



RESEARCH CENTER
Rennes - Bretagne-Atlantique

FIELD

Activity Report 2018

Section Software

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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 EMMATRIX 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.

- Participant: Olivier Sentieys
- Partner: Université de Rennes 1
- Contact: Olivier Sentieys
- 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-bretagne-ouest.fr/zyggie-wbsn-platform>



Figure 2. CAIRN's Zyggie 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>

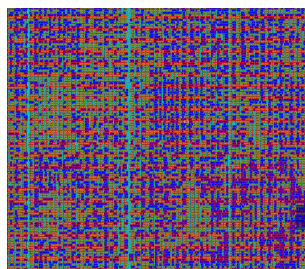


Figure 3. Floorplan of the Comet core ($150\mu\text{m} \times 150\mu\text{m}$ in a 28nm FDSOI technology)

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 Stefanescu
- 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. Its 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 library 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 Language (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 a 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 GPFinder. 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 improve 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 information flows that occurred 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 compromise. 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.

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 Pédro.

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 Pédro.

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 Pédro 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 Zyuizin.

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 Bignum 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 resource 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 Pédro, 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 Pédro

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 Lamercurie 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

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

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 equipped 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 Hérouët
- Contact: Loïc Hérouët
- 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 (Reactive 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 synthesize 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 scheduler 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. It can 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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I4S Project-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/>

SIMSMART Team (section vide)

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) Versioning: 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 multiple 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 link 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 shared 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 consists 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 difficulty 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 produces alternative pathways that could occur 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 tracing 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, Meziame Aite, Guillaume Collet, Nicolas Loira, Sylvain Prigent, Jeanne Got, Anne Siegel and Alejandro Maass
- Partner: University of Chile
- Contact: Meziame 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/lbourneuf/biseau>

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 - Uncertainty - 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 H2OGuide. 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-Carlo

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

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>

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 Bouthemey, Charles Kervrann, Jérôme Boulanger and Jean Salamero
- Partner: UMR 144 CNRS - Institut Curie
- Contact: Patrick Bouthemey
- Publication: [Adaptive spot detection with optimal scale selection in fluorescence microscopy images](#)
- URL: <http://mobylye-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 Bouthemey 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://mobylye-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://mobyte-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 photo-bleaching decay in fluorescence microscopy). The use of such motion models has been proved adequate and efficient for solving problems such as optic flow computation, motion segmentation, detection of independent moving objects, object tracking, or camera motion estimation, and in numerous application domains (video surveillance, visual servoing for robots, video coding, video indexing), including biological imaging (image stack registration, motion compensation in videomicroscopy). Motion2D is an extended and optimized implementation of the robust, multi-resolution and incremental estimation method (exploiting only the spatio-temporal derivatives of the image intensity function). 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 written 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-dimensionnal 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://mobyte-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 using 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 de-jittering 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 platform and software distribution

MobyLe@SERPICO (guest)
set email | sign-in | activate | sign-out
refresh workspace

SERPICO team (INRIA Rennes - Bretagne Atlantique) is partner of France-BioImaging

Search [more]

Programs

- Backwarping
- CRFMovingSpotDetection
- HotSpotDetection
- Hullkground
- KLTracker
- Motion2D
- MS-Detect
- NDSafrir
- OpticalFlow
- OpticalFlowStack

Tutorials

- registration

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.

Logos: SERPICO, FRANCE-BIOIMAGING, Inria

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 developed 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 developed 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).

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++ library. 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 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 wizard 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 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 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 and 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 wizard 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.

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 - Configurators - 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 Alferes 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 chinese 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. InspectorGidget

KEYWORDS: Static analysis - Software testing - User Interfaces

FUNCTIONAL DESCRIPTION: InspectorGidget is a static code analysing tool. InspectorGidget analyses UI (user interface/interaction) code of a software system to extract high level information and metrics. InspectorGidget also finds bad UI coding practices, such as Blob listener instances. InspectorGidget 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/InspectorGidget>

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

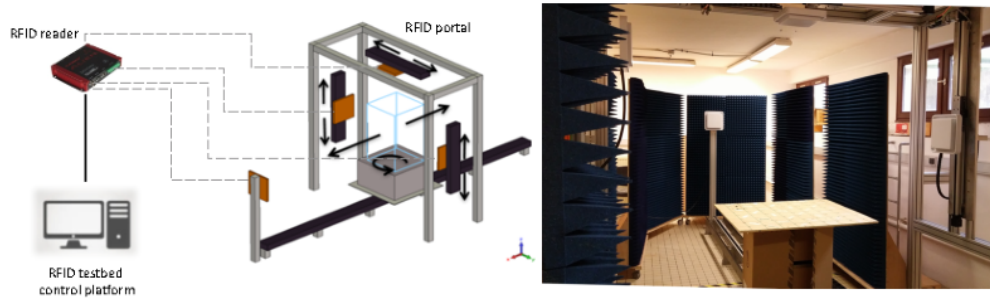


Figure 2. RFID testbed

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 charging 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 VeDeCom⁰.

