

Inria

RESEARCH CENTER
Rennes - Bretagne-Atlantique

FIELD

Activity Report 2019

Section Software

Edition: 2020-03-21

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CAIRN Project-Team

5. New Software and Platforms

5.1. 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>

5.2. 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 in 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 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 optimized 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 constructs an analytic accuracy model of the program, which means it can explore more solutions and thereby produce a much more efficient code.

- Participant: Olivier Sentieys
- Partner: Université de Rennes 1
- Contact: Olivier Sentieys
- URL: <http://idfix.gforge.inria.fr>

5.3. SmartSense

KEYWORDS: Wireless Sensor Networks - Smart building - Non-Intrusive Appliance Load Monitoring

FUNCTIONAL DESCRIPTION: To measure energy consumption by equipment in a building, NILM techniques (Non-Intrusive Appliance Load Monitoring) are based on observation of overall variations in electrical voltage. This avoids having to deploy watt-meters on every device and thus reduces the cost. SmartSense goes a step further to improve on these techniques by combining sensors (light, temperature, electromagnetic wave, vibration and sound sensors, etc.) to provide additional information on the activity of equipment and people. Low-cost sensors can be energy-autonomous too.

- Contact: Olivier Sentieys

5.4. Platforms

5.4.1. Zyggye: a Wireless Body Sensor Network Platform

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

SCIENTIFIC DESCRIPTION: Zyggye 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. Zyggye can be used to determine posture or gestures and mainly has applications in sport, healthcare and the multimedia industry.

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

The Zyggye 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/zyggye-wbsn-platform>

5.4.2. 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.



Figure 2. CAIRN's Zyggie platform for WBSN

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>

5.4.3. *Firopt: a tool for the simultaneous design of digital FIR filters along with the dedicated hardware model*

KEYWORDS: FIR filter design, multiplierless hardware implementation generator

SCIENTIFIC DESCRIPTION: the firopt tool is an open source C++ prototype that produces Finite Impulse Response (FIR) filters that have minimal cost in terms of digital adders needed to implement them. This project aims at fusing the filter design problem from a frequency domain specification with the design of the dedicated hardware architecture. The optimality of the results is ensured by solving appropriate mixed integer linear programming (MILP) models developed for the project. It produces results that are generally more efficient than those of other methods found in the literature or from commercial tools (such as MATLAB).

- Participants: Silviu-Ioan Filip, Martin Kumm, Anastasia Volkova
- Partners: Université de Rennes 1, Université de Nantes, Fulda University of Applied Sciences
- Contact: Silviu-Ioan Filip
- URL: <https://gitlab.com/filteropt/firopt>

5.4.4. *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>

5.4.5. 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 in the core can be done easily at the C level.

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

5.4.6. TypEx

KEYWORDS: Embedded systems, Fixed-point arithmetic, Floating-point, Low power consumption, Energy efficiency, FPGA, ASIC, Accuracy optimization, Automatic floating-point to fixed-point conversion

SCIENTIFIC DESCRIPTION: TypEx is a tool designed to automatically determine custom number representations and word-lengths (i.e., bit-width) for FPGAs and ASIC designs at the C source level. The main goal of TypEx is to explore the design space spanned by possible number formats in the context of High-Level Synthesis. TypEx takes a C code written using floating-point datatypes specifying the application to be explored. The tool also takes as inputs a cost model as well as some user constraints and generates a C code where the floating-point datatypes are replaced by the wordlengths found after exploration. The best set of word-lengths is the one found by the tool that respects the given accuracy constraint and that minimizes a parametrized cost function. Figure 3 presents an overview of the TypEx design flow.

- Participants: Olivier Sentieys, Tomofumi Yuki, Van-Phu Ha
- Partners: Université de Rennes 1
- URL: <https://gitlab.inria.fr/gecos/gecos-float2fix>

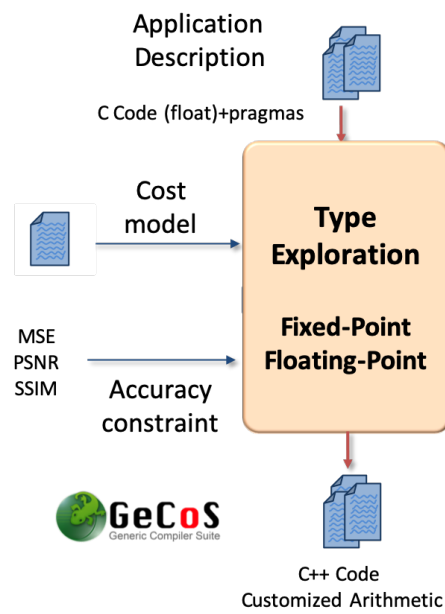


Figure 3. TypEx: a tool for type exploration and automatic floating-point to fixed-point conversion

CELTIQUE Project-Team

3. New Software and Platforms

3.1. 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 : Static Single Assignment meets CompCert](#) - [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/>

3.2. Jacal

JJavaCard AnaLyseur

KEYWORDS: JavaCard - Certification - Static program analysis - AFSCM

FUNCTIONAL DESCRIPTION: Jacal is a JJavaCard 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

3.3. 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/>

3.4. 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/>

3.5. 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/>

3.6. 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>

3.7. 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://gitlab.inria.fr/star-explain/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. GroddDroid

KEYWORDS: Android - Detection - Malware

SCIENTIFIC DESCRIPTION: GroddDroid automates the dynamic analysis of a malware. When a piece of suspicious code is detected, groddDroid interacts with the user interface and eventually forces the execution of the identified code. Using Blare (Information Flow Monitor), GroddDroid monitors how an execution contaminates the operating system. The output of GroddDroid can be visualized in an web browser. GroddDroid is used by the Kharon software.

FUNCTIONAL DESCRIPTION: GroddDroid 1 - locates suspicious code in Android application 2 - computes execution paths towards suspicious code 3 - forces executions of suspicious code 4 - automate the execution of a malware or a regular Android application

NEWS OF THE YEAR: In 2017, GroddDroid has integrated the work of Mourad Leslous, who have implemented 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.

- Authors: Mourad Leslous, Adrien Abraham, Pierre Graux, Jean François Lalande, Valérie Viet Triem Tong and Pierre Wilke
- 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>

5.3. 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](#)

5.4. GroddViewer

KEYWORDS: Android - Detection - Malware

FUNCTIONAL DESCRIPTION: To visualise data from GroddDroid

- Authors: Jean-François Lalande, Valérie Viet Triem Tong, Sébastien Campion, Mathieu Simon and Pierre Wilke
- Contact: Valérie Viet Triem Tong

5.5. Survivor

KEYWORDS: Intrusion Response - Intrusion Recovery - Survivability - Resiliency - Linux - Checkpoint/Restore - Threat Mitigation

FUNCTIONAL DESCRIPTION: Survivor is a set of low-level components to design a Linux-based operating system able to withstand ongoing intrusions and to allow business continuity despite the presence of an active adversary. Survivor provides an Intrusion Response System (IRS) with the low-level components and interfaces needed to orchestrate a per-service checkpoint, recovery, and mitigation actions. It recovers infected services (i.e., their processes and their associated files) to a previous safe state and it protects their state by applying a set of mitigations (e.g., privilege restrictions and resource quotas) aimed at withstanding further reinfections.

- Participants: Ronny Chevalier, Guillaume Hiet, David Plaquin and Chris Dalton
- Partners: CentraleSupélec - HP Labs
- Contact: Ronny Chevalier

5.6. PyMaO

Python Malware Orchestrator

KEYWORDS: Android - Malware

FUNCTIONAL DESCRIPTION: PyMaO chains several analyses that are part of an experiment. An analysis is most of the time, a call to an external tool that returns a result, for example apktool, grep, Androguard, Apkid. An experiment is a collection of analyses that are run one by one, chained, if some conditions hold. For example, if the unpacking of an application with Apktool succeeds, then you can grep the code for searching a string.

PyMaO has a nice old-fashion graphical interface (ncurses).

RELEASE FUNCTIONAL DESCRIPTION: Initial release corresponding to the demo presented at MASCOTS 2019.

NEWS OF THE YEAR: A demo has been presented at the MASCOTS 2019 conference: <https://hal-centralesupelec.archives-ouvertes.fr/hal-02305473>

- Authors: Jean-François Lalande, Pierre Graux and Tomas Javier Concepcion Miranda
- Contact: Jean-François Lalande
- URL: <https://gitlab.inria.fr/cidre-public/pymao>

5.7. OATs'inside

KEYWORDS: Android - Malware - Reverse engineering - Code analysis

FUNCTIONAL DESCRIPTION: OATs'inside is a Android reverse engineering tool that handles all native obfuscation techniques. This tool uses a hybrid approach based on dynamic monitoring and trace-based symbolic execution to output control flow graphs (CFGs) for each method of the analyzed application. These CFGs spare users the need to dive into low-level instructions, which are difficult to reverse engineer.

- Participants: Pierre Graux, Jean-François Lalande, Valérie Viet Triem Tong and Pierre Wilke
- Contact: Pierre Graux

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 8.10 contains two major new features: support for a native fixed-precision integer type and a new sort SProp of strict propositions. It is also the result of refinements and stabilization of previous features, deprecations or removals of deprecated features, cleanups of the internals of the system and API, and many documentation improvements. This release includes many user-visible changes, including deprecations that are documented in the next subsection, and new features that are documented in the reference manual.

Version 8.10 is the fifth release of Coq developed on a time-based development cycle. Its development spanned 6 months from the release of Coq 8.9. Vincent Laporte is the release manager and maintainer of this release. This release is the result of 2500 commits and 650 PRs merged, closing 150+ issues.

