virtual infrastructure of a Cloud environment and reconfigures its components (security probes) accordingly. SAIDS can also reconfigure probes in the case of a change in the list of running services.

- Authors: Anna Giannakou and Jean-Léon Cusinato
- Contact: Christine Morin

6.4. 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/

6.5. DiFFuSE

Distributed framework for cloud-based epidemic simulations
KEYWORDS: Simulation - Cloud
FUNCTIONAL DESCRIPTION: The DiFFuSE framework enables simulations of epidemics to take full advantage of cloud environments. The framework provides design support, reusable code, and tools for building and executing epidemic simulations. Notably, the framework automatically handles failures and supports elastic allocation of resources from multiple clouds.

- Authors: Yvon Jégou, Manh Linh Pham, Nikolaos Parlavantzas and Christine Morin
- Contact: Nikolaos Parlavantzas
- Publication: hal-01612979/
- URL: https://team.inria.fr/myriads/software-and-platforms/diffuse/

Neo Project-Team

6. New Software and Platforms

6.1. marmoteCore

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

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

- Participants: Alain Jean-Marie, 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/

PHOENIX-POST Team

5. New Software and Platforms

5.1. Allen

The Allen DSL for online context detection over binary sensors

KEYWORDS: DSL - Contextual service - Iot - Sensors - Data stream

SCIENTIFIC DESCRIPTION: There is a large variety of binary sensors in use today, and useful context-aware services can be defined using such binary sensors. However, the currently available approaches for programming context-aware services do not conveniently support binary sensors. Indeed, no existing approach simultaneously supports a notion of state, central to binary sensors, offers a complete set of operators to compose states, allows to define reusable abstractions by means of such compositions, and implements efficient online processing of these operators.

The Allen language proposes a new approach for event processing specifically targeted to binary sensors. The central contributions of this language are a native notion of state and semi-causal operators for temporal state composition including: Allen logic's interval relations generalized for handling multiple intervals, and temporal filters for handling delays. Compared to other approaches such as CEP (complex event processing), our language provides less discontinued information, allows less restricted compositions, and supports reusable abstractions. We implemented a compiler for our language and applied it to successfully rewrite a full set of real Ambient Assisted Living services. The performance of our prototype interpreter has been shown to compete well with a commercial CEP engine when expressing the same services.

FUNCTIONAL DESCRIPTION: Main concepts and features: * Signal: formalized as a boolean function of (discrete) time. A signal models either the current state of a physical sensor or a higher-level context depending on such sensors. The "states" of a signal are the time intervals where the signal is 1. * Precise semantics of an Allen program: based on the above model. Allows checking domain properties. * Operators: allow to combine signals for deriving more complex signals. Each operator takes a given number of signals and produces a signal. For instance, the logic operators "and", "or", "not" have their usual meaning, at each time point, unary operators up(s) and down(s) produces the starting/ending events of signal s. Binary operator during(p,q) produces a signal containing the states of p entirely contained in some state of q. * Parameterized operators: take, besides a given number of signals, a given number of scalar (numeric) parameters, such as temporal delays. For instance, the unary operators gt[T](s) and lt[T](s) produces signals containing only the states of s which are longer/shorter than some delay T. * Language constructs for defining new operators. For instance, "def up(s) = gt[1](s)" allows defining operator "up" above, based on the more primitive operator "gt". This feature enables the construction of user-defined abstractions, and thus creating layers of reusable pieces of context logic. * Online context detection: the computation in real time of contexts based on incoming streams of events produces by sensors.

RELEASE FUNCTIONAL DESCRIPTION: First public version.

- Author: Eugène Volanschi
- Contact: Eugène Volanschi
- URL: https://github.com/NicVolanschi/Allen

POEMS-POST Team

6. New Software and Platforms

6.1. XLiFE++

KEYWORDS: Numerical simulations - Finite element modelling - Boundary element method
FUNCTIONAL DESCRIPTION: XLiFE++ is an FEM-BEM C++ code developed by POEMS laboratory and IRMAR laboratory, that can solve 1D/2D/3D, scalar/vector, transient/stationary/harmonic problems. Description: https://uma.ensta-paristech.fr/soft/XLiFE++/

- Contact: Eric Lunéville

6.2. COFFEE

KEYWORDS: Numerical simulations - Wave propagation - Boundary element method
FUNCTIONAL DESCRIPTION: COFFEE is an adapted fast BEM solver to model acoustic and elastic wave propagation (full implementation in Fortran 90). The 3-D acoustic or elastodynamic equations are solved with the boundary element method accelerated by the multi-level fast multipole method or a hierarchical-matrices based representation of the system matrix. The fundamental solutions for the infinite space are used in this implementation. A boundary element-boundary element coupling strategy is also implemented so multi-region problems (strata inside a valley for example) can be solved. In order to accelerate the convergence of the iterative solver, various analytic or algebraic preconditioners are available. Finally, an anisotropic mesh adaptation strategy is used to further reduce the computational times.

- Contact: Stéphanie Chaillat

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.

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/

6.8. 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/

RESIST Team

6. New Software and Platforms

6.1. Distem

KEYWORDS: Large scale - Experimentation - Virtualization - Emulation
FUNCTIONAL DESCRIPTION: Distem is a distributed systems emulator. When conducting research on Cloud, P2P, High Performance Computing or Grid systems, it can be used to transform an homogenenous cluster (composed of identical nodes) into an experimental platform where nodes have different performance, and are linked together through a complex network topology, making it the ideal tool to benchmark applications targetting such environments, or aiming at tolerating performance degradations or variations which are frequent in the Cloud or in other applications distributed at large scale (P2P for example).

RELEASE FUNCTIONAL DESCRIPTION: New features in Distem 1.3 include: (1) New network emulation parameters: loss, duplication, corruption, reordering and jitter, (2) Support for Debian Stretch, (3) Added many tests, (4) Moved project from GForge to GitHub (https://github.com/madynes/distem).
NEWS OF THE YEAR: New version 1.3

- Participants: Luc Sarzyniec, Lucas Nussbaum and Tomasz Buchert
- Partners: CNRS - Université de Lorraine - Loria - Grid'5000 - Inria
- Contact: Lucas Nussbaum
- URL: http://distem.gforge.inria.fr

6.2. Grid'5000

Grid'5000 experimental platform
KEYWORDS: HPC - Cloud - Big data - Testbeds
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.
NEWS OF THE YEAR: This year's highlights include the first joint FIT-Grid'5000 school, and various improvements (update to Debian 9, several new clusters, etc.). More information on https://www.grid5000.fr/w/News

- Participants: Christian Pérez, David Loup, Frédéric Desprez, Laurent Lefèvre, Laurent Pouilloux, Marc Pinhède, Simon Delamare, Lucas Nussbaum, Teddy Valette and Alexandre Merlin
- Contact: Frédéric Desprez
- URL: https://www.grid5000.fr/

6.3. HTTP-NDN gateway

A gateway to transport HTTP over NDN
KEYWORDS: Internet protocols - Interoperability - Named Data Networking - Web - Network gateway
FUNCTIONAL DESCRIPTION: In order to creat an NDN island using our HTTP over NDN architecture, we propose two kinds of gateways: (1) an ingress gateway (iGW), which converts HTTP user requests into NDN messages and converts requested NDN messages into HTTP responses sent to the end-users, and (2) an egress gateway (eGW), the counterpart of the first one, which converts requested NDN messages into HTTP requests towards web sites and converts HTTP responses into NDN messages.

The whole thing can be considered as an HTTP proxy for the outsiders of the NDN network because the gateways represent the input(s) and output(s) of the NDN network island which can store the HTTP responses passing through. The gateway also features intelligent naming and cache management of web contents passing through the NDN network to better use the NDN architecture. Native NDN clients and NDN web servers can be present inside this NDN network, and they can communicate with the same mapping protocol used by the gateways to communicate with regular HTTP/IP clients or servers.
NEWS OF THE YEAR: First release

- Partner: Orange Labs
- Contact: Thibault Cholez
- URL: https://github.com/DOCTOR-ANR/NDN-HTTP-Gateway

6.4. micro-NDN

microservices for NDN
KEYWORDS: Named Data Networking - Network Function Virtualization - Microservices
FUNCTIONAL DESCRIPTION: micro-NDN proposes to split the main functions of an NDN (Named-Data Networking) router into multiple microservices and to orchestrate them. Currently, it implements seven microservices: five are usual functions of an NDN router as in the NFD forwarding deamon (http://named-data.net/doc/NFD/current), and two are proposed to improve security: - Name Router (NR): Route Interest packets to producers that have registered a prefix of the name of the packet, it is like the Forwarding Information Base (FIB) in an NDN router, - Backward Router (BR): Route back Data packets to the consumers that have asked for it, it is like the Pending Interest Table (PIT) in an NDN router, - Packet Dispatcher (PD): Select the right pipeline for each kind of packet, - Content Store (CS): Aims to store Data packets to reuse them later when reasked, like the Content Store (CS) in an NDN router, - Strategy Forwarder (SF): A more general way to apply strategy (fail-over, round-robin, etc.), - Signature Verifier (SV): Verify the signature of the NDN packet based on the trusted keys, - Name Filter (NF): Drop packets based on their name.

We also provide a central manager that can monitor and orchestrate all the microservices. It provides a web-based GUI and a REST API to dynamically manipulate the topology (spawn a microservice, link them, etc.). It can also trigger actions based on predefined rules, for example to scale-up a bottleneck component.
NEWS OF THE YEAR: First release

- Contact: Thibault Cholez
- URL: https://github.com/DOCTOR-ANR/NDN-microservices

6.5. ndnperf

tool for server-side evaluation of NDN throughput
KEYWORDS: Named Data Networking - Performance measure
FUNCTIONAL DESCRIPTION: NDNperf is a tool for NDN server-side performance evaluation and sizing purposes, in order to have an idea of the throughput a server can achieve when it has to generate and transmit NDN Data packets. It is very similar to iPerf and also needs a client and a server to perform the measurements while minimizing the number of instructions between Interest reception and Data emission. It exists in two flavors (Java and C++) and has the following features: - Periodic performance report: end-to-end throughput, latency, processing time, - Multi-threaded (one main thread for event lookup and N threads for NDN Data generation), - Able to use all the available signatures implemented in the NDN library, choose the size of the key, and the transmission size of Data packets, - Message broker implementation (Java version only, currently no update is scheduled).

NDNperf features many options regarding the signing process because we identified it as the main bottleneck of application performances.

NEWS OF THE YEAR: First release

- Contact: Thibault Cholez
- URL: https://github.com/DOCTOR-ANR/ndnperf

6.6. SCUBA

A Tool Suite for the automated security assessment of IoT environments

KEYWORDS: Cybersecurity - Internet of things - Machine learning - Artificial intelligence

FUNCTIONAL DESCRIPTION: IoT devices are used in different fields of application, not only for the general public, but also in industrial environments. SCUBA is tool suite for the security assessment of industrial and general public IoT devices. It mainly relies on collected information through passive and active scanning of a running IoT device in its exploitation environment to build its Security Knowledge Base (SKB). The knowledge base contains all relevant information of the device regarding its network communications extracted from PCAP files, the enumeration of its used hardware and software represented in the CPE (Common Platform Enumeration) format, the list of its known vulnerabilities in the CVE (Common Vulnerabilities and Exposures) format associated to their CWE (Common Weakness Enumeration) and CAPEC (Common Attack Pattern Enumeration and Classification) descriptions. The SKB is used by SCUBA to predict the intrusion chains associated to an IoT device and its environment. SCUBA tries to be as automated as possible to face the large scale and the great heterogeneity of IoT networks.

NEWS OF THE YEAR: First release

- Participants: Abdelkader Lahmadi, Frédéric Beck, Thomas Lacour and Jérôme François
- Contact: Abdelkader Lahmadi

6.7. Platforms

6.7.1. CPS Security Assessment Platform

During 2018, we have extended our Cyber-Physical systems security assessment platform with new hardware components including multiple types of Programmable Logic Controllers (PLCs), a small scale distribution and sorting testbed, and an experimental system modelled after a microgrid system. The physical platform is also extended with several IoT devices dedicated to residential networks (heating control, lightning system, home gateways, etc). The platform will be mainly used for building security assessment and evaluation experimentation on the available devices to identify and validate their associated attack patterns and discover new vulnerabilities. This platform is used as a testbed for the development carried on the SCUBA (see 6.6) tool suite to assess the security of IoT and SCADA systems.

RMOD Project-Team

6. New Software and Platforms

6.1. Moose

Moose: Software and Data Analysis Platform

KEYWORDS: Software engineering - Meta model - Software visualisation

FUNCTIONAL DESCRIPTION: Moose is an extensive platform for software and data analysis. It offers multiple services ranging from importing and parsing data, to modeling, to measuring, querying, mining, and to building interactive and visual analysis tools. The development of Moose has been evaluated to 200 man/year.

Mots-cles : MetaModeling, Program Visualization, Software metrics, Code Duplication, Software analyses, Parsers

- Participants: Anne Etien, Nicolas Anquetil, Olivier Auverlot, Stéphane Ducasse, Julien Delplanque, Guillaume Larcheveque, Cyril Ferlicot-Delbecque and Pavel Krivanek
- Partners: Université de Berne - Sensus - Synectique - Pleiad - USI - Vrije Universiteit Brussel
- Contact: Stéphane Ducasse
- URL: http://www.moosetechnology.org

6.2. Pharo

KEYWORDS: Live programmation objet - Reflective system - Web Application

FUNCTIONAL DESCRIPTION: Pharo is a pure object reflective and dynamic language inspired by Smalltalk. In addition, Pharo comes with a full advanced programming environment developed under the MIT License. It provides a platform for innovative development both in industry and research. By providing a stable and small core system, excellent developer tools, and maintained releases, Pharo's goal is to be a platform to build and deploy mission critical applications, while at the same time continue to evolve. Pharo 60 got 100 contributors world-wide. It is used by around 30 universities, 15 research groups and around 40 companies.

- Participants: Christophe Demarey, Clement Bera, Damien Pollet, Esteban Lorenzano, Marcus Denker, Stéphane Ducasse and Guillermo Polito
- Partners: BetaNine - Reveal - Inceptive - Netstyle - Feenk - ObjectProfile - GemTalk Systems - Greyc Université de Caen - Basse-Normandie - Université de Berne - Yesplan - RMod - Pleiad - Sensus - Université de Bretagne Occidentale - École des Mines de Douai - ENSTA - Uqbar foundation Argentina - LAM Research - ZWEIDENKER - LifeWare - JPMorgan Chase - KnowRoaming - ENIT - Spesenfuchs - FINWorks - Esug - FAST - Ingenieubüro Schmidt - Projector Software - HRWorks - Inspired.org - Palantir Solutions - High Octane - Soops - Osoco - Ta Mère SCRL - University of Yaounde 1 - Software Quality Laboratory, University of Novi Sad - Software Institute Università della Svizzera italiana - Universdad Nacional de Quilmes - UMMISCO IRD - Université technique de Prague
- Contact: Marcus Denker
- URL: http://www.pharo.org

6.3. Pillar

KEYWORDS: HTML - LaTeX - HTML5

FUNCTIONAL DESCRIPTION: Pillar is a markup syntax and associated tools to write and generate documentation and books. Pillar is currently used to write several books and other documentation. It is used in the tools developed by Feenk.com.

- Partner: Feenk
- Contact: Stéphane Ducasse
- URL: https://github.com/Pillar-markup/pillar

ROMA Project-Team

6. New Software and Platforms

6.1. MUMPS

A MUltifrontal Massively Parallel Solver

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

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

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, Aurélia 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 and the web page, and doesn't need to bother about the internal details of the system. fftweb has been developped 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

SPIRALS Project-Team

6. New Software and Platforms

6.1. APISENSE

KEYWORDS: Mobile sensing - Crowd-sensing - Mobile application - Crowd-sourcing - Android
FUNCTIONAL DESCRIPTION: APISENSE platform is a software solution to collect various contextual information from Android devices (client application) and automatically upload collected data to a server (deployed as a SaaS). APISENSE is based on a Cloud computing infrastructure to facilitate datasets collection from significant populations of mobile users for research purposes.

- Participants: Antoine Veuiller, Christophe Ribeiro, Julien Duribreux, Nicolas Haderer, Romain Rouvoy, Romain Sommerard and Lakhdar Meftah
- Partner: Université de Lille
- Contact: Romain Rouvoy
- URL: https://apisense.io

6.2. PowerAPI

KEYWORDS: Energy efficiency - Energy management
FUNCTIONAL DESCRIPTION: PowerAPI is a library for monitoring the energy consumption of software systems.

PowerAPI differs from existing energy process-level monitoring tool in its software orientation, with a fully customizable and modular solution that let the user to precisely define what he/she wants to monitor. PowerAPI is based on a modular and asynchronous event-driven architecture using the Akka library. PowerAPI offers an API which can be used to define requests about energy spent by a process, following its hardware resource utilization (in term of CPU, memory, disk, network, etc.).

- Participants: Adel Noureddine, Loïc Huertas, Maxime Colmant and Romain Rouvoy
- Contact: Romain Rouvoy
- URL: http://powerapi.org

6.3. Saloon

KEYWORDS: Feature Model - Software Product Line - Cloud computing - Model-driven engineering - Ontologies
FUNCTIONAL DESCRIPTION: Saloon is a framework for the selection and configuration of Cloud providers according to application requirements. The framework enables the specification of such requirements by defining ontologies. Each ontology provides a unified vision of provider offers in terms of frameworks, databases, languages, application servers and computational resources (i.e., memory, storage and CPU frequency). Furthermore, each provider is related to a Feature Model (FM) with attributes and cardinalities, which captures its capabilities. By combining the ontology and FMs, the framework is able to match application requirements with provider capabilities and select a suitable one. Specific scripts to the selected provider are generated in order to enable its configuration.

- Participants: Clément Quinton, Daniel Romero Acero, Laurence Duchien, Lionel Seinturier and Romain Rouvoy
- Partner: Université Lille 1
- Contact: Lionel Seinturier
- URL: https://gitlab.irisa.fr/drome00A/saloon

6.4. SPOON

KEYWORDS: Java - Code analysis

FUNCTIONAL DESCRIPTION: Spoon is an open-source library that enables you to transform (see below) and analyze Java source code (see example) . Spoon provides a complete and fine-grained Java metamodel where any program element (classes, methods, fields, statements, expressions...) can be accessed both for reading and modification. Spoon takes as input source code and produces transformed source code ready to be compiled.

- Participants: Gérard Paligot, Lionel Seinturier, Martin Monperrus and Nicolas Petitprez
- Contact: Martin Monperrus
- URL: http://spoon.gforge.inria.fr

STACK 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, Hélène Coullon and Maverick Chardet
- Partners: IMT Atlantique - LS2N - LIP
- Contact: Hélène Coullon
- Publications: Madeus: A formal deployment model - Behavioral interfaces for reconfiguration of component models

6.2. Nitro

KEYWORDS: Cloud storage - Virtual Machine Image - Geo-distribution
SCIENTIFIC DESCRIPTION: Nitro is a storage system that is designed to work in geo-distributed cloud environments (i.e., over WAN) to efficiently manage Virtual Machine Images (VMIs).

Nitro employs fixed-size deduplication to store VMIs. This technique contributes to minimizing the network cost. Also, Nitro incorporates a network-aware scheduling algorithm (based on max flow algorithm) to determine which chunks should be pulled from which site in order to reconstruct the corresponding image on the destination site, with minimal (provisioning) time.
FUNCTIONAL DESCRIPTION: Geo-distributed Storage System to optimize Images (VM, containers, ...) management, in terms of cost and time, in geographically distributed cloud environment (i.e. data centers are connected over WAN).

- Authors: Jad Darrous, Shadi Ibrahim and Christian Pérez
- Contact: Shadi Ibrahim
- URL: https://gitlab.inria.fr/jdarrous/nitro

6.3. VMPlaces

KEYWORDS: Simulation - Virtualization - Scheduling
FUNCTIONAL DESCRIPTION: VMPlaces is a dedicated framework to evaluate and compare VM placement algorithms. This framework is composed of two major components: the injector and the VM placement algorithm. The injector is the generic part of the framework (i.e. the one you can directly use) while the VM placement algorithm is the part you want to study (or compare with available algorithms). Currently, the VMPlaceS is released with three algorithms:

Entropy, a centralized approach using a constraint programming approach to solve the placement/reconfiguration VM problem

Snooze, a hierarchical approach where each manager of a group invokes Entropy to solve the placement/reconfiguration VM problem. Note that in the original implementation of Snooze, it is using a specific heuristic to solve the placement/reconfiguration VM problem. As the sake of simplicity, we have simply reused the entropy scheduling code.

DVMS, a distributed approach that dynamically partitions the system and invokes Entropy on each partition.

- Participants: Adrien Lèbre, Flavien Quesnel, Jonathan Pastor, Mario Südholt and Takahiro Hirofuchi
- Contact: Adrien Lèbre
- URL: http://beyondtheclouds.github.io/VMPlaceS/

6.4. ENOS

Experimental eNvironment for OpenStack
KEYWORDS: OpenStack - Experimentation - Reproducibility
FUNCTIONAL DESCRIPTION: Enos workflow :

A typical experiment using Enos is the sequence of several phases:

- enos up : Enos will read the configuration file, get machines from the resource provider and will prepare the next phase - enos os : Enos will deploy OpenStack on the machines. This phase rely highly on Kolla deployment. - enos init-os : Enos will bootstrap the OpenStack installation (default quotas, security rules, ...) - enos bench : Enos will run a list of benchmarks. Enos support Rally and Shaker benchmarks. - enos backup : Enos will backup metrics gathered, logs and configuration files from the experiment.

- Partner: Orange Labs
- Contact: Adrien Lèbre
- URL: http://enos.readthedocs.io/en/stable/

6.5. Platforms

6.5.1. OpenStack

OpenStack is the de facto open-source management system to operate and use Cloud Computing infrastructures. Started in 2012, the OpenStack foundation gathers 500 organizations including groups such as Intel, AT&T, RedHat, etc. The software platform relies on tens of services with a 6-month development cycle. It is composed of more than 2 millions of lines of code, mainly in Python, just for the core services. While these aspects make the whole ecosystem quite swift, they are also good signs of maturity of this community. We created and animated between 2016 and 2018 the Fog/Edge/Massively Distributed (FEMDC) Special Interest Group [0] and have been contributing to the Performance working group since 2015. The former investigates how OpenStack can address Fog/Edge Computing use cases whereas the latter addresses scalability, reactivity and high-availability challenges. In addition to releasing white papers and guidelines [100], the major result from the academic view point is the aforementioned EnOS solution, a holistic framework to conduct performance evaluations of OpenStack (control and data plane). In May 2018, the FEMDC SiG turned into a larger group under the control of the OpenStack foundation. This group gathers large companies such as Verizon, ATT, etc.

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[0] https://wiki.openstack.org/wiki/Fog_Edge_Massively_Distributed_Clouds

6.5.2. 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. STACK members are strongly involved into the management and the supervision of the testbed, notably through the steering committee or the SeDuCe testbed described hereafter.

6.5.3. SeDuCe

The SeDuCe project aims to deliver a research testbed dedicated to holistic research studies on energetical aspects of datacenters. Part of the Grid’5000 Nantes’ site, this infrastructure is composed of probes that measure the power consumption of each server, each switch and each cooling system, and also measure the temperature at the front and the back of each servers. These sensors enable reasearch to cover a full spectrum of the energetical aspect of datacenters, such as cooling and power consumption depending of experimental conditions.

The testbed should soon be connected to renewqble energy sources (solar panels). This “green” datacenter will enable researchers to perform real experiment-driven studies on fields such as temperature based scheduling or “green” aware software (*i.e.*, software that take into account renewable energies and weather conditions).

6.5.4. SILECS

STACK Members are involved in the definition and bootstrap of the SILECS infrastructure (IR ministère). This infrastructure can be seen as a merge of the Grid’5000 and FIT testbeds with the goal of providing a common platform for experimental computer Science (Next Generation Internet, Internet of things, clouds, HPC, big data, ...).

STORM Project-Team

6. New Software and Platforms

6.1. Chameleon

KEYWORDS: Runtime system - Task-based algorithm - Dense linear algebra - HPC - Task scheduling
SCIENTIFIC DESCRIPTION: Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

We expect advances in three directions based first on strong and closed interactions between the runtime and numerical linear algebra communities. This initial activity will then naturally expand to more focused but still joint research in both fields.

1. Fine interaction between linear algebra and runtime systems. On parallel machines, HPC applications need to take care of data movement and consistency, which can be either explicitly managed at the level of the application itself or delegated to a runtime system. We adopt the latter approach in order to better keep up with hardware trends whose complexity is growing exponentially. One major task in this project is to define a proper interface between HPC applications and runtime systems in order to maximize productivity and expressivity. As mentioned in the next section, a widely used approach consists in abstracting the application as a DAG that the runtime system is in charge of scheduling. Scheduling such a DAG over a set of heterogeneous processing units introduces a lot of new challenges, such as predicting accurately the execution time of each type of task over each kind of unit, minimizing data transfers between memory banks, performing data prefetching, etc. Expected advances: In a nutshell, a new runtime system API will be designed to allow applications to provide scheduling hints to the runtime system and to get real-time feedback about the consequences of scheduling decisions.

2. Runtime systems. A runtime environment is an intermediate layer between the system and the application. It provides low-level functionality not provided by the system (such as scheduling or management of the heterogeneity) and high-level features (such as performance portability). In the framework of this proposal, we will work on the scalability of runtime environment. To achieve scalability it is required to avoid all centralization. Here, the main problem is the scheduling of the tasks. In many task-based runtime environments the scheduler is centralized and becomes a bottleneck as soon as too many cores are involved. It is therefore required to distribute the scheduling decision or to compute a data distribution that impose the mapping of task using, for instance the so-called “owner-compute” rule. Expected advances: We will design runtime systems that enable an efficient and scalable use of thousands of distributed multicore nodes enhanced with accelerators.

3. Linear algebra. Because of its central position in HPC and of the well understood structure of its algorithms, dense linear algebra has often pioneered new challenges that HPC had to face. Again, dense linear algebra has been in the vanguard of the new era of petascale computing with the design of new algorithms that can efficiently run on a multicore node with GPU accelerators. These algorithms are called “communication-avoiding” since they have been redesigned to limit the amount of communication between processing units (and between the different levels of memory hierarchy). They are expressed through Direct Acyclic Graphs (DAG) of fine-grained tasks that are dynamically scheduled. Expected advances: First, we plan to investigate the impact of these principles in the case of sparse applications (whose algorithms are slightly more complicated but often rely on dense kernels). Furthermore, both in the dense and sparse cases, the scalability on thousands of nodes is still limited, new numerical approaches need to be found. We will specifically design sparse hybrid direct/iterative methods that represent a promising approach.

Overall end point. The overall goal of the MORSE associate team is to enable advanced numerical algorithms to be executed on a scalable unified runtime system for exploiting the full potential of future exascale machines.

FUNCTIONAL DESCRIPTION: Chameleon is a dense linear algebra software relying on sequential task-based algorithms where sub-tasks of the overall algorithms are submitted to a Runtime system. A Runtime system such as StarPU is able to manage automatically data transfers between not shared memory area (CPUs-GPUs, distributed nodes). This kind of implementation paradigm allows to design high performing linear algebra algorithms on very different type of architecture: laptop, many-core nodes, CPUs-GPUs, multiple nodes. For example, Chameleon is able to perform a Cholesky factorization (double-precision) at 80 TFlop/s on a dense matrix of order 400 000 (e.i. 4 min).

RELEASE FUNCTIONAL DESCRIPTION: Chameleon includes the following features:

- BLAS 3, LAPACK one-sided and LAPACK norms tile algorithms - Support QUARK and StarPU runtime systems and PaRSEC since 2018 - Exploitation of homogeneous and heterogeneous platforms through the use of BLAS/LAPACK CPU kernels and cuBLAS/MAGMA CUDA kernels - Exploitation of clusters of interconnected nodes with distributed memory (using OpenMPI)

- Participants: Cédric Castagnede, Samuel Thibault, Emmanuel Agullo, Florent Pruvost and Mathieu Faverge
- Partners: Innovative Computing Laboratory (ICL) - King Abdullha University of Science and Technology - University of Colorado Denver
- Contact: Emmanuel Agullo
- URL: https://gitlab.inria.fr/solverstack/chameleon

6.2. hwloc

Hardware Locality

KEYWORDS: NUMA - Multicore - GPU - Affinities - Open MPI - Topology - HPC - Locality

FUNCTIONAL DESCRIPTION: Hardware Locality (hwloc) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices. It builds a widely-portable abstraction of these resources and exposes it to applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

hwloc targets many types of high-performance computing applications, from thread scheduling to placement of MPI processes. Most existing MPI implementations, several resource managers and task schedulers, and multiple other parallel libraries already use hwloc.

- Participants: Brice Goglin and Samuel Thibault
- Partners: Open MPI consortium - Intel - AMD
- Contact: Brice Goglin
- Publications: hwloc: a Generic Framework for Managing Hardware Affinities in HPC Applications - Managing the Topology of Heterogeneous Cluster Nodes with Hardware Locality (hwloc) - A Topology-Aware Performance Monitoring Tool for Shared Resource Management in Multicore Systems - Exposing the Locality of Heterogeneous Memory Architectures to HPC Applications - Towards the Structural Modeling of the Topology of next-generation heterogeneous cluster Nodes with hwloc - On the Overhead of Topology Discovery for Locality-aware Scheduling in HPC
- URL: http://www.open-mpi.org/projects/hwloc/

6.3. KaStORS

The KaStORS OpenMP Benchmark Suite

KEYWORDS: Benchmarking - HPC - Task-based algorithm - Task scheduling - OpenMP - Data parallelism

FUNCTIONAL DESCRIPTION: The KaStORS benchmarks suite has been designed to evaluate implementations of the OpenMP dependent task paradigm, introduced as part of the OpenMP 4.0 specification.

- Participants: François Broquedis, Nathalie Furmento, Olivier Aumage, Philippe Virouleau, Pierrick Brunet, Samuel Thibault and Thierry Gautier
- Contact: Thierry Gautier
- URL: http://kastors.gforge.inria.fr/#!index.md

6.4. KStar

The KStar OpenMP Compiler
KEYWORDS: Source-to-source compiler - OpenMP - Task scheduling - Compilers - Data parallelism
FUNCTIONAL DESCRIPTION: The KStar software is a source-to-source OpenMP compiler for languages C and C++. The KStar compiler translates OpenMP directives and constructs into API calls from the StarPU runtime system or the XKaapi runtime system. The KStar compiler is virtually fully compliant with OpenMP 3.0 constructs. The KStar compiler supports OpenMP 4.0 dependent tasks and accelerated targets.

- Participants: Nathalie Furmento, Olivier Aumage, Philippe Virouleau and Samuel Thibault
- Contact: Olivier Aumage
- Publications: Bridging the gap between OpenMP and task-based runtime systems for the fast multipole method - Bridging the gap between OpenMP 4.0 and native runtime systems for the fast multipole method - Evaluation of OpenMP Dependent Tasks with the KASTORS Benchmark Suite
- URL: http://kstar.gforge.inria.fr/#!index.md

6.5. MAQAO

SCIENTIFIC DESCRIPTION: MAQAO relies on binary codes for Intel x86 and ARM architectures. For x86 architecture, it can insert probes for instrumention directly inside the binary. There is no need to recompile. The static/dynamic approach of MAQAO analysis is the main originality of the tool, combining performance model with values collected through instrumentation.

MAQAO has a static performance model for x86 and ARM architectures. This model analyzes performance of the codes on the architectures and provides some feed-back hints on how to improve these codes, in particular for vector instructions.

The dynamic collection of data in MAQAO enables the analysis of thread interactions, such as false sharing, amount of data reuse, runtime scheduling policy, ...
FUNCTIONAL DESCRIPTION: MAQAO is a performance tuning tool for OpenMP parallel applications. It relies on the static analysis of binary codes and the collection of dynamic information (such as memory traces). It provides hints to the user about performance bottlenecks and possible workarounds.