KEYWORDS: Smart Grid - Intelligent Transport System

- Partner: IMT Atlantique
- Participants: Guillaume Le Gall
- Contact: Jean-Marie Bonnin

⁰<http://www.vedecom.fr/>

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 visualizing 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 Cherièr, Matthieu Dorier and Gabriel Antoniu
- Partner: ENS Rennes
- Contact: Nathanaël Cherièr
- 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 99th percentile latencies by 2x and 3x respectively.

- Contact: Gabriel Antoniu

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 relies 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/](https://hal.archives-ouvertes.fr/hal-01612979/)
- URL: <https://team.inria.fr/myriads/software-and-platforms/diffuse/>

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, H el ene Coullon and Maverick Chardet
- Partners: IMT Atlantique - LS2N - LIP
- Contact: H el ene 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 P erez
- 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 Group⁰ 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.

⁰https://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, ...).

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

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 in collaborative 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).

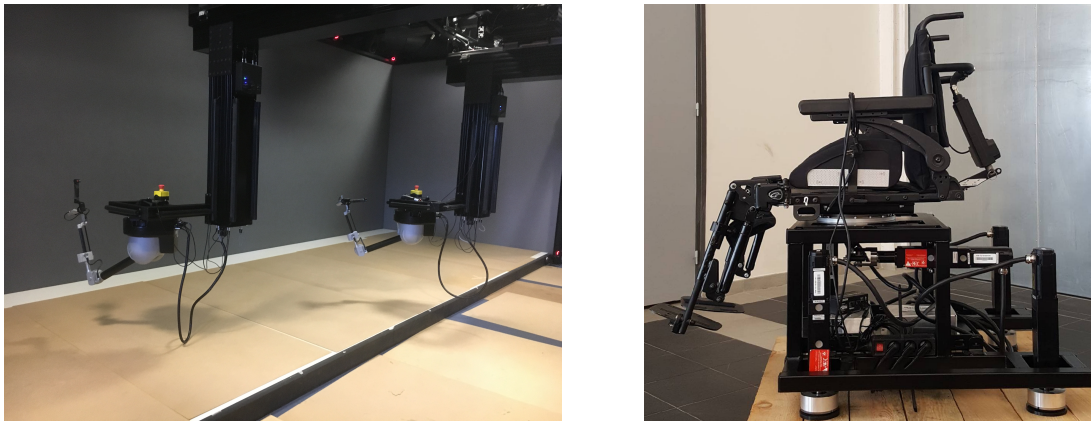


Figure 2. Upgrade of the Immersia platform: two new devices installed. (Left) "Scale-One" Haptic system for one or two users. (Right) Motion platform for powered wheelchair simulation.

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>

LINKMEDIA Project-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 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 or 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: Previsualisation - 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 occlutations 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 environments. 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 automatically 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).

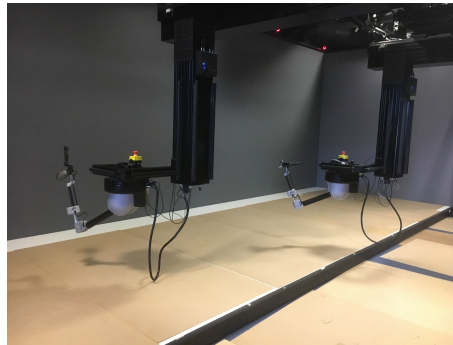


Figure 4. Upgrade of the Immersia platform with the Scale-One Haptic device enabling single-handed or dual-handed haptic feedback in the full space covered by Immersia, with the possibility of carrying the user.

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](#) - [FA_μST: 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:

- Srđan Kitić, Nancy Bertin, Remi Gribonval. Audio Declipping by Cosparsity Hard Thresholding. iTwist - 2nd international - Traveling Workshop on Interactions between Sparse models and Technology, Aug 2014, Namur, Belgium.

- Srđan Kitić, 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, Allgo, 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 Allgo platform.

- Participants: Nancy Bertin, Clement Gaultier, Ewen Camberlein, Romain Lebarbenchon, Alexandre Sanchez, Rémi Gribonval and Srdan Kitic
- Contact: Rémi Gribonval
- Publications: [Audio Declipping by Cosparsity 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](#)

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.

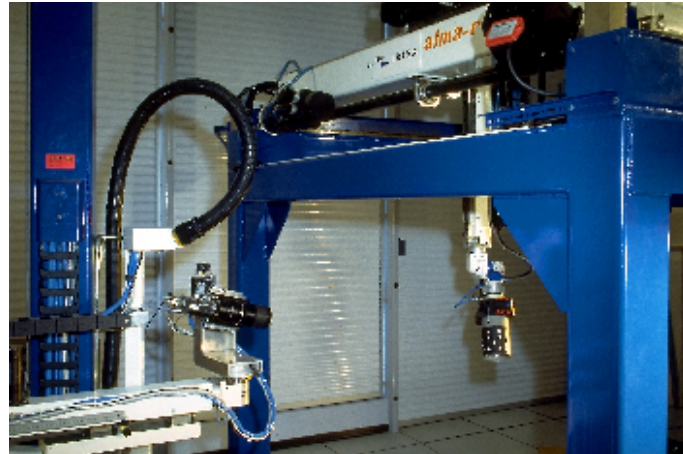


Figure 2. Rainbow robotics platform for vision-based manipulation

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.