See the Zenodo citation for more information on this release: <https://zenodo.org/record/3476303#.Xe54f5NKjOQ>

NEWS OF THE YEAR: Coq 8.10.0 contains:

- some quality-of-life bug fixes, - a critical bug fix related to template polymorphism, - native 63-bit machine integers, - a new sort of definitionally proof-irrelevant propositions: SProp, - private universes for opaque polymorphic constants, - string notations and numeral notations, - a new simplex-based proof engine for the tactics lia, nia, lra and nra, - new introduction patterns for SSReflect, - a tactic to rewrite under binders: under, - easy input of non-ASCII symbols in CoqIDE, which now uses GTK3.

All details can be found in the user manual.

- Participants: Yves Bertot, Frédéric Besson, Maxime Denes, Emilio Jesús Gallego Arias, Gaëtan Gilbert, Jason Gross, Hugo Herbelin, Assia Mahboubi, Érik Martin-Dorel, Guillaume Melquiond, Pierre-Marie Pédro, Michael Soegtrop, Matthieu Sozeau, Enrico Tassi, Laurent Théry, Théo Zimmermann, Theo Winterhalter, Vincent Laporte, Arthur Charguéraud, Cyril Cohen, Christian Doczkal and Chantal Keller
- Partners: CNRS - Université Paris-Sud - ENS Lyon - Université Paris-Diderot
- Contact: Matthieu Sozeau
- URL: <http://coq.inria.fr/>

5.2. Math-Components

Mathematical Components library

KEYWORD: Proof assistant

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

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

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

5.3. 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 Lamercerie and Benoît Caillaud
- Contact: Benoît Caillaud
- Publication: [Surgical Process Mining with Test and Flip Net Synthesis](#)

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
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- URL: <http://www.irisa.fr/s4/tools/mica/>

5.3. IsamDAE

Implicit Structural Analysis of Multimode DAE systems

KEYWORDS: Structural analysis - Differential algebraic equations - Multimode - Scheduling

SCIENTIFIC DESCRIPTION: Modeling languages and tools based on Differential Algebraic Equations (DAE) bring several specific issues that do not exist with modeling languages based on Ordinary Differential Equations. The main problem is the determination of the differentiation index and latent equations. Prior to generating simulation code and calling solvers, the compilation of a model requires a structural analysis step, which reduces the differentiation index to a level acceptable by numerical solvers.

The Modelica language, among others, allows hybrid models with multiple modes, mode-dependent dynamics and state-dependent mode switching. These Multimode DAE (mDAE) systems are much harder to deal with. The main difficulties are (i) the combinatorial explosion of the number of modes, and (ii) the correct handling of mode switchings.

The aim of the software is on the first issue, namely: How can one perform a structural analysis of an mDAE in all possible modes, without enumerating these modes? A structural analysis algorithm for mDAE systems has been designed and implemented, based on an implicit representation of the varying structure of an mDAE. It generalizes J. Pryce's Sigma-method to the multimode case and uses Binary Decision Diagrams (BDD) to represent the mode-dependent structure of an mDAE. The algorithm determines, as a function of the mode, the set of latent equations, the leading variables and the state vector. This is then used to compute a mode-dependent block-triangular decomposition of the system, that can be used to generate simulation code with a mode-dependent scheduling of the blocks of equations.

FUNCTIONAL DESCRIPTION: IsamDAE (Implicit Structural Analysis of Multimode DAE systems) is a software library for testing new structural analysis algorithms for multimode DAE systems, based on an implicit representation of incidence graphs, matchings between equations and variables, and block decompositions. The input of the software is a variable dimension multimode DAE system consisting in a set of guarded equations and guarded variable declarations. It computes a mode-dependent structural index-reduction of the multimode system and produces a mode-dependent graph for the scheduling of blocks of equations. Evaluation functions make it possible to return the lists of leading equations and leading variables, as well as the actual scheduling of blocks, in a specified mode.

IsamDAE is coded in OCaml, and uses the following packages: * MLBDD by Arlen Cox, * Menhir by François Pottier and Yann Régis-Gianas, * Pprint by François Pottier, * XML-Light by Nicolas Cannasse and Jacques Garrigue.

RELEASE FUNCTIONAL DESCRIPTION: Version 0.2: * MEL: ad hoc language for the declaration of variable dimension multi-mode DAE systems * automatic parsing, model checking and model allocation * XML output for the list of evaluation blocks (parameters, equations, unknowns to be computed) * new algorithms for the mode-dependent scheduling and the evaluation of the scheduling in a given mode

NEWS OF THE YEAR: It has been possible to perform the structural analysis of systems with more than 750 equations and 10 to the power 23 modes, therefore demonstrating the scalability of the method.

- Authors: Benoît Caillaud and Mathias Malandain
- 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
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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
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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, CentOS.

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
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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.

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 tool-chains, and can work with a variety of current architectures.

- Participants: Arjun Suresh and Erven Rohou
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- 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.

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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 Caroline Collange
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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 them 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.

FUNCTIONAL 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.

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- 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.

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6.2. 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. From 2015 to 2018, it was used for the P22 collaboration with Asltom Transport, to model metro traffic and evaluate performance of regulation solutions. It is now (2019) at the heart of a collaboration on multi-modal networks with Alstom transport Madrid. 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.

Since then, 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. In 2019, it was extended to include planning-based regulation techniques during a collaboration with Roma 3 University.

RELEASE FUNCTIONAL DESCRIPTION: modeling of continuous vehicles movements

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

TAMIS Project-Team

5. New Software and Platforms

5.1. 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

5.2. 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
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- Contact: Delphine Beaulaton
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5.3. 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>

5.4. AHMA

Automatic Malware Hardware Analysis

KEYWORDS: Side-channel - Deep learning - Malware

FUNCTIONAL DESCRIPTION: This framework is composed of several parts, each one of them taking in charge the generation and the processing of the data at different levels. Drivers have been developed to automatically control the different oscilloscopes we are working with (picoScope 6407 et Infiniium Keysight). We use signal processing tools on the raw data to feed a deep neural network which is in charge of classifying the observed malwares. We are using two different approaches to manage the infection of the system. The first one is to reinitialize it each time we make a measurement to ensure its integrity. We have proposed a method allowing to speed the procedure up a lot. Besides, we developed several malwares, to make our experiments in a controlled environment, to avoid the necessity of cleaning the system up after each measurement.

- Contact: Annelie Heuser

5.5. SABR

Semantic-driven Analysis of Binaries

KEYWORDS: Malware - Semantic - Binary analysis - Unsupervised graph clustering SCDG - Machine learning

FUNCTIONAL DESCRIPTION: Toolchain for binary analysis based on different techniques for capturing binaries' semantics and performing machine learning-assisted analysis. The primary use is malware analysis for malware detection and classification, either based on supervised and unsupervised learning.

This toolchain includes modules of the former BMA toolchain, specifically the SCDG extraction.

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.

- Contact: Olivier Zendra

5.6. ORQAL

ORQchestration of ALgorithms

KEYWORDS: Docker - Orchestration

FUNCTIONAL DESCRIPTION: ORQAL is a simple batch scheduler for docker cluster which can be used to remotely and without overhead in scientific experiment.

- Contact: Olivier Zendra

5.7. Side-channel deep learning evaluation platform

KEYWORDS: Deep learning - Evaluation

FUNCTIONAL DESCRIPTION: Our platform is based on several software. The first software permits to train a deep neural network and evaluate it for side-channel analysis, we evaluate our neural network with guessing entropy metrics. The second software is used for programming and communicating with the target devices, but we also develop a software to communicate with the equipment and made some measurement for side-channel analysis. The last software is used to make some attack and analysis of side-channel (e.g. made Correlation Power Analysis)

- Contact: Annelie Heuser

5.8. E-PAC

Evolving-Packer Classifier

KEYWORDS: Packer classification - Incremental learning - Clustering - Malware - Obfuscation

FUNCTIONAL DESCRIPTION: E-PAC is an Evolving packer classifier that identifies the class of the packer used in a batch of packed binaries given in input. The software has the ability to identify both known packer classes and new unseen packer classes. After each update, the evolving classifier self-updates itself with the predicted packer classes.

The software is based on a semi-supervised machine learning system composed of an offline phase and an online phase. In the offline phase, a set of features is extracted from a collection of packed binaries provided with their ground truth labels, then a density-based clustering algorithm (DBSCAN) is used to group similar packers together with respect to a distance measure. In this step, the similarity threshold is tuned in order to form the clusters that fit the best with the the set of labels provided.

In the online phase, the software reproduces the same operations of features extraction and distances calculation with the incoming packed samples, then uses a customized version of the incremental clustering algorithm DBSCAN in order to classify them, either in knowns packer classes or fom new packer classes, or provisoirely leave them unclassified (notion of noise with DBSCAN).

The clusters formed after each update serve as a baseline for the application to self-evolve.

- Contact: Lamine Noureddine

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 Loic 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.

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- 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.

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- 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 Manual⁰: 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

5. New Software and Platforms

5.1. Platforms

5.1.1. Pegase

PEGASE is the wireless platform developed by the team. The milestones for the PEGASE platform in 2019 are

- finalization of the PEGASE3 hardware and software platform: SDK, decoding FPGA-based GPS frames,
- capacity (demonstrated during work with CEA Lost) of synchronous transmission / reception and ultrasonic wave phase.
- Writing documentation associated with the platform (User Guide ...).
- Start of the valuation process.

A prototype for modal analysis with several PEGASE platforms was developed. To obtain detailed modal information of large and very large structures, many sensors would be required to cover the geometry of the structure with a reasonable accuracy. However, when only a limited amount of sensors is available, large structures can be measured in several sensor setups, where some sensors remain fixed and some are moved between different measurement setups. With the sensors connected to different wireless platforms, the synchronous acquisition of data is required. A solution of data acquisition synchronization, as well as signal processing for merging the information taking into account the change of sensor positions and environmental variability has been developed and presented at IWSHM [31].