- Participants: Christopher Haine, Denis Barthou, James Tombi A Mba and Olivier Aumage
- Contact: Denis Barthou

6.6. StarPU

The StarPU Runtime System
KEYWORDS: Multicore - GPU - Scheduling - HPC - Performance

SCIENTIFIC DESCRIPTION: Traditional processors have reached architectural limits which heterogeneous multicore designs and hardware specialization (eg. coprocessors, accelerators, ...) intend to address. However, exploiting such machines introduces numerous challenging issues at all levels, ranging from programming models and compilers to the design of scalable hardware solutions. The design of efficient runtime systems for these architectures is a critical issue. StarPU typically makes it much easier for high performance libraries or compiler environments to exploit heterogeneous multicore machines possibly equipped with GPGPUs or Cell processors: rather than handling low-level issues, programmers may concentrate on algorithmic concerns.Portability is obtained by the means of a unified abstraction of the machine. StarPU offers a unified offloadable task abstraction named "codelet". Rather than rewriting the entire code, programmers can encapsulate existing functions within codelets. In case a codelet may run on heterogeneous architectures, it is possible to specify one function for each architectures (eg. one function for CUDA and one function for CPUs). StarPU takes care to schedule and execute those codelets as efficiently as possible over the entire machine. In order to relieve programmers from the burden of explicit data transfers, a high-level data management library enforces memory coherency over the machine: before a codelet starts (eg. on an accelerator), all its data are transparently made available on the compute resource.Given its expressive interface and portable scheduling policies, StarPU obtains portable performances by efficiently (and easily) using all computing resources at the same time. StarPU also takes advantage of the heterogeneous nature of a machine, for instance by using scheduling strategies based on auto-tuned performance models.

StarPU is a task programming library for hybrid architectures

The application provides algorithms and constraints: - CPU/GPU implementations of tasks - A graph of tasks, using either the StarPU's high level GCC plugin pragmas or StarPU's rich C API

StarPU handles run-time concerns - Task dependencies - Optimized heterogeneous scheduling - Optimized data transfers and replication between main memory and discrete memories - Optimized cluster communications

Rather than handling low-level scheduling and optimizing issues, programmers can concentrate on algorithmic concerns!
FUNCTIONAL DESCRIPTION: StarPU is a runtime system that offers support for heterogeneous multicore machines. While many efforts are devoted to design efficient computation kernels for those architectures (e.g. to implement BLAS kernels on GPUs), StarPU not only takes care of offloading such kernels (and implementing data coherency across the machine), but it also makes sure the kernels are executed as efficiently as possible.

- Participants: Corentin Salingue, Andra Hugo, Benoît Lize, Cédric Augonnet, Cyril Roelandt, François Tessier, Jérôme Clet-Ortega, Ludovic Courtes, Ludovic Stordeur, Marc Sergent, Mehdi Juhoor, Nathalie Furmento, Nicolas Collin, Olivier Aumage, Pierre-André Wacrenier, Raymond Namyst, Samuel Thibault, Simon Archipoff, Xavier Lacoste, Terry Cojean, Yanis Khorsi, Philippe Virouleau, LOïC JOUANS and Leo Villeveygoux
- Contact: Olivier Aumage
- Publications: Achieving High Performance on Supercomputers with a Sequential Task-based Programming Model - The StarPU Runtime System at Exascale ? - Analyzing Dynamic Task-Based Applications on Hybrid Platforms: An Agile Scripting Approach - Resource aggregation for task-based Cholesky Factorization on top of heterogeneous machines - Resource aggregation in task-based applications over accelerator-based multicore machines - Controlling the Memory Subscription of Distributed Applications with a Task-Based Runtime System - Exploiting Two-Level Parallelism by Aggregating Computing Resources in Task-Based Applications Over Accelerator-Based Machines - Exploiting Two-Level Parallelism by Aggregating Computing Resources in Task-Based Applications Over Accelerator-Based Machines - Achieving High Performance on Supercomputers with a Sequential Task-based Programming Model - Bridging the gap between OpenMP 4.0 and native runtime systems for the fast multipole method - Scalability of a task-based runtime system for dense linear algebra applications - Faithful Performance Prediction of a Dynamic Task-Based Runtime

System for Heterogeneous Multi-Core Architectures - Towards seismic wave modeling on heterogeneous many-core architectures using task-based runtime system - Bridging the Gap between Performance and Bounds of Cholesky Factorization on Heterogeneous Platforms - Composing multiple StarPU applications over heterogeneous machines: A supervised approach - Evaluation of OpenMP Dependent Tasks with the KASTORS Benchmark Suite - A runtime approach to dynamic resource allocation for sparse direct solvers - Modeling and Simulation of a Dynamic Task-Based Runtime System for Heterogeneous Multi-Core Architectures - Toward OpenCL Automatic Multi-Device Support - Harnessing clusters of hybrid nodes with a sequential task-based programming model - Taking advantage of hybrid systems for sparse direct solvers via task-based runtimes - Modulariser les ordonnanceurs de tâches : une approche structurelle - Overview of Distributed Linear Algebra on Hybrid Nodes over the StarPU Runtime - StarPU-MPI: Task Programming over Clusters of Machines Enhanced with Accelerators - Modeling and Simulation of a Dynamic Task-Based Runtime System for Heterogeneous Multi-Core Architectures - Taking advantage of hybrid systems for sparse direct solvers via task-based runtimes - Adaptive Task Size Control on High Level Programming for GPU/CPU Work Sharing - Composing multiple StarPU applications over heterogeneous machines: a supervised approach - Implementation of FEM Application on GPU with StarPU - Le problème de la composition parallèle : une approche supervisée - Support exécutif scalable pour les architectures hybrides distribuées - SOCL: An OpenCL Implementation with Automatic Multi-Device Adaptation Support - C Language Extensions for Hybrid CPU/GPU Programming with StarPU - Programming Models and Runtime Systems for Heterogeneous Architectures - Programmation unifiée multi-accélérateur OpenCL - StarPU-MPI: Task Programming over Clusters of Machines Enhanced with Accelerators - Parallelization on Heterogeneous Multicore and Multi-GPU Systems of the Fast Multipole Method for the Helmholtz Equation Using a Runtime System - High-Level Support for Pipeline Parallelism on Many-Core Architectures - Programmability and Performance Portability Aspects of Heterogeneous Multi-/Manycore Systems - Programmation des architectures hétérogènes à l'aide de tâches divisibles - StarPU: a unified platform for task scheduling on heterogeneous multicore architectures - PEPPHER: Efficient and Productive Usage of Hybrid Computing Systems - The PEPPHER Approach to Programmability and Performance Portability for Heterogeneous many-core Architectures - Flexible runtime support for efficient skeleton programming on hybrid systems - LU Factorization for Accelerator-based Systems - QR Factorization on a Multicore Node Enhanced with Multiple GPU Accelerators - Programmation multi-accélérateurs unifiée en OpenCL - Détection optimale des coins et contours dans des bases d'images volumineuses sur architectures multicœurs hétérogènes - Association de modèles de programmation pour l'exploitation de clusters de GPUs dans le calcul intensif - Programming heterogeneous, accelerator-based multicore machines:current situation and main challenges - Scheduling Tasks over Multicore machines enhanced with acelerators: a Runtime System's Perspective - Composabilité de codes parallèles sur architectures hétérogènes - Data-Aware Task Scheduling on Multi-Accelerator based Platforms - Dynamically scheduled Cholesky factorization on multicore architectures with GPU accelerators. - StarPU: a Runtime System for Scheduling Tasks over Accelerator-Based Multicore Machines - StarPU : un support exécutif unifié pour les architectures multicoeurs hétérogènes - Automatic Calibration of Performance Models on Heterogeneous Multicore Architectures - StarPU: A Unified Platform for Task Scheduling on Heterogeneous Multicore Architectures - Exploiting the Cell/BE architecture with the StarPU unified runtime system - Bridging the gap between OpenMP and task-based runtime systems for the fast multipole method

- URL: http://starpu.gforge.inria.fr/

6.7. PARCOACH

PARallel Control flow Anomaly CHecker

KEYWORDS: High-Performance Computing - Program verification - Debug - MPI - OpenMP - Compilation

SCIENTIFIC DESCRIPTION: PARCOACH verifies programs in two steps. First, it statically verifies applications with a data- and control-flow analysis and outlines execution paths leading to potential deadlocks. The code is then instrumented, displaying an error and synchronously interrupting all processes if the actual scheduling leads to a deadlock situation.

FUNCTIONAL DESCRIPTION: Supercomputing plays an important role in several innovative fields, speeding up prototyping or validating scientific theories. However, supercomputers are evolving rapidly with now millions of processing units, posing the questions of their programmability. Despite the emergence of more widespread and functional parallel programming models, developing correct and effective parallel applications still remains a complex task. As current scientific applications mainly rely on the Message Passing Interface (MPI) parallel programming model, new hardwares designed for Exascale with higher node-level parallelism clearly advocate for an MPI+X solutions with X a thread-based model such as OpenMP. But integrating two different programming models inside the same application can be error-prone leading to complex bugs - mostly detected unfortunately at runtime. PARallel COntrol flow Anomaly CHecker aims at helping developers in their debugging phase.

- Participants: Emmanuelle Saillard, Denis Barthou and Pierre Huchant
- Partner: CEA
- Contact: Emmanuelle Saillard
- URL: https://esaillar.github.io/PARCOACH/

6.8. AFF3CT

A Fast Forward Error Correction Toolbox

KEYWORDS: High-Performance Computing - Signal processing - Error Correction Code

FUNCTIONAL DESCRIPTION: AFF3CT proposes high performance Error Correction algorithms for Polar, Turbo, LDPC, RSC (Recursive Systematic Convolutional), Repetition and RA (Repeat and Accumulate) codes. These signal processing codes can be parameterized in order to optimize some given metrics, such as Bit Error Rate, Bandwidth, Latency, ...using simulation. For the designers of such signal processing chain, AFF3CT proposes also high performance building blocks so to develop new algorithms. AFF3CT compiles with many compilers and runs on Windows, Mac OS X, Linux environments and has been optimized for x86 (SSE, AVX instruction sets) and ARM architectures (NEON instruction set).

- Authors: Adrien Cassagne, Bertrand Le Gal, Camille Leroux, Denis Barthou and Olivier Aumage
- Partner: IMS
- Contact: Adrien Cassagne
- URL: https://aff3ct.github.io/

6.9. MORSE

KEYWORDS: High performance computing - Matrix calculation - Fast multipole method - Runtime system

FUNCTIONAL DESCRIPTION: MORSE (Matrices Over Runtime Systems @ Exascale) is a scientific project, its objectives are to solve matrix problems on complex architectures, using runtime systems. More specifically, the goal is to write codes that reach a high level of performance for all architectures. The algorithms are written independently of the architecture, and the runtime system dispatches the different computational parts to the different computing units. This methodology has been validated on three classes of problems: dense linear algebra, sparse and dense, and fast multipole methods. The corresponding codes have been incorporated into several softwares, MAGMA, Pastix and ScalFMM.

- Contact: Emmanuel Agullo
- URL: http://icl.cs.utk.edu/morse/

6.10. SwLoc

Software Contexts for Locality

KEYWORDS: HPC - Locality - Contexts - Multicore - GPU

FUNCTIONAL DESCRIPTION: SwLoc is a library for flexible and generic partitioning of computing resources (processors, accelerators) to be able to co-excute confined parallel regions which can rely on different runtime systems (e.g. OpenMP, Intel TBB, StarPU, etc.). With all different hypervisor strategies, It is possible to adapt dynamically the computing resources of each context, in order to match each parallel region's need as closely as possible.

- Contact: Corentin Salingue
- URL: http://swloc.gforge.inria.fr/

6.11. VITE

Visual Trace Explorer

KEYWORDS: Visualization - Execution trace

FUNCTIONAL DESCRIPTION: ViTE is a trace explorer. It is a tool made to visualize execution traces of large parallel programs. It supports Pajé, a trace format created by Inria Grenoble, and OTF and OTF2 formats, developed by the University of Dresden and allows the programmer a simpler way to analyse, debug and/or profile large parallel applications.

- Participant: Mathieu Faverge
- Contact: Mathieu Faverge
- URL: http://vite.gforge.inria.fr/

TADAAM Project-Team

6. New Software and Platforms

6.1. Hsplit

Hierarchical communicators split

KEYWORDS: MPI communication - Topology - Hardware platform

SCIENTIFIC DESCRIPTION: Hsplit is a library that implements an abstraction allowing the programmer using MPI in their parallel applications to access the underlying hardware structure through a hierarchy of communicators. Hsplit is based on the MPI_Comm_split_type routine and provides a new value for the split_type argument that specifically creates a hierarchy a subcommunicators where each new subcommunicator corresponds to a meaningful hardware level. The important point is that only the structure o the hardware is exploited and the number of levels or the levels names are not fixed so as to propose a solution independent from future hardware evolutions (such as new levels for instance). Another flavor of this MPI_Comm_split_type function is provided that creates a roots communicators at the same time a subcommunicator is produced, in order to ease the collective communication and/or synchronization among subcommunicators.

FUNCTIONAL DESCRIPTION: Hsplit implements an abstraction that allows the programmer using MPI in their parallel applications to access the underlying hardware structure through a hierarchy of communicators. Hsplit is based on the MPI_Comm_split_type routine and provides a new value for the split_type argument that specifically creates a hierarchy a subcommunicators where each new subcommunicator corresponds to a meaningful hardware level. The important point is that only the structure o the hardware is exploited and the number of levels or the levels names are not fixed so as to propose a solution independent from future hardware evolutions (such as new levels for instance). Another flavor of this MPI_Comm_split_type function is provided that creates a roots communicators at the same time a subcommunicator is produced, in order to ease the collective communication and/or synchronization among subcommunicators.

NEWS OF THE YEAR: A new working group in the MPI Forum to champion the integration of this proposal in the MPI standard has been created. This working group includes Inria, CEA, Atos/Bull, Paratools, the University of Tennessee - Knoxville and many other institutions/companies are interested to join in.

- Participants: Guillaume Mercier, Brice Goglin, Emmanuel Jeannot and Farouk Mansouri
- Contact: Guillaume Mercier
- Publications: A hierarchical model to manage hardware topology in MPI applications - A Hierarchical Model to Manage Hardware Topology in MPI Applications
- URL: http://mpi-topology.gforge.inria.fr/

6.2. hwloc

Hardware Locality

KEYWORDS: NUMA - Multicore - GPU - Affinities - Open MPI - Topology - HPC - Locality

FUNCTIONAL DESCRIPTION: Hardware Locality (hwloc) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices. It builds a widely-portable abstraction of these resources and exposes it to applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

hwloc targets many types of high-performance computing applications, from thread scheduling to placement of MPI processes. Most existing MPI implementations, several resource managers and task schedulers, and multiple other parallel libraries already use hwloc.

- Participants: Brice Goglin and Samuel Thibault
- Partners: Open MPI consortium - Intel - AMD
- Contact: Brice Goglin
- Publications: hwloc: a Generic Framework for Managing Hardware Affinities in HPC Applications - Managing the Topology of Heterogeneous Cluster Nodes with Hardware Locality (hwloc) - A Topology-Aware Performance Monitoring Tool for Shared Resource Management in Multicore Systems - Exposing the Locality of Heterogeneous Memory Architectures to HPC Applications - Towards the Structural Modeling of the Topology of next-generation heterogeneous cluster Nodes with hwloc - On the Overhead of Topology Discovery for Locality-aware Scheduling in HPC
- URL: http://www.open-mpi.org/projects/hwloc/

6.3. NetLoc

Network Locality
KEYWORDS: Topology - Locality - Distributed networks - HPC - Parallel computing - MPI communication
FUNCTIONAL DESCRIPTION: netloc (Network Locality) is a library that extends hwloc to network topology information by assembling hwloc knowledge of server internals within graphs of inter-node fabrics such as Infiniband, Intel OmniPath or Cray networks.

Netloc builds a software representation of the entire cluster so as to help applications properly place their tasks on the nodes. It may also help communication libraries optimize their strategies according to the wires and switches.

Netloc targets the same challenges as hwloc but focuses on a wider spectrum by enabling cluster-wide solutions such as process placement. It interoperates with the Scotch graph partitioner to do so.

Netloc is distributed within hwloc releases starting with hwloc 2.0.

- Participants: Brice Goglin, Clement Foyer and Cyril Bordage
- Contact: Brice Goglin
- Publications: netloc: Towards a Comprehensive View of the HPC System Topology - Netloc: a Tool for Topology-Aware Process Mapping
- URL: http://www.open-mpi.org/projects/netloc/

6.4. NewMadeleine

NewMadeleine: An Optimizing Communication Library for High-Performance Networks
KEYWORDS: High-performance calculation - MPI communication
FUNCTIONAL DESCRIPTION: NewMadeleine is the fourth incarnation of the Madeleine communication library. The new architecture aims at enabling the use of a much wider range of communication flow optimization techniques. Its design is entirely modular: drivers and optimization strategies are dynamically loadable software components, allowing experimentations with multiple approaches or on multiple issues with regard to processing communication flows.

The optimizing scheduler SchedOpt targets applications with irregular, multi-flow communication schemes such as found in the increasingly common application conglomerates made of multiple programming environments and coupled pieces of code, for instance. SchedOpt itself is easily extensible through the concepts of optimization strategies (what to optimize for, what the optimization goal is) expressed in terms of tactics (how to optimize to reach the optimization goal). Tactics themselves are made of basic communication flows operations such as packet merging or reordering.

The communication library is fully multi-threaded through its close integration with PIOMan. It manages concurrent communication operations from multiple libraries and from multiple threads. Its MPI implementation MadMPI fully supports the MPI_THREAD_MULTIPLE multi-threading level.

- Participants: Alexandre Denis, Clement Foyer, Nathalie Furmento, Raymond Namyst and ADRIEN GUILBAUD
- Contact: Alexandre Denis
- Publications: NewMadeleine: a Fast Communication Scheduling Engine for High Performance Networks - Ordonnancement et qualité de service pour réseaux rapides - Improving Reactivity and Communication Overlap in MPI using a Generic I/O Manager - PIOMan : un gestionnaire d'entrées-sorties générique - A multithreaded communication engine for multicore architectures - A multicore-enabled multirail communication engine - About the interactions between communication and thread scheduling in clusters of multicore machines - An analysis of the impact of multi-threading on communication performance - A scalable and generic task scheduling system for communication libraries - A Generic and High Performance Approach for Fault Tolerance in Communication Library - A High-Performance Superpipeline Protocol for InfiniBand - A sampling-based approach for communication libraries auto-tuning - High performance checksum computation for fault-tolerant MPI over InfiniBand - pioman: a Generic Framework for Asynchronous Progression and Multithreaded Communications - pioman: a pthread-based Multithreaded Communication Engine - Updating MadMPI to MPI-3: Remote Memory Access - Portage de StarPU sur la bibliothèque de communication NewMadeleine
- URL: http://pm2.gforge.inria.fr/newmadeleine/

6.5. PaMPA

Parallel Mesh Partitioning and Adaptation

KEYWORDS: Dynamic load balancing - Unstructured heterogeneous meshes - Parallel remeshing - Subdomain decomposition - Parallel numerical solvers

SCIENTIFIC DESCRIPTION: PaMPA is a parallel library for handling, redistributing and remeshing unstructured meshes on distributed-memory architectures. PaMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes. It provides solver writers with a distributed mesh abstraction and an API to: - describe unstructured and possibly heterogeneous meshes, on the form of a graph of interconnected entities of different kinds (e.g. elements, faces, edges, nodes), - attach values to the mesh entities, - distribute such meshes across processing elements, with an overlap of variable width, - perform synchronous or asynchronous data exchanges of values across processing elements, - describe numerical schemes by means of iterators over mesh entities and their connected neighbors of a given kind, - redistribute meshes so as to balance computational load, - perform parallel dynamic remeshing, by applying adequately a user-provided sequential remesher to relevant areas of the distributed mesh.

PaMPA runs concurrently multiple sequential remeshing tasks to perform dynamic parallel remeshing and redistribution of very large unstructured meshes. E.g., it can remesh a tetrahedral mesh from 43Melements to more than 1Belements on 280 Broadwell processors in 20 minutes.

FUNCTIONAL DESCRIPTION: Parallel library for handling, redistributing and remeshing unstructured, heterogeneous meshes on distributed-memory architectures. PaMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes.

NEWS OF THE YEAR: PaMPA has been used to remesh an industrial mesh of a helicopter turbine combustion chamber, up to more than 1 billion elements.

- Participants: Cécile Dobrzynski, Cedric Lachat and François Pellegrini
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: François Pellegrini
- URL: http://project.inria.fr/pampa/

6.6. TreeMatch

KEYWORDS: Intensive parallel computing - High-Performance Computing - Hierarchical architecture - Placement

SCIENTIFIC DESCRIPTION: TreeMatch embeds a set of algorithms to map processors/cores in order to minimize the communication cost of the application.

Important features are : the number of processors can be greater than the number of applications processes , it assumes that the topology is a tree and does not require valuation of the topology (e.g. communication speeds) , it implements different placement algorithms that are switched according to the input size.

Some core algorithms are parallel to speed-up the execution. Optionally embeds scotch for fix-vertex mapping. enable exhaustive search if required. Several metric mapping are computed. Allow for oversubscribing of ressources. multithreaded.

TreeMatch is integrated into various software such as the Charm++ programming environment as well as in both major open-source MPI implementations: Open MPI and MPICH2.
FUNCTIONAL DESCRIPTION: TreeMatch is a library for performing process placement based on the topology of the machine and the communication pattern of the application.

- Participants: Adele Villiermet, Emmanuel Jeannot, François Tessier, Guillaume Mercier and Pierre Celor
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: Emmanuel Jeannot
- URL: http://treematch.gforge.inria.fr/

6.7. SCOTCH

KEYWORDS: Mesh partitioning - Domain decomposition - Graph algorithmics - High-performance calculation - Sparse matrix ordering - Static mapping

FUNCTIONAL DESCRIPTION: Scotch is a graph partitioner. It helps optimise the division of a problem, by means of a graph, into a set of independent sub-problems of equivalent sizes. These sub-problems can also be solved in parallel.

RELEASE FUNCTIONAL DESCRIPTION: Version 6.0 offers many new features:

sequential graph repartitioning

sequential graph partitioning with fixed vertices

sequential graph repartitioning with fixed vertices

new, fast, direct k-way partitioning and mapping algorithms

multi-threaded, shared memory algorithms in the (formerly) sequential part of the library

exposure in the API of many centralized and distributed graph handling routines

embedded pseudo-random generator for improved reproducibility and even more...

- Participants: François Pellegrini, Sébastien Fourestier, Jun-Ho Her and Cédric Chevalier
- Partners: Université de Bordeaux - IPB - CNRS - Region Aquitaine
- Contact: François Pellegrini
- Publications: Process Mapping onto Complex Architectures and Partitions Thereof - Multi-criteria Graph Partitioning with Scotch - Adaptation au repartitionnement de graphes d'une méthode d'optimisation globale par diffusion - Contributions au partitionnement de graphes parallèle multi-niveaux - A parallelisable multi-level banded diffusion scheme for computing balanced partitions with smooth boundaries - PT-Scotch: A tool for efficient parallel graph ordering - Design and implementation of efficient tools for parallel partitioning and distribution of very large numerical problems - Improvement of the Efficiency of Genetic Algorithms for Scalable Parallel Graph Partitioning in a Multi-Level Framework - PT-Scotch : Un outil pour la renumérotation parallèle efficace de grands graphes dans un contexte multi-niveaux - PT-Scotch: A tool for efficient parallel graph ordering
- URL: http://www.labri.fr/~pelegrin/scotch/

6.8. disk-revolve

KEYWORDS: Automatic differentiation - Gradients - Machine learning

FUNCTIONAL DESCRIPTION: This software provides several algorithms (Disk-Revolve, 1D-Revolve, Periodic-Disk-Revolve,...) computing the optimal checkpointing strategy when executing a adjoin chain with limited memory. The considered architecture has a level of limited memory that is free to access (writing and reading costs are negligible) and a level of unlimited memory with non-negligible access costs. The algorithms describe which data should be saved in the memory to minimize the number of re-computation during the execution.

- Authors: Guillaume Aupy and Julien Herrmann
- Contact: JULIEN HERRMANN
- Publications: Periodicity in optimal hierarchical checkpointing schemes for adjoint computations - Optimal Multistage Algorithm for Adjoint Computation
- URL: https://gitlab.inria.fr/adjoint-computation/disk-revolve-public

WHISPER Project-Team

6. New Software and Platforms

6.1. Coccinelle

KEYWORDS: Code quality - Evolution - Infrastructure software
FUNCTIONAL DESCRIPTION: Coccinelle is a tool for code search and transformation for C programs. It has been extensively used for bug finding and evolutions in Linux kernel code.

- Participants: Gilles Muller, Julia Lawall, Nicolas Palix, Rene Rydhof Hansen and Thierry Martinez
- Partners: LIP6 - IRILL
- Contact: Julia Lawall
- URL: http://coccinelle.lip6.fr

6.2. Prequel

KEYWORDS: Code search - Git
SCIENTIFIC DESCRIPTION: The commit history of a code base such as the Linux kernel is a gold mine of information on how evolutions should be made, how bugs should be fixed, etc. Nevertheless, the high volume of commits available and the rudimentary filtering tools provided mean that it is often necessary to wade through a lot of irrelevant information before finding example commits that can help with a specific software development problem. To address this issue, we propose Prequel (Patch Query Language), which brings the descriptive power of code matching to the problem of querying a commit history.
FUNCTIONAL DESCRIPTION: Prequel is a tool for searching for complex patterns in the commits of software managed using git.

- Participants: Gilles Muller and Julia Lawall
- Partners: LIP6 - IRILL
- Contact: Julia Lawall
- URL: http://prequel-pql.gforge.inria.fr/

6.3. Usuba

KEYWORDS: Cryptography - Optimizing compiler - Synchorous language
FUNCTIONAL DESCRIPTION: Usuba is a programming language for specifying block ciphers as well as a bitslicing compiler, for producing high-throughput and secure code.

- Contact: Pierre-Evariste Dagand
- Publication: Usuba, Optimizing & Trustworthy Bitslicing Compiler
- URL: https://github.com/DadaIsCrazy/usuba/

WIDE Project-Team

5. New Software and Platforms

5.1. WebGC

Web-based Gossip Communication
KEYWORDS: Epidemic protocols - Gossip protocols - Peer-to-peer - Web - Personalized systems - Decentralized architectures - Recommendation systems - WebRTC - Decentralized web
SCIENTIFIC DESCRIPTION: The library currently includes the implementation of two peer sampling protocols, Cyclon and the generic peer-sampling protocol from, as well as a clustering protocol. All protocols implement a common GossipProtocol "interface"
FUNCTIONAL DESCRIPTION: WebGC consists of a WebRTC-based library that supports gossip-based communication between web browsers and enables them to operate with Node-JS applications. WebGC comprises the implementation of standard gossip protocols such as Peer Sampling or Clustering, and simplifies the development of new protocols. It comprises a decentralized signaling service that makes it easier to build completely decentralized browser-based applications.

- Participants: Anne-Marie Kermarrec, Davide Frey, Matthieu Simonin and Raziel Carvajal Gomez
- Contact: Davide Frey

5.2. YALPS

KEYWORDS: Traffic-shaping - Nat traversal - Experimentation - Peer-to-peer - Simulator - Deployment
FUNCTIONAL DESCRIPTION: YALPS is an open-source Java library designed to facilitate the development, deployment, and testing of distributed applications. Applications written using YALPS can be run both in simulation and in real-world mode without changing a line of code or even recompiling the sources. A simple change in a configuration file will load the application in the proper environment. A number of features make YALPS useful both for the design and evaluation of research prototypes and for the development of applications to be released to the public. Specifically, YALPS makes it possible to run the same application as a simulation or in a real deployment. Applications communicate by means of application-defined messages which are then routed either through UDP/TCP or through YALPS's simulation infrastructure. In both cases, YALPS's communication layer offers features for testing and evaluating distributed protocols and applications. Communication channels can be tuned to incorporate message losses or to constrain their outgoing bandwidth. Finally, YALPS includes facilities to support operation in the presence of NATs and firewalls using relaying and NAT-traversal techniques. The implementation of YALPS includes approximately 16K lines of code, and is used in several projects by ASAP, including HEAP, AllYours-P2P, and Behave.

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

5.3. KIFF

KIFF: An impressively fast and efficient JAVA library for KNN construction
KEYWORD: KNN
FUNCTIONAL DESCRIPTION: This package implements the KIFF algorithm reported in [1]. KIFF is a generic, fast and scalable K-Nearest-Neighbor graph construction algorithm. This algorithm connects each object to its k most similar counterparts, according to a given similarity metric. In term of comparison, this package implements also HYREC [2] and NN-DESCENT [3]. The standalone program implements cosine similarity only, however this library supports arbitrary similarity measures.

[1] Antoine Boutet, Anne-Marie Kermarrec, Nupur Mittal, Francois Taiani. Being prepared in a sparse world: the case of KNN graph construction. ICDE 2016, Finland.

- Partner: LIRIS
- Contact: Antoine Boutet

ALICE Project-Team

6. New Software and Platforms

6.1. Graphite

Graphite: The Numerical Geometry Workbench
KEYWORDS: 3D modeling - Numerical Geometry - Texturing - Lighting - CAD - Visualization
SCIENTIFIC DESCRIPTION: Graphite is an experimental 3D modeler, built on top of the Geogram programming library. It has data structures and efficient OpenGL visualization for pointsets, surfacic meshes (triangles and polygons), volumetric meshes (tetrahedra and hybrid meshes). It has state-of-the-art mesh repair, remeshing, reconstruction algorithms. It also has an interface to the Tetgen tetrahedral mesh generator (by Hang Si). This year, Graphite3 was released. It is a major rewrite, based on Geogram, with increased software quality standards (zero warnings on all platforms, systematic documentation of all classes / all functions / all parameters, dramatically improved performances). It embeds Geogram (and optionally Vorpaline) with an easy-to-use Graphic User Interface.
FUNCTIONAL DESCRIPTION: Graphite is a dedicated software platform in numerical geometry that enables, among other things, 3D modelling and texture baking.

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

6.2. GEOGRAM

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

- Participant: Bruno Lévy
- Contact: Bruno Lévy
- URL: http://alice.loria.fr

6.3. OpenNL

Open Numerical Library
KEYWORDS: 3D modeling - Numerical algorithm
FUNCTIONAL DESCRIPTION: Open Numerical Library is a library for solving sparse linear systems, especially designed for the Computer Graphics community. The goal for OpenNL is to be as small as possible, while offering the subset of functionalities required by this application field. The Makefiles of OpenNL can generate a single .c + .h file, very easy to integrate in other projects. The distribution includes an implementation of the Least Squares Conformal Maps parameterization method.

RELEASE FUNCTIONAL DESCRIPTION: Latest version available as part of GEOGRAM:
∗ OpenMP parallel solver
∗ more compact data structures, X2 acceleration

∗ SuperLU weak coupling (dynamically loads SuperLU .so if available)

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

6.4. IceSL

KEYWORD: Additive manufacturing
FUNCTIONAL DESCRIPTION: IceSL allows to model complex shapes through CSG boolean operations. Objects can be directly prepared and sent to a 3d printer for fabrication, without the need to compute an intermediate 3D mesh.

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

6.5. LibSL

Simple Library For Graphics
KEYWORDS: 3D - Graphics
FUNCTIONAL DESCRIPTION: LibSL is a toolbox for rapid prototyping of computer graphics algorithms, under both OpenGL, DirectX 9 - 10, Windows and Linux.

- Participant: Sylvain Lefebvre
- Contact: Sylvain Lefebvre

6.6. 3DPrintScaffoldings

KEYWORDS: 3D - 3D modeling - Additive manufacturing
FUNCTIONAL DESCRIPTION: Support generation for additive manufacturing. Optimizes scaffolding made of vertical pillars and horizontal bars that are optimized to use minimal material, be easily removed and support the part at all stages of the fabrication process.

- Participants: Jean Hergel, Jérémie Dumas and Sylvain Lefebvre
- Partner: Université de Lorraine
- Contact: Sylvain Lefebvre
- URL: http://shapeforge.loria.fr/icesl/

6.7. VORPALINE

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

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

ALMAnaCH Team

5. New Software and Platforms

5.1. Enqi

- Author: Benoît Sagot
- Contact: Benoît Sagot

5.2. SYNTAX

KEYWORD: Parsing
FUNCTIONAL DESCRIPTION: Syntax system includes various deterministic and non-deterministic CFG parser generators. It includes in particular an efficient implementation of the Earley algorithm, with many original optimizations, that is used in several of Alpage's NLP tools, including the pre-processing chain Sx Pipe and the LFG deep parser SxLfg . This implementation of the Earley algorithm has been recently extended to handle probabilistic CFG (PCFG), by taking into account probabilities both during parsing (beam) and after parsing (n-best computation).

