RESEARCH CENTER
Rennes - Bretagne-Atlantique

FIELD

Activity Report 2015

Section Software

Edition: 2016-03-21

ALGORITHMICS, PROGRAMMING, SOFTWARE AND ARCHITECTURE

APPLIED MATHEMATICS, COMPUTATION AND SIMULATION

DIGITAL HEALTH, BIOLOGY AND EARTH

NETWORKS, SYSTEMS AND SERVICES, DISTRIBUTED COMPUTING

PERCEPTION, COGNITION AND INTERACTION

ALF Project-Team

6. New Software and Platforms

6.1. ATC

Address Trace Compression

KEYWORDS: Compressing - Decompressing - Address traces

FUNCTIONAL DESCRIPTION

ATC is a utility and a C library for compressing/decompressing address traces. It implements a new lossless transformation, Bytesort, that exploits spatial locality in address traces. ATC leverages existing general-purpose compressors such as gzip and bzip2. ATC also provides a lossy compression mode that yields higher compression ratios while preserving certain important characteristics of the original trace.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/alf/software/atc/

6.2. ATMI

Modeling microprocessor 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.

We have developed an ad hoc temperature model, ATMI (Analytical model of Temperature in MIcroprocessors), 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.

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

6.3. Barra

Modelisation of a GPU architecture

KEYWORDS: Simulator - GPU - Computer architecture

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 simulates CUDA programs at the assembly language level (Tesla ISA). Its ultimate goal is to provide a 100 % bit-accurate simulation, offering bug-for-bug compatibility with NVIDIA G80-based GPUs. It works directly with CUDA executables, neither source modification nor recompilation is required.

Barra is primarily intended as a tool for research in computer architecture, although it can also be used to debug, profile and optimize CUDA programs at the lowest level.

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

6.4. HEPTANE

Static analyser of Worst-Case Execution Time
KEYWORD: WCET
FUNCTIONAL DESCRIPTION

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.
Status: Registered with APP (Agence de Protection des Programmes). Available under GNU General Public License v3, with number IDDN.FR.001.510039.000.S.P.2003.000.10600.

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

6.5. If-memo

KEYWORD: Performance, function memoization, dynamic optimization
Status: Ongoing development, early prototype. Registered with APP (Agence de Protection des Programmes) under number IDDN.FR.001.250013.000.S.P.2015.000.10800.

SCIENTIFIC DESCRIPTION

Memoization is the technique of saving result of executions so that future executions can be omitted when the inputs repeat. Memoization has been proposed in previous literature at the instruction level, basic block level and function level using hardware as well as pure software level approaches including changes to programming language.

We proposed software memoization of pure functions for procedural languages. We rely on the operating system loader, taking advantage of the LD_PRELOAD feature of UNIX systems. By setting this variable to the path of a shared library, we instruct the loader to first look to missing symbols in that library. Our library redefines the functions we wish to intercept. The interception code is very straightforward: it receives the same parameter as the target function and checks in a table (a software cache) if this value is readily available. In the favorable case, the result value is immediately returned. Otherwise, we invoke the original function, and store the result in the cache before returning it.

Our technique does not require the availability of source code and thus can be applied even 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. We validated If-memo with x86-64 platform using both GCC and icc compiler tool-chains, and ARM cortex-A9 platform using GCC.

- Participants: Erven Rohou and Arjun Suresh
- Contact: Erven Rohou

6.6. Padrone

KEYWORDS: Legacy code - Optimization - Performance analysis - Dynamic Optimization
Status: Registered with APP (Agence de Protection des Programmes) under number IDDN.FR.001.250013.000.S.P.2015.000.1080

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: Erven Rohou and Emmanuel Riou
- Contact: Erven Rohou
- https://team.inria.fr/alf/software/Padrone/

6.7. STiMuL

Steady temperature in Multi-Layers components
FUNCTIONAL DESCRIPTION

STiMuL is a C library for modeling steady-state heat conduction in microprocessors. It can be used to obtain temperature from power density or power density from temperature. It can also be used to model stacked dies. STiMuL does not model time-varying temperature. For time-varying temperature, other models must be used, such as ATMI.

- Participant: Pierre Michaud
- Contact: Pierre Michaud
- URL: https://team.inria.fr/alf/software/stimul/

6.8. TPCalc

Throughput calculator
KEYWORDS: Architecture - Performance analysis
FUNCTIONAL DESCRIPTION

TPCalc is a throughput calculator for microarchitecture studies concerned with multi-program workloads consisting of sequential programs. Because microarchitecture simulators are slow, it is difficult to simulate throughput experiments where a multicore executes many jobs that enter and leave the system. The usual practice of measuring instantaneous throughput on independent coschedules chosen more or less randomly is not a rigorous practice because it assumes that all the coschedules are equally important, which is not always true. TPCalc can compute the average throughput of a throughput experiment without actually doing the throughput experiment. The user first defines the workload heterogeneity (number of different job types), the multicore configuration (number of cores and symmetries). TPCalc provides a list of base coschedules. The user then simulates these coschedules, using some benchmarks of his choice, and feeds back to TPCalc the measured execution rates (e.g., instructions per cycle or instructions per second).TPCalc eventually outputs the average throughput.