MINGUS Project-Team

5. New Software and Platforms

5.1. 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 Project-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) migration to github, (2) complete re-engineering for cleaning the successive layers and accomodating further extensions, (3) integration of the Corese triplestore (<https://corese.inria.fr/>) in addition to fuseki and virtuoso, (4) improved user interface, (5) capability to save queries for sharing and reusing them, (6) automatic generation of askomics-compliant graph of entity types (abstraction), (7) capability to use askomics to query remote endpoints (including Uniprot and neXtProt), (8) support for federated queries involving remote endpoints and local data

- 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. 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.

RELEASE FUNCTIONAL DESCRIPTION: - Reworking padmet and padmet-utils to allow full-python workflow in the future - Adding new script padmet-utils/exploration/prot2genome with exonerate - Fixing minor errors

NEWS OF THE YEAR: (1) Pantograph replaced by OrthoFinder (2) Create a readthedocs for AuReMe, padmet and padmet-utils (3) Reworking padmet and padmet-utils to allow full python workflow (4) Adding new script padmet-utils/exploration/prot2genome with exonerate (5) Modify template data structure (6) Fixing errors

- Participants: Marie Chevallier, Meziane Aite, Guillaume Collet, Nicolas Loira, Sylvain Prigent, Jeanne Cambefort, Anne Siegel and Alejandro Maass
- Partner: University of Chile
- Contact: Meziane Aite
- Publication: [Traceability, reproducibility and wiki-exploration for "à-la-carte" reconstructions of genome-scale metabolic models](#)
- URL: <http://aureme.genouest.org/>

6.3. biseau

KEYWORDS: ASP - Answer Set Programming - Graph - Formal concept analysis

SCIENTIFIC DESCRIPTION: Use ASP as a Domain Specific Language to specify dot-based visualizations.

NEWS OF THE YEAR: First release.

- Contact: Lucas Bourneuf
- Publication: [An Answer Set Programming Environment for High-Level Specification and Visualization of FCA](#)
- URL: <https://gitlab.inria.fr/lbourneu/biseau>

6.4. Metage2Metabo

KEYWORDS: Metabolic networks - Microbiota - Metagenomics - Workflow

FUNCTIONAL DESCRIPTION: Metabolic networks are graphs which nodes are compounds and edges are biochemical reactions. To study the metabolic capabilities of microbiota, Metage2Metabo uses multiprocessing to reconstruct metabolic networks at large-scale. The individual and collective metabolic capabilities (number of compounds producible) are computed and compared. From these comparisons, a set of compounds only producible by the community is created. These newly producible compounds are used to find minimal communities that can produce them. From these communities, the keystone species in the production of these compounds are identified.

NEWS OF THE YEAR: First release.

- Contact: Anne Siegel
- Publication: [Metage2Metabo: metabolic complementarity applied to genomes of large-scale microbiotas for the identification of keystone species](#)
- URL: <https://github.com/AuReMe/metage2metabo>

6.5. 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 difficulties when dealing with pathways in non-model organism is their incomplete conservation during evolution. To deal with this problem, we developed a prototype inferring new biochemical reactions using reactions and metabolites from known metabolic pathways and metabolomics data. This method produce alternative pathway that could occurred in the species of interest.

RELEASE FUNCTIONAL DESCRIPTION: Fix an issue with test data.

NEWS OF THE YEAR: (1) Add a container in Singularity Hub (<https://singularity-hub.org/collections/3758>). (2) Rewrite data files (sterol and MAA). (3) Add creation of pictures of new molecules from MZ. (4) Add new output files to ease understanding of PathModel output. (5) Rewrite the Readme.

- 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://github.com/pathmodel>

6.6. 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.

We recently developed a framework that integrates an updated version of the CADBIOM core software and visualization tools. We provided a command line interface allowing users to translate the interactions between biomolecules described in data sources in BioPAX format into the formalism based on the guarded transitions used by CADBIOM. The command line also makes it easy to search for scenarios based on the constraints of a model, to compare scenarios with each other and to visualize interaction graphs facilitating the biologist's expertise (Vignet et al 2019 JOBIM)

- Participants: Geoffroy Andrieux, Michel Le Borgne, Nathalie Theret, Nolwenn Le Meur, Pierre Vignet and Anne Siegel
- Contact: Anne Siegel
- URL: <http://cadbiom.genouest.org>

EMPENN 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 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 Duché 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 Empenn 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: <https://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. 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 : search, 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 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 regard to security, the system requires authentication and user rights are tunable for each hosted study. 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, Inès Fakhfakh, Justine Guillaumont, Michael Kain and Yao Yao
- Contact: Christian Barillot
- URL: <http://shanoir.gforge.inria.fr>

6.7. Anima medInria plugins

KEYWORDS: IRM - Medical imaging - Diffusion imaging

FUNCTIONAL DESCRIPTION: Plugins for the medInria software based on the open source software Anima developed in the Visages / Empenn team. These plugins are interfaces between anima and medinria allowing to use Anima functionalities within the clinical user interface provided by medInria. The current functionalities included in the plugins are right now: image registration, denoising, quantitative image (relaxometry), and model estimation and visualization from diffusion imaging.

- Participants: Olivier Commowick, René-Paul Debroize and Guillaume Pasquier
- Contact: Olivier Commowick

6.8. Platforms

6.8.1. The Neurinfo Platform

Empenn 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, CNRS 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 (<https://www.neurinfo.org>).

Concerning the Neurinfo Platform, the activity domain is a continuum between methodological and technological research built around specific clinical research projects. 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 central nervous system 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. A new 3T Siemens Prisma MRI scanner was installed at the Neurinfo platform in February 2018. In 2014, an 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 High Performance Computing environment made of one large computing cluster and a data center that is shared and operated by the Inria center and IRISA (UMR CNRS 6074). The computation cluster (480 cores) and the data center (up to 150 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 60 sites). In 2019, an MRI and EEG-compatible fNIRS system was acquired through a co-funding from the INS2I institute of CNRS and FEDER. At the end of 2019, GIS IBISA awarded the Neurinfo platform with a complementary funding that will be dedicated to supplement the current system with additional sensors (from 8x8 optodes to 16x16 optodes).

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

KEYWORD: Fluid mechanics

FUNCTIONAL DESCRIPTION: Typhoon is a fluid motion estimator from image sequences. It is almost real-time dedicated to the measurement of LIDAR sequences, multi-scale, fast and precise to make a fine scale analysis of fluid flows with applications in the fields of energy, transport and environment.

- Participants: Christopher Mauzey, Étienne Mémin and Pierre Dérian
- Partner: CSU Chico
- Contact: Étienne Mémin
- URL: <https://phys.csuchico.edu/lidar/typhoon/>

5.6. H2OLab

KEYWORDS: Simulation - Energy - Contamination - Groundwater - Hydrogeology - Heterogeneity - Uncertainly - Multiscale

SCIENTIFIC DESCRIPTION: The software platform contains a database which is interfaced through the web portal H2OWeb. It contains also software modules which can be used through the interface 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
- 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. SVJedi

KEYWORDS: High throughput sequencing - Structural Variation - Genome analysis

FUNCTIONAL DESCRIPTION: SVJedi is a structural variation (SV) genotyper for long read data. Based on a representation of the different alleles, it estimates the genotype of each variant in a given individual sample based on allele-specific alignment counts. SVJedi takes as input a variant file (VCF), a reference genome (fasta) and a long read file (fasta/fastq) and outputs the initial variant file with an additional column containing genotyping information (VCF).

- Participants: Claire Lemaitre, Lolita Lecompte, Pierre Peterlongo and Dominique Lavenier
- Contact: Claire Lemaitre
- URL: <https://github.com/llecompte/SVJedi>

6.2. MinYS

MineYourSymbiont

KEYWORDS: High throughput sequencing - Genome assembly - Metagenomics

FUNCTIONAL DESCRIPTION: MinYS allows targeted assembly of a bacterial genome of interest in a metagenomic short read sequencing sample using a reference-guided pipeline. First, taking advantage of a potentially distant reference genome, a subset of the metagenomic reads is assembled into a set of backbone contigs. Then, this first draft assembly is completed using the whole metagenomic readset in a de novo manner. The resulting assembly is output as a genome graph, allowing to distinguish different strains with potential structural variants coexisting in the sample.

- Contact: Claire Lemaitre
- URL: <https://github.com/cguyomar/MinYS>

6.3. Simka

KEYWORDS: Comparative metagenomics - K-mer - Distance - Ecology

FUNCTIONAL DESCRIPTION: Simka is a comparative metagenomics method dedicated to NGS datasets. It computes a large collection of distances classically used in ecology to compare communities by approximating species counts by k-mer counts. The method scales to a large number of datasets thanks to an efficient and parallel kmer-counting strategy that processes all datasets simultaneously. SimkaMin is distributed also with Simka. SimkaMin is a faster and more resource-frugal version of Simka. It outputs approximate (but very similar) results by subsampling the kmer space.

RELEASE FUNCTIONAL DESCRIPTION: Since release version 1.5.0, SimkaMin is distributed alongside Simka. SimkaMin is also a de novo comparative metagenomics tool. It is a faster and more resource-frugal version of Simka. It outputs approximate (but very similar) results as Simka by subsampling the kmer space. With this strategy, and with default parameters, SimkaMin is an order of magnitude faster, uses 10 times less memory and 70 times less disk than Simka.