- Participants: Benoît Sagot and Pierre Boullier
- Contact: Pierre Boullier
- URL: http://syntax.gforge.inria.fr/

5.3. FRMG

KEYWORDS: Parsing - French
FUNCTIONAL DESCRIPTION: FRMG is a large-coverage linguistic meta-grammar of French. It can be compiled (using MGCOMP) into a Tree Adjoining Grammar, which, in turn, can be compiled (using DyALog) into a parser for French.

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

5.4. MElt

Maximum-Entropy lexicon-aware tagger
KEYWORD: Part-of-speech tagger
FUNCTIONAL DESCRIPTION: MElt is a freely available (LGPL) state-of-the-art sequence labeller that is meant to be trained on both an annotated corpus and an external lexicon. It was developed by Pascal Denis and Benoît Sagot within the Alpage team, a joint Inria and Université Paris-Diderot team in Paris, France. MElt allows for using multiclass Maximum-Entropy Markov models (MEMMs) or multiclass perceptrons (multitrons) as underlying statistical devices. Its output is in the Brown format (one sentence per line, each sentence being a space-separated sequence of annotated words in the word/tag format).

MElt has been trained on various annotated corpora, using Alexina lexicons as source of lexical information. As a result, models for French, English, Spanish and Italian are included in the MElt package.

MElt also includes a normalization wrapper aimed at helping processing noisy text, such as user-generated data retrieved on the web. This wrapper is only available for French and English. It was used for parsing web data for both English and French, respectively during the SANCL shared task (Google Web Bank) and for developing the French Social Media Bank (Facebook, twitter and blog data).

- Contact: Benoît Sagot
- URL: https://team.inria.fr/almanach/melt/

5.5. dyalog-sr

KEYWORDS: Parsing - Deep learning - Natural language processing
FUNCTIONAL DESCRIPTION: DyALog-SR is a transition-based dependency parser, built on top of DyALog system. Parsing relies on dynamic programming techniques to handle beams. Supervised learning exploit a perceptron and aggressive early updates. DyALog-SR can handle word lattice and produce dependency graphs (instead of basic trees). It was tested during several shared tasks (SPMRL'2013 and SEMEVAL'2014). It achieves very good accuracy on French TreeBank, alone or by coupling with FRMG parser. In 2017, DyALog-SR has been extended into DyALog-SRNN by adding deep neuronal layers implemented with the Dynet library. The new version has participated to the evaluation campaigns CONLL UD 2017 (on more than 50 languages) and EPE 2017.

- Contact: Éric De La Clergerie

5.6. Crapbank

French Social Media Bank
KEYWORDS: Treebank - User-generated content
FUNCTIONAL DESCRIPTION: The French Social Media Bank is a treebank of French sentences coming from various social media sources (Twitter(c), Facebook(c)) and web forums (JeuxVidéos.com(c), Doctissimo.fr(c)). It contains different kind of linguistic annotations: - part-of-speech tags - surface syntactic representations (phrase-based representations) as well as normalized form whenever necessary.

- Contact: Djamé Seddah

5.7. DyALog

KEYWORD: Logic programming
FUNCTIONAL DESCRIPTION: DyALog provides an environment to compile and execute grammars and logic programs. It is essentially based on the notion of tabulation, i.e. of sharing computations by tabulating traces of them. DyALog is mainly used to build parsers for Natural Language Processing (NLP). It may nevertheless be used as a replacement for traditional PROLOG systems in the context of highly ambiguous applications where sub-computations can be shared.

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

5.8. SxPipe

KEYWORD: Surface text processing
SCIENTIFIC DESCRIPTION: Developed for French and for other languages, Sx Pipe includes, among others, various named entities recognition modules in raw text, a sentence segmenter and tokenizer, a spelling corrector and compound words recognizer, and an original context-free patterns recognizer, used by several specialized grammars (numbers, impersonal constructions, quotations...). It can now be augmented with modules developed during the former ANR EDyLex project for analysing unknown words, this involves in particular (i) new tools for the automatic pre-classification of unknown words (acronyms, loan words...) (ii) new morphological analysis tools, most notably automatic tools for constructional morphology (both derivational and compositional), following the results of dedicated corpus-based studies. New local grammars for detecting new types of entities and improvement of existing ones, developed in the context of the PACTE project, will soon be integrated within the standard configuration.

FUNCTIONAL DESCRIPTION: SxPipe is a modular and customizable processing chain dedicated to applying to raw corpora a cascade of surface processing steps (tokenisation, wordform detection, non-deterministic spelling correction…). It is used as a preliminary step before ALMAnaCH's parsers (e.g., FRMG) and for surface processing (named entities recognition, text normalization, unknown word extraction and processing...).

- Participants: Benoît Sagot, Djamé Seddah and Éric Villemonte De La Clergerie
- Contact: Benoît Sagot
- URL: http://lingwb.gforge.inria.fr/

5.9. Mgwiki

KEYWORDS: Parsing - French
FUNCTIONAL DESCRIPTION: Mgwiki is a linguistic wiki that may used to discuss linguistic phenomena with the possibility to add annotated illustrative sentences. The work is essentially devoted to the construction of an instance for documenting and discussing FRMG, with the annotations of the sentences automatically provided by parsing them with FRMG. This instance also offers the possibility to parse small corpora with FRMG and an interface of visualization of the results. Large parsed corpora (like French Wikipedia or Wikisource) are also available. The parsed corpora can also be queried through the use of the DPath language.

- Participant: Éric Villemonte De La Clergerie
- Contact: Éric Villemonte De La Clergerie
- URL: http://alpage.inria.fr/frmgwiki/

5.10. WOLF

WOrdnet Libre du Français (Free French Wordnet)
KEYWORDS: WordNet - French - Semantic network - Lexical resource
FUNCTIONAL DESCRIPTION: The WOLF (Wordnet Libre du Français, Free French Wordnet) is a free semantic lexical resource (wordnet) for French.

The WOLF has been built from the Princeton WordNet (PWN) and various multilingual resources.

- Contact: Benoît Sagot
- URL: http://alpage.inria.fr/~sagot/wolf-en.html

5.11. vera

KEYWORD: Text mining
FUNCTIONAL DESCRIPTION: Automatic analysis of answers to open-ended questions based on NLP and statistical analysis and visualisation techniques (vera is currently restricted to employee surveys).

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

5.12. Alexina

Atelier pour les LEXiques INformatiques et leur Acquisition
KEYWORD: Lexical resource
FUNCTIONAL DESCRIPTION: Alexina is ALMAnaCH's framework for the acquisition and modeling of morphological and syntactic lexical information. The first and most advanced lexical resource developed in this framework is the Lefff, a morphological and syntactic lexicon for French.

- Participant: Benoît Sagot
- Contact: Benoît Sagot
- URL: http://gforge.inria.fr/projects/alexina/

5.13. FQB

French QuestionBank
KEYWORD: Treebank
FUNCTIONAL DESCRIPTION: The French QuestionBanks is a corpus of around 2000 questions coming from various domains (TREC data set, French governmental organisation, NGOs, etc..) it contains different kind of annotations - morpho-syntactic ones (POS, lemmas) - surface syntaxe (phrase based and dependency structures) with long-distance dependency annotations.

The TREC part is aligned with the English QuestionBank (Judge et al, 2006).

- Contact: Djamé Seddah

5.14. Sequoia corpus

KEYWORD: Treebank
FUNCTIONAL DESCRIPTION: The Sequoia corpus contains French sentences, annotated with various linguistic information: - parts-of-speech - surface syntactic representations (both constituency trees and dependency trees) - deep syntactic representations (which are deep syntactic dependency graphs)

- Contact: Djamé Seddah

AUCTUS Team

6. New Software and Platforms

6.1. HuMoSoft

Human Motion Analysis Software
KEYWORDS: Movement analysis - 3D movement
FUNCTIONAL DESCRIPTION: HuMoSoft is based on the ROS platform. The acquisition data can come from different depth sensors, for example Kinect, via the Nuitrack JDK. An extended Kalman filter has been implemented, and motion analysis uses the RULA method.

- Authors: Jessica Colombel and David Daney
- Contact: Sylvain Pion
- URL: https://gitlab.inria.fr/auctus/kombos-server

AVIZ Project-Team

5. New Software and Platforms

5.1. Cartolabe

KEYWORD: Information visualization
FUNCTIONAL DESCRIPTION: The goal of Cartolabe is to build a visual map representing the scientific activity of an institution/university/domain from published articles and reports. Using the HAL Database and building upon the AnHALytics processing chain, Cartolabe provides the user with a map of the thematics, authors and articles and their dynamics along time. ML techniques are used for dimensionality reduction, cluster and topics identification, visualisation techniques are used for a scalable 2D representation of the results.
NEWS OF THE YEAR: Improvement of the graphical interface

- Contact: Philippe Caillou
- URL: http://cartolabe.lri.fr/

5.2. BitConduite

BitConduite Bitcoin explorer
KEYWORDS: Data visualization - Clustering - Financial analysis - Cryptocurrency
FUNCTIONAL DESCRIPTION: BitConduite is a web-based visual tool that allows for a high level explorative analysis of the Bitcoin blockchain. It offers a data transformation back end that gives us an entity-based access to the blockchain data and a visualization front end that supports a novel high-level view on transactions over time. In particular, it facilitates the exploration of activity through filtering and clustering interactions. This gives analysts a new perspective on the data stored on the blockchain.

- Contact: Petra Isenberg

CEDAR Project-Team

6. New Software and Platforms

6.1. Tatooine

KEYWORDS: RDF - JSon - Knowledge database - Databases - Data integration - Polystore
FUNCTIONAL DESCRIPTION: Tatooine allows to jointly query data sources of heterogeneous formats and data models (relations, RDF graphs, JSON documents etc.) under a single interface. It is capable of evaluating conjunctive queries over several such data sources, distributing computations between the underlying single-data model systems and a Java-based integration layer based on nested tuples.

- Participants: François Goasdoué, Ioana Manolescu, Javier Letelier Ruiz, Michaël Thomazo, Oscar Santiago Mendoza Rivera, Raphael Bonaque, Swen Ribeiro, Tien Duc Cao and Xavier Tannier
- Contact: Ioana Manolescu

6.2. AIDES

KEYWORDS: Data Exploration - Active Learning
FUNCTIONAL DESCRIPTION: AIDES is a data exploration software. It allows a user to explore a huge (tabular) dataset and discover tuples matching his or her interest. Our system repeatedly proposes the most informative tuples to the user, who must annotate them as “interesting” / “not-interesting”, and as iterations progress an increasingly accurate model of the user’s interest region is built. Our system also focuses on supporting low selectivity, high-dimensional interest regions.

- Contact: Yanlei Diao

6.3. OntoSQL

KEYWORDS: RDF - Semantic Web - Querying - Databases
FUNCTIONAL DESCRIPTION: OntoSQL is a tool providing three main functionalities: - Loading RDF graphs (consisting of data triples and possibly a schema or ontology) into a relational database, - Saturating the data based on the ontology. Currently, RDF Schema ontologies are supported. - Querying the loaded data using conjunctive queries. Data can be loaded either from distinct files or from a single file containing them both. The loading process allows to choose between two storage schemas: - One triples table. - One table per role and concept. Querying provides an SQL translation for each conjunctive query according to the storage schema used in the loading process, then the SQL query is evaluated by the underlying relational database.

- Participants: Ioana Manolescu, Michaël Thomazo and Tayeb Merabti
- Partner: Université de Rennes 1
- Contact: Ioana Manolescu
- URL: https://ontosql.inria.fr/

6.4. ConnectionLens

KEYWORDS: Data management - Big data - Information extraction - Semantic Web

FUNCTIONAL DESCRIPTION: ConnectionLens treats a set of heterogeneous, independently authored data sources as a single virtual graph, whereas nodes represent fine-granularity data items (relational tuples, attributes, key-value pairs, RDF, JSON or XML nodes…) and edges correspond either to structural connections (e.g., a tuple is in a database, an attribute is in a tuple, a JSON node has a parent…) or to similarity (sameAs) links. To further enrich the content journalists work with, we also apply entity extraction which enables to detect the people, organizations etc. mentioned in text, whether full-text or text snippets found e.g. in RDF or XML. ConnectionLens is thus capable of finding and exploiting connections present across heterogeneous data sources without requiring the user to specify any join predicate.

- Contact: Manolescu Ioana
- Publication: ConnectionLens: Finding Connections Across Heterogeneous Data Sources

6.5. INSEE-Extract

Spreadsheets extractor
KEYWORDS: RDF - Data extraction
FUNCTIONAL DESCRIPTION: Extract content of spreadsheets automatically and store it as RDF triples

- Participants: Ioana Manolescu, Xavier Tannier and Tien Duc Cao
- Contact: Tien Duc Cao
- Publication: Extracting Linked Data from statistic spreadsheets
- URL: https://gitlab.inria.fr/cedar/excel-extractor

6.6. INSEE-Search

KEYWORDS: Document ranking - RDF
FUNCTIONAL DESCRIPTION: Searching for relevant data cells (or data row/column) given a query in natural language (French)

- Participants: Ioana Manolescu, Xavier Tannier and Tien Duc Cao
- Contact: Tien Duc Cao
- Publications: Extracting Linked Data from statistic spreadsheets - Searching for Truth in a Database of Statistics

6.7. RDFQuotient

Quotient summaries of RDF graphs
KEYWORDS: RDF - Graph algorithmics - Graph visualization - Graph summaries - Semantic Web
FUNCTIONAL DESCRIPTION: RDF graphs can be large and heterogeneous, making it hard for users to get acquainted with a new graph and understand whether it may have interesting information. To help users figure it out, we have devised novel equivalence relations among RDF nodes, capable of recognizing them as equivalent (and thus, summarize them together) despite the heterogeneity often exhibited by their incoming and outgoing node properties. From these relations, we derive four novel summaries, called Weak, Strong, Typed Weak and Typed Strong, and show how to obtain from them compact and enticing visualizations.

- Partner: Université de Rennes 1
- Contact: Manolescu Ioana
- Publications: Compact Summaries of Rich Heterogeneous Graphs - Structural Summarization of Semantic Graphs

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 managment 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. Therefoe 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

Simultion 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 Philppe 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

COML Team

5. New Software and Platforms

5.1. abkhazia

KEYWORDS: Speech recognition - Speech-text alignment
FUNCTIONAL DESCRIPTION: The Abkhazia sofware makes it easy to obtain simple baselines for supervised ASR (using Kaldi) and ABX tasks (using ABXpy) on the large corpora of speech recordings typically used in speech engineering, linguistics or cognitive science research.

- Contact: Emmanuel Dupoux
- URL: https://github.com/bootphon/abkhazia

5.2. TDE

Term Discovery Evaluation
KEYWORDS: NLP - Speech recognition - Speech
SCIENTIFIC DESCRIPTION: This toolbox allows the user to judge of the quality of a word discovery algorithm. It evaluates the algorithms on these criteria : - Boundary : efficiency of the algorithm to found the actual boundaries of the words - Group : efficiency of the algorithm to group similar words - Token/Type: efficiency of the algorithm to find all words from the corpus (types), and to find all occurences (token) of these words. - NED : Mean of the edit distance across all the word pairs found by the algorithm - Coverage : efficiency of the algorithm to find every discoverable phone in the corpus
FUNCTIONAL DESCRIPTION: Toolbox to evaluate algorithms that segment speech into words. It allows the user to evaluate the efficiency of algorithms to segment speech into words, and create clusters of similar words.

- Contact: Emmanuel Dupoux
- URL: https://github.com/bootphon/TDE

5.3. ABXpy

KEYWORDS: Evaluation - Speech recognition - Machine learning
FUNCTIONAL DESCRIPTION: The ABX package gives a performance score to speech recognition systems by measuring their capacity to discriminate linguistic contrasts (accents, phonemes, speakers, etc...)

- Contact: Emmanuel Dupoux
- URL: https://github.com/bootphon/ABXpy

5.4. h5features

KEYWORD: File format
FUNCTIONAL DESCRIPTION: The h5features python package provides easy to use and efficient storage of large features data on the HDF5 binary file format.

- Contact: Emmanuel Dupoux
- URL: https://github.com/bootphon/h5features

DEFROST Project-Team

6. New Software and Platforms

6.1. SOFA

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

- Participants: Christian Duriez, François Faure, Hervé Delingette and Stéphane Cotin
- Partner: IGG
- Contact: Stéphane Cotin
- URL: http://www.sofa-framework.org

6.2. SoftRobots

SoftRobots plugin for Sofa
KEYWORDS: Numerical simulations - Problem inverse - Soft robotics
FUNCTIONAL DESCRIPTION: This plugin allows the modeling of deformable robots in the Sofa platform. It allows the modeling of different actuators, such as cable, pneumatic pressure, hydraulics and other simpler types of actuation. It also contains useful tools for animation design or communication with the robot. Coupled with the SoftRobots.Inverse plugin, it also allows the control of these robots. More information can be found on the dedicated website https://project.inria.fr/softrobot/.

- Participants: Christian Duriez, Olivier Goury, Jérémie Dequidt, Damien Marchal, Eulalie Coevoet, Erwan Douaille and Félix Vanneste
- Contact: Christian Duriez
- URL: https://project.inria.fr/softrobot/

6.3. Model Order Reduction Plugin for SOFA

KEYWORDS: Model Order Reduction - Sofa - Finite element modelling
SCIENTIFIC DESCRIPTION: This plugin allows speed-up of SOFA simulations by providing tools to create a reduced version of the SOFA simulation that runs at much higher rates but remains accurate. Starting with a snapshot of the object deformations on a high-dimensional Finite Element mesh, Proper Orthogonal Decomposition (POD) is used to compute a reduced basis of small dimension representing correctly all the possible deformations of the object. The original system describing the object motion is then greatly reduced. To keep numerical efficiency, a hyper-reduction method is used to speed-up the construction of the reduced system.

FUNCTIONAL DESCRIPTION: This plugin allows to dramatically reduce computational time in mechanical simulation in the SOFA framework. A reduced simulation, of much smaller dimension but still accurate is created in an automatic way by the plugin. Building the reduced model may take time, but this operation is made once only. The user can then benefit from a reduced and interactive version of his/her simulation without significant loss of accuracy.

RELEASE FUNCTIONAL DESCRIPTION: This is the first version of the plugin.
NEWS OF THE YEAR: Publication using this plugin accepted dans IEEE Transactions on Robotics

- Participants: Olivier Goury, Félix Vanneste, Christian Duriez and Eulalie Coevoet
- Contact: Olivier Goury
- Publication: Fast, generic and reliable control and simulation of soft robots using model order reduction
- URL: https://project.inria.fr/modelorderreduction/

6.4. SoftRobots.Inverse

KEYWORDS: Sofa - SoftRobots
FUNCTIONAL DESCRIPTION: This plugin builds on the plugin SoftRobots (https://project.inria.fr/softrobot/). Inside the plugin, there is some constraint components that are used to describe the robot (effectors, actuators, sensors). An optimisation algorithm is provided to find the efforts to put on actuators in order to place the robot in a the closest possible configuration than the one described by "effectors", or to a state described by "sensors". This method used to control the soft-robots in the task space is patented.

- Partners: CNRS - Université de Lille - Ecole Centrale de Lille
- Contact: Christian Duriez
- URL: https://project.inria.fr/softrobot.inverse

EX-SITU Project-Team

6. New Software and Platforms

6.1. Platforms

6.1.1. WildOS

Participant: Michel Beaudouin-Lafon [correspondant].

WildOS is middleware designed to support applications that run in an interactive room, such as our WILD and WILDER rooms, with various interaction resources, including a tiled wall display, a motion tracking system, interactive tabletops, tablets, smartphones and custom-made or 3d printed interactive devices. The conceptual model of WildOS is a *platform*, such as the WILD or WILDER room, that can be described as a set of devices on which one or more applications can be run.

WildOS consists of a server running on a machine that has network access to all the machines involved in the platform, and a set of clients running on the various interaction resources, such as a display cluster or a tablet. Once *WildOS* is running, applications can be started and stopped and devices can be added to or removed from the platform.

WildOS relies on Web technologies, most notably Javascript and node.js, as well as node-webkit and HTML5. This makes it inherently portable (it is currently tested on Mac OS X and Linux). While applications can be developed only with these Web technologies, it is also possible to bridge to existing applications developed in other environments if they provide sufficient access for remote control. Sample applications include a web browser, an image viewer, a window manager, and the BrainTwister application developed in collaboration with neuroanatomists at NeuroSpin.

WildOS is used for several research projects at ExSitu and by other partners of the Digiscope project. It was also deployed on several of Google's interactive rooms in Mountain View, Dublin and Paris. It is available under on Open Source licence at https://bitbucket.org/mblinsitu/wildos.

- ACM: H.5.2 [User Interfaces]: Graphical user interfaces (GUI)
- Software benefit: helps development of multisurface applications.
- OS/Middleware: Crossplatform
- Required library or software: node.js, node-webkit
- Programming language: Javascript

6.1.2. Unity Cluster

Participants: Cédric Fleury [correspondant], Olivier Gladin [SED-SAC].

Unity Cluster is middleware to distribute any Unity 3D (https://unity3d.com/) application on a cluster of computers that run in interactive rooms, such as our WILD and WILDER rooms, or immersive CAVES (Computer-Augmented Virtual Environments). Users can interact the the application with various interaction resources.

Unity Cluster provides an easy solution for running existing Unity 3D applications on any display that requires a rendering cluster with several computers. *Unity Cluster* is based on a master-slave architecture: The master computer runs the main application and the physical simulation as well as manages the input; the slave computers receive updates from the master and render small parts of the 3D scene. *Unity Cluster* manages data distribution and synchronization among the computers to obtain a consistent image on the entire wall-sized display surface.

Unity Cluster can also deform the displayed images according to the user's position in order to match the viewing frustum defined by the user's head and the four corners of the screens. This respects the motion parallax of the 3D scene, giving users a better sense of depth.

Unity Cluster is composed of a set of C Sharp scripts that manage the network connection, data distribution, and the deformation of the viewing frustum. In order to distribute an existing application on the rendering cluster, all scripts must be embedded into a Unity package that is included in an existing Unity project.

- ACM: C.2.4 [Distributed Systems]: Distributed applications, I.3.7 [3D Graphics and Realism]: Virtual reality
- Software benefit: adapts existing Unity 3D application to a rendering cluster of an interactive room.
- OS/Middleware: Crossplatform
- Required library or software: Unity 3D
- Programming language: C Sharp

6.1.3. WILDER

Participants: Michel Beaudouin-Lafon [correspondant], Cédric Fleury, Olivier Gladin.

WILDER (Figure 1) is our second experimental ultra-high-resolution interactive environment, which follows the WILD platform developed in 2009. It features a wall-sized display with seventy-five 20" LCD screens, i.e. a 5m50 x 1m80 (18’ x 6’) wall displaying 14 400 x 4 800 = 69 million pixels, powered by a 10-computer cluster and two front-end computers. The platform also features a camera-based motion tracking system that lets users interact with the wall, as well as the surrounding space, with various mobile devices. The display uses a multitouch frame (the largest of its kind in the world) to make the entire wall touch sensitive.

WILDER was inaugurated in June, 2015. It is one of the ten platforms of the Digiscope Equipment of Excellence and, in combination with WILD and the other Digiscope rooms, provides a unique experimental environment for collaborative interaction.

In addition to using WILD and WILDER for our research, we have also developed software architectures and toolkits, such as WildOS and Unity Cluster, that enable developers to run applications on these multi-device, cluster-based systems.

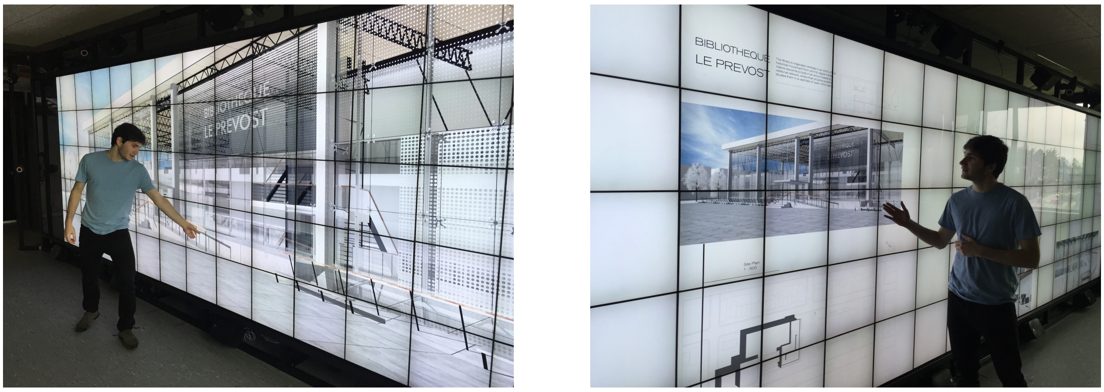


Figure 1. The WILDER platform.

FLOWERS Project-Team

6. New Software and Platforms

6.1. 3rd hand infrastructure

KEYWORDS: Interaction - Robotics - Infrastructure software - Framework - Robot Operating System (ROS)
FUNCTIONAL DESCRIPTION: The infrastructure is predicate-based to handle relational actions and covers perception (scene description generation, human actions recognition), decision making (teleoperated, scripted or learning from demonstrations), interaction with end users (GUI, voice, gestures) and parallel executions of robotic actions (hold, pick, grasp, bring, ...).

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

6.2. Aversive++

FUNCTIONAL DESCRIPTION: Aversive++ is a C++ library that eases micro-controller programming. Its aim is to provide an interface simple enough to be able to create complex applications, and optimized enough to enable small micro-controllers to execute these applications. The other aspect of this library is to be multiplatform. Indeed, it is designed to provide the same API for a simulator (named SASIAE) and for AVR-based and ARM-based micro-controllers.

- Contact: Loïc Dauphin
- URL: https://github.com/AversivePlusPlus

6.3. DMP-BBO

Black-Box Optimization for Dynamic Movement Primitives
KEYWORD: -
FUNCTIONAL DESCRIPTION: The DMP-BBO Matlab library is a direct consequence of the insight that black-box optimization outperforms reinforcement learning when using policies represented as Dynamic Movement Primitives. It implements several variants of the PIBB algorithm for direct policy search. The dmp-bbo C++ library has been extended to include the “unified model for regression”. The implementation of several of the function approximators have been made real-time compatible.

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

6.4. Explauto

an autonomous exploration library
KEYWORD: Exploration

SCIENTIFIC DESCRIPTION: An important challenge in developmental robotics is how robots can be intrinsically motivated to learn efficiently parametrized policies to solve parametrized multi-task reinforcement learning problems, i.e. learn the mappings between the actions and the problem they solve, or sensory effects they produce. This can be a robot learning how arm movements make physical objects move, or how movements of a virtual vocal tract modulates vocalization sounds. The way the robot will collects its own sensorimotor experience have a strong impact on learning efficiency because for most robotic systems the involved spaces are high dimensional, the mapping between them is non-linear and redundant, and there is limited time allowed for learning. If robots explore the world in an unorganized manner, e.g. randomly, learning algorithms will be often ineffective because very sparse data points will be collected. Data are precious due to the high dimensionality and the limited time, whereas data are not equally useful due to non-linearity and redundancy. This is why learning has to be guided using efficient exploration strategies, allowing the robot to actively drive its own interaction with the environment in order to gather maximally informative data to optimize the parametrized policies. In the recent year, work in developmental learning has explored various families of algorithmic principles which allow the efficient guiding of learning and exploration.

Explauto is a framework developed to study, model and simulate curiosity-driven learning and exploration in real and simulated robotic agents. Explauto's scientific roots trace back from Intelligent Adaptive Curiosity algorithmic architecture [122], which has been extended to a more general family of autonomous exploration architectures by [1] and recently expressed as a compact and unified formalism [113]. The library is detailed in [114]. In Explauto, interest models are implementing the strategies of active selection of particular problems / goals in a parametrized multi-task reinforcement learning setup to efficiently learn parametrized policies. The agent can have different available strategies, parametrized problems, models, sources of information, or learning mechanisms (for instance imitate by mimicking vs by emulation, or asking help to one teacher or to another), and chooses between them in order to optimize learning (a processus called strategic learning [118]). Given a set of parametrized problems, a particular exploration strategy is to randomly draw goals/ RL problems to solve in the motor or problem space. More efficient strategies are based on the active choice of learning experiments that maximize learning progress using bandit algorithms, e.g. maximizing improvement of predictions or of competences to solve RL problems [122]. This automatically drives the system to explore and learn first easy skills, and then explore skills of progressively increasing complexity. Both random and learning progress strategies can act either on the motor or on the problem space, resulting in motor babbling or goal babbling strategies.

- Motor babbling consists in sampling commands in the motor space according to a given strategy (random or learning progress), predicting the expected effect, executing the command through the environment and observing the actual effect. Both the parametrized policies and interest models are finally updated according to this experience.
- Goal babbling consists in sampling goals in the problem space and to use the current policies to infer a motor action supposed to solve the problem (inverse prediction). The robot/agent then executes the command through the environment and observes the actual effect. Both the parametrized policies and interest models are finally updated according to this experience.It has been shown that this second strategy allows a progressive solving of problems much more uniformly in the problem space than with a motor babbling strategy, where the agent samples directly in the motor space [1].

FUNCTIONAL DESCRIPTION: This library provides high-level API for an easy definition of:

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

The library comes with several built-in environments. Two of them corresponds to simulated environments: a multi-DoF arm acting on a 2D plan, and an under-actuated torque-controlled pendulum. The third one allows to control real robots based on Dynamixel actuators using the Pypot library. Learning parametrized policies involves machine learning algorithms, which are typically regression algorithms to learn forward models,

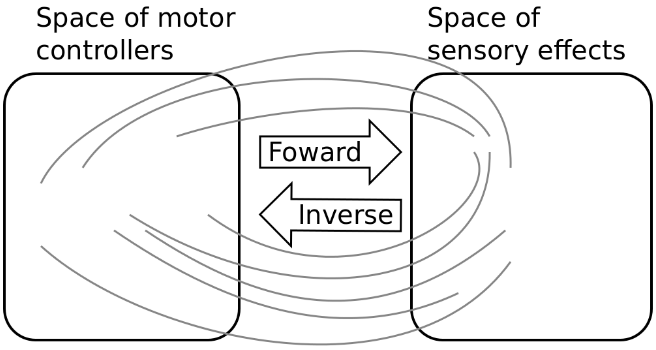


Figure 1. Complex parametrized policies involve high dimensional action and effect spaces. For the sake of visualization, the motor M and sensory S spaces are only 2D each in this example. The relationship between M and S is non-linear, dividing the sensorimotor space into regions of unequal stability: small regions of S can be reached very precisely by large regions of M, or large regions in S can be very sensitive to variations in M.: s as well as a non-linear and redundant relationship. This non-linearity can imply redundancy, where the same sensory effect can be attained using distinct regions in M.

from motor controllers to sensory effects, and optimization algorithms to learn inverse models, from sensory effects, or problems, to the motor programs allowing to reach them. We call these sensorimotor learning algorithms sensorimotor models. The library comes with several built-in sensorimotor models: simple nearest-neighbor look-up, non-parametric models combining classical regressions and optimization algorithms, online mixtures of Gaussians, and discrete Lidstone distributions. Explauto sensorimotor models are online learning algorithms, i.e. they are trained iteratively during the interaction of the robot in theenvironment in which it evolves. Explauto provides also a unified interface to define exploration strategies using the InterestModel class. The library comes with two built-in interest models: random sampling as well as sampling maximizing the learning progress in forward or inverse predictions.

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

This library has been used in many experiments including:

- the control of a 2D simulated arm,
- the exploration of the inverse kinematics of a poppy humanoid (both on the real robot and on the simulated version),
- acoustic model of a vocal tract.

Explauto is crossed-platform and has been tested on Linux, Windows and Mac OS. It has been released under the GPLv3 license.

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

6.5. HiPi Board

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

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

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

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

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

6.6. IKPy

Inverse Kinematics Python Library

FUNCTIONAL DESCRIPTION: IKPy is a Python Inverse Kinematics library, designed to be simple to use and extend. It provides Forward and Inverse kinematics functionality, bundled with helper tools such as 3D plotting of the kinematics chains. Being written entirely in Python, IKPy is lightweight and is based on numpy and scipy for fast optimization. IKPy is compatible with many robots, by automatically parsing URDF files. It also supports other (such as DH-parameters) and custom representations. Moreover, it provides a framework to easily implement new Inverse Kinematics strategies. Originally developed for the Poppy project, it can also be used as a standalone library.