- Participant: Pierre Michaud
- Partner: Ghent University
- Contact: Pierre Michaud
- URL: http://www.irisa.fr/alf/downloads/michaud/tpcalc.html

6.9. tiptop

KEYWORDS: Performance, hardware counters, analysis tool.
SCIENTIFIC DESCRIPTION

Status: Registered with APP (Agence de Protection des Programmes). Available under GNU General Public License v2, with number IDDN.FR.001.450006.000.S.P.2011.000.10800. Current version is 2.3, released June 2015.

Tiptop is a new simple and flexible user-level tool that collects hardware counter data on Linux platforms (version 2.6.31+). Tiptop has been integrated in major Linux distributions, such as Fedora, Debian, Ubuntu. FUNCTIONAL DESCRIPTION The goal is to make the collection of performance and bottleneck data as simple as possible, including simple installation and usage. In particular, we stress the following points.

- 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.
- No privilege is required, any user can run *tiptop* — non-privileged users can only watch processes they own, ability to monitor anybody's process opens the door to side-channel attacks.
- The usage is similar to *top*. There is no need for the source code of the applications of interest, making it possible to monitor proprietary applications or libraries. And since there is no probe to insert in the application, understanding of the structure and implementation of complex algorithms and code bases is not required.
- Applications do not need to be restarted, and monitoring can start at any time (obviously, only events that occur after the start of *tiptop* are observed).
- Events can be counted per thread, or per process.
- Any expression can be computed, using the basic arithmetic operators, constants, and counter values.
- A configuration file lets users define their prefered setup, as well as custom expressions.
- Participant: Erven Rohou
- Contact: Erven Rohou
- URL: http://tiptop.gforge.inria.fr

6.10. Parasuite

Participants: Sylvain Collange, Thibault Person, Erven Rohou, André Seznec.

Parasuite: parallel benchmarks for multi-core CPUs, clusters and accelerators

Despite the ubiquity of parallel architectures in all computing segments, the research community often lacks benchmarks representative of parallel applications. The Inria Parallel Benchmark Suite (Parasuite) seeks to address this need by providing a set of representative parallel benchmarks for the architecture, compiler and system research communities. Parasuite targets the main contemporary parallel programming technologies: shared-memory multi-thread parallelism for multi-core, message-passing parallelism for clusters and fine-grained data-level parallelism for GPU architectures and SIMD extensions.

All benchmarks come with input datasets of various sizes, to accommodate use cases ranging from microarchitecture simulation to large-scale performance evaluation. Correctness checks on the computed results enable automated regression testing. In order to support computer arithmetic optimization and approximate computing research scenarios, the correctness checks favor accuracy metrics evaluating domain-specific relevance rather than bit-exact comparisons against an arbitrary reference output.

Visit http://parasuite.inria.fr/

CAIRN Project-Team

6. New Software and Platforms

6.1. Panorama

With the ever raising complexity of embedded applications and platforms, the need for efficient and customizable compilation flows is stronger than ever. This need of flexibility is even stronger when it comes to research compiler infrastructures that are necessary to gather quantitative evidence of the performance/energy or cost benefits obtained through the use of reconfigurable platforms. From a compiler point of view, the challenges exposed by these complex reconfigurable platforms are quite significant, since they require the compiler to extract and to expose an important amount of coarse and/or fine grain parallelism, to take complex resource constraints into consideration while providing efficient memory hierarchy and power management.

Because they are geared toward industrial use, production compiler infrastructures do not offer the level of flexibility and productivity that is required for compiler and CAD tool prototyping. To address this issue, we have designed an extensible source-to-source compiler infrastructure that takes advantage of leading edge model-driven object-oriented software engineering principles and technologies.