- Participants: Claire Lemaitre, Dominique Lavenier, Gaëtan Benoit and Pierre Peterlongo
- Contact: Claire Lemaitre
- URL: <https://gatb.inria.fr/software/simka/>

6.4. DiscoSnpRad

*DISCO*vering Single Nucleotide Polymorphism, Indels in RAD seq data

KEYWORD: RAD-seq

FUNCTIONAL DESCRIPTION: Software discoSnpRad is designed for discovering Single Nucleotide Polymorphism (SNP) and insertions/deletions (indels) from raw set(s) of RAD-seq data. Note that number of input read sets is not constrained, it can be one, two, or more. Note also that no other data as reference genome or annotations are needed. The software is composed of several modules. First module, kissnp2, detects SNPs from read sets. A second module, kissreads2, enhances the kissnp2 results by computing per read set and for each variant found i/ its mean read coverage and ii/ the (phred) quality of reads generating the polymorphism. Then, variants are grouped by RAD locus, and a VCF file is finally generated. We also provide several scripts to further filter and select informative variants for downstream population genetics studies.

This tool relies on the GATB-Core library.

RELEASE FUNCTIONAL DESCRIPTION: * Substantive improvements: better quality of results (accuracy and recall), better filtering of obtained results * Formal improvements: better organization of scripts, better presentation of results

- Participants: Pierre Peterlongo and Claire Lemaitre
- Contact: Pierre Peterlongo
- URL: <https://github.com/GATB/DiscoSnp>

SERPICO Project-Team

6. New Software and Platforms

6.1. 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. Colocalization amounts here 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 - Hollings Cancer Center at the Medical University of South Carolina, Charleston SC, USA
- Contact: Charles Kervrann
- Publication: [Testing independence between two random sets for the analysis of colocalization in bioimaging](#)
- URL: <http://icy.bioimageanalysis.org/plugin/GcoPS>

6.2. THOTH

Testing Hypotheses for diffusion TricHotomy

KEYWORDS: Photonic imaging - Fluorescence microscopy - Biomedical imaging - Classification - Statistical categorisation techniques - Statistics - Image sequence - Visual tracking

FUNCTIONAL DESCRIPTION: The THOTH software classifies biomolecule trajectories of biomolecules (computed with tracking algorithms) into three groups of diffusion: (i) free diffusion, (ii) subdiffusion or (iii) superdiffusion. Brownian motion corresponds to the NULL hypothesis. THOTH is a nonparametric three-decision test whose alternatives are subdiffusion and superdiffusion. Single and multiple testing procedures control respectively the type I error and the false discovery rate. THOTH 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: [Statistical analysis of particle trajectories in living cells](#)
- URL: <https://team.inria.fr/serpico/software/thot/>

6.3. SparseVolution

Sparse Variation for 2D Image Deconvolution

KEYWORDS: Fluorescence microscopy - Image processing - Deconvolution - Inverse problem

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 the first (Total Variation) or second (Hessian Variation) derivatives to favor 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 algorithm has been dedicated to deconvolve very large 2D (e.g. 20 000 x 20 000) images or 3D images.

- Participants: Hoai Nam Nguyen, Charles Kervrann, Sylvain Prigent and Cesar Augusto Valades Cruz
- Partners: Innopsys - UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann

6.4. AiryscanJ

Reconstruction of AiryScan microscopy images

KEYWORDS: Image reconstruction - Fluorescence microscopy - Photonic imaging - Deconvolution - Image analysis

FUNCTIONAL DESCRIPTION: The AiryscanJ software enables to reconstruct a high resolution image from an array of multiple raw images acquired with the Airyscan technology (32 detectors). Airyscanning is a recent technique based on confocal laser scanning microscopy. The AiryscanJ software gathers four reconstruction methods (ISM, IFED, ISFED, ISM-Deconvolution) to compute a high resolution image: 1/ ISM amounts to summing the preliminarily registered raw images. 2/ IFED is the weighted difference between the inner detectors and the outer detector. 3/ ISFED is the weighted difference between the registered outer detectors and the original outer detectors. AiryscanJ automatically estimates the parameter controlling the IFED and ISFED algorithms. 4/ ISM-Deconvolution allows reconstructing a high resolution image by applying a deconvolution algorithm on the ISM image.

- Participants: Sylvain Prigent, Stephanie Dutertre and Charles Kervrann
- Partners: Université de Rennes 1 - CNRS
- Contact: Charles Kervrann
- URL: https://gitlab.inria.fr/serpico/airyscanj_bin

6.5. DeepFinder

Deep learning for macromolecule identification within 3D cellular cryo-electron tomograms

KEYWORDS: Image analysis - Deep learning - Cryo-electron microscopy - Object detection

FUNCTIONAL DESCRIPTION: DeepFinder is a computational approach that uses artificial neural networks to accurately and jointly localize multiple types and/or states of macromolecules in 3D cellular cryo-electron tomograms. DeepFinder leverages deep learning and outperforms the commonly-used template matching method on ideal data. On synthetic image data (SHREC 2019 challenge), DeepFinder is very fast and produces superior detection results when compared to other competitive deep learning methods, especially on small macromolecules. On experimental cryo-ET data depicting ribosomes, the detection results obtained by DeepFinder are consistent with expert annotations. We have got a high overlap of 86% and a similar structure resolution determined by subtomogram averaging.

- Participants: Emmanuel Moebel, Antonio Martinez and Charles Kervrann
- Partners: Max Planck Institute Martinsried - Fondation Fourmentin-Guilbert
- Contact: Charles Kervrann
- URL: <https://gitlab.inria.fr/serpico/deep-finder>

6.6. CPAnalysis

Change point detection algorithm for detecting switches of diffusion along 2D-3D single particle trajectories

KEYWORDS: Statistical modeling - Statistical physics - Fluorescence microscopy - Motion analysis

FUNCTIONAL DESCRIPTION: The change point detection algorithm is designed for detecting switches of diffusion along a given 2D-3D particle trajectory. We consider that the particle can switch between three main motion modes: 1/ Superdiffusion which occurs when the particle is transported via molecular motors along the cytoskeleton, 2/ Free diffusion (or Brownian motion) which arises when the particle evolves freely inside the cytosol, 3/ Subdiffusion observed when the particle is confined in a domain or evolves in a crowded area. The algorithm is a sequential nonparametric procedure based on a nonparametric three-decision test computed on local sliding windows along the trajectory.

- Participants: Antoine Salomon, Vincent Briane, Myriam Vimond, Jean Salamero and Charles Kervrann
- Partners: ENSAI - UMR 144 CNRS - Institut Curie
- Contact: Charles Kervrann
- Publication: [A sequential algorithm to detect diffusion switching along intracellular particle trajectories](#)
- URL: <https://team.inria.fr/serpico/software/cpanalysis/>

6.7. FlowScope

Optical flow computation for 3D fluorescence microscopy

KEYWORDS: Motion analysis - Fluorescence microscopy - Image analysis - Data visualization

FUNCTIONAL DESCRIPTION: The FLOWSCOPE software is able to estimate 3D motion between two fluorescence microscopy volumes. The underlying variational method amounts to minimizing an energy functional made up of two terms: a data term and a regularization term. The data term is derived from the continuous form of Census signature and the smoothness of the flow field is imposed by a L2 regularization term. The method is implemented for a single core CPU. FLOWSCOPE outputs three separate files corresponding to the motion vector components. The flow fields can be visualized with an appropriate color code named 3PHS. The 3PHS map projects the flow field onto the three orthogonal planes selected by the user. The projections of the vector field is color coded in the Hue (direction) and the Saturation (amplitude) spaces.

- Participants: Patrick Bouthemy, Charles Kervrann, Sylvain Prigent, Leo Maury and Philippe Roudot
- Partner: Danuser lab, University of Texas Southwestern, Dallas, USA
- Contact: Sandeep Manandhar
- Publication: [3D Flow Field Estimation and Assessment for Live Cell Fluorescence Microscopy](#)
- URL: <https://gitlab.inria.fr/smanandh/flowscope>

6.8. MWR

Missing Wedge Restoration (MWR) and Noise Removal in 3D Cryo-Tomography

KEYWORDS: Image analysis - Inverse problem - Cryo-electron microscopy - Monte-Carlo methods - Bayesian estimation

FUNCTIONAL DESCRIPTION: The Missing Wedge Restoration (MWR) software enables to reduce the high amount of noise and artifacts observed in 3D cellular cryo-tomograms, induced by the presence of a missing wedge (MW) in the spectral domain. MWR takes as input a 3D tomogram derived from limited-angle tomography, and gives as output a 3D denoised and artifact compensated volume. The artifact compensation is achieved by filling up the MW with meaningful information. A Minimum Mean Square Error (MMSE) estimator is computed by applying a dedicated Markov Chain Monte-Carlo (MCMC) sampling procedure based on the Metropolis-Hasting algorithm. MWR can be used to enhance visualization or as a pre-processing step for image analysis, including segmentation and classification of macromolecules.

- Participants: Emmanuel Moebel and Antonio Martinez
- Partners: Max Planck Institute Martinsried - Fondation Fourmentin-Guilbert
- Contact: Charles Kervrann
- Publication: [A Monte Carlo framework for missing wedge restoration and noise removal in cryo-electron tomography](#)
- URL: <https://gitlab.inria.fr/serpico/mwr>

6.9. Platforms

6.9.1. Moby@serpico platform and software distribution

Participants: Sylvain Prigent, Léo Maury, Charles Kervrann.

Moby@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 available

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

Tutorials

- registration

Welcome to Moby, 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

Moby 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.

SERPICO FRANCE-BIOIMAGING Inria

Figure 2. Moby@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/>). A few of them are freely available on the team website <https://team.inria.fr/serpico/software/> under a proprietary license.

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[9], ATLAS[1], HULLKGROUND[48], KLTRACKER[52], MOTION2D[51], MS-DETECT[49], ND-SAFIR[4], OPTICALFLOW and FLUX ESTIMATION [9]. The web interface makes our image processing methods available for biologists at Mobyle@serpico 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 [4], HULLKGROUND [48], MOTION2D [51], ATLAS [1]. The C-CRAFT [9], QUANTEV and GCOPS [19] algorithms have been developed for the image processing ICY platform (<http://icy.bioimageanalysis.org/>).