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

6.7. KERAS-QR

KERAS with Quick Reset

KEYWORDS: Library - Deep learning

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

6.8. KidBreath

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

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

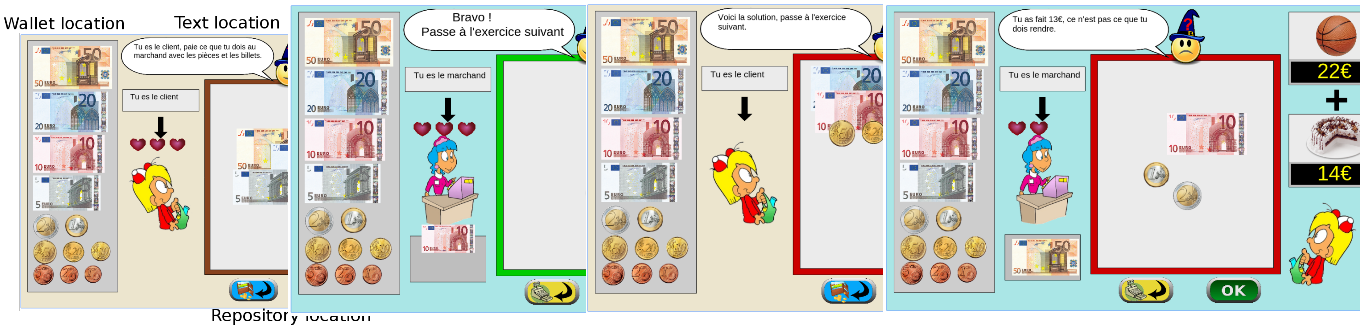


Figure 2. Four principal regions are defined in the graphical interface. The first is the wallet location where users can pick and drag the money items and drop them on the repository location to compose the correct price. The object and the price are present in the object location. Four different types of exercises exist: M : customer/one object, R : merchant/one object, MM : customer/two objects, RM : merchant/two objects.

6.9. Kidlearn: money game application

FUNCTIONAL DESCRIPTION: The games is instantiated in a browser environment where students are proposed exercises in the form of money/token games (see Figure 2). For an exercise type, one object is presented with a given tagged price and the learner has to choose which combination of bank notes, coins or abstract tokens need to be taken from the wallet to buy the object, with various constraints depending on exercises parameters. The games have been developed using web technologies, HTML5, javascript and Django.

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

6.10. Kidlearn: script for Kidbreath use

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

Github link to explanation about it : https://github.com/flowersteam/kidlearn/.

- Contact: Benjamin Clement
- URL: https://github.com/flowersteam/kidlearn/

6.11. KidLearn

KEYWORD: Automatic Learning
FUNCTIONAL DESCRIPTION: KidLearn is a software which adaptively personalize sequences of learning activities to the particularities of each individual student. It aims at proposing to the student the right activity at the right time, maximizing concurrently his learning progress and its motivation.

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

6.12. Kinect 2 Server

Kinect 2 server
KEYWORDS: Depth Perception - Speech recognition - Gesture recognition - Kinect
FUNCTIONAL DESCRIPTION: The server written in C# uses the Kinect SDK v2 to get the RGBD raw image, skeleton tracking information, recognized speech. It also uses the text-to-speech from Microsoft. Then it streams JSON data over the network using the Publisher/Subscriber pattern from the ZeroMQ network library. A Linux client has been written in Python but it can be written in any other language that is compatible with ZeroMQ. Features are controllable through a Graphical User Interface on Windows, or through the code from any Linux/Windows client. The clients can for instance enable features (speech recognition on, skeleton tracking off, . . .) and parameters (set new speech to recognize, change language, . . .) from remote.

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

6.13. Multimodal

FUNCTIONAL DESCRIPTION: The python code provides a minimum set of tools and associated libraries to reproduce the experiments in [98] , together with the choreography datasets. The code is primarily intended for reproduction of the mulimodal learning experiment mentioned above. It has already been reused in several experimentations by other member of the team and is expected to play an important role in further collaborations. It is also expected that the public availability of the code encourages further experimentation by other scientists with data coming from other domains, thus increasing both the impact of the aforementioned publication and the knowledge on the algorithm behaviors.

- Participant: Olivier Mangin
- Contact: Olivier Mangin
- URL: https://github.com/omangin/multimodal

6.14. OptiTrack

FUNCTIONAL DESCRIPTION: This python library allows you to connect to an OptiTrack from NaturalPoint. This camera permits the tracking of 3D markers efficiently and robustly. With this library, you can connect to the Motive software used by the OptiTrack and retrieve the 3D position and orientation of all your tracked markers directly from python.

- Participant: Pierre Rouanet
- Contact: Pierre Rouanet
- URL: http://www.optitrack.com/

6.15. Pixl Board

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

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

The board is used in the Poppy Ergo Jr robot.

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

6.16. Poppy

FUNCTIONAL DESCRIPTION: The Poppy Project team develops open-source 3D printed robots platforms based on robust, flexible, easy-to-use and reproduce hardware and software. In particular, the use of 3D printing and rapid prototyping technologies is a central aspect of this project, and makes it easy and fast not only to reproduce the platform, but also to explore morphological variants. Poppy targets three domains of use: science, education and art.

In the Poppy project we are working on the Poppy System which is a new modular and open-source robotic architecture. It is designed to help people create and build custom robots. It permits, in a similar approach as Lego, building robots or smart objects using standardized elements.

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

- Unified mechanical interfaces, simplifying the assembly process and the design of 3D printable parts.
- Unified communication between elements using the same connector and bus for each module.
- Unified software, making it easy to program each module independently.

Our ambition is to create an ecosystem around this system so communities can develop custom modules, following the Poppy System standards, which can be compatible with all other Poppy robots.

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

6.17. Poppy Ergo Jr

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

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

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

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

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

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

6.18. Poppy Ergo Jr Installer

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

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

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

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

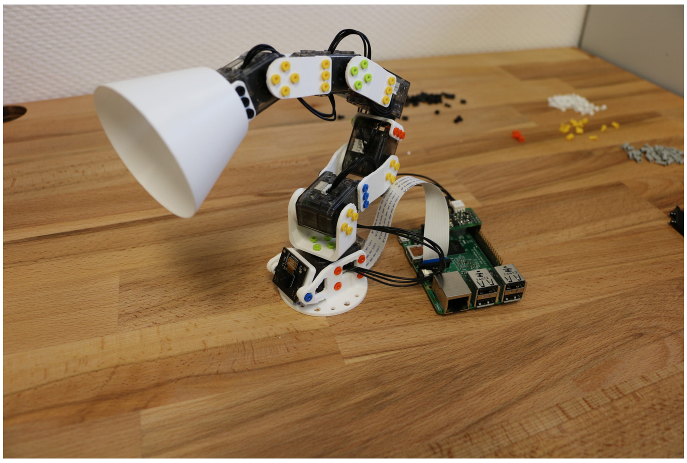


Figure 3. Poppy Ergo Jr, 6-DoFs arm robot for education

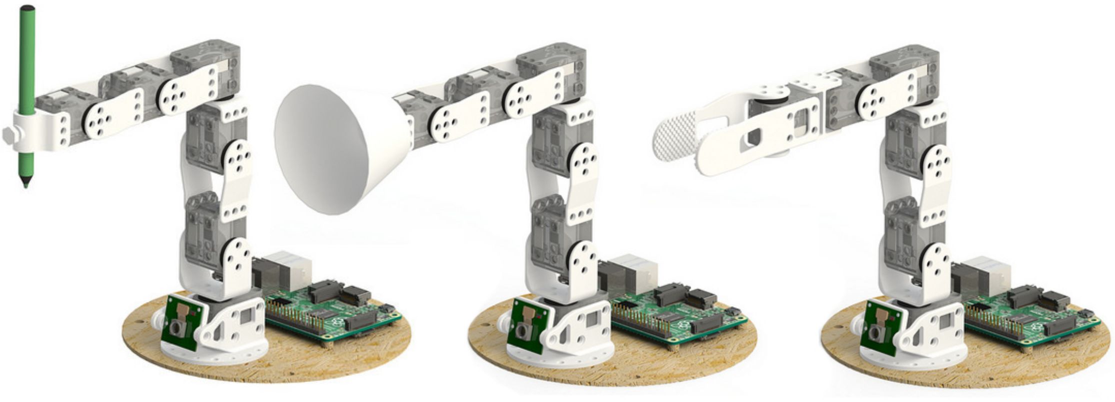


Figure 4. The available Ergo Jr tools: a pen holder, a lampshade and a gripper

6.19. Poppy Ergo Jr Simulator

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

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

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

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

6.20. ProMP

Probabilistic Movement Primitives
KEYWORDS: Interaction - Robotics - Probability - Motion model - Robot Operating System (ROS)
FUNCTIONAL DESCRIPTION: Joint-space primitives with a task-space constraint: The primitives are stored in joint-space but demonstrations are provided both in joint space and task space, context. Thanks to this context, task-space goals can be requested to these joint-space primitives. The benefit is that requesting a new task-space goal does not require to call an IK method which would return demonstrations-agnostic joint configurations.

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

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

6.21. PyPot

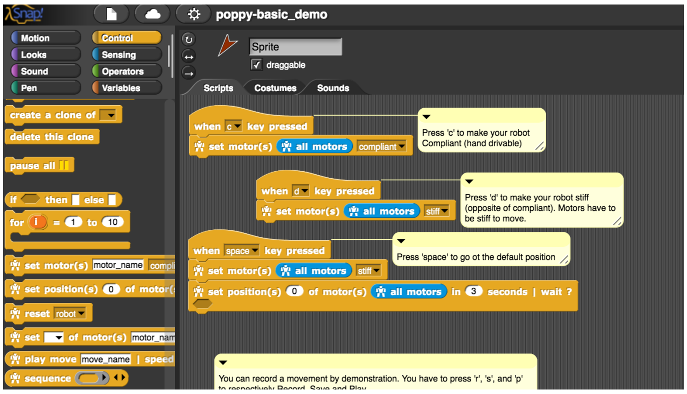
SCIENTIFIC DESCRIPTION: Pypot is a framework developed to make it easy and fast to control custom robots based on Dynamixel motors. This framework provides different levels of abstraction corresponding to different types of use. Pypot can be used to:

- control Robotis motors through a USB2serial device,
- define the structure of a custom robot and control it through high-level commands,
- define primitives and easily combine them to create complex behavior.

Pypot is part of the Poppy project. It is the core library used by the Poppy robots. This abstraction layer allows to seamlessly switch from a given Poppy robot to another. It also provides a common set of tools, such as forward and inverse kinematics, simple computer vision, recording and replaying moves, or easy access to the autonomous exploration library Explauto.

To extend pypot application domains and connection to outside world, it also provides an HTTP API. On top of providing an easy way to connect to smart sensors or connected devices, it is notably used to connect to Snap!, a variant of the well-known Scratch visual programming language.

FUNCTIONAL DESCRIPTION: Pypot is entirely written in Python to allow for fast development, easy deployment and quick scripting by non-expert developers. It can also benefit from the scientific and machine learning libraries existing in Python. The serial communication is handled through the standard library and offers high performance (10ms sensorimotor loop) for common Poppy uses. It is cross-platform and has been tested on Linux, Windows and Mac OS.



```
when c key pressed
set motor(s) all motors compliant

when d key pressed
set motor(s) all motors stiff

when space key pressed
set motor(s) all motors stiff
set position(s) 0 of motor(s) all motors in 3 seconds | wait ?
```

Press 'c' to make your robot Compliant (hand drivable)

Press 'd' to make your robot stiff (opposite of compliant). Motors have to be stiff to move.

Press 'space' to go ot the default position

You can record a movement by demonstration. You have to press 'r', 's', and 'p'

Figure 5. Example of using pypot to program a robot to reproduce a drawn shape

Pypot is also compatible with the V-REP simulator. This allows the transparent switch from a real robot to its simulated equivalent with a single code base.

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

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

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

Thanks to the Snap! HTTP block, a connection can be made to pypot allowing users to directly control robots through their visual interfaces. A set of dedicated Snap! blocks have been designed, such as *set motor position* or *get motor temperature*. Thanks to the Snap! HTTP block, users can control robots through this visual interfaces connecting to Pypot. A set of dedicated Snap! blocks has been designed, such as *set motor position* or *get motor temperature*.

Snap! is also used as a tool to program the robot by demonstration. Using the *record* and *play* blocks, users can easily trigger kinesthetic recording of the whole robot or only a specific subpart, such as an arm. These records can then be played or "mixed" - either played in sequence or simultaneously - with other recordings to compose complex choreographies. The moves are encoded as a model of mixture of gaussians (GMM) which allows the definition of clean mathematical operators for combining them.

This recording tool has been developed and used in collaboration with artists who show interest in the concept of robotic moves.

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

6.22. PyQMC

Python library for Quasi-Metric Control

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

Figure 6. Using Snap! to program a robot by demonstration and create complex choreographies

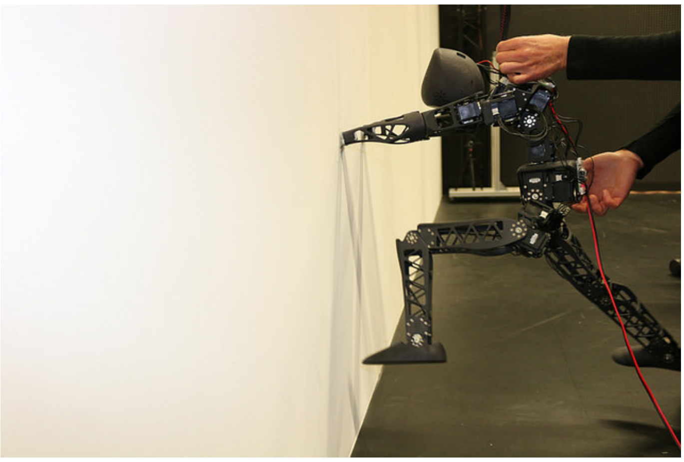


Figure 7. Artistic project exploring the concept of robotic move.

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

6.23. ROS Optitrack Publisher

KEYWORDS: Target tracking - Robot Operating System (ROS)
FUNCTIONAL DESCRIPTION: This package allows to publish optitrack markers declared as rigid bodies as TF transforms. Data is gathered through the embedded VRPN server of Motive/Arena. Only rigid bodies are requested to the server, thus single points in 2D/3D are ignored. VRPN server can be enable in View > Data streaming in Motive.

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

6.24. ThifloNet

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

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

By using this combination of systems, the architecture as a whole requires significantly fewer data samples than other systems (which exclusively utilize neural networks). This makes the approach more feasible to real-life applciation with actual live demonstration.
FUNCTIONAL DESCRIPTION: The neural network consists of ResNet-50 (the currently best-performing computer vision system), with 50 layers, 2 layers for converting the output of ResNet to predicates and a varying amount of output neurons, corresponding to the estimated number of n-arity predicates. The network was pretrained on the ImageNet dataset. The policy learning module incorporates the ACE tree learning tool and a wrapper in Prolog.

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

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

6.25. S-RL Toolbox

Reinforcement Learning (RL) and State Representation Learning (SRL) for Robotics
KEYWORDS: Machine learning - Robotics

FUNCTIONAL DESCRIPTION: This repository was made to evaluate State Representation Learning methods using Reinforcement Learning. It integrates (automatic logging, plotting, saving, loading of trained agent) various RL algorithms (PPO, A2C, ARS, ACKTR, DDPG, DQN, ACER, CMA-ES, SAC, TRPO) along with different SRL methods (see SRL Repo) in an efficient way (1 Million steps in 1 Hour with 8-core cpu and 1 Titan X GPU).

- Partner: ENSTA
- Contact: David Filliat
- URL: https://github.com/araffin/robotics-rl-srl

6.26. Sets

KEYWORD: Data structures
FUNCTIONAL DESCRIPTION: The sets library allow to manipulate and operate on sets.

Those can be simple sets: + Empty: + Singleton: ’a’ + Finite: ’a’, ’b’ + Integer subset: |[1, 10]| + Reals subset: [1, inf[Or, they can be cartesian product of sets: + ’a’, ’b’ x |[0, 10]| x]-inf, inf[Or, they can be incomplete unions of sets: + ’a’,’b’ x |[0, 5]| U ’c’ x -|[0, 10]|

In particular, every set is hashable. This operation is non-trivial in the case of an incomplete union (equivalent to an orthogonal polyhedron). An extreme vertices representations, corresponding to the state-of-the-art, is used to implement it.

Various operations are available: + Product (Cartesian) + Measure + Partition + Belonging test + Subset test (Proper) + Equality test + Union + Intersection + Exclusion

- Contact: Alexandre Pere

6.27. Deep-Explauto

KEYWORDS: Deep learning - Unsupervised learning - Learning - Experimentation
FUNCTIONAL DESCRIPTION: Until recently, curiosity driven exploration algorithms were based on classic learning algorithms, unable to handle large dimensional problems (see explauto). Recent advances in the field of deep learning offer new algorithms able to handle such situations.

Deep explauto is an experimental library, containing reference implementations of curiosity driven exploration algorithms. Given the experimental aspect of exploration algorithms, and the low maturity of the libraries and algorithms using deep learning, proposing black-box implementations of those algorithms, enabling a blind use of those, seem unrealistic.

Nevertheless, in order to quickly launch new experiments, this library offers an set of objects, functions and examples, allowing to kickstart new experiments.

- Contact: Alexandre Pere

6.28. Orchestra

KEYWORD: Experimental mechanics
FUNCTIONAL DESCRIPTION: Ochestra is a set of tools meant to help in performing experimental campaigns in computer science. It provides you with simple tools to:

+ Organize a manual experimental workflow, leveraging git and lfs through a simple interface. + Collaborate with other peoples on a single experimental campaign. + Execute pieces of code on remote hosts such as clusters or clouds, in one line. + Automate the execution of batches of experiments and the presentation of the results through a clean web ui.

A lot of advanced tools exists on the net to handle similar situations. Most of them target very complicated workflows, e.g. DAGs of tasks. Those tools are very powerful but lack the simplicity needed by newcomers. Here, we propose a limited but very simple tool to handle one of the most common situation of experimental campaigns: the repeated execution of an experiment on variations of parameters.

In particular, we include three tools: + expegit: a tool to organize your experimental campaign results in a git repository using git-lfs (large file storage). + runaway: a tool to execute code on distant hosts parameterized with easy to use file templates. + orchestra: a tool to automate the use of the two previous tools on large campaigns.

- Contact: Alexandre Pere

GRAPHDECO Project-Team

5. New Software and Platforms

5.1. SGTDGP

Synthetic Ground Truth Data Generation Platform

KEYWORD: Graphics

FUNCTIONAL DESCRIPTION: The goal of this platform is to render large numbers of realistic synthetic images for use as ground truth to compare and validate image-based rendering algorithms and also to train deep neural networks developed in our team.

This pipeline consists of tree major elements that are:

- Scene exporter
- Assisted point of view generation
- Distributed rendering on Inria's high performance computing cluster

The scene exporter is able to export scenes created in the widely-used commercial modeler 3DSMAX to the Mitsuba opensource renderer format. It handles the conversion of complex materials and shade trees from 3DSMAX including materials made for VRay. The overall quality of the produced images with exported scenes have been improved thanks to a more accurate material conversion. The initial version of the exporter was extended and improved to provide better stability and to avoid any manual intervention.

From each scene we can generate a large number of images by placing multiple cameras. Most of the time those points of view has to be placed with a certain coherency. This task could be long and tedious. In the context of image-based rendering, cameras have to be placed in a row with a specific spacing. To simplify this process we have developed a set of tools to assist the placement of hundreds of cameras along a path.

The rendering is made with the open source renderer Mitsuba. The rendering pipeline is optimised to render a large number of point of view for single scene. We use a path tracing algorithm to simulate the light interaction in the scene and produce hight dynamic range images. It produces realistic images but it is computationally demanding. To speed up the process we setup an architecture that takes advantage of the Inria cluster to distribute the rendering on hundreds of CPUs cores.

The scene data (geometry, textures, materials) and the cameras are automatically transfered to remote workers and HDR images are returned to the user.

We already use this pipeline to export tens of scenes and to generate several thousands of images, which have been used for machine learning and for ground-truth image production.

We have recently integrated the platform with the SIBR software library, allowing us to read mitsuba scenes. We have written a tool to allow camera placement to be used for rendering and for reconstruction of synthetic scenes, including alignment of the exact and reconstructed version of the scenes. This dual-representation scenes can be used for learning and as ground truth. We can also perform various operations on the ground truth data within SIBR, e.g., compute shadow maps of both exact and reconstructed representations etc.

- Contact: George Drettakis

5.2. Unity IBR

KEYWORD: Graphics

FUNCTIONAL DESCRIPTION: Unity IBR (for Image-Based Rendering in Unity) This is a software module that proceeds the development of IBR algorithms in Unity. In this case, algorithms are developed for the context of EMOTIVE EU project. The rendering technique was changed during the year to evaluate and compare which one produces better results suitable for Game Development with Unity (improvement of image quality and faster rendering). New features were also added such as rendering of bigger datasets and some debugging utilities. Software was also updated to keep compatibility with new released versions of Unity game engine. In addition, in order to develop a demo showcasing the technology, a multiplayer VR scene was created proving the integration of IBR with the rest of the engine.

- Contact: George Drettakis

5.3. SIBR

Simple Image-Based Rendering
KEYWORD: Graphics
FUNCTIONAL DESCRIPTION: This is a framework containing libraries and tools used internally for research projects based on Image-Base Rendering. It includes both preprocessing tools (computing data used for rendering) and rendering utilities and serves as the basis for many research projects in the group.

It includes basic support for a large set of computer graphics and computer vision functionalities and includes implementations of several image-based rendering algorithms. The code base has become quite mature and is in the process of being used for tech transfer.

- Contact: George Drettakis

5.4. SynthDraw

KEYWORDS: Non-photorealistic rendering - Vector-based drawing
FUNCTIONAL DESCRIPTION: The SynthDraw library extracts occluding contours and sharp features over a 3D shape, computes all their intersections using a binary space partitionning algorithm, and finally makes a raycast to determine each sub-contour visibility. The resulting lines can then be exported as an SVG file for subsequent processing, for instance to stylize the drawing with different brush strokes. The library can also export various attributes for each line, such as its visibility and type. SynthDraw is based on the geometry processing library libIGL.

RELEASE FUNCTIONAL DESCRIPTION: This first version extracts occluding contours and creases, and computes their visibility with brute-force ray casting.

- Contact: Bastien Wailly

5.5. DeepSketch

KEYWORDS: 3D modeling - Sketching - Deep learning
FUNCTIONAL DESCRIPTION: DeepSketch is a sketch-based modeling system that runs in a web browser. It relies on deep learning to recognize geometric shapes in line drawings. The system follows a client/server architecture, based on the Node.js and WebGL technology. The application's main targets are iPads or Android tablets equipped with a digital pen, but it can also be used on desktop computers.

RELEASE FUNCTIONAL DESCRIPTION: This first version is built around a client/server Node.js application whose job is to transmit a drawing from the client's interface to the server where the deep networks are deployed, then transmit the results back to the client where the final shape is created and rendered in a WebGL 3D scene thanks to the THREE.js JavaScript framework. Moreover, the client is able to perform various camera transformations before drawing an object (change position, rotate in place, scale on place) by interacting with the touch screen. The user also has the ability to draw the shape's shadow to disambiguate depth/height. The deep networks are created, trained and deployed with the Caffe framework.

- Contact: Adrien Bousseau

GRAPHIK Project-Team

6. New Software and Platforms

6.1. Cogui

KEYWORDS: Knowledge database - Ontologies - GUI (Graphical User Interface)
SCIENTIFIC DESCRIPTION: Cogui is a visual tool for building and verifying graphical knowledge bases (KB). Knowledge bases are represented under graphical form (close to conceptual graphs). There is a complete correspondence with the logical existential rule (or Datalog+) framework.
FUNCTIONAL DESCRIPTION: Cogui is a freeware written in Java. It allows to graphically create a KB, to handle its structure and content, and to control it. Currently, it supports Conceptual Graphs and import/export in RDFS and Datalog+. Wizards allow to analyze and check facts with respect to some constraints, as well as to query them while taking into account inferences enabled by the ontology.

RELEASE FUNCTIONAL DESCRIPTION: Plugin-extensible architecture, multi-project management, automatic construction of a web documentation of the ontology, adoption of semantic web conventions (IRIs and namespaces), integration of some Graal functionalities (homomorphisms and OWL 2 import), improvement of the import/export between Cogui knowledge bases and Graal dlgp format.
NEWS OF THE YEAR: Release of a new version (V3) resulting from heavy refactoring to benefit from NetBeans plugin-extensible platform architecture and graphical libraries (total replacement of the graphical editors).

This new version requires to completely revise the user documentation, which is in progress.

- Participants: Alain Gutierrez, Michel Chein, Marie-Laure Mugnier, Michel Leclère and Madalina Croitoru
- Partner: LIRMM
- Contact: Michel Chein
- URL: http://www.lirmm.fr/cogui/

6.2. DAGGER

KEYWORDS: Graph algorithmics - Logic programming
FUNCTIONAL DESCRIPTION: We introduce DAGGER: a generator for logic based argumentation frameworks instantiated from inconsistent knowledge bases expressed using Datalog. The tool allows to import a knowledge base in DLGP format and the generation and visualisation of the corresponding argumentation graph. Furthermore, the argumentation framework can also be exported in the Aspartix format.

- Contact: Madalina Croitoru
- URL: http://www.lirmm.fr/~yun/tools.html

6.3. Eldr

Existential Logic for Defeasible Reasoning
KEYWORDS: Knowledge representation - Logic programming
FUNCTIONAL DESCRIPTION: Eldr is an open source defeasible reasoning tool that allows the use of different semantics (ambiguity blocking/propagating with or without team defeat) in order to reason with incoherent or inconsistent knowledge. It allows the reasoning about preferences and their justification between different agents with a final aim of producing justified preferences on different outcomes (alternatives). These preferences are then used with a voting module (given certain voting strategy) to break ties and establish the chosen alternative. It is applied within the GLOPACK and NOAW projects.

- Contact: Madalina Croitoru
- URL: https://github.com/hamhec/graal-elder

6.4. GRAAL

KEYWORDS: Knowledge database - Ontologies - Querying - Data management
SCIENTIFIC DESCRIPTION: Graal is a Java toolkit dedicated to querying knowledge bases within the framework of existential rules, aka Datalog+/-.
FUNCTIONAL DESCRIPTION: Graal has been designed in a modular way, in order to facilitate software reuse and extension. It should make it easy to test new scenarios and techniques, in particular by combining algorithms. The main features of Graal are currently the following: (1) a data layer that provides generic interfaces to store various kinds of data and query them with (union of) conjunctive queries, currently: MySQL, PostgreSQL, Sqlite, in memory graph and linked list structures, (2) an ontological layer, where an ontology is a set of existential rules, (3) a knowledge base layer, where a knowledge base is composed of a fact base (abstraction of the data via generic interfaces) and an ontology, (4) algorithms to process ontology-mediated queries, based on query rewriting and/or forward chaining (or chase), (5) a rule analyzer, which performs a syntactic and structural analysis of an existential rule set, (6) several IO formats, including imports from OWL 2.

RELEASE FUNCTIONAL DESCRIPTION: Version 1.3.0 (2017) fixes some bugs, makes the dlgp parser more flexible (dlgp being our serialization format for existential rules) and improves the efficiency of the forward chaining (chase) algorithms.

Version 1.3.1 (2018) provides minor optimizations and small bug fixes.
NEWS OF THE YEAR: 2018: Version 1.3.1, with small bug fixes and minor improvements. Several new functionalities were developed by internships in 2018 but the code is not integrated to Graal yet. 2017: New stable version (1.3.0) realised. Moreover, Graal website has been deeply restructured and enriched with new tools, available online or for download, and documentation including tutorials, examples of use, and technical documentation about all Graal modules.

- Participants: Marie-Laure Mugnier, Clément Sipieter, Jean-François Baget, Mélanie König, Michel Leclère and Swan Rocher
- Contact: Marie-Laure Mugnier
- Publications: Graal: A Toolkit for Query Answering with Existential Rules - Datalog+, RuleML and OWL 2: Formats and Translations for Existential Rules
- URL: https://github.com/graphik-team

HEPHAISTOS Project-Team

6. New Software and Platforms

6.1. ALIAS

Algorithms Library of Interval Analysis for Systems
FUNCTIONAL DESCRIPTION: The ALIAS library whose development started in 1998, is a collection of procedures based on interval analysis for systems solving and optimization.

ALIAS is made of two parts:

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

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

- Participants: Jean-Pierre Merlet and Odile Pourtallier
- Contact: Jean-Pierre Merlet

6.2. PALGate

KEYWORDS: Health - Home care - Handicap

- Contact: David Daney

6.3. Platforms

6.3.1. ALIAS, Algorithms Library of Interval Analysis for Systems

Participants: Hiparco Lins Vieira, Jean-Pierre Merlet [correspondant], Yves Papegay.

URL: http://www-sop.inria.fr/hephaistos/developpements/main.html

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

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6.3.2. Hardware platforms

We describe here only the new platforms that have been developed or improved in 2018 while we maintain a very large number of platforms (e.g. the cable-driven parallel robots of the MARIONET family, the ANG family of walking aids or our experimental flat).

6.3.2.1. REVMED: virtual reality and rehabilitation

Inria and Université Côte d'Azur have agreed to fund us for developing the platform REVMED whose purpose is to introduce end-user motion and their analysis in a virtual reality environment in order to make rehabilitation exercises more attractive and more appropriate for the rehabilitation process. For example we have developed an active treadmill whose slope change according to the user place in the virtual world while the lateral inclination may be changed in order to regulate the load between the left and right leg. Such a system may be used in rehabilitation to simulate a walk in the mountain while increasing on-demand the load on an injured leg (that is usually avoided by the user) for a shorter rehabilitation time. At the same time the walking pattern is analyzed by using lidar, kinect and distance sensor in order to assess the efficiency of the rehabilitation exercise.

The motion system is composed of two vertical columns whose height may be adjusted (they are used for actuating the treadmill), a 6 d.o.f motion base and a cable-driven parallel robot which may lift the user (in the walking experiment this robot may be used to support partly the user while he is walking allowing frail people to start the rehabilitation earlier). We intend to develop sailing and ski simulators as additional rehabilitation environment. Currently the columns and instrumented treadmill are effective and we have completed at the end of this year the coupling between the subject motion and the 2D visualization of a walk in a nice-looking environment, including basic sound (figure 1). Walking analysis is performed using a lidar, a kinect and a distance sensor at the head of the treadmill.

Figure 1. Our rehabilitation station in a configuration with a treadmill, 2 columns for changing its slope and inclination and lidar and kinect for motion analysis

6.3.2.2. Activities detection platform

For non intrusive activities detection we use low cost distance and motion sensors that are incorporated in a 3D printed box and constitute a detection station. Several such station are implemented at appropriate place in the location that has to be monitored. Currently we have 15 such stations deployed at Valrose EHPAD since end of 2016 and 17 (which amount to 77 different sensors) deployed at Institut Claude Pompidou since the end of 2017.

HYBRID Project-Team

6. New Software and Platforms

6.1. #FIVE

Framework for Interactive Virtual Environments
KEYWORDS: Virtual reality - 3D - 3D interaction - Behavior modeling
SCIENTIFIC DESCRIPTION: #FIVE (Framework for Interactive Virtual Environments) is a framework for the development of interactive and collaborative virtual environments. #FIVE was developed to answer the need for an easier and a faster design and development of virtual reality applications. #FIVE provides a toolkit that simplifies the declaration of possible actions and behaviours of objects in a VE. It also provides a toolkit that facilitates the setting and the management of collaborative interactions in a VE. It is compliant with a distribution of the VE on different setups. It also proposes guidelines to efficiently create a collaborative and interactive VE. The current implementation is in C# and comes with a Unity3D engine integration, compatible with MiddleVR framework.
FUNCTIONAL DESCRIPTION: #FIVE contains software modules that can be interconnected and helps in building interactive and collaborative virtual environments. The user can focus on domain-specific aspects for his/her application (industrial training, medical training, etc) thanks to #FIVE's modules. These modules can be used in a vast range of domains using virtual reality applications and requiring interactive environments and collaboration, such as in training for example.