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.

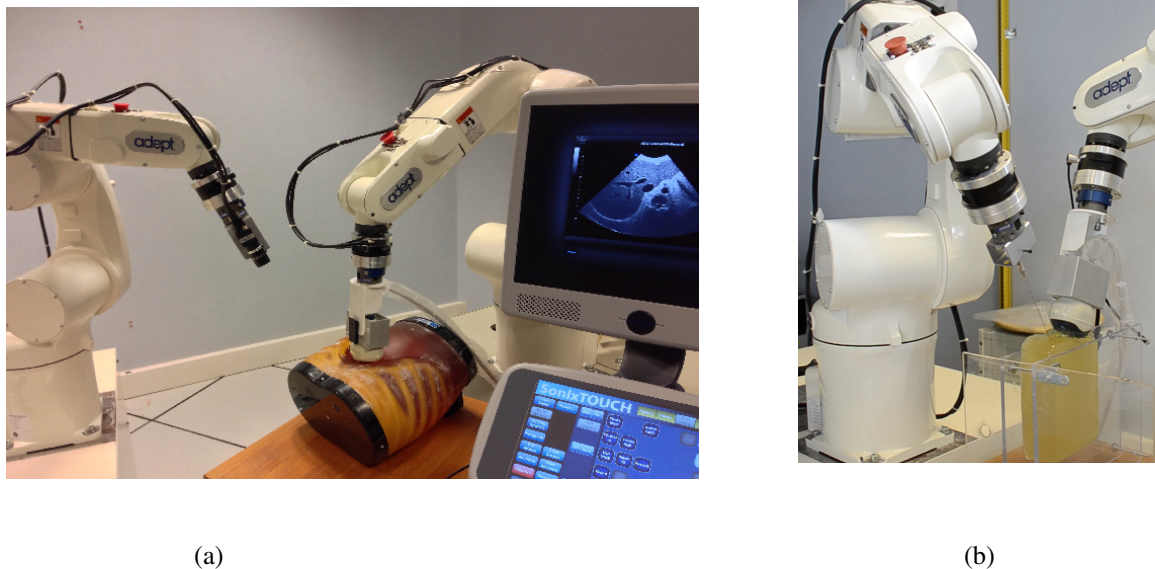


Figure 4. Rainbow medical robotic platforms. a) On the right Viper S850 robot arm equipped with a SonixTouch 3D ultrasound probe. On the left Viper S650 equipped with a tool changer that allows to attach a classical camera or biopsy needles. b) Robotic setup for autonomous needle insertion by visual 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].

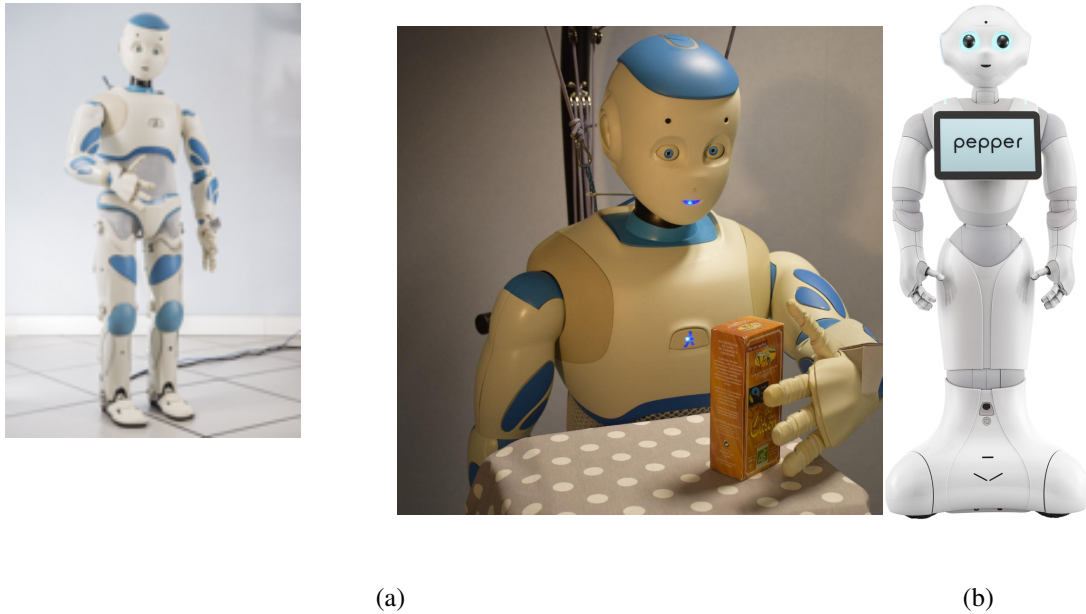


Figure 6. Humanoid Robots Platform. a) Romeo experimental platform, b) Pepper human-shaped robot

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 Virtuoso 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 **qrobotics** 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 XLI 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

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/fv360>. 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>