Partners: CNRS-UMR 144 Institut Curie & France-BioImaging (UMS 3714 CEMIBIO).

6.9.2. Bioimage-IT for bioimage management and processing

Participants: Sylvain Prigent, Cesar Augusto Valades Cruz, Léo Maury, Jean Salamero, Charles Kervrann.

New image acquisition systems generate large number of images and large volume images. Such data sets are hard to store, to process and to analyze for one user in a workstation. Many solutions exist for data management (e.g. Omero, OpenImadis), image analysis (e.g. Fiji, Icy, CellProfiler) and statistics (e.g. R). Each of them has its specificities and several bridges have been developed between pieces of software. Nevertheless, in many use-cases, we need to perform analysis using tools that are available in different pieces of software and different languages. It is then tedious to create a workflow that brings the data from one tool to another. It needs programming skills and most of the time, a dedicated script using a dedicated file system for processed data management is developed. The aim of BioImage-IT is to create a “bandmaster” application that allow any scientist to annotate, process, and analyze data using only one single high level application. This BioImage-IT application is based on 3 components:

- an image annotation method based on a JSON file system,
- an image processing and analysis tools integration method based on Docker and XML commands description,
- an application with a graphical interface to easily annotate data, run processing tools, and visualize data and results.

This software architecture has three main goals. First, data are annotated using a file system. This means that data are not dependent on any software like a SQL database, and each experiment can then be stored in a different directory and can be moved from one server to another or to any drive with a simple copy pasting operation. Second, the processing tools are used as binary packages managed by the Docker technology. Docker enables to gently handle dependencies and several versions of the same tool. Any existing tool can then be integrated in its native programming language. Third, using a single “bandmaster” application allows one to automatically generate metadata for any processed data, improving the traceability and the repeatability of any experimental result.

BioImage-IT (<https://project.inria.fr/bioimageit>) is developed in the context of the France-BioImaging research infrastructure in coordination with the IPDM-FBI (Image Processing and Data Management) node in order to provide a standardized image processing tool set and data management for the imaging facilities.

Partners: CNRS-UMR 144 and U1143 INSERM/CNRS-UMR 3666, Institut Curie & France-BioImaging (UMS 3714 CEMIBIO).

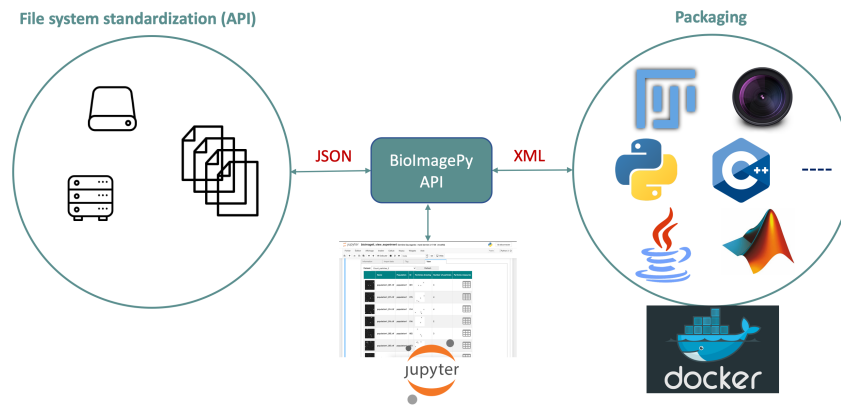


Figure 3. Scheme of the BioImage-IT components interactions.

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 detail 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 detail 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.

- Panopticlick <https://panopticlick.eff.org/>
- BrowserSpy <http://browserspy.dk/>

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 100,000 unique visitors in one year.

FUNCTIONAL DESCRIPTION: This web site aims at informing visitors about browser fingerprinting and possible tools to mitigate its effect, as well as at collecting data about the fingerprints that can be found on the web. It collects browser fingerprints with the explicit agreement of the users (they have to click on a button on the home page). Fingerprints are composed of 17 attributes, which include regular HTTP headers as well as the most recent state of the art techniques (canvas fingerprinting, WebGL information).

- Participants: Benoit Baudry and Pierre Laperdrix
- Partner: INSA Rennes
- Contact: Benoit Baudry
- URL: <https://amiunique.org/>

5.2. FAMILIAR

KEYWORDS: Software line product - Configators - Customisation

SCIENTIFIC DESCRIPTION: FAMILIAR (for FeAture Model scrIpt Language for manipulation and Automatic Reasoning) is a language for importing, exporting, composing, decomposing, editing, configuring, computing "diffs", refactoring, reverse engineering, testing, and reasoning about (multiple) feature models. All these operations can be combined to realize complex variability management tasks. A comprehensive environment is proposed as well as integration facilities with the Java ecosystem.

FUNCTIONAL DESCRIPTION: Familiar is an environment for large-scale product customisation. From a model of product features (options, parameters, etc.), Familiar can automatically generate several million variants. These variants can take many forms: software, a graphical interface, a video sequence or even a manufactured product (3D printing). Familiar is particularly well suited for developing web configurators (for ordering customised products online), for providing online comparison tools and also for engineering any family of embedded or software-based products.

- Participants: Aymeric Hervieu, Benoit Baudry, Didier Vojtisek, Edward Mauricio Alferez Salinas, Guillaume Bécan, Joao Bosco Ferreira-Filho, Julien Richard-Foy, Mathieu Acher, Olivier Barais and Sana Ben Nasr
- Contact: Mathieu Acher
- URL: <http://familiar-project.github.com>

5.3. GEMOC Studio

KEYWORDS: DSL - Language workbench - Model debugging

SCIENTIFIC DESCRIPTION: The language workbench put together the following tools seamlessly integrated to the Eclipse Modeling Framework (EMF):

- Melange, a tool-supported meta-language to modularly define executable modeling languages with execution functions and data, and to extend (EMF-based) existing modeling languages.
- MoCCML, a tool-supported meta-language dedicated to the specification of a Model of Concurrency and Communication (MoCC) and its mapping to a specific abstract syntax and associated execution functions of a modeling language.
- GEL, a tool-supported meta-language dedicated to the specification of the protocol between the execution functions and the MoCC to support the feedback of the data as well as the callback of other expected execution functions.
- BCOoL, a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models.
- Sirius Animator, an extension to the model editor designer Sirius to create graphical animators for executable modeling languages.

FUNCTIONAL DESCRIPTION: The GEMOC Studio is an eclipse package that contains components supporting the GEMOC methodology for building and composing executable Domain-Specific Modeling Languages (DSMLs). It includes the two workbenches: The GEMOC Language Workbench: intended to be used by language designers (aka domain experts), it allows to build and compose new executable DSMLs. The GEMOC Modeling Workbench: intended to be used by domain designersto create, execute and coordinate models conforming to executable DSMLs. The different concerns of a DSML, as defined with the tools of the language workbench, are automatically deployed into the modeling workbench. They parametrize a generic execution framework that provide various generic services such as graphical animation, debugging tools, trace and event managers, timeline, etc.

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

5.4. Kevoree

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/doc/1.4/frascati-userguide.html>).
- 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).

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. 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>

5.7. 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/>

5.8. 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: [hal-01499106v5](#) - [hal-01308625v2](#)
- URL: <https://github.com/diverse-project/InspectorGidget>

5.9. Descartes

KEYWORDS: Software testing - Mutation analysis

FUNCTIONAL DESCRIPTION: Descartes evaluates the capability of your test suite to detect bugs using extreme mutation testing.

Descartes is a mutation engine plugin for PIT which implements extreme mutation operators as proposed in the paper *Will my tests tell me if I break this code?*.

- Participants: Oscar Luis Vera Perez, Benjamin Danglot, Benoit Baudry and Martin Monperrus
- Partner: KTH Royal Institute of Technology
- Contact: Benoit Baudry
- Publications: [Descartes: a PITest engine to detect pseudo-tested methods - Tool Demonstration - A Comprehensive Study of Pseudo-tested Methods](#)
- URL: <https://github.com/STAMP-project/pitest-descartes>

5.10. PitMP

PIT for Multi-module Project

KEYWORDS: Mutation analysis - Mutation testing - Java - JUnit - Maven

FUNCTIONAL DESCRIPTION: PIT and Descartes are mutation testing systems for Java applications, which allows you to verify if your test suites can detect possible bugs, and so to evaluate the quality of your test suites. They evaluate the capability of your test suite to detect bugs using mutation testing (PIT) or extreme mutation testing (Descartes). Mutation testing does it by introducing small changes or faults into the original program. These modified versions are called mutants. A good test suite should be able to kill or detect a mutant. Traditional mutation testing works at the instruction level, e.g., replacing ">" by "<=", so the number of generated mutants is huge, as the time required to check the entire test suite. That's why Extreme Mutation strategy appeared. In Extreme Mutation testing, the whole body of a method under test is removed. Descartes is a mutation engine plugin for PIT which implements extreme mutation operators. Both provide reports combining, line coverage, mutation score and list of weaknesses in the source.