- Participants: Florian Nouviale, Valérie Gouranton, Bruno Arnaldi, Vincent Goupil, Carl-Johan Jorgensen, Emeric Goga, Adrien Reuzeau and Alexandre Audinot
- Contact: Valérie Gouranton
- Publication: #FIVE : High-Level Components for Developing Collaborative and Interactive Virtual Environments
- URL: https://bil.inria.fr/fr/software/view/2527/tab

6.2. #SEVEN

Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environments
KEYWORDS: Virtual reality - Interactive Scenarios - 3D interaction
SCIENTIFIC DESCRIPTION: #SEVEN (Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environments) is a model and an engine based on petri nets extended with sensors and effectors, enabling the description and execution of complex and interactive scenarios
FUNCTIONAL DESCRIPTION: #SEVEN enables the execution of complex scenarios for driving Virtual Reality applications. #SEVEN's scenarios are based on an enhanced Petri net model which is able to describe and solve intricate event sequences. #SEVEN comes with an editor for creating, editing and remotely controlling and running scenarios. #SEVEN is implemented in C# and can be used as a stand-alone application or as a library. An integration to the Unity3D engine, compatible with MiddleVR, also exists.

- Participants: Florian Nouviale, Valérie Gouranton, Bruno Arnaldi, Vincent Goupil, Emeric Goga, Carl-Johan Jorgensen, Adrien Reuzeau and Alexandre Audinot
- Contact: Valérie Gouranton
- Publications: Versatile Scenario Guidance for Collaborative Virtual Environments - Roles in Collaborative Virtual Environments for Training - Actions sequencing incollaborative virtual environment - Short Paper: #SEVEN, a Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environment
- URL: https://bil.inria.fr/fr/software/view/2528/tab

6.3. OpenVIBE

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

FUNCTIONAL DESCRIPTION: OpenViBE is a free and open-source software platform devoted to the design, test and use of Brain-Computer Interfaces (BCI). The platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. The key features of OpenViBE software are its modularity, its high-performance, its portability, its multiple-users facilities and its connection with high-end/VR displays. The designer of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge under the terms of the AGPL licence, and it was officially released in June 2009. Since then, the OpenViBE software has already been downloaded more than 60000 times, and it is used by numerous laboratories, projects, or individuals worldwide. More information, downloads, tutorials, videos, documentations are available on the OpenViBE website.

- Participants: Cédric Riou, Thierry Gaugry, Anatole Lécuyer, Fabien Lotte, Jussi Tapio Lindgren, Laurent Bougrain, Maureen Clerc and Théodore Papadopoulo
- Partners: INSERM - GIPSA-Lab
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

6.4. Platforms

6.4.1. Platform: Immerstar

- Participants: Florian Nouviale, Ronan Gaugne
- URL: http://www.irisa.fr/immersia/

With the two virtual reality technological platforms Immersia and Immermove, grouped under the name Immerstar, the team has access to high-level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform was granted by an Inria funding for the 2015-2019 period which enables several important evolutions. In particular, in 2018, an haptic system covering the entire volume of the Immersia platform has been installed, allowing various configurations from single haptic device usage to dual haptic devices usage with either one or two users. In addition, a motion platform designed to introduce motion feedback in powered wheelchair simulations has also been incorporated (see Figure 2).

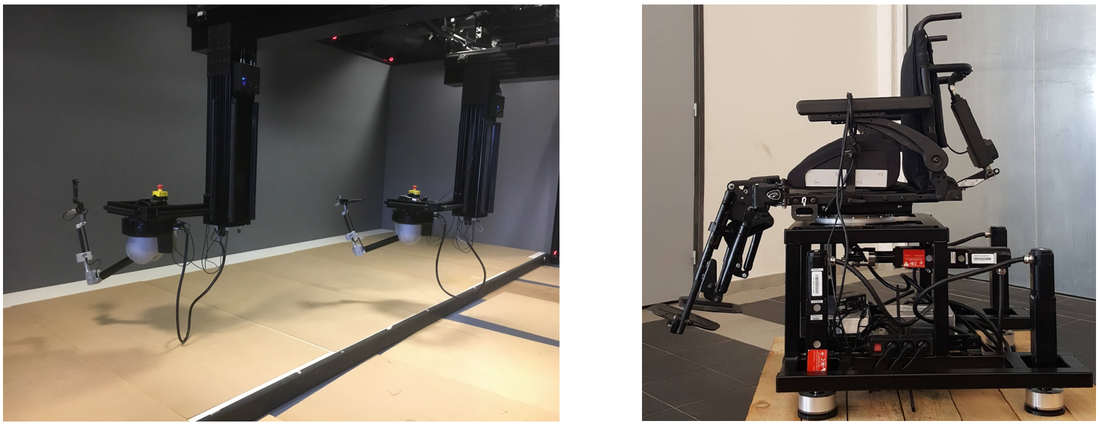


Figure 2. Upgrade of the Immersia platform: two new devices installed. (Left) "Scale-One" Haptic system for one or two users. (Right) Motion platform for powered wheelchair simulation.

ILDA Project-Team

5. New Software and Platforms

5.1. Smarties

FUNCTIONAL DESCRIPTION: The Smarties system provides an easy way to add mobile interactive support to collaborative applications for wall displays.

It consists of (i) a mobile interface that runs on mobile devices for input, (ii) a communication protocol between the mobiles and the wall application, and (iii) libraries that implement the protocol and handle synchronization, locking and input conflicts. The library presents the input as an event loop with callback functions and handles all communication between mobiles and wall application. Developpers can customize the mobile interface from the wall application without modifying the mobile interface code.

On each mobile we find a set of cursor controllers associated with keyboards, widgets and clipboards. These controllers (pucks) can be shared by multiple collaborating users. They can control simple cursors on the wall application, or specific content (objects or groups of them). The developper can decide the types of widgets associated to pucks from the wall application side.

- Contact: Olivier Chapuis
- URL: http://smarties.lri.fr/

5.2. ZVTM

Zoomable Visual Transformation Machine
KEYWORDS: Big data - Visualization - Data visualization - Information visualization - Graph visualization
FUNCTIONAL DESCRIPTION: ZVTM is a toolkit enabling the implementation of multi-scale interfaces for interactively navigating in large datasets displayed as 2D graphics.

ZVTM is used for browsing large databases in multiple domains: geographical information systems, control rooms of complex facilitites, astronomy, power distribution systems.

The toolkit also enables the development of applications running on ultra-high-resolution wall-sized displays.

- Participants: Caroline Appert, Olivier Chapuis and Emmanuel Pietriga
- Contact: Emmanuel Pietriga
- Publications: Rapid Development of User Interfaces on Cluster-Driven Wall Displays with jBricks - A Toolkit for Addressing HCI Issues in Visual Language Environments
- URL: http://zvtm.sf.net

5.3. MapMosaic

KEYWORDS: Geo-visualization - Data visualization
SCIENTIFIC DESCRIPTION: GIS software applications and other mapping tools enable users to correlate data from multiple layers and gain insight from the resulting visualizations. However, most of these applications only feature basic, monolithic layer compositing techniques. These techniques do not always support users effectively in their tasks, as we observed during interviews with GIS experts. MapMosaic is a novel approach based on dynamic visual compositing that enables users to interactively create and manipulate local composites of multiple vector and raster map layers, taking into account the semantics and attribute values of objects and fields in the composit-ing process. We evaluated MapMosaic's interaction model against that of QGIS (a widely-used desktop GIS) and MAPublisher (a professional cartography tool) using the "Cognitive Dimensions" framework and through an analytical comparison, showing that MapMosaic's model is more flexible and can support users more effectively in their tasks.

FUNCTIONAL DESCRIPTION: MapMosaic is a novel approach to combine geographical layers based on dynamic visual compositing that enables users to interactively create and manipulate local composites of multiple vector and raster map layers. It takes into account the semantics and attribute values of objects and fields in the compositing process. MapMosaic aims at better supporting GIS users in their tasks such as correlating data from multiple layers and gaining insight from the resulting visualizations.

RELEASE FUNCTIONAL DESCRIPTION: First public release.

- Participants: Maria Jesus Lobo Gunther, Caroline Appert and Emmanuel Pietriga
- Contact: Emmanuel Pietriga
- Publications: MapMosaic: Dynamic Layer Compositing for Interactive Geovisualization - An Evaluation of Interactive Map Comparison Techniques
- URL: http://ilda.saclay.inria.fr/mapmuxing/mapmosaic/index.html

5.4. Baia

Before-and-after satellite image animation
KEYWORDS: Geo-visualization - 2D animation
SCIENTIFIC DESCRIPTION: Before-and-after image pairs show how entities in a given region have evolved over a specific period of time. Satellite images are a major source of such data, that capture how natural phenomena or human activity impact a geographical area. These images are used both for data analysis and to illustrate the resulting findings to diverse audiences. The simple techniques used to display them, including juxtaposing, swapping and monolithic blending, often fail to convey the underlying phenomenon in a meaningful manner. Baia is a framework to create advanced animated transitions, called animation plans, between before-and-after images. Baia relies on a pixel-based transition model that gives authors much expressive power, while keeping animations for common types of changes easy to create thanks to predefined animation primitives.
FUNCTIONAL DESCRIPTION: Baia is a framework to create advanced animated transitions, called animation plans, between before-and-after satellite images.

Before-and-after image pairs show how entities in a given region have evolved over a specific period of time. Satellite images are a major source of such data, that capture how natural phenomena or human activity impact a geographical area. These images are used both for data analysis and to illustrate the resulting findings to diverse audiences. The simple techniques used to display them, including juxtaposing, swapping and monolithic blending, often fail to convey the underlying phenomenon in a meaningful manner.

Baia relies on a pixel-based transition model that gives authors much expressive power. The animation editor enables authors to easily represent common types of changes thanks to predefined animation primitives and to sequence different changes across time.

RELEASE FUNCTIONAL DESCRIPTION: First public release

- Participants: Maria Jesus Lobo Gunther, Caroline Appert and Emmanuel Pietriga
- Contact: Emmanuel Pietriga
- Publication: Animation Plans for Before-and-After Satellite Images
- URL: http://ilda.saclay.inria.fr/mapmuxing/baia/index.html

5.5. LODAtlas

KEYWORDS: LOD - Linked open data - Semantic Web

SCIENTIFIC DESCRIPTION: The Web of Data is growing fast, as exemplified by the evolution of the Linked Open Data (LOD) cloud over the last ten years. One of the consequences of this growth is that it is becoming increasingly difficult for application developers and end-users to find the datasets that would be relevant to them. Semantic Web search engines, open data catalogs , datasets and frameworks such as LODStats and LOD Laundromat, are all useful but only give partial, even if complementary, views on what datasets are available on the Web. LODAtlas is a portal that enables users to find datasets of interest. Users can make different types of queries about both the datasets' metadata and contents, aggregated from multiple sources. They can then quickly evaluate the matching datasets' relevance, thanks to LODAtlas' summary visualizations of their general metadata, connections and contents.

FUNCTIONAL DESCRIPTION: The Web of Data is growing fast, as exemplified by the evolution of the Linked Open Data (LOD) cloud over the last ten years. One of the consequences of this growth is that it is becoming increasingly difficult for application developers and end-users to find the datasets that would be relevant to them. Semantic Web search engines, open data catalogs, datasets and frameworks such as LODStats and LOD Laundromat, are all useful but only give partial, even if complementary, views on what datasets are available on the Web. LODAtlas is a portal that enables users to find datasets of interest. Users can make different types of queries about both the datasets' metadata and contents, aggregated from multiple sources. They can then quickly evaluate the matching datasets' relevance, thanks to LODAtlas' summary visualizations of their general metadata, connections and contents.

- Participants: Caroline Appert, Marie Destandau, Ioana Manolescu, François Goasdoué, Sejla Cebiric, Hande Gozukan and Emmanuel Pietriga
- Contact: Emmanuel Pietriga
- Publication: Browsing Linked Data Catalogs with LODAtlas
- URL: http://lodatlas.lri.fr

5.6. TouchTokens

KEYWORDS: Tangible interface - HCI

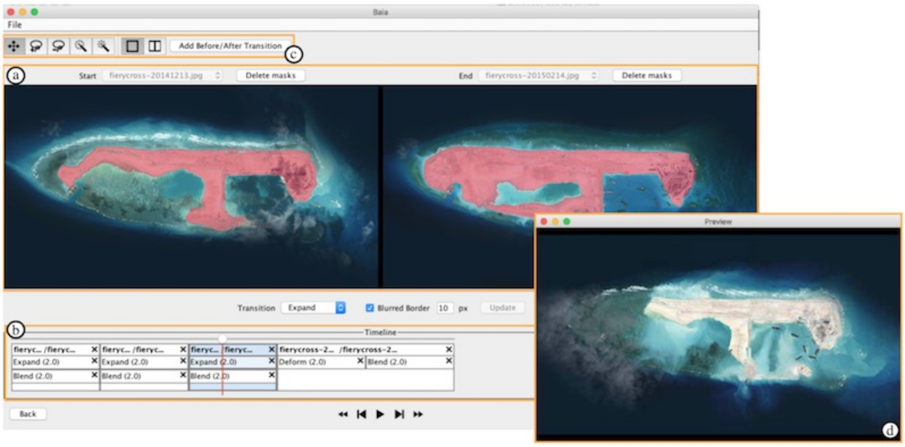
SCIENTIFIC DESCRIPTION: TouchTokens make it possible to easily build interfaces that combine tangible and gestural input using passive tokens and a regular multi-touch surface. The tokens constrain users' grasp, and thus, the relative spatial configuration of fingers on the surface, theoretically making it possible to design algorithms that can recognize the resulting touch patterns. See associated scientific articles below.

FUNCTIONAL DESCRIPTION: TouchTokens allow interface designers to build low-cost tangible interfaces. The technique consists in recognizing multi-touch patterns that are associated with specific passive tokens. Those physical tokens can be made out of any material to get tracked on any touch-sensitive surface. Implementations of the recognizer (in both TUIO and Android) and vector descriptions of the tokens ready for 3D-printing or laser-cutting are available

- Participants: Caroline Appert, Rafael Morales Gonzalez, Emmanuel Pietriga and Gilles Bailly
- Contact: Caroline Appert
- Publications: TouchTokens: Guiding Touch Patterns with Passive Tokens - Passive yet Expressive TouchTokens - Custom-made Tangible Interfaces with TouchTokens
- URL: https://www.lri.fr/~appert/touchtokens/

5.7. Platforms

5.7.1. Platform: WILDER



Start fierycross-20141213.jpg

End fierycross-20150214.jpg

Transition Expand

☑ Blurred Border 10 px

fieryc... /fieryc... Expand (2.0) Blend (2.0)

fieryc... /fieryc... Expand (2.0) Blend (2.0)

fieryc... /fieryc... Expand (2.0) Blend (2.0)

fierycross-2... /fierycross-2... Deform (2.0) Blend (2.0)

Figure 2. Baia is a framework to create advanced animated transitions between before-and-after satellite images. Before-and-after image pairs show how entities in a given region have evolved over a specific period of time. Baia relies on a pixel-based transition model to convey the underlying phenomenon that caused this evolution in a meaningful manner. The animation editor pictured here enables authors to easily represent common types of changes thanks to predefined animation primitives and to sequence different changes across time.

Figure 3. Multiple asteroid-generated tsunami simulations running simultaneously on the WILDER ultra-wall. The high display capacity of this interactive surface makes it possible to show, for each of the simulations: a planet-wide view showing the propagation of the tsunami on the globe, a close-up on the region of impact, showing a simulation of one or more scalar fields, parameters of the simulation.

Ultra-high-resolution wall-sized displays [39] feature a very high pixel density over a large physical surface. Such platforms have properties that make them well-suited to the visualization of very large datasets. They can represent the data with a high level of detail while at the same time retaining context: users can transition from an overview of the data to a detailed view simply by physically moving in front of the wall display. Wall displays also offer good support for collaborative work, enabling multiple users to simultaneously visualize and interact with the displayed data. To make them interactive, wall-sized displays are increasingly coupled with input devices such as touch frames, motion-tracking systems and wireless multitouch devices, in order to enable multi-device and multi-user interaction with the displayed data. Application areas for such visualization platforms range from the monitoring of complex infrastructures and crisis management situations to tools for the exploratory visualization of scientific data.

WILDER is the latest ultra-high-resolution wall-sized display set up at Inria Saclay, and is one of the nodes of the Digiscope EquipEx. We use this platform for multiple projects, both fundamental HCI research, and research and development activities for specific application areas such as geographical informations systems (Figure 3) and astronomy.

WILDER was used in the projects that led to the following publications this year: [23], [31].

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 definitiion (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 developped by Maxime Garcia as part of his PhD thesis, which incorporates several shape modleing and animation tools developped 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.

LACODAM Project-Team

6. New Software and Platforms

6.1. REMI

Mining Intuitive Referring Expressions in Knowledge Bases
KEYWORDS: RDF - Knowledge database - Referring expression
FUNCTIONAL DESCRIPTION: REMI takes an RDF knowledge base stored as an HDT file, and a set of target entities and returns a referring expression that is intuitive, i.e., the user is likely to understand it.

- Contact: Luis Galarraga Del Prado
- URL: http://gitlab.inria.fr/lgalarra/remi

6.2. HIPAR

Hierarchical Interpretable Pattern-aided Regression
KEYWORDS: Regression - Pattern extraction
FUNCTIONAL DESCRIPTION: Given a (tabular) dataset with categorical and numerical attributes, HIPAR is a Python library that can extract accurate hybrid rules that offer a trade-off between (a) interpretability, (b) accuracy, and (c) data coverage.

- Contact: Luis Galarraga Del Prado
- URL: https://gitlab.inria.fr/opelgrin/hipar

6.3. NegPSpan

Negative pattern mining with PrefixSpan
KEYWORDS: Pattern discovery - Data mining - Sequential patterns - Traces
SCIENTIFIC DESCRIPTION: Mining frequent sequential patterns consists in extracting recurrent behaviors, modeled as patterns, in a big sequence dataset. Such patterns inform about which events are frequently observed in sequences, i.e. what does really happen. Sometimes, knowing that some specific event does not happen is more informative than extracting a lot of observed events. Negative sequential patterns (NSP) formulate recurrent behaviors by patterns containing both observed events and absent events. Few approaches have been proposed to mine such NSPs. In addition, the syntax and semantics of NSPs differ in the different methods which makes it difficult to compare them. This article provides a unified framework for the formulation of the syntax and the semantics of NSPs. Then, we introduce a new algorithm, NegPSpan, that extracts NSPs using a PrefixSpan depth-first scheme and enabling maxgap constraints that other approaches do not take into account. The formal framework allows for highlighting the differences between the proposed approach wrt to the methods from the literature, especially wrt the state of the art approach eNSP. Intensive experiments on synthetic and real datasets show that NegPSpan can extract meaningful NSPs and that it can process bigger datasets than eNSP thanks to significantly lower memory requirements and better computation times.
FUNCTIONAL DESCRIPTION: NegPSpan is software to extract patterns from sequential data (traces, sequences of events, client pathways, etc.). The NegPSpan software extracts two types of patterns: the classical sequential patterns and the negative sequential patterns. Sequential patterns describe recurrent behaviors described as a sequence of events (e.g. event A occurs, then event B occurs and finally C occurs) while negative sequential patterns hold information about absent event (e.g. event A occurs, then event B occurs but without any C in between).

The user has to provide a dataset in the IBM sequence format and, at least, a parameters corresponding to the minimal number of occurrences in the dataset (and possible additional parameters). The software efficiently extracts the patterns and output them (in a text or JSON format). The software can use different strategies for exploring negative sequential patterns, and also specify some constraints about the expected patterns.
NEWS OF THE YEAR: NegPSpan has been developed in 2018.

- Participants: Thomas Guyet and René Quiniou
- Contact: Thomas Guyet
- Publication: NegPSpan: efficient extraction of negative sequential patterns with embedding constraints
- URL: http://people.irisa.fr/Thomas.Guyet/negativepatterns/evalnegpat.php

LARSEN Project-Team

6. New Software and Platforms

6.1. Limbo

LIbrary for Model-based Bayesian Optimization
KEYWORDS: Black-box optimization - C++ - Global optimization - Machine learning - Policy Learning - Bayesian optimization - Gaussian processes
FUNCTIONAL DESCRIPTION: Limbo is an open-source C++11 library for Gaussian processes and Bayesian Optimization which is designed to be both highly flexible and very fast. It can be used to optimize functions for which the gradient is unknown, evaluations are expensive, and where runtime cost matters (e.g., on embedded systems or robots). Benchmarks on standard functions show that Limbo is about 2 times faster than BayesOpt (another C++ library) for a similar accuracy.
NEWS OF THE YEAR: - publication of a paper in the Journal of Open Source Software - several bug fixes and performance improvement

- Partners: UPMC - Imperial College London
- Contact: Jean-Baptiste Mouret
- Publication: Limbo: A Flexible High-performance Library for Gaussian Processes modeling and Data-Efficient Optimization
- URL: http://www.resibots.eu/limbo

6.2. sferes2

A lightweight generic C++ framework for evolutionary computation
KEYWORDS: Evolutionary Algorithms - Evolution - Global optimization - Multi-objective optimisation
FUNCTIONAL DESCRIPTION: Sferes2 is a high-performance, multi-core, lightweight, generic C++11 framework for evolutionary computation. It is intently kept small to stay reliable and understandable.

Sferes2 relies heavily on template-based meta-programming in C++ to get both abstraction and execution speed.
NEWS OF THE YEAR: - integration of a new set of classes for quality diversity, based on Antoine Cully's paper (IEEE TEC, 2018) - new documentation in Sphinx - new random generator (more thread safe, C++11) - drop the C++98 support (now C++11 only)

- Partner: UPMC
- Contact: Jean-Baptiste Mouret
- Publication: Sferes_v2: Evolvin' in the Multi-Core World
- URL: http://github.com/sferes2/sferes2/

6.3. xsens_driver

KEYWORD: IMU driver
FUNCTIONAL DESCRIPTION: This is a driver for the third and fourth generation of Xsens IMU devices. The driver is in two parts, a small implementation of most of the MT protocol in Python and a ROS node. It works both on serial and USB interfaces.

These MT* devices can store their configuration and will retrieve it at each boot and then stream data according to this configuration. The node only forwards the data streamed onto ROS topics. In order to configure your device, you can use the mtdevice.py script (or the vendor tool on Windows).

RELEASE FUNCTIONAL DESCRIPTION: bug fixes

NEWS OF THE YEAR: version 2.1.0 (2017-04-14) - several bugfixes and a new option.

- Contact: Francis Colas
- URL: https://github.com/ethz-asl/ethzasl_xsens_driver

6.4. SeekPlans

KEYWORDS: Robotics - Depth map
FUNCTIONAL DESCRIPTION: The SeekPlanes software is a high-performance C99 micro library which seeks planes in a depth image. It provides the height, the pitch and the roll of the camera that takes the image, in order to use the same orthonormal model for multi-camera acquisition. In addition, this library provides all the image planes: walls, ceiling, but also the top of a table or a bed, etc. Ultra fast, written in full portable C99 with optional X86 vectorizations (SSE and/or AVX), it has been tested on Linux and Windows, in 32 and 64 bits, and also on a Raspberry PI model 3.

- Contact: François Charpillet

LINKMEDIA Project-Team (section vide)

LINKS Project-Team

6. New Software and Platforms

6.1. ShEx validator

Validation of Shape Expression schemas
KEYWORDS: Data management - RDF
FUNCTIONAL DESCRIPTION: Shape Expression schemas is a formalism for defining constraints on RDF graphs. This software allows to check whether a graph satisfies a Shape Expressions schema.

RELEASE FUNCTIONAL DESCRIPTION: ShExJava now uses the Commons RDF API and so support RDF4J, Jena, JSON-LD-Java, OWL API and Apache Clerezza. It can parse ShEx schema in the ShEcC, ShEJ, ShExR formats and can serialize a schema in ShExJ.

To validate data against a ShExSchema using ShExJava, you have two different algorithms: - the refine algorithm: compute once and for all the typing for the whole graph - the recursive algorithm: compute only the typing required to answer a validate(node,ShapeLabel) call and forget the results.

- Contact: Iovka Boneva
- URL: http://shexjava.lille.inria.fr/

6.2. gMark

gMark: schema-driven graph and query generation
KEYWORDS: Semantic Web - Data base
FUNCTIONAL DESCRIPTION: gMark allow the generation of graph databases and an associated set of query from a schema of the graph.gMark is based on the following principles: - great flexibility in the schema definition - ability to generate big size graphs - ability to generate recursive queries - ability to generate queries with a desired selectivity

- Contact: Aurélien Lemay
- URL: https://github.com/graphMark/gmark

6.3. SmartHal

KEYWORD: Bibliography
FUNCTIONAL DESCRIPTION: SmartHal is a better tool for querying the HAL bibliography database, while is based on Haltool queries. The idea is that a Haltool query returns an XML document that can be queried further. In order to do so, SmartHal provides a new query language. Its queries are conjunctions of Haltool queries (for a list of laboratories or authors) with expressive Boolean queries by which answers of Haltool queries can be refined. These Boolean refinement queries are automatically translated to XQuery and executed by Saxon. A java application for extraction from the command line is available. On top of this, we have build a tool for producing the citation lists for the evaluation report of the LIFL, which can be easily adapter to other Labs.

- Contact: Joachim Niehren
- URL: http://smarthal.lille.inria.fr/

6.4. QuiXPath

KEYWORDS: XML - NoSQL - Data stream

SCIENTIFIC DESCRIPTION: The QuiXPath tools supports a very large fragment of XPath 3.0. The QuiXPath library provides a compiler from QuiXPath to FXP, which is a library for querying XML streams with a fragment of temporal logic.
FUNCTIONAL DESCRIPTION: QuiXPath is a streaming implementation of XPath 3.0. It can query large XML files without loading the entire file in main memory, while selecting nodes as early as possible.

- Contact: Joachim Niehren
- URL: https://project.inria.fr/quix-tool-suite/

6.5. X-FUN

KEYWORDS: Programming language - Compilers - Functional programming - Transformation - XML
FUNCTIONAL DESCRIPTION: X-FUN is a core language for implementing various XML, standards in a uniform manner. X-Fun is a higher-order functional programming language for transforming data trees based on node selection queries.

- Participants: Joachim Niehren and Pavel Labath
- Contact: Joachim Niehren

LOKI Team

6. New Software and Platforms

6.1. ParkEvolution

Longitudinal analysis of fine motor movement in an ecological context for patients with Parkinson disease
KEYWORD: Parkinson disease
FUNCTIONAL DESCRIPTION: The originality of this application relies on the acquisition of data in an ecological context. Thanks to this application that patients download on their personal computer, the data corresponding to cursor displacement on screen and raw input from pointing devices are collected, encrypted and sent to a server. The analysis of this data allows to compute a motor score according to the parameters of movement, in order to identify alterations in fine motor control. We ensure a realistic score based on the important quantity of data collected. This software is written in C++ and runs on Windows. It uses the libpointing library to access raw data from pointing devices.

RELEASE FUNCTIONAL DESCRIPTION: Fixed bugs and developed new features.
NEWS OF THE YEAR: Release of the 1.3.0 version fixing a number of bugs and introducing a number of new small features. An APP request is close of getting approved.

- Participants: Géry Casiez and Laure Fernandez
- Partners: Aix-Marseille Université - CNRS Laboratoire de Psychologie Cognitive - UMR 7290 - Team ‘Perception and attention’ - Institut de Neurosciences de la Timone
- Contact: Géry Casiez
- URL: http://parkevolution.org/

6.2. liblag

Library implementing latency compensation techniques for interactive systems
KEYWORDS: Interaction - Latency
FUNCTIONAL DESCRIPTION: The library comprises the management of a set of multitouch input devices, the implementation of latency compensation techniques from the state-of-the-art and new latency compensation techniques developed in the project, and a system to handle artificial latency.

The library is developed in C++ using the Qt framework to allow compiling the same code on a wide range of devices and platforms.
NEWS OF THE YEAR: Finished the work on the latency compensation algorithm "TurboTouch predictor" and development of the demonstrator presented at Euratechnologies. Development of an on-line interactive demo available at http://ns.inria.fr/loki/TTp/

- Contact: Géry Casiez
- Publications: Dispositif à affichage prédictif - Next-Point Prediction for Direct Touch Using Finite-Time Derivative Estimation
- URL: http://mjolnir.lille.inria.fr/turbotouch/

MAGNET Project-Team

6. New Software and Platforms

6.1. CoRTeX

Python library for noun phrase COreference Resolution in natural language TEXts
KEYWORD: Natural language processing
FUNCTIONAL DESCRIPTION: CoRTex is a LGPL-licensed Python library for Noun Phrase coreference resolution in natural language texts. This library contains implementations of various state-of-the-art coreference resolution algorithms, including those developed in our research. In addition, it provides a set of APIs and utilities for text pre-processing, reading the CONLL2012 and CONLLU annotation formats, and performing evaluation, notably based on the main evaluation metrics (MUC, B-CUBED, and CEAF). As such, CoRTex provides benchmarks for researchers working on coreference resolution, but it is also of interest for developers who want to integrate a coreference resolution within a larger platform. It currently supports use of the English or French language.

- Participant: Pascal Denis
- Partner: Orange Labs
- Contact: Pascal Denis
- URL: https://gitlab.inria.fr/magnet/CoRTeX

6.2. Mangoes

MAgnet liNGuistic wOrd vEctorS
KEYWORDS: Word embeddings - NLP
FUNCTIONAL DESCRIPTION: Process textual data and compute vocabularies and co-occurrence matrices. Input data should be raw text or annotated text. Compute word embeddings with different state-of-the art unsupervised methods. Propose statistical and intrinsic evaluation methods, as well as some visualization tools.

- Contact: Nathalie Vauquier
- URL: https://gitlab.inria.fr/magnet/mangoes

6.3. metric-learn

KEYWORDS: Machine learning - Python - Metric learning
FUNCTIONAL DESCRIPTION: Distance metrics are widely used in the machine learning literature. Traditionally, practicioners would choose a standard distance metric (Euclidean, City-Block, Cosine, etc.) using a priori knowledge of the domain. Distance metric learning (or simply, metric learning) is the sub-field of machine learning dedicated to automatically constructing optimal distance metrics.

This package contains efficient Python implementations of several popular metric learning algorithms.

- Partner: Parietal
- Contact: William De Vazelhes
- URL: https://github.com/metric-learn/metric-learn

6.4. MyLocalInfo

KEYWORDS: Privacy - Machine learning - Statistics
FUNCTIONAL DESCRIPTION: Decentralized algorithms for machine learning and inference tasks which (1) perform as much computation as possible locally and (2) ensure privacy and security by avoiding personal data leaves devices.

- Contact: Nathalie Vauquier
- URL: https://gitlab.inria.fr/magnet/mylocalinfo

MAGRIT Project-Team

6. New Software and Platforms

6.1. PoLAR

Portable Library for Augmented Reality

FUNCTIONAL DESCRIPTION: PoLAR (Portable Library for Augmented Reality) is a framework which aims to help creating graphical applications for augmented reality, image visualization and medical imaging. PoLAR was designed to offer powerful visualization functionalities without the need to be a specialist in Computer Graphics. The framework provides an API to state-of-the-art libraries: Qt to build GUIs and OpenSceneGraph for high-end visualization, for researchers and engineers with a background in Computer Vision to be able to create beautiful AR applications, with little programming effort. The framework is written in C++ and published under the GNU GPL license

- Contact: Erwan Kerrien
- URL: http://polar.inria.fr

6.2. Fast>VP

KEYWORDS: Vanishing points - Image rectification

FUNCTIONAL DESCRIPTION: Fast>VP is a fast and effective tool to detect vanishing points in uncalibrated images of urban or indoor scenes.

This tool also allows automatic rectification of the vertical planes in the scene, namely generating images where these planes appear as if they were observed from a fronto-parallel view.

It is the Matlab implementation of the algorithm described in [6].

- Contact: Gilles Simon
- URL: https://members.loria.fr/GSimon/fastvp/

6.3. NoLoDuDoCT

A non-local dual-domain cartoon and texture decomposition

KEYWORDS: Image analysis - Cartoon and texture decomposition

FUNCTIONAL DESCRIPTION: This is an algorithm decomposing images into cartoon and texture components. Spectrum components of textures are detected on the basis of a statistical hypothesis test, the null hypothesis modeling a purely cartoon patch. Statistics are estimated in a non-local way.