- Partners: CSQE - KTH Royal Institute of Technology - ENGINEERING
- Contact: Caroline Landry
- URL: <https://github.com/STAMP-project/pitmp-maven-plugin>

EASE Project-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 Alexis Girard (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

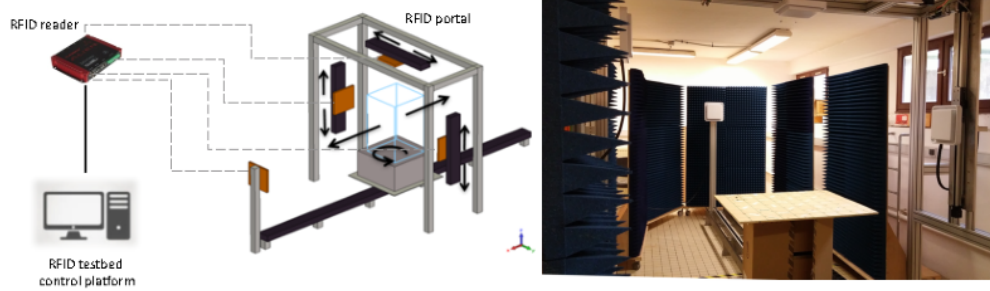


Figure 2. RFID testbed

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
- Contact: Jean-Marie Bonnin

⁰<http://www.vedecom.fr/>

KERDATA Project-Team

6. New Software and Platforms

6.1. 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/>

6.2. 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

6.3. 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: [hal-01886351](#)
- URL: <https://gitlab.inria.fr/Puffertools/Pufferbench/wikis/home>

6.4. 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

6.5. 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/>

6.6. 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

6.7. 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. 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/>

6.2. 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

6.3. SimGrid

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

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

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

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

NEWS OF THE YEAR: There were 3 major releases in 2019: Python bindings were introduced, SMPI now partially supports some of the MPI/IO functions, a new model for Wifi networks was proposed, and the API for the simulation of storage resources was completely revisited. We also pursued our efforts to improve the documentation of the software, simplified the web site, and made a lot of bug fixing and code refactoring.

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

6.4. 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/>

6.5. 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>

6.6. libcvss

KEYWORD: Cybersecurity

FUNCTIONAL DESCRIPTION: libcvss is a Rust implementation of the CVSS specification. The supported versions of CVSS are 2.0, 3.0 and 3.1.

The official CVSS website describes CVSS this way: "The Common Vulnerability Scoring System (CVSS) provides a way to capture the principal characteristics of a vulnerability and produce a numerical score reflecting its severity. The numerical score can then be translated into a qualitative representation (such as low, medium, high, and critical) to help organizations properly assess and prioritize their vulnerability management processes."

libcvss provides Rust users with a native way to manipulate CVSS-formatted vulnerability data. Rust is leveraged to provide a CVSS implementation focused on both performance and correctness.

- Participant: Clement El Baz
- Contact: Clement El Baz
- URL: <https://crates.io/crates/libcvss>

STACK Project-Team

6. New Software and Platforms

6.1. MAD

Madeus Application Deployer

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

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

RELEASE FUNCTIONAL DESCRIPTION: Initial submission with basic functionalities of MAD

NEWS OF THE YEAR: Operational prototype.

- Participants: Christian Pérez, Dimitri Pertin, H 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, Jonathan Pastor and Mario Südholt
- 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. EnOSlib

EnOSlib is a library to help you with your experiments

KEYWORDS: Distributed Applications - Distributed systems - Evaluation - Grid Computing - Cloud computing - Experimentation - Reproducibility - Linux - Virtualization

FUNCTIONAL DESCRIPTION: EnOSlib is a library to help you with your distributed application experiments. The main parts of your experiment logic is made reusable by the following EnOSlib building blocks:

- Reusable infrastructure configuration: The provider abstraction allows you to run your experiment on different environments (locally with Vagrant, Grid'5000, Chameleon and more) - Reusable software provisioning: In order to configure your nodes, EnOSlib exposes different APIs with different level of expressivity - Reusable experiment facilities: Tasks help you to organize your experimentation workflow.

EnOSlib is designed for experimentation purpose: benchmark in a controlled environment, academic validation ...

- Contact: Matthieu Simonin
- Publications: [Toward a Holistic Framework for Conducting Scientific Evaluations of OpenStack - EnosStack: A LAMP-like stack for the experimenter](#)
- URL: <https://discovery.gitlabpages.inria.fr/enoslib/>

6.6. Concerto

KEYWORDS: Reconfiguration - Distributed Software - Component models - Dynamic software architecture

FUNCTIONAL DESCRIPTION: Concerto is an implementation of the formal model Concerto written in Python. Concerto allows to : 1. describe the life-cycle and the dependencies of software components, 2. describe a components assembly that forms the overall life-cycle of a distributed software, 3. automatically reconfigure a Concerto assembly of components by using a set of reconfiguration instructions as well as a formal operational semantics.

- Partners: IMT Atlantique - LS2N - LIP
- Contact: Maverick Chardet
- URL: <https://gitlab.inria.fr/VeRDi-project/concerto>

6.7. Platforms

6.7.1. 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 [96], 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.

6.7.2. 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.

6.7.3. 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 research to cover a full spectrum of the energetical aspect of datacenters, such as cooling and power consumption depending of experimental conditions.

The testbed is connected to renewable 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).

⁰https://wiki.openstack.org/wiki/Fog_Edge_Massively_Distributed_Clouds

6.7.4. SILECS

STACK Members are involved in the definition and bootstrap of the SILECS infrastructure. 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, etc.).

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 Noviale, 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 enhanced Petri net and state machine models 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.

RELEASE FUNCTIONAL DESCRIPTION: Adding state machine handling for scenario description in addition to the already existing petri net format. Improved scenario editor

- Participants: Florian Noviale, Valérie Gouranton, Bruno Arnaldi, Vincent Goupil, Emeric Goga, Carl-Johan Jorgensen, Adrien Reuzeau and Alexandre Audinot
- Contact: Valérie Gouranton
- Publications: [Versatile Scenario Guidance for Collaborative Virtual Environments - Roles in Collaborative Virtual Environments for Training - Actions sequencing incollaborative virtual environment - Short Paper: #SEVEN, a Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environment](#)
- URL: <https://bil.inria.fr/fr/software/view/2528/tab>

6.3. OpenViBE

KEYWORDS: Neurosciences - Interaction - Virtual reality - Health - Real time - Neurofeedback - Brain-Computer Interface - EEG - 3D interaction

FUNCTIONAL DESCRIPTION: OpenViBE is a free and open-source software platform devoted to the design, test and use of Brain-Computer Interfaces (BCI). The platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. The key features of OpenViBE software are its modularity, its high-performance, its portability, its multiple-users facilities and its connection with high-end/VR displays. The designer of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge under the terms of the AGPL licence, and it was officially released in June 2009. Since then, the OpenViBE software has already been downloaded more than 60000 times, and it is used by numerous laboratories, projects, or individuals worldwide. More information, downloads, tutorials, videos, documentations are available on the OpenViBE website.

- Participants: Cedric 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. 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 had enabled several important evolutions. In particular, in 2018, a haptic system covering the entire volume of the Immersia platform was 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 for powered wheelchair simulations has also been incorporated (see Figure 2).

We celebrated the twentieth anniversary of the Immersia platform in November 2019 by inaugurating the new haptic equipment. We proposed scientific presentations and received 150 participants, and visits for the support services in which we received 50 persons.

Immersia hosted and supported several projects and experiments during the year such as the Adapt [34], Sunset [2] or Introspect ([19], [29]) projects. Moreover, the platform was involved in the multidisciplinary project LSI led by the invited professor Franz Fischnaller from the Academy of Fine Arts of Torino. The project was implemented in Immersia with the support of the Immersia staff and deployed in the Ars Electronica center 3



Figure 2. Immersia platform: (Left) “Scale-One” Haptic system for one or two users. (Right) Motion platform for a powered wheelchair simulation.



Figure 3. (Left) The LSI project in Immersia. (Right) The LSI project in Ars Electronica.

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. PyChronicle

KEYWORDS: Sequence - Sequential patterns - Pattern matching

FUNCTIONAL DESCRIPTION: Python library containing classes for representing sequences and chronicles, ie a representation of a temporal pattern. It implements efficient recognition algorithms to match chronicles in a long sequence.

- Participant: Thomas Guyet
- Contact: Thomas Guyet
- Publication: [Énumération des occurrences d'une chronique](#)
- URL: <https://gitlab.inria.fr/tguyet/pychronicles>

LINKMEDIA Project-Team

6. New Software and Platforms

6.1. Lookinlabs-Global

KEYWORD: Search Engine

FUNCTIONAL DESCRIPTION: Lookinlabs allows you to find, among teams/individuals/publications, those best matching your query.

- Authors: William Kokou Dedzoe and Jean Hany
- Contact: Vincent Claveau

6.2. TagEx

Yet another Part-of-Speech Tagger for French

KEYWORD: Natural language processing

FUNCTIONAL DESCRIPTION: TagEx is available as a web-service on <https://allgo.inria.fr> . Refer to Allgo for its usage.

- Contact: Vincent Claveau
- URL: <https://allgo.inria.fr/app/tagex>

6.3. NegDetect

Negation Detection

KEYWORD: Natural language processing

FUNCTIONAL DESCRIPTION: NegDetect relies on several layers of machine learning techniques (CRF, neural networks).

- Contact: Vincent Claveau

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: Previzualisation - Virtual camera - 3D animation

FUNCTIONAL DESCRIPTION: Directors Lens Motion Builder is a software plugin for Autodesk's Motion Builder animation tool. This plugin features a novel workflow to rapidly prototype cinematographic sequences in a 3D scene, and is dedicated to the 3D animation and movie previzualization 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 Ergonomics 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 occlusions 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: [hal-01612939v1](#) - [hal-01393066v1](#) - [hal-01332716v1](#) - [hal-01332711v2](#) - [hal-01095084v1](#)

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, Georges Dumont, Pierre Puchaud, Anthony Sorel, Claire Livet and Louise Demestre
- Contact: Charles Pontonnier
- Publications: [Motion-based prediction of external forces and moments and back loading during manual material handling tasks - A case study with custom : a comparison of normal and altered gait with an ankle brace](#) - [Motion-based prediction of hands and feet contact efforts during asymmetric handling tasks](#) - [MusIC method enhancement by a sensitivity study of its performance: application to a lower limbs musculoskeletal model](#) - [Ground Reaction Forces and Moments Prediction of Challenging Motions: Fencing Lunges](#) - [CusToM: a Matlab toolbox for musculoskeletal simulation](#) - [The MusIC method: a fast and quasi-optimal solution to the muscle forces estimation problem](#)

6.8. 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 one side, for Immermove, the addition of a third face to the immersive space, and the extension of the Vicon tracking system have been realized and continued this year with 23 new cameras. And, on the second 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, one or two handed haptic feedback in the full space covered by Immersia and possibility of carrying the user.

We celebrated the twentieth anniversary of the Immersia platform in November 2019 by inaugurating the new haptic equipment. We proposed scientific presentations and received 150 participants, and visits for support services where we received 50 persons.

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 \$\mu\$ ST: 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

5. New Software and Platforms

5.1. 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

5.2. 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 2D and 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 acquiring 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 and Fabien Spindler
- Partners: Inria - Université de Rennes 1
- Contact: Alexandre Krupa
- URL: <https://ustk.inria.fr>

5.3. 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 designing vision-based tasks for eye-in-hand and eye-to-hand systems from 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 408 examples and 88 tutorials are proposed to the user. ViSP is released under a dual licensing model. It is open-source with a GNU GPLv2 or GPLv3 license. A professional edition license that replaces GNU GPL is also available.

- Participants: Éric Marchand, Fabien Spindler and François Chaumette
- Partners: Inria - Université de Rennes 1
- Contact: Fabien Spindler
- URL: <http://visp.inria.fr>

5.4. Platforms

5.4.1. Robot Vision Platform

Participants: François Chaumette, Alexandre Krupa, Eric Marchand, Fabien Spindler [contact].

We exploit two industrial robotic systems built by Afma Robots in the nineties to validate our research 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 monocular RGB cameras. The Gantry robot also allows mounting grippers on its end-effector. Attached to this platform, we can also find a collection of various RGB and RGB-D cameras used to validate vision-based real-time tracking algorithms (see Sections 6.1.1 and 6.1.2). Note that four papers [32], [14], [52], [53] published by Rainbow in 2019 include results validated on this platform.

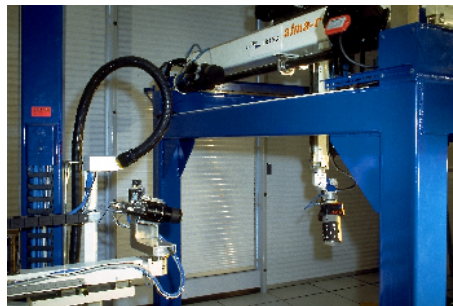


Figure 2. Rainbow robotics platform for vision-based manipulation

5.4.2. Mobile Robots

Participants: Marie Babel, Solenne Fortun, François Pasteau, Julien Pettré, Quentin Delamare, 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 6.4.4), 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, ultrasound and time of flight 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 a virtual reality environment (see Fig. 3 (c)).

Pepper, a human-shaped robot designed by SoftBank Robotics to be a genuine day-to-day companion (see Fig. 3 .d) 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 6.2.6).

Note that 2 papers and 1 PhD Thesis exploiting the mobile robots were published this year [42], [54], [1].

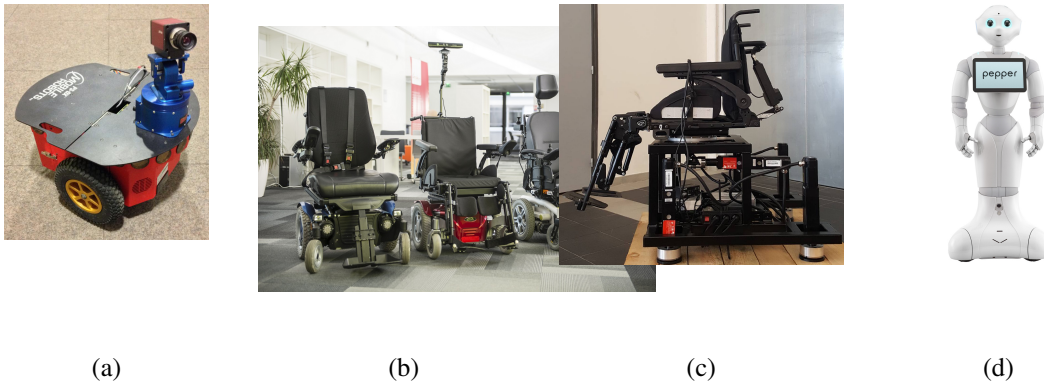


Figure 3. Mobile Robot Platform. a) Pioneer P3-DX robot, b) wheelchairs from Permobil, Sunrise and YouQ, c) Wheelchair haptic simulator, d) Pepper human-shaped robot

5.4.3. Medical Robotic Platform

Participants: Alexandre Krupa, Fabien Spindler [contact].

This platform is composed of two 6 DoF Adept Viper arms (see Figs. 4 .a–b). Ultrasound probes connected either to a SonoSite 180 Plus or an Ultrasonix SonixTouch 2D and 3D imaging system can be mounted on a force torque sensor attached to each robot end-effector. The haptic Virtuose 6D or Omega 6 device (see Fig. 7 .a) can also be used within this platform.

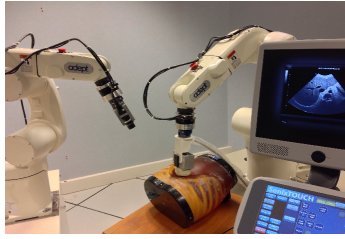
This year this platform was extended with a new ATI Nano43 force/torque sensor dedicated to needle insertion applications.

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 Sect. 6.4.3 and Sect. 6.4.2).

This platform was used to obtain experimental results presented in 4 new papers [6], [23], [38], [51].

5.4.4. Advanced Manipulation Platform

Participants: François Chaumette, Claudio Pacchierotti, Paolo Robuffo Giordano, Fabien Spindler [contact].



(a)



(b)

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

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 **qrobotics** can be mounted on the robot end-effector (see Fig. 5 .a) to validate our researches in coupling force and vision for controlling robot manipulators (see Section 6.2.12) and in shared control for remote manipulation (see Section 6.4.1). Other haptic devices (see Section 5.4.6) can also be coupled to this platform.

This year this platform was extended with a new Reflex TakkTile 2 gripper from **RightHand Labs** (see Fig. 5 .b). A new force/torque sensor from **Alberobotics** that can be mounted on the robot end-effector to get more precision during torque control was also bought.

Two new papers published this year include experimental results obtained with this platform [50], [66].



Figure 5. Rainbow advanced manipulation platform. a) One of the two Panda lightweight arms from Franka Emika, with mounted the Pisa SoftHand, b) the Reflex TakkTile 2 gripper that could be mounted on the Panda robot end-effector.

5.4.5. Unmanned Aerial Vehicles (UAVs)

Participants: Joudy Nader, Paolo Robuffo Giordano, Claudio Pacchierotti, Fabien Spindler [contact].

Rainbow is involved in several activities involving perception and control for single and multiple quadrotor UAVs. To this end, we purchased four quadrotors from Mikrokopter GmbH, Germany (see Fig. 6 .a), and one quadrotor from 3DRobotics, USA (see Fig. 6 .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 2 papers [20], [25] and 2 PhD Theses [3] contain simulative and experimental results obtained with this platform [1].

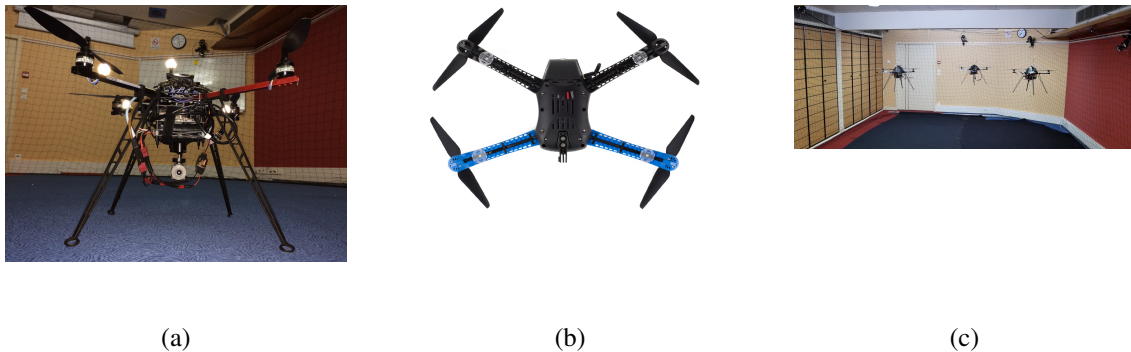


Figure 6. Unmanned Aerial Vehicles Platform. a) Quadrotor XL1 from Mikrokopter, b) Quadrotor Iris from 3DRobotics, c) Formation control with 3 XL1 from Mikrokopter.

5.4.6. Haptics and Shared Control Platform

Participants: Claudio Pacchierotti, Paolo Robuffo Giordano, Fabien Spindler [contact].

Various haptic devices are used to validate our research in shared control. We have a Virtuose 6D device from **Haption** (see Fig. 7 .a). This device is used as master device in many of our shared control activities (see Sections 6.4.2 and 6.4.3). It could also be coupled to the **Haption** haptic glove in loan from the University of Birmingham. An Omega 6 (see Fig. 7 .b) from **Force Dimension** and devices in loan from **Ultrahaptics** complete this platform that could be coupled to the other robotic platforms.

This platform was used to obtain experimental results presented in 9 papers [6], [50], [43], [44], [38], [45], [11], [51], [5] published this year.