- Contact: Frédéric Sur
- URL: https://members.loria.fr/FSur/software/NoLoDuDoCT/

6.4. BSpeckleRender

A Boolean model for deformed speckle rendering

KEYWORDS: Boolean model - Monte Carlo estimation - Experimental mechanics - Displacement fields

FUNCTIONAL DESCRIPTION: This library implements a new method for synthesizing speckle images deformed by an arbitrary deformation field set by the user. Such images are very useful for assessing the different methods based on digital image correlation (DIC) for estimating displacement fields in experimental mechanics. Since the deformations are very small, it is necessary to ensure that no additional bias is introduced by the image synthesis algorithm. The proposed method is based on the Monte Carlo evaluation of images generated by a Boolean model.

- Contact: Frédéric Sur
- URL: https://members.loria.fr/FSur/software/BSpeckleRender/

MANAO Project-Team

6. New Software and Platforms

6.1. Eigen

KEYWORD: Linear algebra
FUNCTIONAL DESCRIPTION: Eigen is an efficient and versatile C++ mathematical template library for linear algebra and related algorithms. In particular it provides fixed and dynamic size matrices and vectors, matrix decompositions (LU, LLT, LDLT, QR, eigenvalues, etc.), sparse matrices with iterative and direct solvers, some basic geometry features (transformations, quaternions, axis-angles, Euler angles, hyperplanes, lines, etc.), some non-linear solvers, automatic differentiations, etc. Thanks to expression templates, Eigen provides a very powerful and easy to use API. Explicit vectorization is performed for the SSE, AltiVec and ARM NEON instruction sets, with graceful fallback to non-vectorized code. Expression templates allow to perform global expression optimizations, and to remove unnecessary temporary objects.

RELEASE FUNCTIONAL DESCRIPTION: In 2017, we released three revisions of the 3.3 branch with few fixes of compilation and performance regressions, some doxygen documentation improvements, and the addition of transpose, adjoint, conjugate methods to SelfAdjointView to ease writing generic code.

- Participant: Gaël Guennebaud
- Contact: Gaël Guennebaud
- URL: http://eigen.tuxfamily.org/

6.2. Elasticity Skinning

KEYWORD: 3D animation
FUNCTIONAL DESCRIPTION: Geometric skinning techniques are very popular in the industry for their high performances, but fail to mimic realistic deformations. With elastic implicit skinning the skin stretches automatically (without skinning weights) and the vertices distribution is more pleasing. Our approach is more robust, for instance the angle's range of joints is larger than implicit skinning.

This software has been ported as a plugin for the Modo software (The Foundry) in collaboration with Toulouse Tech Transfer. This plugin has been bought by The Foundry, which maintains and sells it.

- Participants: Brian Wyvill, Damien Rohmer, Florian Canezin, Gaël Guennebaud, Loïc Barthe, Marie-Paule Cani, Mathias Paulin, Olivier Gourmel and Rodolphe Vaillant
- Partners: Université de Bordeaux - CNRS - INP Bordeaux - Université de Toulouse - Institut Polytechnique de Grenoble - Ecole Supérieure de Chimie Physique Electronique de Lyon
- Contact: Gaël Guennebaud
- URL: https://www.irit.fr/~Loic.Barthe/transfer.php

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 crowdy scenes (which are rigid, for the moment). The principle is to represent data on the GPU as a Sparse Voxel Octree which multiscale voxels bricks are produced on demand only when necessary and only at the required resolution, and kept in a LRU cache. User defined producer lays accross CPU and GPU and can load, transform, or procedurally create the data. Another user defined function is called to shade each voxel according to the user-defined voxel content, so that it is user choice to distribute the appearance-making at creation (for faster rendering) or on the fly (for storageless thin procedural details). The efficient rendering is done using a GPU differential cone-tracing using the scale corresponding to the 3D-MIPmapping LOD, allowing quality rendering with one single ray per pixel. Data is produced in case of cache miss, and thus only whenever visible (accounting for view frustum and occlusion). Soft-shadows and depth-of-field is easily obtained using larger cones, and are indeed cheaper than unblurred rendering. Beside the representation, data management and base rendering algorithm themself, we also worked on realtime light transport, and on quality prefiltering of complex data. Ongoing researches are addressing animation. GigaVoxels is currently used for the quality real-time exploration of the detailed galaxy in ANR RTIGE. Most of the work published by Cyril Crassin (and al.) during his PhD (see http://maverick.inria.fr/Members/Cyril.Crassin/) is related to GigaVoxels. GigaVoxels is available for Windows and Linux under the BSD-3 licence.

- Participants: Cyril Crassin, 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 developpement of new algorithms for global illumination, those benefiting from the existing algorithms for handling materials, geometry and light sources.

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

6.5. 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 Hétroy-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/

MFX Team (section vide)

MIMETIC Project-Team

6. New Software and Platforms

6.1. AsymGait

Asymmetry index for clinical gait analysis based on depth images

KEYWORDS: Motion analysis - Kinect - Clinical analysis

SCIENTIFIC DESCRIPTION: The system uses depth images delivered by the Microsoft Kinect to retrieve the gait cycles first. To this end it is based on a analyzing the knees trajectories instead of the feet to obtain more robust gait event detection. Based on these cycles, the system computes a mean gait cycle model to decrease the effect of noise of the system. Asymmetry is then computed at each frame of the gait cycle as the spatial difference between the left and right parts of the body. This information is computed for each frame of the cycle.

FUNCTIONAL DESCRIPTION: AsymGait is a software package that works with Microsoft Kinect data, especially depth images, in order to carry-out clinical gait analysis. First it identifies the main gait events using the depth information (footstrike, toe-off) to isolate gait cycles. Then it computes a continuous asymmetry index within the gait cycle. Asymmetry is viewed as a spatial difference between the two sides of the body.

- Participants: Edouard Auvinet and Franck Multon
- Contact: Franck Multon

6.2. Cinematic Viewpoint Generator

KEYWORD: 3D animation

FUNCTIONAL DESCRIPTION: The software, developed as an API, provides a mean to automatically compute a collection of viewpoints over one or two specified geometric entities, in a given 3D scene, at a given time. These viewpoints satisfy classical cinematographic framing conventions and guidelines including different shot scales (from extreme long shot to extreme close-up), different shot angles (internal, external, parallel, apex), and different screen compositions (thirds,fifths, symmetric of di-symmetric). The viewpoints allow to cover the range of possible framings for the specified entities. The computation of such viewpoints relies on a database of framings that are dynamically adapted to the 3D scene by using a manifold parametric representation and guarantee the visibility of the specified entities. The set of viewpoints is also automatically annotated with cinematographic tags such as shot scales, angles, compositions, relative placement of entities, line of interest.

- Participants: Christophe Lino, Emmanuel Badier and Marc Christie
- Partners: Université d'Udine - Université de Nantes
- Contact: Marc Christie

6.3. Directors Lens Motion Builder

KEYWORDS: Previzualisation - Virtual camera - 3D animation

FUNCTIONAL DESCRIPTION: Directors Lens Motion Builder is a software plugin for Autodesk's Motion Builder animation tool. This plugin features a novel workflow to rapidly prototype cinematographic sequences in a 3D scene, and is dedicated to the 3D animation and movie previsualization industries. The workflow integrates the automated computation of viewpoints (using the Cinematic Viewpoint Generator) to interactively explore different framings of the scene, proposes means to interactively control framings in the image space, and proposes a technique to automatically retarget a camera trajectory from one scene to another while enforcing visual properties. The tool also proposes to edit the cinematographic sequence and export the animation. The software can be linked to different virtual camera systems available on the market.

- Participants: Christophe Lino, Emmanuel Badier and Marc Christie
- Partner: Université de Rennes 1
- Contact: Marc Christie

6.4. Kimea

Kinect IMprovement for Egronomics Assessment
KEYWORDS: Biomechanics - Motion analysis - Kinect
SCIENTIFIC DESCRIPTION: Kimea consists in correcting skeleton data delivered by a Microsoft Kinect in an ergonomics purpose. Kimea is able to manage most of the occlultations that can occur in real working situation, on workstations. To this end, Kimea relies on a database of examples/poses organized as a graph, in order to replace unreliable body segments reconstruction by poses that have already been measured on real subject. The potential pose candidates are used in an optimization framework.
FUNCTIONAL DESCRIPTION: Kimea gets Kinect data as input data (skeleton data) and correct most of measurement errors to carry-out ergonomic assessment at workstation.

- Participants: Franck Multon, Hubert Shum and Pierre Plantard
- Partner: Faurecia
- Contact: Franck Multon
- Publications: Usability of corrected Kinect measurement for ergonomic evaluation in constrained environment - Validation of an ergonomic assessment method using Kinect data in real workplace conditions - Ergonomics Measurements using Kinect with a Pose Correction Framework - Filtered Pose Graph for Efficient Kinect Pose Reconstruction - Reliability of Kinect measurements for assessing the movement of operators in ergonomic studies

6.5. Populate

KEYWORDS: Behavior modeling - Agent - Scheduling
SCIENTIFIC DESCRIPTION: The software provides the following functionalities:

- A high level XML dialect that is dedicated to the description of agents activities in terms of tasks and sub activities that can be combined with different kind of operators: sequential, without order, interlaced. This dialect also enables the description of time and location constraints associated to tasks.

- An XML dialect that enables the description of agent’s personal characteristics.

- An informed graph describes the topology of the environment as well as the locations where tasks can be performed. A bridge between TopoPlan and Populate has also been designed. It provides an automatic analysis of an informed 3D environment that is used to generate an informed graph compatible with Populate.

- The generation of a valid task schedule based on the previously mentioned descriptions.

With a good configuration of agents characteristics (based on statistics), we demonstrated that tasks schedules produced by Populate are representative of human ones. In conjunction with TopoPlan, it has been used to populate a district of Paris as well as imaginary cities with several thousands of pedestrians navigating in real time.
FUNCTIONAL DESCRIPTION: Populate is a toolkit dedicated to task scheduling under time and space constraints in the field of behavioral animation. It is currently used to populate virtual cities with pedestrian performing different kind of activities implying travels between different locations. However the generic aspect of the algorithm and underlying representations enable its use in a wide range of applications that need to link activity, time and space. The main scheduling algorithm relies on the following inputs: an informed environment description, an activity an agent needs to perform and individual characteristics of this agent. The algorithm produces a valid task schedule compatible with time and spatial constraints imposed by the activity description and the environment. In this task schedule, time intervals relating to travel and task fulfillment are identified and locations where tasks should be performed are automatically selected.

- Participants: Carl-Johan Jorgensen and Fabrice Lamarche
- Contact: Fabrice Lamarche

6.6. The Theater

KEYWORDS: 3D animation - Interactive Scenarios
FUNCTIONAL DESCRIPTION: The Theater is a software framework to develop interactive scenarios in virtual 3D environements. The framework provides means to author and orchestrate 3D character behaviors and simulate them in real-time. The tools provides a basis to build a range of 3D applications, from simple simulations with reactive behaviors, to complex storytelling applications including narrative mechanisms such as flashbacks.

- Participant: Marc Christie
- Contact: Marc Christie

6.7. CusToM

Customizable Toolbox for Musculoskeletal simulation
KEYWORDS: Biomechanics - Dynamic Analysis - Kinematics - Simulation - Mechanical multi-body systems
SCIENTIFIC DESCRIPTION: The present toolbox aims at performing a motion analysis thanks to an inverse dynamics method.

Before performing motion analysis steps, a musculoskeletal model is generated. Its consists of, first, generating the desire anthropometric model thanks to models libraries. The generated model is then kinematical calibrated by using data of a motion capture. The inverse kinematics step, the inverse dynamics step and the muscle forces estimation step are then successively performed from motion capture and external forces data. Two folders and one script are available on the toolbox root. The Main script collects all the different functions of the motion analysis pipeline. The Functions folder contains all functions used in the toolbox. It is necessary to add this folder and all the subfolders to the Matlab path. The Problems folder is used to contain the different study. The user has to create one subfolder for each new study. Once a new musculoskeletal model is used, a new study is necessary. Different files will be automaticaly generated and saved in this folder. All files located on its root are related to the model and are valuable whatever the motion considered. A new folder will be added for each new motion capture. All files located on a folder are only related to this considered motion.
FUNCTIONAL DESCRIPTION: Inverse kinematics Inverse dynamics Muscle forces estimation External forces prediction

- Participants: Antoine Muller, Charles Pontonnier and Georges Dumont
- Contact: Antoine Muller

6.8. MotionGraphVR

KEYWORDS: Virtual reality - Motion capture - Movement analysis
FUNCTIONAL DESCRIPTION: MotionGraphVR is a tool enabling users to automatically create motion graphs in Unity. It is particularly targeting Virtual Reality applications, where with the development of Head Mounted Displays users are now unable to see their real body unless they use expensive motion capture system, or animation techniques (e.g., Inverse Kinematics) which suffer from a lack of visual realism. To lever these limitations, MotionGraphVR automatically builds a graph of human motions from a set of examples captured on a real actor, and identify which motion path is the graph is closest to the user's actions. Additionally, this plugin also provides analysing tools to allow developers of VR applications to visualise similarities between movements to use in their applications before seamlessly connecting them in Motion Graphs.

- Participants: Tiffany Luong, Ludovic Hoyet and Fernando Argelaguet Sanz
- Contact: Ludovic Hoyet

6.9. Platforms

6.9.1. Immerstar Platform

Participants: Georges Dumont [contact], Ronan Gaugne, Anthony Sorel, Richard Kulpa.

With the two platforms of virtual reality, Immersia (http://www.irisa.fr/immersia/) and Immermove (http://m2slab.com/index.php/facilities-4/), grouped under the name Immerstar, the team has access to high level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform is granted by a Inria CPER funding for 2015-2019 that enables important evolutions of the equipment. In 2016, the first technical evolutions have been decided and, in 2017, these evolutions have been implemented. On the one side, for Immermove, a third face to the immersive space was added. Moreover, 23 new Qualisys cameras were bought to complete the Vicon motion capture system for a total budget of 160k€half funded by Rennes Métropole. Both systems can interoperate to cover all the gymnasium but can also be used separately. On the other side, for Immersia, the installation of WQXGA laser projectors with augmented global resolution, of a new tracking system with higher frequency and of new computers for simulation and image generation in 2017. In 2018, a Scale One haptic device has been installed,. It allows, as in the CPER proposal, single-handed or dual-handed haptic feedback in the full space covered by Immersia, with the possibility of carrying the user (see Figure 2).

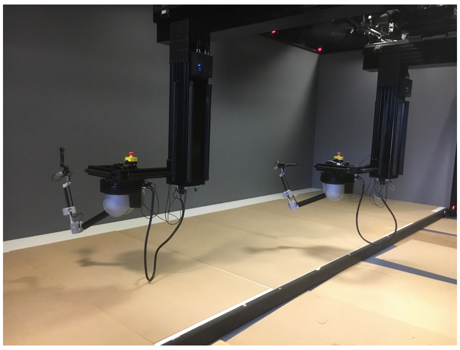


Figure 4. Upgrade of the Immersia platform with the Scale-One Haptic device enabling single-handed or dual-handed haptic feedback in the full space covered by Immersia, with the possibility of carrying the user.

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 AMSELEM
- 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

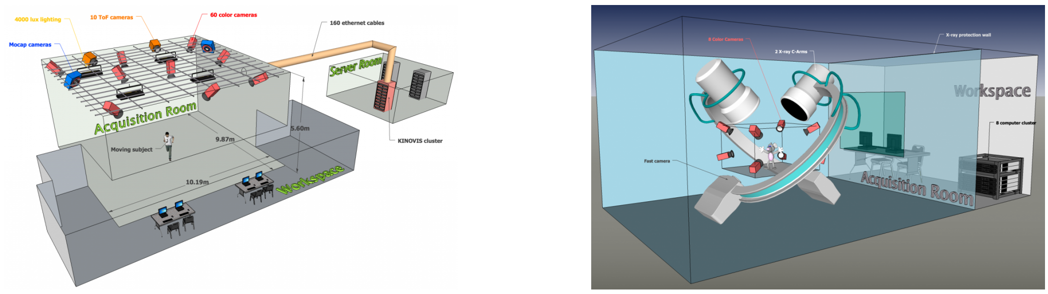


Figure 2. Kinovis platforms: on the left the Inria platform; on the right Grenoble Hospital platform.

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.

MULTISPEECH Project-Team

6. New Software and Platforms

6.1. dnnsep

Multichannel audio source separation with deep neural networks
KEYWORDS: Audio - Source Separation - Deep learning
SCIENTIFIC DESCRIPTION: dnnsep is the only source separation software relying on multichannel Wiener filtering based on deep learning. Deep neural networks are used to initialize and reestimate the power spectrum of the sources at every iteration of an expectation-maximization (EM) algorithm. This results in state-of-the-art separation quality for both speech and music.
FUNCTIONAL DESCRIPTION: Combines deep neural networks and multichannel signal processing for speech enhancement and separation of musical recordings.

RELEASE FUNCTIONAL DESCRIPTION: This version derives from version 1.0 (not 1.9). Differences concerns the use of a bidirectional long short-term memory (BLSTM) neural network, smoothing of the multichannel Wiener filter (MWF) over time and frequency, usage of the principal component of the MWF filter, adding a new generalized eigenvector beamformer with blind analytical normalization (GEVB) filter, and normalizing the training and test signals.

- Participants: Aditya Nugraha, Emmanuel Vincent and Antoine Liutkus
- Contact: Emmanuel Vincent

6.2. Dynalips-Player

High realistic lip synchronization for 3d animated characters
KEYWORDS: 3D animation - Graphics - Speech Synthesis
FUNCTIONAL DESCRIPTION: Dynalips provides a solution to synchronize precisely and automatically the movements of the lips of a 3D character with speech (we address 3D animation movies and video games). We have developed a demonstrator that illustrates the whole process: from audio + text to the generation of the animation trajectory, and controlling the animation of a 3D model (e.g. an avatar). The demonstrator is composed mainly by the player developed in Unity 3D (but can be used with any other system) and plays the animation synchronously with speech in realtime. It is possible to generate an animation for Autodesk Maya 3D.
NEWS OF THE YEAR: The whole lip-sync demonstrator is fully operational. From text and recorded speech, the system allows animating two different 3D models. The player is running on Unity 3D.

- Partners: Université de Lorraine - Sayens (SATT Grand Est)
- Contact: Slim Ouni
- URL: http://www.dynalips.com

6.3. KATS

Kaldi-based Automatic Transcription System
KEYWORD: Speech recognition
FUNCTIONAL DESCRIPTION: KATS is a multipass system for transcribing audio data, and in particular radio or TV shows in French, English or Arabic. It is based on the Kaldi speech recognition tools. It relies on Deep Neural Network (DNN) modeling for speech detection and acoustic modeling of the phones (speech sounds). Higher order statistical language models and recurrent neural network language models can be used for improving performance through rescoring of multiple hypotheses.

NEWS OF THE YEAR: New models have been trained for British English and evaluated on MGB data

- Contact: Dominique Fohr

6.4. VisArtico

Visualization of multimodal speech data
KEYWORDS: Data visualization - 3D movement - Speech processing - Videos
SCIENTIFIC DESCRIPTION: VisArtico is a multimodal data visualization software acquired by several systems: articulograph, motion capture, depth camera. This software makes it possible to visualize the positions of real or virtual sensors and to animate them simultaneously with acoustics. Regarding the articulatory data, the user has the possibility to visualise the contour of the tongue and the lips. It also makes it possible to find the midsagittal plane of the speaker, and to deduce the position of the palate, if this information is absent during the acquisition. The software makes it possible to display the segmentation at the level of sentences, words or phonemes. The goal is to provide an effective multimodal data visualization tool that can be useful to anyone studying speech production, audio-visual synthesis, or animation in a more general way.
FUNCTIONAL DESCRIPTION: VisArtico is a user-friendly software which allows visualizing multimodal data acquired by several systems : an articulograph (AG500, AG501 or NDI Wave), motion capture system, depth camera. This visualization software has been designed so that it can directly use the data provided by the different systems to display the spatial and temporal positions of the sensors (real and virtual), synchronized with the corresponding acoustic recordings. Moreover, for articulatory data, VisArtico not only allows viewing the sensors but also enriches the visual information by indicating clearly and graphically the data for the tongue, lips and jaw. Finally, it is possible to generate a movie for any articulatory-acoustic sequence. This software can be useful for researchers in speech production, audiovisual speech synthesis or articulatory speech analysis.

RELEASE FUNCTIONAL DESCRIPTION: The main improvement in this version is the ability to view a video that was recorded along with the articulatory or motion capture data. The software also allows for automatic speech segmentation.
NEWS OF THE YEAR: This year, we have added the possibility to visualize a video simultaneously with the multimodal data and the acoustic data. Several bugs have been fixed.

- Participants: Ilef Ben Farhat, Loïc Mangeonjean and Slim Ouni
- Partners: CNRS - Université de Lorraine
- Contact: Slim Ouni
- Publication: VisArtico: a visualization tool for articulatory data
- URL: http://visartico.loria.fr

6.5. Xarticulators

KEYWORDS: Medical imaging - Natural language processing
FUNCTIONAL DESCRIPTION: The Xarticulators software is intended to delineate contours of speech articulators in X-ray and MR images, construct articulatory models and synthesize speech from X-ray films. This software provides tools to track contours automatically, semi-automatically or by hand, to make the visibility of contours easier, to add anatomical landmarks to speech articulators and to synchronize images with the sound. In addition we also added the possibility of processing digitized manual delineation results made on sheets of papers when no software is available. Xarticulators also enables the construction of adaptable linear articulatory models from the X-ray or MR images and incorporates acoustic simulation tools to synthesize speech signals from the vocal tract shape. Recent work was on the possibility of synthesizing speech from 2D-MRI films, and on the construction of better articulatory models for the velum, lips and epiglottis.

RELEASE FUNCTIONAL DESCRIPTION: The new version allows MRI films to be processed and, above all, it offers a better transition from the shape of the vocal tract to the area function, which corresponds to an approximation of the vocal tract using a series of elementary tubes from the glottis to the lips.

NEWS OF THE YEAR: Improvements to the articulatory model which now takes into account "small" filiform articulators such as the epiglottis and velum using models using the central line. Improvement of the transition from the medio-sagittal 2D form of the vocal tract to the function of area.

- Contact: Yves Laprie
- Publication: Articulatory model of the epiglottis

ORPAILLEUR Project-Team

6. New Software and Platforms

6.1. ARPEnTAge

Analyse de Régularités dans les Paysages : Environnement, Territoires, Agronomie
KEYWORDS: Stochastic process - Hidden Markov Models
FUNCTIONAL DESCRIPTION: ARPEnTAge is a software based on stochastic models (HMM2 and Markov Field) for analyzing spatio-temporal data-bases. ARPEnTAge is built on top of the CarottAge system to fully take into account the spatial dimension of input sequences. It takes as input an array of discrete data in which the columns contain the annual land-uses and the rows are regularly spaced locations of the studied landscape. It performs a Time-Space clustering of a landscape based on its time dynamic Land Uses (LUS). Displaying tools and the generation of Time-dominant shape files have also been defined.

- Partner: INRA
- Contact: Jean-François Mari
- URL: http://carottage.loria.fr/index_in_english.html

6.2. CarottAge

KEYWORDS: Stochastic process - Hidden Markov Models
FUNCTIONAL DESCRIPTION: The system CarottAge is based on Hidden Markov Models of second order and provides a non supervised temporal clustering algorithm for data mining and a synthetic representation of temporal and spatial data. CarottAge is currently used by INRA researchers interested in mining the changes in territories related to the loss of biodiversity (projects ANR BiodivAgrim and ACI Ecoger) and/or water contamination. CarottAge is also used for mining hydromorphological data. Actually a comparison was performed with three other algorithms classically used for the delineation of river continuum and CarottAge proved to give very interesting results for that purpose.

- Participants: Florence Le Ber and Jean-François Mari
- Partner: INRA
- Contact: Jean-François Mari
- URL: http://carottage.loria.fr/index_in_english.html

6.3. CORON

KEYWORDS: Data mining - Closed itemset - Frequent itemset - Generator - Association rule - Rare itemset
FUNCTIONAL DESCRIPTION: The Coron platform is a KDD toolkit organized around three main components: (1) Coron-base, (2) AssRuleX, and (3) pre- and post-processing modules.

The Coron-base component includes a complete collection of data mining algorithms for extracting itemsets such as frequent itemsets, closed itemsets, generators and rare itemsets. In this collection we can find APriori, Close, Pascal, Eclat, Charm, and, as well, original algorithms such as ZART, Snow, Touch, and Talky-G. AssRuleX generates different sets of association rules (from itemsets), such as minimal non-redundant association rules, generic basis, and informative basis. In addition, the Coron system supports the whole life-cycle of a data mining task and proposes modules for cleaning the input dataset, and for reducing its size if necessary.

- Participants: Adrien Coulet, Aleksey Buzmakov, Amedeo Napoli, Florent Marcuola, Jérémie Bourseau, Laszlo Szathmary, Mehdi Kaytoue, Victor Codocedo and Yannick Toussaint
- Contact: Amedeo Napoli
- URL: http://coron.loria.fr/site/index.php

6.4. LatViz: Visualization of Concept Lattices

- Contact: Amedeo Napoli
- URL: http://latviz.loria.fr/
- KEYWORDS: Formal Concept Analysis, Pattern Structures, Concept Lattice, Implications, Visualization

FUNCTIONAL DESCRIPTION.

LatViz is a tool allowing the construction, the display and the exploration of concept lattices. LatViz proposes some noticeable improvements over existing tools and introduces various functionalities focusing on interaction with experts, such as visualization of pattern structures for dealing with complex non-binary data, AOC-poset which is composed of the core elements of the lattice, concept annotations, filtering based on various criteria and a visualization of implications [70]. This way the user can effectively perform interactive exploratory knowledge discovery as often needed in knowledge engineering.

The LatViz platform can be associated with the Coron platform and extends its visualization capabilities (see http://coron.loria.fr). Recall that the Coron platform includes a complete collection of data mining algorithms for extracting itemsets and association rules.

6.5. OrphaMine: Data Mining Platform for Orphan Diseases

- Contact: Chedy Raïssi
- URL: http://orphamine.inria.fr/
- KEYWORDS: Bioinformatics, data mining, biology, health, data visualization, drug development.

FUNCTIONAL DESCRIPTION.

The OrphaMine platform enables visualization, data integration and in-depth analytics in the domain of “orphan diseases”, where data is extracted from the OrphaData ontology (http://www.orpha.net/consor/cgi-bin/index.php). At present, we aim at building a true collaborative portal that will serve different actors: (i) a general visualization of OrphaData data for physicians working, maintaining and developing this knowledge database about orphan diseases. (ii) the integration of analytics (data mining) algorithms developed by the different academic actors. (iii) the use of these algorithms to improve our general knowledge of rare diseases.

6.6. Siren: Interactive and Visual Redescription Mining

- Contact: Esther Catherine Galbrun
- URL: http://siren.gforge.inria.fr/main/
- KEYWORDS: Redescription mining, Interactivity, Visualization.

FUNCTIONAL DESCRIPTION.

Siren is a tool for interactive mining and visualization of redescriptions. Redescription mining aims to find distinct common characterizations of the same objects and, vice versa, to identify sets of objects that admit multiple shared descriptions. The goal is to provide domain experts with a tool allowing them to tackle their research questions using redescription mining. Merely being able to find redescriptions is not enough. The expert must also be able to understand the redescriptions found, adjust them to better match his domain knowledge and test alternative hypotheses with them, for instance. Thus, Siren allows mining redescriptions in an anytime fashion through efficient, distributed mining, to examine the results in various linked visualizations, to interact with the results either directly or via the visualizations, and to guide the mining algorithm toward specific redescriptions.

New features, such as a visualization of the contribution of individual literals in the queries and the simplification of queries as a post-processing, have been added to the tool.

PANAMA Project-Team

6. New Software and Platforms

6.1. FAuST

KEYWORDS: Learning - Sparsity - Fast transform - Multilayer sparse factorisation
SCIENTIFIC DESCRIPTION: FAuST allows to approximate a given dense matrix by a product of sparse matrices, with considerable potential gains in terms of storage and speedup for matrix-vector multiplications.
FUNCTIONAL DESCRIPTION: Faust 1.x contains Matlab routines to reproduce experiments of the PANAMA team on learned fast transforms.

Faust 2.x contains a C++ implementation with Matlab / Python wrappers (work in progress).
NEWS OF THE YEAR: A Software Development Initiative (ADT REVELATION) started in April 2018 for the maturation of FAuST. A first step achieved this year was to complete and robustify Matlab wrappers, to code Python wrappers with the same functionality, and to setup a continuous integration process. A second step was to simplify the parameterization of the main algorithms. The roadmap for next year includes showcasing examples and optimizing computational efficiency. – In 2017, new Matlab code for fast approximate Fourier Graph Transforms have been included. based on the approach described in the papers:

-Luc Le Magoarou, Rémi Gribonval, "Are There Approximate Fast Fourier Transforms On Graphs?", ICASSP 2016 .

-Luc Le Magoarou, Rémi Gribonval, Nicolas Tremblay, "Approximate fast graph Fourier transforms via multi-layer sparse approximations", IEEE Transactions on Signal and Information Processing over Networks,2017.

- Participants: Luc Le Magoarou, Nicolas Tremblay, Rémi Gribonval, Nicolas Bellot, Adrien Leman and Hakim Hadj-Djilani
- Contact: Rémi Gribonval
- Publications: Approximate fast graph Fourier transforms via multi-layer sparse approximations - Analyzing the Approximation Error of the Fast Graph Fourier Transform - Flexible Multi-layer Sparse Approximations of Matrices and Applications - Are There Approximate Fast Fourier Transforms On Graphs? - Efficient matrices for signal processing and machine learning - FAμST: speeding up linear transforms for tractable inverse problems - Chasing butterflies: In search of efficient dictionaries - Multi-layer Sparse Matrix Factorization
- URL: http://faust.inria.fr/

6.2. SPADE

Sparse Audio Declipper
KEYWORDS: Audio - Sparse regularization - Declipping
SCIENTIFIC DESCRIPTION: SPADE (the Sparse Audio Declipper) allows to reproduce audio declipping experiments from the papers:

- Srdan Kitic, Nancy Bertin, Remi Gribonval. Audio Declipping by Cosparse Hard Thresholding. iTwist - 2nd international - Traveling Workshop on Interactions between Sparse models and Technology, Aug 2014, Namur, Belgium.

- Srdan Kitic, Nancy Bertin, Remi Gribonval. Sparsity and cosparsity for audio declipping: a flexible non-convex approach. LVA/ICA 2015 - The 12th International Conference on Latent Variable Analysis and Signal Separation, Aug 2015, Liberec, Czech Republic.
FUNCTIONAL DESCRIPTION: SPADE is a declipping algorithm developed by the PANAMA project-team. To the best of our knowledge SPADE achieves state-of-the-art audio declipping quality. Real-time processing of audio streams is possible.

The web site http://spade.inria.fr provides example audio files and allows users to test SPADE on their own files, either by downloading Matlab routines or using Inria's software demonstration platform, A||go, to test it on the web.
NEWS OF THE YEAR: In 2018, the code has been robustified with the help of InriaTech for a potential industrial transfer. – In 2017, a web interface to demonstrate the potential of SPADE has been setup using the A||go platform.

- Participants: Nancy Bertin, Clement Gaultier, Ewen Camberlein, Romain Lebarbenchon, Alexandre Sanchez, Rémi Gribonval and Srdan Kitic
- Contact: Rémi Gribonval
- Publications: Audio Declipping by Cosparse Hard Thresholding - Sparsity and cosparsity for audio declipping: a flexible non-convex approach
- URL: http://spade.inria.fr/

6.3. FASST

Flexible Audio Source Separation Toolbox
KEYWORD: Audio signal processing
SCIENTIFIC DESCRIPTION: FASST is a Flexible Audio Source Separation Toolbox, designed to speed up the conception and automate the implementation of new model-based audio source separation algorithms.

FASST 1.0 development was achieved by the METISS team in Rennes and is now deprecated.

FASST 2.1 development was jointly achieved by the PAROLE team in Nancy and the (former) TEXMEX team in Rennes through an Inria funded ADT (Action de Développement Technologique). PANAMA contributed to the development by coordinating and performing user tests, and to the dissemination in a Show-and-Tell ICASSP poster [58]. While the first implementation was in Matlab, the new implementation is in C++ (for core functions), with Matlab and Python user scripts. Version 2, including speedup and new features was released in 2014 and can be downloaded from http://bass-db.gforge.inria.fr/fasst/ .

Version 2.2.2 (current version) has been released in May 2018. This version was developed in the PANAMA team through the Inria funded ADT "FFWD" (FASST For Wider Dissemination). A version 3.0 is currently under development and will be released in 2019.
FUNCTIONAL DESCRIPTION: FASST is a Flexible Audio Source Separation Toolbox designed to speed up the conception and automate the implementation of new model-based audio source separation algorithms. It is the only audio source separation software available to the public (QPL licence) which simultaneously exploits spatial and spectral cues on the sources to separate.
NEWS OF THE YEAR: Version 2.2.2 (current version) has been released in May 2018. This version was developed in the PANAMA team through the Inria funded ADT FFWD (FASST For Wider Dissemination). A version 3.0 is currently under development and will be released in 2019.

- Participants: Alexey Ozerov, Nancy Bertin, Ewen Camberlein, Romain Lebarbenchon, Emmanuel Vincent, Frédéric Bimbot and Yann Salaun
- Contact: Emmanuel Vincent
- URL: http://bass-db.gforge.inria.fr/fasst/

6.4. Multi-channel BSS Locate Basic

KEYWORDS: Audio - Localization - Signal processing - Multichannel signal
SCIENTIFIC DESCRIPTION: Multi-Channel BSS Locate is a Matlab toolbox to estimate Direction Of Arrival (expressed both in azimuth and elevation) of multiple sources in a multi-channel audio signal recorded by an array of microphones. This toolbox implements the previous 8 angular spectrum methods presented in BSS Locate (GCC-PHAT, GCC-NONLIN, MUSIC and several SNR-based spectra).

NEWS OF THE YEAR: In 2018, with the help of InriaTech, selected parts of Multi-channel BSS Locate were ported to C++ in the perspective of a transfer

- Authors: Charles Blandin, Ewen Camberlein, Romain Lebarbenchon, Emmanuel Vincent, Alexey Ozerov and Nancy Bertin
- Contact: Emmanuel Vincent
- URL: http://bass-db.gforge.inria.fr/bss_locate/

6.5. VoiceHome-2

KEYWORDS: Speech processing - Audio signal processing - Source Separation - Source localization
SCIENTIFIC DESCRIPTION: New, extended version of the voiceHome corpus for distant-microphone speech processing in domestic environments. This 5-hour corpus includes short reverberated, noisy utterances (smart home commands) spoken in French by 12 native French talkers in diverse realistic acoustic conditions and recorded by an 8-microphone device at various angles and distances and in various noise conditions. Noise-only segments before and after each utterance are included in the recordings. Clean speech and spontaneous speech recorded in 12 real rooms distributed in 4 different homes are also available. All data have been fully annotated.

- Participants: Nancy Bertin, Ewen Camberlein, Romain Lebarbenchon, Emmanuel Vincent, Sunit Sivasankaran, Irina Illina and Frédéric Bimbot
- Contact: Nancy Bertin
- Publication: VoiceHome-2, an extended corpus for multichannel speech processing in real homes

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

- Authors: 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.

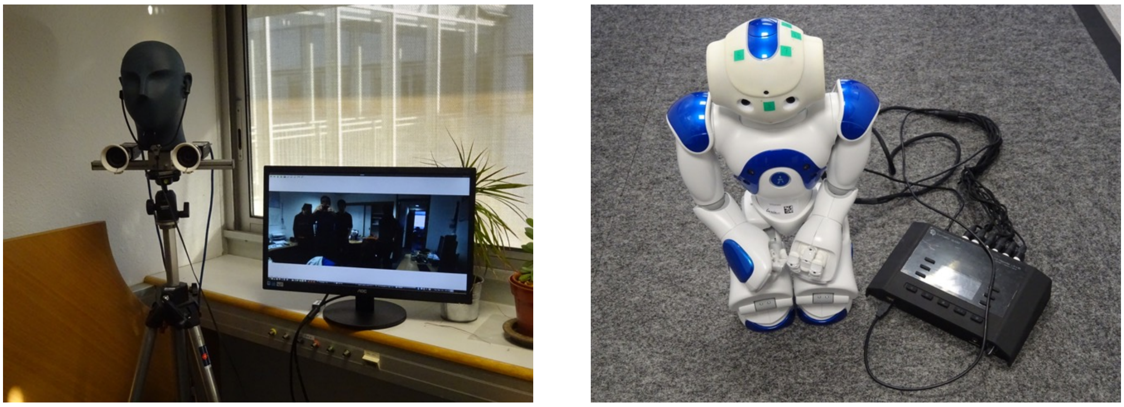


Figure 2. The Popeye+ audio-visual platform (left) delivers high-quality, high-resolution and wide-angle images at 30FPS. The NAO prototype used by PERCEPTION in the EARS STREP project has a twelve-channel spherical microphone array synchronized with a stereo camera pair.

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.

PETRUS Project-Team

6. New Software and Platforms

6.1. PLUG-DB ENGINE

KEYWORDS: Databases - Personal information - Privacy - Hardware and Software Platform
FUNCTIONAL DESCRIPTION: en PlugDB is a complete platform dedicated to a secure and ubiquitous management of personal data. It aims at providing an alternative to a systematic centralization of personal data. The PlugDB engine is a personal database server capable of storing data (tuples and documents) in tables and BLOBs, indexing them, querying them in SQL, sharing them through assertional access control policies and enforcing transactional properties (atomicity, integrity, durability).

The PlugDB engine is embedded in a tamper-resistant hardware device combining the security of smartcard with the storage capacity of NAND Flash. The personal database is hosted encrypted in NAND Flash and the PlugDB engine code runs in the microcontroller. Complementary modules allow to pre-compile SQL queries for the applications, communicate with the DBMS from a remote Java program, synchronize local data with remote servers (typically used for recovering the database in the case of a broken or lost devices) and participate in distributed computation (e.g., global queries). PlugDB runs both on secure devices provided by Gemalto and on specific secure devices designed by PETRUS and assembled by electronic SMEs. Mastering the hardware platform opens up new research and experiment opportunities (e.g., support for wireless communication, secure authentication, sensing capabilities, battery powered ...). PlugDB engine has been registered first at APP (Agence de Protection des Programmes) in 2009 - a new version being registered every two years - and the hardware datasheets in 2015.

PlugDB has been experimented in the field, notably in the healthcare domain. We also recently set up an educational platform on top of PlugDB, named SIPD (Système d'Information Privacy-by-Design) and used at ENSIIE, INSA CVL and UVSQ through the Versailles Sciences Lab fablab, to raise students awareness of privacy protection problems and embedded programming. As a conclusion, PlugDB combines several research contributions from the team, at the crossroads of flash data management, embedded data processing and secure distributed computations. It then strongly federates all members of our team (permanent members, PhD students and engineers). It is also a vector of visibility, technological transfer and dissemination and gives us the opportunity to collaborate with researchers from other disciplines around a concrete privacy-enhancing platform.

PlugDB is now being industrialized in the context of the OwnCare Inria Innovation Lab (II-Lab). In OwnCare, PlugDB acts as a secure personal cloud to manage medical/social data for people receiving care at home. It should be deployed over 10.000 patient in the Yvelines district. The industrialization process covers the development of a complete testing environment, the writing of a detailed documentation and the development of additional features (e.g., embedded ODBC driver, TPM support, flexible access control model and embedded code upgrade notably). It has also required the design of a new hardware platform equipped with a battery power supply, introducing new energy consumption issues for the embedded software.

- Participants: Aydogan Ersoz, Laurent Schneider, Luc Bouganim, Nicolas Anciaux and Philippe Pucheral
- Contact: Nicolas Anciaux
- URL: https://project.inria.fr/plugdb/

POTIOC Project-Team

6. New Software and Platforms

6.1. Aïana

KEYWORD: Multimedia player
FUNCTIONAL DESCRIPTION: This software aims to make accessible the playing of a MOOC composed of various information flows (boards, videos, subtitles ...). It is not intended to be "reserved" for people with disabilities but rather to be open to as many as possible by allowing each user to adapt the interface, and therefore the use, to its users own capabilities and needs.

- Authors: Damien Caselli, Pierre-Antoine Cinquin, Pascal Guitton and Hélène Sauzéon
- Partner: Université de Bordeaux
- Contact: Pascal Guitton
- Publications: Towards Truly Accessible MOOCs for Persons with Cognitive Disabilities: Design and Field Assessment - Online e-learning and cognitive disabilities: A systematic review

6.2. HybridOptics : Hybrid Optical Platform

KEYWORDS: Augmented reality - Education - Tangible interface
FUNCTIONAL DESCRIPTION: The software platform - gets the values of the sensors - computes in real-time the result of the simulation - generates pedagogical supports that are directly linked to the simulation (projected on the work table) - allows the user to control several parameters from a dedicated application on a tablet

- Participants: Benoît Coulais, Lionel Canioni, Bruno Bousquet, Martin Hachet and Jean-Paul Guillet
- Contact: Martin Hachet
- URL: https://project.inria.fr/hobit/

6.3. Platforms

6.3.1. HOBIT

In 2018, we have continued working on the HOBIT platform dedicated to teaching and training of Optics at University. We have notably improved the hardware side, as illustrated in Figure 3 .

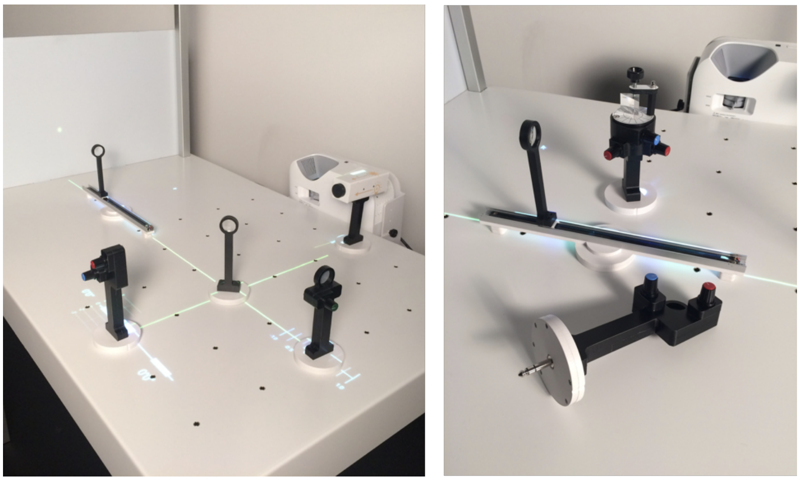


Figure 3. The new version of HOBIT. Users can easily plug fake optical components (e.g. source lights, mirrors and lens) anywhere on the table to build their optical experiment.

RAINBOW Project-Team

6. New Software and Platforms

6.1. bib2html

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

- Partners: Inria - Université de Rennes 1
- Contact: Éric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html

6.2. HandiViz

Driving assistance of a wheelchair
KEYWORDS: Health - Persons attendant - Handicap
FUNCTIONAL DESCRIPTION: The HandiViz software proposes a semi-autonomous navigation framework of a wheelchair relying on visual servoing.

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

- Participants: François Pasteau and Marie Babel
- Partner: INSA Rennes
- Contact: Marie Babel

6.3. SINATRACK

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

- Participants: Antoine Guillaume Petit, Éric Marchand and François Chaumette
- Partners: Inria - Université de Rennes 1
- Contact: Éric Marchand

6.4. UsTk

Ultrasound toolkit for medical robotics applications guided from ultrasound images
KEYWORDS: Echographic imagery - Image reconstruction - Medical robotics - Visual tracking - Visual servoing (VS) - Needle insertion

FUNCTIONAL DESCRIPTION: UsTK, standing for Ultrasound Toolkit, is a cross-platform extension of ViSP software dedicated to two- (2D) and three-dimensional (3D) ultrasound image processing and visual servoing based on ultrasound images. Written in C++, UsTK architecture provides a core module that implements all the data structures at the heart of UsTK, a grabber module that allows to acquire ultrasound images from an Ultrasonix or a Sonosite device, a GUI module to display data, an IO module for providing functionalities to read/write data from a storage device, and a set of image processing modules to compute the confidence map of ultrasound images, generate elastography images, track a flexible needle in sequences of 2D and 3D ultrasound images and track a target image template in sequences of 2D ultrasound images. All these modules were implemented on several robotic demonstrators to control the motion of an ultrasound probe or a flexible needle by ultrasound visual servoing.

- Participants: Alexandre Krupa, Marc Pouliquen, Fabien Spindler and Pierre Chatelain
- Partners: Inria - Université de Rennes 1
- Contact: Alexandre Krupa
- URL: https://ustk.inria.fr

6.5. ViSP

Visual servoing platform

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

SCIENTIFIC DESCRIPTION: Since 2005, we develop and release ViSP [1], an open source library available from https://visp.inria.fr. ViSP standing for Visual Servoing Platform allows prototyping and developing applications using visual tracking and visual servoing techniques at the heart of the Rainbow research. ViSP was designed to be independent from the hardware, to be simple to use, expandable and cross-platform. ViSP allows to design vision-based tasks for eye-in-hand and eye-to-hand visual servoing that contains the most classical visual features that are used in practice. It involves a large set of elementary positioning tasks with respect to various visual features (points, segments, straight lines, circles, spheres, cylinders, image moments, pose...) that can be combined together, and image processing algorithms that allow tracking of visual cues (dots, segments, ellipses...) or 3D model-based tracking of known objects or template tracking. Simulation capabilities are also available.

[1] E. Marchand, F. Spindler, F. Chaumette. ViSP for visual servoing: a generic software platform with a wide class of robot control skills. IEEE Robotics and Automation Magazine, Special Issue on "Software Packages for Vision-Based Control of Motion", P. Oh, D. Burschka (Eds.), 12(4):40-52, December 2005.

FUNCTIONAL DESCRIPTION: ViSP provides simple ways to integrate and validate new algorithms with already existing tools. It follows a module-based software engineering design where data types, algorithms, sensors, viewers and user interaction are made available. Written in C++, ViSP is based on open-source cross-platform libraries (such as OpenCV) and builds with CMake. Several platforms are supported, including OSX, iOS, Windows and Linux. ViSP online documentation allows to ease learning. More than 300 fully documented classes organized in 17 different modules, with more than 380 examples and 82 tutorials are proposed to the user. ViSP is released under a dual licensing model. It is open-source with a GNU GPLv2 or more recent license. A professional edition license that replaces GNU GPLv2 is also available.

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

6.6. Platforms

6.6.1. Robot Vision Platform

Participants: François Chaumette, Fabien Spindler [contact].

We exploit two industrial robotic systems built by Afma Robots in the nineties to validate our researches in visual servoing and active vision. The first one is a 6 DoF Gantry robot, the other one is a 4 DoF cylindrical robot (see Fig. 2). These robots are equipped with cameras. The Gantry robot also allows embedding grippers on its end-effector.

Note that 3 papers [53], [78], [10] and 1 PhD Thesis [2] published by Rainbow in 2018 include results validated on this platform.

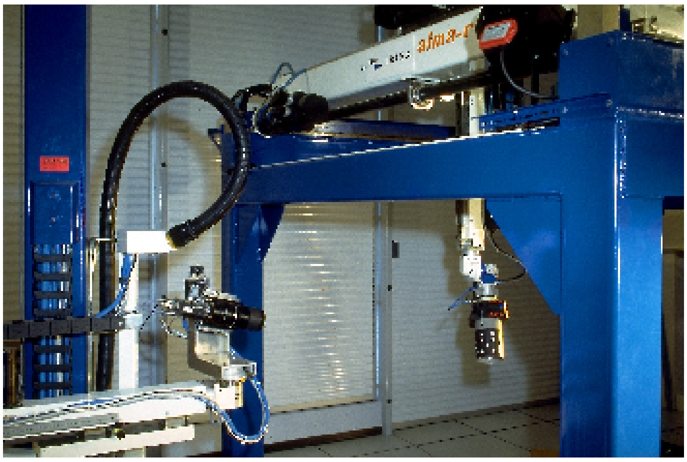


Figure 2. Rainbow robotics platform for vision-based manipulation

6.6.2. Mobile Robots

Participants: Marie Babel, Solenne Fortun, François Pasteau, Fabien Spindler [contact].

For fast prototyping of algorithms in perception, control and autonomous navigation, the team uses a Pioneer 3DX from Adept (see Fig. 3 .a). This platform is equipped with various sensors needed for autonomous navigation and sensor-based control.

Moreover, to validate our research in personally assisted living topic (see Section 7.4.3), we have three electric wheelchairs, one from Permobil, one from Sunrise and the last from YouQ (see Fig. 3 .b). The control of the wheelchair is performed using a plug and play system between the joystick and the low level control of the wheelchair. Such a system lets us acquire the user intention through the joystick position and control the wheelchair by applying corrections to its motion. The wheelchairs have been fitted with cameras and ultrasound sensors to perform the required servoing for assisting handicapped people. This year we also bought a wheelchair haptic simulator to develop new human interaction strategies in an virtual reality environment (Fig. 3 (c)).

Note that 4 papers exploiting the mobile robots were published this year [23], [60], [79], [80].

6.6.3. Medical Robotic Platform

Participants: Alexandre Krupa, Marc Pouliquen, Fabien Spindler [contact].

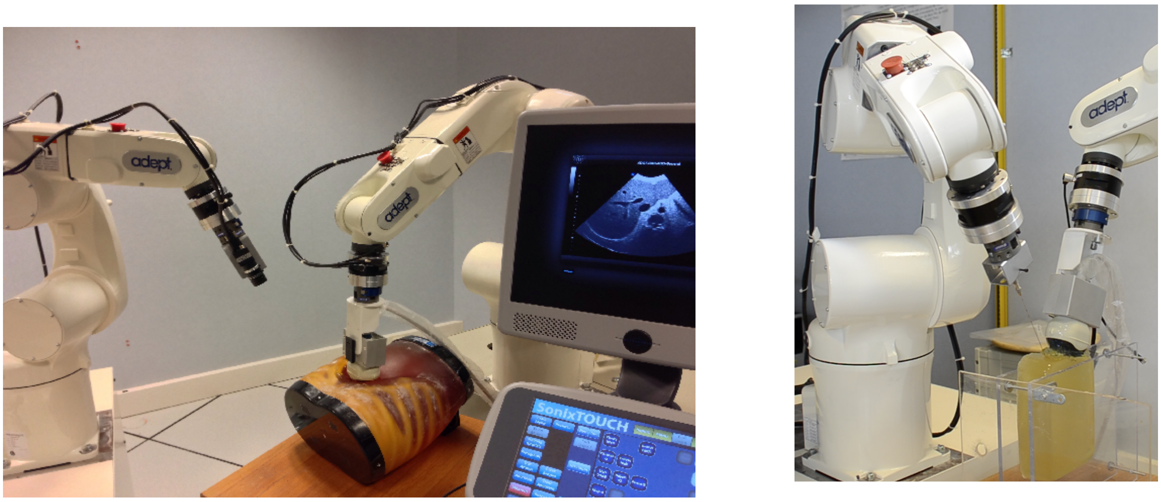
This platform is composed of two 6 DoF Adept Viper arms (see Fig. 4 .a). Ultrasound probes connected either to a SonoSite 180 Plus or an Ultrasonix SonixTouch imaging system can be mounted on a force torque sensor attached to each robot end-effector. The haptic Virtuose 6D device (see Fig. 8 .a) can also be used within this platform.

(a) (b) (c)

Figure 3. Mobile Robot Platform. a) Pioneer P3-DX robot, b) wheelchairs from Permobil, Sunrise and YouQ, c) the wheelchair haptic simulator.

This testbed is of primary interest for researches and experiments concerning ultrasound visual servoing applied to probe positioning, soft tissue tracking, elastography or robotic needle insertion tasks (see Section 7.2.9).

This platform was used to obtain experimental results presented in 6 articles [18], [61], [12], [10], [36], [51] and in 2 PhD manuscripts [4], [5] published this year.



(a) (b)

Figure 4. Rainbow medical robotic platforms. a) On the right Viper S850 robot arm equipped with a SonixTouch 3D ultrasound probe. On the left Viper S650 equipped with a tool changer that allows to attach a classical camera or biopsy needles. b) Robotic setup for autonomous needle insertion by visual servoing.

6.6.4. Advanced Manipulation Platform

Participants: François Chaumette, Claudio Pacchierotti, Paolo Robuffo Giordano, Fabien Spindler [contact].

This new platform is composed by 2 Panda lightweight arms from Franka Emika equipped with torque sensors in all seven axes. An electric gripper, a camera or a soft hand from qbrobotics can be mounted on the robot end-effector (see Fig. 5) to validate our researches in coupling force and vision for controlling robot manipulators (see Section 7.2.13) and in shared control for remote manipulation (see Section 7.4.1). Other haptic devices (see Section 6.6.7) can also be coupled to this platform.

Note that 1 paper published this year include experimental results obtained with new platform [77].

Figure 5. Rainbow advanced manipulation platform. One of the two Panda lightweight arms from Franka Emika, with mounted the Pisa SoftHand.

6.6.5. Humanoid Robots

Participants: François Chaumette, Julien Pettré, Fabien Spindler [contact].

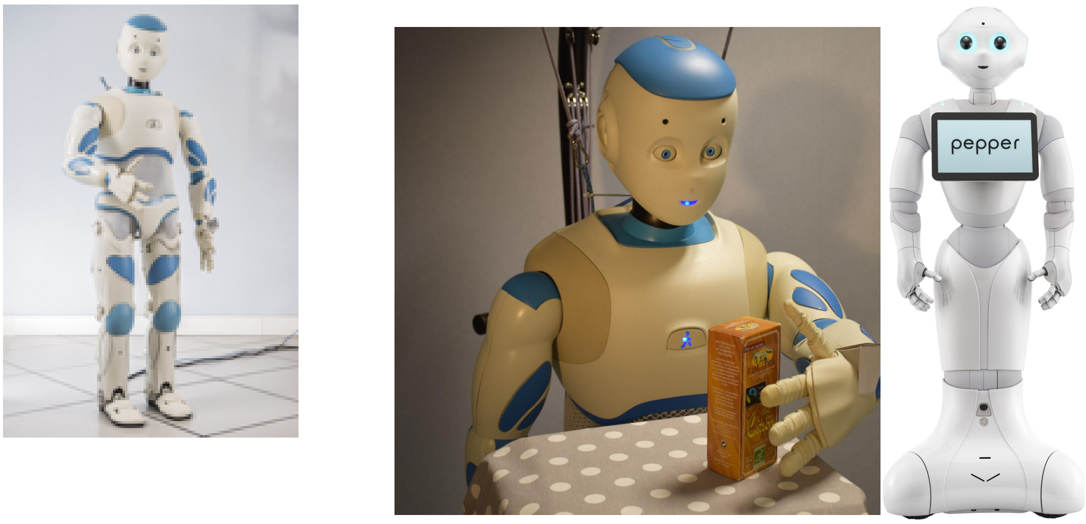
Romeo is a humanoid robot from SoftBank Robotics which is intended to be a genuine personal assistant and companion. Only the upper part of the body (trunk, arms, neck, head, eyes) is working. This research platform is used to validate our researches in visual servoing and visual tracking for object manipulation (see Fig. 6 .a).

Pepper, another human-shaped robot designed by SoftBank Robotics to be a genuine day-to-day companion (see Fig. 6 .b) is also part of this platform. It has 17 DoF mounted on a wheeled holonomic base and a set of sensors (cameras, laser, ultrasound, inertial, microphone) that makes this platform interesting for robot-human interactions during locomotion (see Section 7.2.5).

Note that 2 papers published this year include experimental results obtained with this platform [24], [23].

6.6.6. Unmanned Aerial Vehicles (UAVs)

Participants: Pol Mordel, Paolo Robuffo Giordano, Fabien Spindler [contact].



(a) (b)

Figure 6. Humanoid Robots Platform. a) Romeo experimental platform, b) Pepper human-shaped robot

From 2014, Rainbow also started some activities involving perception and control for single and multiple quadrotor UAVs, especially thanks to the ANR project "SenseFly" (see Section 9.2.1). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (see Fig. 7 .a), and one quadrotor from 3DRobotics, USA (see Fig. 7 .b). The Mikrokopter quadrotors have been heavily customized by: (i) reprogramming from scratch the low-level attitude controller onboard the microcontroller of the quadrotors, (ii) equipping each quadrotor with a NVIDIA Jetson TX2 board running Linux Ubuntu and the TeleKyb-3 software based on genom3 framework developed at LAAS in Toulouse (the middleware used for managing the experiment flows and the communication among the UAVs and the base station), and (iii) purchasing the Flea Color USB3 cameras together with the gimbal needed to mount them on the UAVs. The quadrotor group is used as robotic platforms for testing a number of single and multiple flight control schemes with a special attention on the use of onboard vision as main sensory modality.

This year 7 papers [33], [34], [65], [67], [72], [17], [71] and 1 PhD Thesis [7] contain experimental results obtained with this platform.

6.6.7. Haptics and Shared Control Platform

Participants: Claudio Pacchierotti, Paolo Robuffo Giordano, Fabien Spindler [contact].

Various haptic devices are used to validate our research in shared control. We have a Virtuose 6D device from Haption (see Fig. 8 .a). This device is used as master device in many of our shared control activities (see Sections 9.3.1.3 , 7.2.10 , and 7.3.1). It could also be coupled to the Haption haptic glove in loan from the University of Birmingham. An Omega 6 (see Fig. 8 .b) from Force Dimension, devices in loan from Ultrahaptics as well as a soft hand from qbrobotics complete this platform that could be coupled to the other robotic platforms.

This platform was used to obtain experimental results presented in 2 articles [51], [36] and in 1 PhD manuscript [5] published this year.

(a) (b)

Figure 7. Unmanned Aerial Vehicles Platform. a) Quadrotor XL1 from Mikrokopter, b) Quadrotor Iris from 3DRobotics

(a) (b)

Figure 8. Haptics and Shared Control Platform. a) Virtuose 6D and b) Omega 6 haptic devices

RITS Project-Team

6. New Software and Platforms

6.1. PML-SLAM

KEYWORD: Localization

SCIENTIFIC DESCRIPTION: Simultaneous Localization and Mapping method based on 2D laser data.

- Participants: Fawzi Nashashibi and Zayed Alsayed
- Contact: Fawzi Nashashibi

6.2. V2Provue

Vehicle-to-Pedestrian

FUNCTIONAL DESCRIPTION: It is a software developed for the Vehicle-to-Pedestrian (V2P) communications, risk calculation, and alarming pedestrians of collision risk. This software is made of an Android application dedicated to pedestrians and RtMaps modules for the vehicles.

On the pedestrian side, the application is relying on GPS data to localize the user and Wi-Fi communications are used to receive messages about close vehicles and send information about the pedestrian positioning. Besides, a service has been developed to evaluate the collision risk with the vehicles near the pedestrian and an HMI based on OpenStreetMap displays all the useful information such as pedestrian and vehicles localization and, collision risk.

On the vehicle side, RtMaps modules allowing V2X communications have been developed. These modules contain features such as TCP/UDP socket transmissions, broadcast, multicast, unicast communications, routing, forwarding algorithms, and application specific modules. In the V2ProVu software, a particular application module has been implemented to create data packets containing information about the vehicle state (position, speed, yaw rate,...) and the V2X communication stack is used to broadcast these packets towards pedestrians. Moreover, the V2proVu application can also receive data from pedestrians and create objects structures that can be shared with the vehicle perception tools.

- Contact: Fawzi Nashashibi

6.3. SimConVA

Connected Autonomous Vehicles Simulator

FUNCTIONAL DESCRIPTION: The software provides an interface between the network simulator ns-3 (https://www.nsnam.org/) and the modular prototyping framework RTMaps (https://intempora.com/).

This code allows to create an RTMaps component which activates and controls the ns-3 simulator. The component handles the sending and reception of data packets between ns-3 and RTMaps for each vehicle. It also handles the mobility of vehicles in ns-3 using their known position in RTMaps.

- Authors: Pierre Merdrignac, Oyunchimeg Shagdar and Jean-Marc Lasgouttes
- Contact: Jean-Marc Lasgouttes

SEMAGRAMME Project-Team

5. New Software and Platforms

5.1. ACGtk

Abstract Categorial Grammar Development Toolkit
KEYWORDS: Natural language processing - NLP - Syntactic analysis - Semantics
SCIENTIFIC DESCRIPTION: Abstract Categorial Grammars (ACG) are a grammatical formalism in which grammars are based on typed lambda-calculus. A grammar generates languages: the abstract language (the language of parse structures), and the object language (the language of the surface forms, e.g., strings, or higher-order logical formulas), which is the realization of the abstract language.

ACGtk provides two softwares to develop and to use ACGs: acgc, which is a grammar compiler, and acg, which is an interpreter of a command language that allows us, for instance, to parse and realize terms.
FUNCTIONAL DESCRIPTION: ACGtk provides softwares for developing and using Abstract Categorial Grammars (ACG).
NEWS OF THE YEAR: The new version extends the syntax for defining operators that can be used in grammars and removes dependencies to obsolete libraries. It also introduces some light optimizations compared to the previous one.

- Participants: Philippe De Groote, Jiri Marsik, Sylvain Pogodalla and Sylvain Salvati
- Contact: Sylvain Pogodalla
- Publications: A syntax-semantics interface for Tree-Adjoining Grammars through Abstract Categorial Grammars - ACGTK: un outil de développement et de test pour les grammaires catégorielles abstraites - Discourse Modeling with Abstract Categorial Grammars - On the expressive power of Abstract Categorial Grammars: Representing context-free formalisms - Towards abstract categorial grammars
- URL: http://acg.loria.fr/

5.2. Dep2pict

KEYWORDS: Syntactic analysis - Semantics
FUNCTIONAL DESCRIPTION: Dep2pict is a program for drawing graphical representation of dependency structures of natural language sentences. Dep2pict takes into account the modified format mixing surface and deep syntactic information used in deep-sequoia.
NEWS OF THE YEAR: The software was adapted to some extensions of the CoNLL format. A new Graphical User Interface (based on PyQt5) was built to replaced the previous one (https://gitlab.inria.fr/dep2pict/gui). It can be installed through PyPI (https://pypi.org/project/dep2pict-gui/)

- Contact: Bruno Guillaume
- URL: http://dep2pict.loria.fr/

5.3. Grew

Graph Rewriting
KEYWORDS: Semantics - Syntactic analysis - Natural language processing - Graph rewriting
FUNCTIONAL DESCRIPTION: Grew is a Graph Rewriting tool dedicated to applications in NLP. Grew takes into account confluent and non-confluent graph rewriting and it includes several mechanisms that help to use graph rewriting in the context of NLP applications (built-in notion of feature structures, parametrization of rules with lexical information).

NEWS OF THE YEAR: In 2018, the version 1.0 of Grew was released. The major novelties are a new implementation of lexical rules and the introduction of a Python binding (described in the book: Application of Graph Rewriting to Natural Language Processing)

- Participants: Bruno Guillaume, Guy Perrier and Guillaume Bonfante
- Contact: Bruno Guillaume
- Publications: Application de la réécriture de graphes au traitement automatique des langues - Application of Graph Rewriting to Natural Language Processing
- URL: http://grew.fr/

5.4. ZombiLingo

KEYWORDS: Syntactic analysis - Natural language processing - Lexical resource - Collaborative science
FUNCTIONAL DESCRIPTION: ZombiLingo is a prototype of a GWAP (Game With A Purpose) where gamers have to give linguistic information about the syntax of natural language sentence, currently in French, and later to other languages.
NEWS OF THE YEAR: The code was factorized and 3 independant librairies where built (available in the github project: https://github.com/gwaps4nlp/ to facilitate their usage in other projects.

- Authors: Bruno Guillaume, Karën Fort, Nicolas Lefebvre and Valentin Stern
- Contact: Karën Fort
- URL: http://zombilingo.org/

SIROCCO Project-Team

6. New Software and Platforms

6.1. QuantizationAE

KEYWORDS: Compression - Machine learning
FUNCTIONAL DESCRIPTION: This code learns an autoencoder to compress images. The learning is performed under a rate-distortion criterion, and jointly learns a transform (the autoencoder) and the quantization step for target rate points.The code is organized as follows. It first builds a set of luminance images (B1) for the auto-encoder training, a set of luminance images (B2) to analyze how the auto-encoder training advances and a set of luminance images (B3) to evaluate the auto-encoders in terms of rate-distortion. It then trains several auto-encoders using a rate-distortion criterion on the set B1. The quantization can be either fixed or learned during this training stage. The set B2 enables to periodically compute indicators to detect overfitting. It finally compares the auto-encoders in terms of rate-distortion on the set B3. The quantization can be either fixed or variable during this test.