(a)



(b)

Figure 7. Haptics and Shared Control Platform. a) Virtuose 6D and b) Omega 6 haptic devices

SIROCCO Project-Team

6. New Software and Platforms

6.1. 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>

6.2. Context-adaptive neural network based prediction for image compression

KEYWORDS: Deep learning - Image compression - Intra prediction - Neural networks

FUNCTIONAL DESCRIPTION: This code implements (i) the learning of deep neural networks for intra-prediction of video compression and (ii) a video coder/decoder integrating the learned deep neural networks. This code allows to reproduce the results of the paper "Thierry Dumas, Aline Roumy and Christine Guillemot. Context-adaptive neural network based prediction for image compression, IEEE Transactions on Image Processing, 2019." To this end, the code implements the pre-processing of an image database (i.e. extraction of a set of pairs containing a block to be predicted and its context) to yield a training set. Then, from this learning set, the code implements the learning of one deep neural network per block size (fully-connected network at size 8x8 and smaller, and convolutional network at bigger size). The code contains the parameters of all deep networks learned from the preprocessed ILSVRC2012 training database. Then, the code contains a modified version of the HEVC video compression test model (HM 16.9), which integrates the learned prediction functions and the signalling of the intra prediction mode (for both classical HEVC intra prediction modes and the learned neural networks).

- Contact: Aline Roumy
- URL: https://github.com/thierrydumas/context_adaptive_neural_network_based_prediction

6.3. LFDE-FLEX

LFDE-FLEX: A Framework for Learning Based Depth from a Flexible Subset of Dense and Sparse Light Field Views

KEYWORDS: Light fields - Depth estimation - Deep learning

FUNCTIONAL DESCRIPTION: The code implements a learning based depth estimation framework suitable for both densely and sparsely sampled light fields. The proposed framework consists of three processing steps: initial depth estimation, fusion with occlusion handling, and refinement. The estimation can be performed from a flexible subset of input views. The fusion of initial disparity estimates, relying on two warping error measures, allows us to have an accurate estimation in occluded regions and along the contours. In contrast with methods relying on the computation of cost volumes, the proposed approach does not need any prior information on the disparity range.

- Participants: Jinglei Shi, Xiaoran Jiang and Christine Guillemot
- Contact: Jinglei Shi

6.4. EPI-SENet

EPI-based light field view extrapolation network

KEYWORDS: Light fields - Deep learning - View synthesis

FUNCTIONAL DESCRIPTION: This code implements a learning based algorithm for light field view extrapolation from axial volumes of sheared epipolar plane images (EPIs). The learned SENet network is based on tensorflow backend. The inputs of this network are multiple views in a row of a structured dense light field. The network predicts novel views in order to extend the light field baseline by a factor which can go up to 4 times the initial baseline. The code also performs digital refocusing with the original and extrapolated views. As with extended numerical aperture in classical imaging, the extrapolated light field gives refocused images with a shallower depth of field (DOF), leading to more accurate refocusing results.

- Participants: Zhaolin Xiao, Jinglei Shi, Xiaoran Jiang and Christine Guillemot
- Contact: Xiaoran Jiang

6.5. 4D-SFE

4D-SFE: 4D Scene Flow Estimator from Light Fields

KEYWORDS: Light fields - Scene Flow - Motion analysis - Depth estimation

FUNCTIONAL DESCRIPTION: This software implements a method for scene flow estimation from light fields by computing an optical flow, a disparity map and a disparity variation map for the whole light field. It takes as inputs two consecutive frames from a light field video, as well as optical flow and disparity maps estimated for each view of the light field (e.g. with a deep model like PWC-Net) and saved as .flo files. First the light field is divided into 4D clusters called superrays, then a neighboring weighted graph is built between the different clusters and finally a 4D affine model is fitted for every cluster, using the initial estimations from the optical flow and disparity estimations that are contained in the cluster and in the neighboring clusters.

- Participants: Pierre David and Christine Guillemot
- Contact: Christine Guillemot

6.6. LMVS-Net

LMVS-Net: Lightweight Neural Network for Monocular View Synthesis with Occlusion Handling

KEYWORDS: Light fields - View synthesis - Deep learning

FUNCTIONAL DESCRIPTION: This code implements the method described in A Lightweight Neural Network for Monocular View Synthesis with Occlusion Handling, allowing to perform monocular view synthesis in a stereo setting. From one input image, it computes a view laterally located, left-side or right-side, and with the required disparity range depending on user input. It is also able to retrieve a disparity map from the input image, as well as a confidence map to distinguish the occluded regions, as well as to evaluate the pixelwise accuracy of the prediction. The code was developed using Keras and TensorFlow.

- Participants: Simon Evain and Christine Guillemot
- Contact: Simon Evain

6.7. 4D-LFDE

KEYWORDS: Light fields - Depth estimation

FUNCTIONAL DESCRIPTION: This code implements a learning based solution for disparity estimation for either densely or sparsely sampled light fields from 4 corner input views. The code contains two parts "DispEstim" and "DispPropa". The DispEstim module (implemented in tensorflow) takes the 4 corner views of a light field, and estimates the disparity information for these input view positions. The DispPropa module (implemented in Matlab) then generates one disparity map per target view position by propagating corner disparity maps and by applying an occlusion-aware soft 3D reconstruction method. The final output is a .mat file which contains disparity maps for every view positions of a light field.

- Participants: Xiaoran Jiang, Christine Guillemot and Jinglei Shi
- Contact: Xiaoran Jiang

6.8. Compression of omnidirectional images on the sphere

KEYWORDS: Image compression - Omnidirectional image

FUNCTIONAL DESCRIPTION: This code implements a compression scheme of omnidirectional images. The approach operates directly on the sphere, without the need to project the data on a 2D image. More specifically, from the sphere pixelization, called healpix, the code implements the partition of the set of pixels into blocks, a block scanning order, an intra prediction between blocks, and a Graph Fourier Transform for each block residual. Finally, the image to be displayed in the viewport is generated.

- Contact: Aline Roumy

6.9. Performance evaluation of interactive video compression schemes and navigation model for omnidirectional images

KEYWORDS: Image compression - Omnidirectional image

FUNCTIONAL DESCRIPTION: This code consists of two parts. First, the code generates typical navigation paths of users viewing omnidirectional images. This generation relies on Markov modeling of the user behavior (probability to choose a first viewing direction to start the navigation, probability to choose a head motion direction, probability of continuing the head motion in the same direction, probability to stop the head motion). The second part of the code implements various criteria to evaluate the compression performance. Three criteria are computed: the distortion averaged along a set of typical navigation paths, the transmission rate related to these navigation paths, and also the storage cost of the compressed image to be able to serve any possible image request. From these 3 criteria, weighted Bjontegaard metric, and iso values are computed.

- Contact: Aline Roumy

6.10. Interactive compression for omnidirectional images and texture maps of 3D models

KEYWORDS: Image compression - Random access

FUNCTIONAL DESCRIPTION: This code implements a new image compression algorithm that allows to navigate within a static scene. To do so, the code provides access in the compressed domain to any block and therefore allows extraction of any subpart of the image. This codec implements this interactive compression for two image modalities: omnidirectional images and texture maps of 3D models. For omnidirectional images the input is a 2D equirectangular projection of the 360 image. The output is the image seen in the viewport. For 3D models, the input is a texture map and the 3D mesh. The output is also the image seen in the viewport.

The code consists of three parts: (A) an offline encoder (B) an online bit extractor and (C) a decoder. The offline encoder (i) partitions the image into blocks, (ii) optimizes the positions of the access blocks, (iii) computes a set of geometry aware predictions for each block (to cover all possible navigation paths), (iv) implements transform quantization for all blocks and their predictions, and finally (v) evaluates the encoding rates. The online bit extractor (Part B) first computes the optimal and geometry aware scanning order. Then it extracts in the bitstream, the sufficient amount of information to allow the decoding of the requested blocks. The last part of the code is the decoder (Part C). The decoder reconstructs the same scanning order as the one computed at the online bit extractor. Then, the blocks are decoded (inverse transform, geometry aware predictions, ...) and reconstructed. Finally the image in the viewport is generated.

- Contact: Aline Roumy

6.11. Platforms

6.11.1. Acquisition of multi-view sequences for Free viewpoint Television

Participants: 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, user can choose in real time its view angle from which he 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 context of the project ADT ATeP 2016-2018 (funded by Inria), such datasets were acquired and some calibration tools have been developed. First 40 omnidirectional cameras and their associated equipments have been acquired by the team (thanks to Rennes Metropole funding). We have first focused on the calibration of this camera, *i.e.*, the development of the relationship between a 3D point and its projection in the omnidirectional image. In particular, we have shown that the unified spherical model fits the acquired omnidirectional cameras. Second, we have developed tools to calibrate the cameras in relation to each other. Finally, we have made a capture of 3 multiview sequences that have been made available to the community via a public web site. In 2019, we have published and presented our dataset at the ACM MMSys conference [28].

6.11.2. CLIM processing toolbox

Participants: Pierre Allain, Christine Guillemot, Laurent Guillo.

As part of the ERC Clim project, the EPI Sirocco is developing a light field processing toolbox. The toolbox and libraries are developed in C++ and the graphical user interface relies on Qt. As input data, this tool accepts both sparse light fields acquired with High Density Camera Arrays (HDCA) and denser light fields captured with plenoptic cameras using microlens arrays (MLA). At the time of writing, in addition to some simple functionalities, such as re-focusing, change of viewpoints, with different forms of visualization, the toolbox integrates more advanced tools for scene depth estimation from sparse and dense light fields, for super-ray segmentation and scene flow estimation, and for light field denoising and angular interpolation using anisotropic diffusion in the 4D ray space. The toolbox is now being interfaced with the C/C++ API of the tensorflow platform, in order to execute deep models developed in the team for scene depth and scene flow estimation, view synthesis, and axial super-resolution.