- Participants: Aline Roumy, Christine Guillemot and Thierry Dumas
- Contact: Aline Roumy

6.2. LF-Inpainting

Light field inpainting based on a low rank model
KEYWORDS: Light fields - Low rank models - Inpainting
FUNCTIONAL DESCRIPTION: This code implements a method for propagating the inpainting of the central view of a light field to all the other views. To this end, it also implements a new matrix completion algorithm, better suited to the inpainting application than existing methods. A first option does not require any depth prior, unlike most existing light field inpainting algorithms. The code also implements an extended version to better handle the case where the area to inpaint contains depth discontinuities.

- Participants: Mikael Le Pendu and Christine Guillemot
- Contact: Christine Guillemot

6.3. LF-HLRA

Light fields homography-based low rank approximation
KEYWORDS: Compression - Light fields - Low rank models - Dimensionality reduction
FUNCTIONAL DESCRIPTION: This code jointly searches for homographies to align the views of an input light field together with the components of its low rank approximation model. The code either uses a global homography per view or multiple homographies, one per region, the region being extracted using depth information.

- Participants: Xiaoran Jiang, Mikael Le Pendu and Christine Guillemot
- Contact: Christine Guillemot

6.4. GBR-MVimages

Graph-based representation for multi-view and light field images
KEYWORDS: Light fields - Multi-View reconstruction - Graph

FUNCTIONAL DESCRIPTION: Graph-Based Representation (GBR) describes color and geometry of multiview or light field image content using a graph. The graph vertices represent the color information, while the edges represent the geometry information, i.e., the disparity, by connecting corresponding pixels in neighboring images.

- Participants: Xin Su and Thomas Maugey
- Contact: Thomas Maugey

6.5. FastLFInpainting

Fast light field inpainting
KEYWORDS: Inpainting - Light fields
FUNCTIONAL DESCRIPTION: This software implements a method for fast and efficient inpainting of light fields. It computes disparity based on smoothed structure tensors, that is then used for propagating, by angular warping, the inpainted texture of one view to the entire light field. The code allows inpainting a light field of 80 views in a few seconds (from 4 to 15s, depending on the size of the region to be inpainted). The software has been registered at APP under the number IDDN.FR.001.290017.000.S.P.2018.000.21000.

- Participants: Pierre Allain, Laurent Guillo and Christine Guillemot
- Contact: Laurent Guillo

6.6. M360CT

Multi-360 Calibration Toolkit
KEYWORDS: Omnidirectional camera - Calibration - FTV - 6DoF
FUNCTIONAL DESCRIPTION: Based on multiple synchronized sequences of a chessboard pattern moving in the scene, the algorithm computes the internal and external camera parameters of the different cameras under the unified spherical model. This software is composed of two executables, the first one for the individual calibration of each camera, the second one for the fusion of all the outputs of the first executable. The work has been submitted at APP with the number IDNN.FR.001.510008.S.P.2018.000.10800.

- Participants: Cédric Le Cam, Thomas Maugey and Laurent Guillo
- Contact: Thomas Maugey
- URL: http://project.inria.fr/ftv360

6.7. Platforms

6.7.1. Light field editor

Participants: Pierre Allain, Laurent Guillo, Christine Guillemot.

As part of the ERC Clim project, the EPI Sirocco is developing a light field editor, a tool analogous to traditional image editors such as the GNU image manipulation program Gimp or the raster graphic editor Photoshop but dedicated to light fields. As input data, this tool accepts for instance sparse light fields acquired with High Density Camera Arrays (HDCA) or denser light fields captured with microlens array (MLA). Two kinds of features are provided. Traditional features such as changing the angle of view, refocusing or depth map extraction are or will be soon supported. More advanced features are being integrated in our tool as libraries we have developed, such as inpainting to support light field manipulations like object removal, and denoising in the 4D ray space. The next steps are to integrate libraries enabling scene depth estimation and view synthesis. The tool and libraries are developed in C++ and the graphical user interface relies on Qt.

6.7.2. Acquisition of multi-view sequences for Free viewpoint Television

Participants: Cédric Le Cam, Laurent Guillo, Thomas Maugey.

The scientific and industrial community is nowadays exploring new multimedia applications using 3D data (beyond stereoscopy). In particular, Free viewpoint Television (FTV) has attracted much attention in the recent years. In those systems, the user can choose in real time its view angle from which he/she wants to observe the scene. Despite the great interest for FTV, the lack of realistic and ambitious datasets penalizes the research effort. The acquisition of such sequences is very costly in terms of hardware and working effort, which explains why no multi-view videos suitable for FTV has been proposed yet.

In the project ATeP (funded by Inriahub), we have developed a novel acquisition procedure relying on forty synchronized omnidirectional cameras. The captured content allows an omni-directional visualization of the scene at a set of discrete viewpoints corresponding to the pre-defined camera positions. We also propose a calibration technique to estimate the position and orientation of each camera with respect to a same reference. This solution relies on a calibration of each individual camera, and a graph-based synchronization of all the estimated parameters.

Based on these developed tools, we have built a complete dataset that we share on the following website *https://project.inria.fr/ftv360*. Our dataset is made of two different captures (indoor and outdoor), with, in total 8 different sequences (each of them having 40 synchronized videos of 1 to 4 min long). The calibration parameters are shared with the calibration toolkit that was developed during the project. These data can serve for the development of new tools for FTV, such as: view synthesis, depth estimation, super resolution, inpainting, etc.

6.7.3. Light fields datasets

Participants: Pierre Allain, Christine Guillemot, Laurent Guillo.

The EPI Sirocco makes extensive use of light field datasets with sparse or dense contents provided by the scientific community to run tests. However, it has also generated its own natural and synthetic contents.

Natural content has been created with Lytro cameras (the original first generation Lytro and the Lytro Illum). The team also owns a R8 Raytrix plenoptic cameras with which still and video contents have been captured. Applications taking advantage of the Raytrix API have been developed to extract views from the Raytrix lightfield. The number of views per frame is configurable and can be set for instance to 3x3 or 9x9 according to the desired sparsity. A dataset of video light fields captured by our raytrix R8 camera has been proposed to the MPEG-I standardization group and retained for test purposes [24].

Synthetic content exists for dense light fields with small baselines. To address issues of scene depth estimation and of view synthesis in more difficult configurations like in the case of large baselines, we have produced two datasets that we use for training neural networks for scene depth estimation from light fields with small and large baselines. Most of our rendered light field scenes are indoor scenes, with light reflection and diffusion on the object surfaces to make them more realistic. Both dense and sparse light fields of 9×9 views of 512×512 pixels have been rendered from the input 3D models, with a disparity range of $[-20, +20]$ for sparse light fields and $[-4, +4]$ for dense light fields. The dense and sparse light fields datasets contains 43 and 53 scene respectively. They are provided together with the ground truth depth maps.

Similarly, as no publicly available dataset exist for video light fields, we have produced our own data set from the Sintel film (https://durian.blender.org/download/), which is a short computer animated film by the Blender institute, part of the Blender Foundation. A specific Blender add-on is used to extract views from a frame. As previously, the number of views is configurable. Synthetic contents present the advantage to provide a ground truth useful to evaluate how accurate our algorithms are to compute, for instance, the depth maps and the scene flows. At the moment, the dataset contains two synthetic video light fields of 50 frames.

All these contents are made available via the project web site: http://clim.inria.fr/DataSoftware.html

STARS Project-Team

6. New Software and Platforms

6.1. SUP

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

- Participants: Etienne Corvée, François Brémond, Thanh Hung Nguyen and Vasanth Bathrinarayanan
- Partners: CEA - CHU Nice - USC Californie - Université de Hamburg - I2R
- Contact: François Brémond
- URL: https://team.inria.fr/stars/software

6.2. VISEVAL

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

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

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

TITANE Project-Team

6. New Software and Platforms

6.1. CGAL Barycentric_coordinates_2

Module CGAL : Barycentric coordinates 2D
KEYWORD: Computational geometry
FUNCTIONAL DESCRIPTION: This package offers an efficient and robust implementation of two-dimensional closed-form generalized barycentric coordinates defined for simple two-dimensional polygons.

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

6.2. dtk-nurbs-probing

KEYWORDS: Algorithm - CAD - Numerical algorithm - Geometric algorithms
FUNCTIONAL DESCRIPTION: This library offers tools for computing intersection between linear primitives and the constitutive elements of CAD objects (curves and surfaces). It is thus possible to compute intersections between a linear primitive with a trimmed or untrimmed NURBS surface, as well with Bezier surfaces. It is also possible, in the xy plane, to compute the intersections between linear primitives and NURBS curves as well as Bezier curves.

- Participants: Come Le Breton, Laurent Busé and Pierre Alliez
- Contact: Come Le Breton

6.3. MeshMantics

KEYWORDS: Classification - 3D modeling
FUNCTIONAL DESCRIPTION: This software component enables the classification of surface meshes in accordance to common outdoor urban classes such as ground, facades, walls, roofs and vegetation.

- Participants: Florent Lafarge, Pierre Alliez and Yannick Verdié
- Contact: Pierre Alliez

6.4. Module CGAL : Point Set Processing

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

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

6.5. Module CGAL : Scale space surface reconstruction

KEYWORD: Geometric algorithms

SCIENTIFIC DESCRIPTION: This CGAL package implements a surface reconstruction method which takes as input an unordered point set and computes a triangulated surface mesh interpolating the point set. We assume that the input points were sampled from the surface of an object. The method can also process point sets sampled from the interior of the object, although we cannot provide guarantees on the output. This method can handle a decent amount of noise and outliers. The point set may greatly undersample the object in occluded regions, although no surface will be reconstructed to fill these regions.
FUNCTIONAL DESCRIPTION: This method allows to reconstruct a surface that interpolates a set of 3D points. This method provides an efficient alternative to the Poisson surface reconstruction method. The main difference in output is that this method reconstructs a surface that interpolates the point set (as opposed to approximating the point set). How the surface connects the points depends on a scale variable, which can be estimated semi-automatically.

- Participants: Pierre Alliez and Thijs Van Lankveld
- Contact: Pierre Alliez

6.6. Skeleton-Blockers

Skeleton-Blockers data-structure
KEYWORDS: C++ - Mesh - Triangulation - Topology - 3D
FUNCTIONAL DESCRIPTION: Skeleton-Blockers is a compact, efficient and generic data-structure that can represent any simplicial complex. The implementation is in C++11.

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

6.7. Structure-preserving decimation

KEYWORDS: Mesh - 3D - Multi-View reconstruction
FUNCTIONAL DESCRIPTION: Structure-preserving decimation is a software that can simplify 3D meshes while preserving some of their structure. Simplification can be done either with a command line or with a graphical user interface that allows to combine several operations including several simplification methods.

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

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 perfomances 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 choses 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

VALDA Project-Team

5. New Software and Platforms

5.1. ProvSQL

KEYWORDS: Databases - Provenance - Probability
FUNCTIONAL DESCRIPTION: The goal of the ProvSQL project is to add support for (m-)semiring provenance and uncertainty management to PostgreSQL databases, in the form of a PostgreSQL extension/module/plugin.
NEWS OF THE YEAR: Support for where-provenance has been completed. Numerous bug fixes. A docker version has been produced, for ease of installation. Demonstration scenarios are included.

- Participants: Pierre Senellart and Yann Ramusat
- Contact: Pierre Senellart
- Publications: Provenance and Probabilities in Relational Databases: From Theory to Practice - ProvSQL: Provenance and Probability Management in PostgreSQL
- URL: https://github.com/PierreSenellart/provsql

5.2. WAE

Web archive explorer
KEYWORDS: Information extraction - Web archives
FUNCTIONAL DESCRIPTION: The Web archive explorer is a system for extracting, fragmenting and exploring Web archives.

- Contact: Quentin Lobbe
- Publications: Archives, Web fragments and diasporas. For a disaggregated exploration of web archives related to online representations of diasporas - Where the dead blogs are. A Disaggregated Exploration of Web Archives to Reveal Extinct Online Collectives - Revealing Historical Events out of Web Archives
- URL: https://github.com/lobbeque/archive-miner

5.3. apxproof

KEYWORD: LaTeX
FUNCTIONAL DESCRIPTION: apxproof is a LaTeX package facilitating the typesetting of research articles with proofs in appendix, a common practice in database theory and theoretical computer science in general. The appendix material is written in the LaTeX code along with the main text which it naturally complements, and it is automatically deferred. The package can automatically send proofs to the appendix, can repeat in the appendix the theorem environments stated in the main text, can section the appendix automatically based on the sectioning of the main text, and supports a separate bibliography for the appendix material.

RELEASE FUNCTIONAL DESCRIPTION: Numerous bug fixes and robustness enhancements, link theorems to their repeated Versions, proper management of equations in repeated theorems
NEWS OF THE YEAR: Major 1.1.0 release adding several features (link theorems to their repeated versions, proper management of equations in repeated theorems), beyond this, bug fixes, robustness enhancements, better support for some document classes.

- Participant: Pierre Senellart
- Contact: Pierre Senellart
- URL: https://github.com/PierreSenellart/apxproof

5.4. Sgvizler2

KEYWORDS: SPARQL - Data visualization - JavaScript
FUNCTIONAL DESCRIPTION: This project is the reboot in Typescript of project Sgvizler of Martin G. Skjæveland.

- Partners: LRI - Laboratoire de Recherche en Informatique - BorderCloud
- Contact: Karima Rafes
- URL: https://github.com/BorderCloud/sgvizler2

5.5. SPARQL-PHP

KEYWORDS: SPARQL - PHP
FUNCTIONAL DESCRIPTION: Very simple SPARQL client for PHP.

- Partners: LRI - Laboratoire de Recherche en Informatique - BorderCloud
- Contact: Karima Rafes
- URL: https://github.com/BorderCloud/SPARQL

5.6. TFT

Tester for Triplestore
KEYWORDS: PHP - SPARQL
FUNCTIONAL DESCRIPTION: TFT (Tester for Triplestore) is a script PHP to pass tests through a SPARQL service.

- Partners: LRI - Laboratoire de Recherche en Informatique - BorderCloud
- Contact: Karima Rafes
- URL: https://github.com/BorderCloud/TFT

WILLOW Project-Team

6. New Software and Platforms

6.1. NCNet

Neighbourhood Consensus Networks
KEYWORDS: Computer vision - Machine learning
FUNCTIONAL DESCRIPTION: Open source release of the software package for the NIPS'18 paper by Rocco et al. "Neighbourhood Consensus Networks". This release provides a full implementation of the method, including code for training models, and testing on standard datasets, as well as trained models.

- Participants: Ignacio Rocco Spremolla, Mircea Cimpoi, Akihiko Torii, Relja Arandjelovic, Tomas Pajdla and Josef Sivic
- Contact: Ignacio Rocco Spremolla
- Publication: Neighbourhood Consensus Networks
- URL: https://www.di.ens.fr/willow/research/ncnet/

6.2. Mixture-of-Embedding-Experts

KEYWORD: Computer vision
FUNCTIONAL DESCRIPTION: Joint understanding of video and language is an active research area with many applications. Prior work in this domain typically relies on learning text-video embeddings. One difficulty with this approach, however, is the lack of large-scale annotated video-caption datasets for training. To address this issue, we aim at learning text-video embeddings from heterogeneous data sources. To this end, we propose a Mixture-of-Embedding-Experts (MEE) model with ability to handle missing input modalities during training. As a result, our framework can learn improved text-video embeddings simultaneously from image and video datasets. We also show the generalization of MEE to other input modalities such as face descriptors.

- Participants: Ivan Laptev and Josef Sivic
- Contact: Antoine Miech
- Publication: Learning a Text-Video Embedding from Incomplete and Heterogeneous Data
- URL: https://www.di.ens.fr/willow/research/mee/

6.3. BodyNet

BodyNet: Volumetric Inference of 3D Human Body Shapes
KEYWORDS: Computer vision - Machine learning
FUNCTIONAL DESCRIPTION: BodyNet has the code to train multi-task neural networks for 2D/3D pose estimation, 2D body part segmentation, and 3D volumetric shape estimation of human bodies given single RGB images as input. The release also contains pre-trained models.

- Participants: Gül Varol Simsekli, Ivan Laptev and Cordelia Schmid
- Contact: Gül Varol Simsekli
- Publication: BodyNet: Volumetric Inference of 3D Human Body Shapes
- URL: https://www.di.ens.fr/willow/research/bodynet/

6.4. FlexWLoc

Flexible Weakly supervised action Localization model
KEYWORDS: Computer vision - Machine learning

FUNCTIONAL DESCRIPTION: Open source release of the software package for the NIPS'18 paper by Chéron et al. "A flexible model for training action localization with varying levels of supervision". This release provides a full implementation of the method, including code for training and testing.

- Participants: Guilhem Chéron, Jean-Baptiste Alayrac, Ivan Laptev and Cordelia Schmid
- Contact: Guilhem Chéron
- Publication: A flexible model for training action localization with varying levels of supervision
- URL: https://www.di.ens.fr/willow/research/weakactionloc/

6.5. Pinocchio

KEYWORDS: Robotics - Biomechanics - Mechanical multi-body systems
FUNCTIONAL DESCRIPTION: Pinocchio instantiates state-of-the-art Rigid Body Algorithms for poly-articulated systems based on revisited Roy Featherstone's algorithms. In addition, Pinocchio instantiates analytical derivatives of the main Rigid-Body Algorithms like the Recursive Newton-Euler Algorithms or the Articulated-Body Algorithm. Pinocchio is first tailored for legged robotics applications, but it can be used in extra contexts. It is built upon Eigen for linear algebra and FCL for collision detection. Pinocchio comes with a Python interface for fast code prototyping.

- Partner: CNRS
- Contact: JUSTIN CARPENTIER
- URL: https://github.com/stack-of-tasks/pinocchio

6.6. weakalign

End-to-end weakly-supervised semantic alignment
KEYWORDS: Computer vision - Machine learning
FUNCTIONAL DESCRIPTION: Open source release of the software package for the CVPR'18 paper by Rocco et al. "End-to-end weakly-supervised semantic alignment". This release provides a full implementation of the method, including code for training models, and testing on standard datasets, as well as trained models.

- Participants: Ignacio Rocco Spremolla, Relja Arandjelovic and Josef Sivic
- Contact: Ignacio Rocco Spremolla
- Publication: End-to-end weakly-supervised semantic alignment
- URL: https://www.di.ens.fr/willow/research/weakalign/

6.7. InLoc

Indoor Visual Localization with Dense Matching and View Synthesis
KEYWORD: Computer vision
FUNCTIONAL DESCRIPTION: Open source release of the software package for the CVPR'18 paper by Taira et al. "Indoor Visual Localization with Dense Matching and View Synthesis". This release provides a full implementation of the method.

- Participants: Hajime Taira, Masatoshi Okutomi, Torsten Sattler, Mircea Cimpoi, Marc Pollefeys, Josef Sivic, Tomas Pajdla and Akihiko Torii
- Contact: Josef Sivic
- Publication: InLoc: Indoor Visual Localization with Dense Matching and View Synthesis
- URL: https://github.com/HajimeTaira/InLoc_demo

WIMMICS Project-Team

6. New Software and Platforms

6.1. CORESE

COnceptual REsource Search Engine
KEYWORDS: Semantic Web - Search Engine - RDF - SPARQL
FUNCTIONAL DESCRIPTION: Corese is a Semantic Web Factory, it implements W3C RDF, RDFS, SPARQL 1 .1 Query and Update as well as RDF Inference Rules.

Furthermore, Corese query language integrates original features such as approximate search and extended Property Path. It provides STTL: SPARQL Template Transformation Language for RDF graphs. It also provides LDScript: a Script Language for Linked Data. Corese provides distributed federated query processing.

- Participants: Erwan Demairy, Fabien Gandon, Fuqi Song, Olivier Corby, Olivier Savoie and Virginie Bottollier
- Partners: I3S - Mnemotix
- Contact: Olivier Corby
- URL: http://wimmics.inria.fr/corese

6.2. DBpedia

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

RELEASE FUNCTIONAL DESCRIPTION: The new release is based on updated Wikipedia dumps and the inclusion of the DBpedia history extraction of the pages.

- Participants: Fabien Gandon and Elmahdi Korfed
- Contact: Fabien Gandon
- URL: http://wiki.dbpedia.org/

6.3. Discovery Hub

Discovery Hub Exploratory Search Engine
KEYWORD: Search Engine
FUNCTIONAL DESCRIPTION: Recommandation system on top of DBpedia

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

6.4. Fuzzy labelling argumentation module

Fuzzy labelling algorithm for abstract argumentation
KEYWORDS: Artificial intelligence - Multi-agent - Knowledge representation - Algorithm

FUNCTIONAL DESCRIPTION: The goal of the algorithm is to compute the fuzzy acceptability degree of a set of arguments in an abstract argumentation framework. The acceptability degree is computed from the trustworthiness associated with the sources of the arguments.

- Participant: Serena Villata Milanesio
- Contact: Serena Villata Milanesio

6.5. Qakis

Question-Answering wiki framework based system

KEYWORD: Natural language

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

- Participants: Alessio Palmero Aprosio, Amine Hallili, Elena Cabrio, Fabien Gandon, Julien Cojan and Serena Villata Milanesio
- Contact: Elena Cabrio
- URL: http://www.qakis.org/

ZENITH Project-Team

6. New Software and Platforms

6.1. Pl@ntNet

KEYWORDS: Plant identification - Deep learning - Citizen science

FUNCTIONAL DESCRIPTION: Pl@ntNet is a participatory platform and information system dedicated to the production of botanical data through deep learning-based plant identification. It includes 3 main front-ends, an Android app (the most advanced and the most used one), an iOs app (being currently re-developed) and a web version. The main feature of the application is to return the ranked list of the most likely species providing an image or an image set of an individual plant. In addition, Pl@ntNet's search engine returns the images of the dataset that are the most similar to the queried observation allowing interactive validation by the users. The back-office running on the server side of the platform is based on Snoop visual search engine (a software developed by ZENITH) and on NewSQL technologies for the data management. The application is distributed in more than 180 countries (10M downloads) and allows identifying about 20K plant species at present time.

- Participants: Antoine Affouard, Jean-Christophe Lombardo, Pierre Bonnet, Hervé Goëau, Mathias Chouet and Julien Champ
- Contact: Alexis Joly
- Publication: Pl@ntNet app in the era of deep learning

6.2. ThePlantGame

KEYWORD: Crowd-sourcing

FUNCTIONAL DESCRIPTION: ThePlantGame is a participatory game whose purpose is the production of big taxonomic data to improve our knowledge of biodiversity. One major contribution is the active training of the users based on innovative sub-task creation and assignment processes that are adaptive to the increasing skills of the user. Thousands of players are registered and produce on average about tens new validated plant observations per day. The accuracy of the produced taxonnomic tags is very high (about 95

- Participants: Maximilien Servajean and Alexis Joly
- Contact: Alexis Joly
- Publication: Crowdsourcing Thousands of Specialized Labels: A Bayesian Active Training Approach

6.3. Snoop

KEYWORDS: Content-based Image Retrieval - Deep learning

FUNCTIONAL DESCRIPTION: Snoop is a C++ framework dedicated to large-scale content-based image retrieval. Its main features are (i) the extraction and efficient indexing of visual features (hand-crafted or learned through deep learning), (ii) the search of similar images through approximate k-nearest neighbors and (iii), the supervised recognition of trained visual concepts. The framework can be used either as a set of C++ libraries or as a set of web services through a RESTFUL API. Snoop is the visual search engine used by the Pl@ntNet applications (very large audience).

- Participants: Alexis Joly, Jean-Christophe Lombardo and Olivier Buisson
- Partner: INA (Institut National de l'Audiovisuel)
- Contact: Alexis Joly
- Publication: Random Maximum Margin Hashing

6.4. Chiaroscuro

KEYWORDS: Privacy - P2P - Data mining
FUNCTIONAL DESCRIPTION: Chiaroscuro is a complete solution for clustering personal data with strong privacy guarantees. The execution sequence produced by Chiaroscuro is massively distributed on personal devices, coping with arbitrary connections and disconnections. Chiaroscuro builds on our novel data structure, called Diptych, which allows the participating devices to collaborate privately by combining encryption with differential privacy. Our solution yields a high clustering quality while minimizing the impact of the differentially private perturbation.

- Participants: Tristan Allard, Georges Hebrail, Florent Masseglia and Esther Pacitti
- Contact: Florent Masseglia
- Publication: Chiaroscuro: Transparency and Privacy for Massive Personal Time-Series Clustering

6.5. DfAnalyzer

Dataflow Analysis
KEYWORDS: Data management - Monitoring - Runtime Analysis
FUNCTIONAL DESCRIPTION: DfAnalyzer is a tool for monitoring, debugging, steering, and analysis of dataflows while being generated by scientific applications. It works by capturing strategic domain data, registering provenance and execution data to enable queries at runtime. DfAnalyzer provides lightweight dataflow monitoring components to be invoked by high performance applications. It can be plugged in scripts, or Spark applications, in the same way users already plug visualization library components.

- Participants: Vítor Sousa Silva, Daniel De Oliveira, Marta Mattoso and Patrick Valduriez
- Partners: COPPE/UFRJ - Uff
- Contact: Patrick Valduriez
- Publication: DfAnalyzer: Runtime Dataflow Analysis of Scientific Applications using Provenance
- URL: https://github.com/vssousa/dfanalyzer-spark

6.6. CloudMdsQL Compiler

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

- Participants: Boyan Kolev, Oleksandra Levchenko and Patrick Valduriez
- Contact: Patrick Valduriez
- Publication: CloudMdsQL: Querying Heterogeneous Cloud Data Stores with a Common Language

6.7. Savime

Simulation And Visualization IN-Memory
KEYWORDS: Data management. - Distributed Data Management

FUNCTIONAL DESCRIPTION: SAVIME is a multi-dimensional array DBMS for scientific applications. It supports a novel data model called TARS (Typed ARray Schema), which extends the basic array data model with typed arrays. In TARS, the support of application dependent data characteristics is provided through the definition of TAR objects, ready to be manipulated by TAR operators. This approach provides much flexibility for capturing internal data layouts through mapping functions, which makes data ingestion independent of how simulation data has been produced, thus minimizing ingestion time.

- Participants: Hermano Lustosa, Fabio Porto and Patrick Valduriez
- Partner: LNCC - Laboratório Nacional de Computação Científica
- Contact: Patrick Valduriez
- Publication: TARS: An Array Model with Rich Semantics for Multidimensional Data

6.8. OpenAlea

KEYWORDS: Bioinformatics - Biology

FUNCTIONAL DESCRIPTION: OpenAlea is an open source project primarily aimed at the plant research community. It is a distributed collaborative effort to develop Python libraries and tools that address the needs of current and future works in Plant Architecture modeling. It includes modules to analyze, visualize and model the functioning and growth of plant architecture. It was formally developed in the Inria VirtualPlants team.

RELEASE FUNCTIONAL DESCRIPTION: OpenAlea 2.0 adds to OpenAlea 1.0 a high-level formalism dedicated to the modeling of morphogenesis that makes it possible to use several modeling paradigms (Blackboard, L-systems, Agents, Branching processes, Cellular Automata) expressed with different languages (Python, L-Py, R, Visual Porgramming, ...) to analyse and simulate shapes and their development.

- Participants: Christian Fournier, Christophe Godin, Christophe Pradal, Frédéric Boudon, Patrick Valduriez, Esther Pacitti and Yann Guedon
- Partners: CIRAD - INRA
- Contact: Christophe Pradal
- Publications: OpenAlea: Scientific Workflows Combining Data Analysis and Simulation - OpenAlea: A visual programming and component-based software platform for plant modeling

6.9. FP-Hadoop

Fast Parallel Hadoop

KEYWORDS: Hadoop - Data parallelism

FUNCTIONAL DESCRIPTION: FP-Hadoop makes the reduce side of Hadoop MapReduce more parallel and efficiently deals with the problem of data skew in the reduce side. In FP-Hadoop, there is a new phase, called intermediate reduce (IR), in which blocks of intermediate values, constructed dynamically, are processed by intermediate reduce workers in parallel. Our experiments using FP-Hadoop using synthetic and real benchmarks have shown excellent performance gains compared to native Hadoop, e.g. more than 10 times in reduce time and 5 times in total execution time.

- Participants: Reza Akbarinia, Miguel Liroz-Gistau and Patrick Valduriez
- Contact: Reza Akbarinia
- Publication: FP-Hadoop: Efficient Execution of Parallel Jobs Over Skewed Data

6.10. Hadoop_g5k

KEYWORD: Cluster

FUNCTIONAL DESCRIPTION: Hadoop_g5k is a tool that makes it easier to manage Hadoop and Spark clusters and prepare reproducible experiments in the Grid 5000 platform. Hadoop_g5k offers a set of scripts to be used in command-line interfaces and a Python API to interact with the clusters. It is currently active within the G5k community, facilitating the preparation and execution of experiments in the platform.

- Participants: Reza Akbarinia, Miguel Liroz-Gistau and Patrick Valduriez
- Contact: Reza Akbarinia
- URL: https://www.grid5000.fr/mediawiki/index.php/Hadoop_On_Execo

6.11. Triton Server

End-to-end Graph Mapper

KEYWORD: Web Application

FUNCTIONAL DESCRIPTION: A server for managing graph data and applications for mobile social networks. The server is built on top of the OrientDB graph database system and a distributed middleware. It provides an End-to-end Graph Mapper (EGM) for modeling the whole application as (i) a set of graphs representing the business data, the in-memory data structure maintained by the application and the user interface (tree of graphical components), and (ii) a set of standardized mapping operators that maps these graphs with each other.

- Participants: Didier Parigot, Patrick Valduriez and Benjamin Billet
- Contact: Didier Parigot
- Publication: End-to-end Graph Mapper

6.12. SON

Shared-data Overlay Network

KEYWORDS: Sharing - Ibuted exchange - Peer-to-peer.

FUNCTIONAL DESCRIPTION: SON is a development platform for P2P networks using web services, JXTA and OSGi. The development of a SON application is done through the design and implementation of a set of components. Each component includes a technical code that provides the component services and a code component that provides the component logic (in Java). The complex aspects of asynchronous distributed programming are separated from code components and automatically generated from an abstract description of services for each component by the component generator.

- Participants: Didier Parigot, Esther Pacitti and Patrick Valduriez
- Contact: Didier Parigot
- Publication: A Lightweight Middleware for developing P2P Applications with Component and Service-Based Principles
- URL: http://www-sop.inria.fr/members/Didier.Parigot/pmwiki/SON/index.php

6.13. SciFloware

Scientific Workflow Middleware

KEYWORDS: Bioinformatics - Distributed Data Management

FUNCTIONAL DESCRIPTION: SciFloware is a middleware for the execution of scientific workflows in a distributed and parallel way. It capitalizes on our experience with the Shared-Data Overlay Network and an innovative algebraic approach to the management of scientific workflows. SciFloware provides a development environment and a runtime environment for scientific workflows, interoperable with existing systems. We validate SciFloware with workflows for analyzing biological data provided by our partners CIRAD, INRA and IRD.

- Participants: Didier Parigot, Dimitri Dupuis and Patrick Valduriez
- Contact: Didier Parigot
- Publication: InfraPhenoGrid: A scientific workflow infrastructure for Plant Phenomics on the Grid
- URL: http://www-sop.inria.fr/members/Didier.Parigot/pmwiki/Scifloware

6.14. WebSmatch

Web Schema Matching
KEYWORD: Data integration
FUNCTIONAL DESCRIPTION: WebSmatch is a flexible, open environment for discovering and matching complex schemas from heterogeneous Web data sources. It provides three basic functions: (1) metadata extraction from data sources, (2) schema matching, (3) schema clustering to group similar schemas together. WebSmatch is delivered through Web services, to be used directly by data integrators or other tools with RIA clients. It is implemented in Java, delivered as Open Source Software (under LGPL). WebSmatch has been used by Data Publica and CIRAD to integrate public and private data sources.

- Participants: Emmanuel Castanier, Patrick Valduriez and Rémi Coletta
- Contact: Patrick Valduriez
- Publication: WebSmatch: a tool for Open Data
- URL: http://websmatch.gforge.inria.fr/