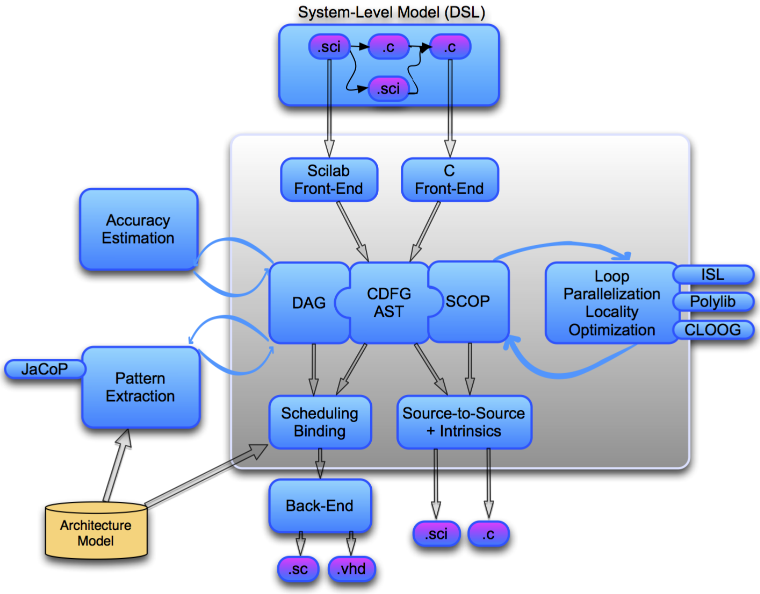

Figure 2. CAIRN's general software development framework.

Figure 2 shows the global framework that is being developed in the group. Our compiler flow mixes several types of intermediate representations. The baseline representation is a simple tree-based model enriched with control flow information. This model is mainly used to support our source-to-source flow, and serves as the backbone for the infrastructure. We use the extensibility of the framework to provide more advanced representations along with their corresponding optimizations and code generation plug-ins. For example, for our pattern selection and accuracy estimation tools, we use a data dependence graph model in all basic blocks instead of the tree model. Similarly, to enable polyhedral based program transformations and analysis, we introduced a specific representation for affine control loops that we use to derive a Polyhedral Reduced Dependence Graph (PRDG). Our current flow assumes that the application is specified as a hierarchy of communicating tasks, where each task is expressed using C or Matlab/Scilab, and where the system-level representation and the target platform model are often defined using Domain Specific Languages (DSL).

Gecos (Generic Compiler Suite) is the main backbone of CAIRN's flow. It is an open source Eclipse-based flexible compiler infrastructure developed for fast prototyping of complex compiler passes. Gecos is a 100% Java based implementation and is based on modern software engineering practices such as Eclipse plugin or model-driven software engineering with EMF (Eclipse Modeling Framework). As of today, our flow offers the following features:

- An automatic floating-point to fixed-point conversion flow (for HLS and embedded processors). **ID.Fix** is an infrastructure for the automatic transformation of software code aiming at the conversion of floating-point data types into a fixed-point representation. http://idfix.gforge.inria.fr.
- A polyhedral-based loop transformation and parallelization engine (mostly targeted at HLS). http://gecos.gforge.inria.fr.
- A custom instruction extraction flow (for ASIP and dynamically reconfigurable architectures). **Durase** and **UPaK** are developed for the compilation and the synthesis targeting reconfigurable platforms and the automatic synthesis of application specific processor extensions. They use advanced technologies, such as graph matching and graph merging together with constraint programming methods.
- Several back-ends to enable the generation of VHDL for specialized or reconfigurable IPs, and SystemC for simulation purposes (e.g., fixed-point simulations).

6.2. Gecos

Participants: Steven Derrien [corresponding author], Nicolas Simon, Nicolas Estibals, Ali Hassan El-Moussawi.

Keywords: source-to-source compiler, model-driven software engineering, retargetable compilation.

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 100% 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 at http://gecos.gforge.inria.fr.

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 since 2012 it is used in the context of the ALMA European project. The Gecos infrastructure will also be used by the EMMTRIX start-up, a spin-off from tha ALMA project which aims at commercializing the results of the project.

Recent developments in Gecos have focused on polyhedral loop transformations and efficient SIMD code generation for fixed point arithmetic data-types as a part of the ALMA project. Significant efforts were also put to provide a coarse-grain parallelization engine targeting the data-flow actor model in the context of the COMPA ANR project.

6.3. ID.Fix: Infrastructure for the Design of Fixed-point Systems

Participants: Olivier Sentieys [corresponding author], Nicolas Simon.

Keywords: fixed-point arithmetic, source-to-source code transformation, accuracy optimization, dynamic range evaluation

The different techniques proposed by the team for fixed-point conversion are implemented on the ID.Fix infrastructure. The application is described with a C code using floating-point data types and different pragmas, used to specify parameters (dynamic, input/output word-length, delay operations) for the fixed-point conversion. This tool determines and optimizes the fixed-point specification and then, generates a C code using fixed-point data types (ac_fixed) from Mentor Graphics. The infrastructure is made-up of two main modules corresponding to the fixed-point conversion (ID.Fix-Conv) and the accuracy evaluation (ID.Fix-Eval). The last developments allowed to have a complete compatibility with GeCos and to avoid the use of Matlab for LTI and recursive systems. In the context of the ANR DEFIS project, the ID.Fix tool has been reorganized to be integrated in the DEFIS toolflow.

6.4. PowWow: Power Optimized Hardware and Software FrameWork for Wireless Motes

Participants: Olivier Sentieys [corresponding author], Arnaud Carer.

Keywords: Wireless Sensor Networks, Low Power, Preamble Sampling MAC Protocol, Hardware and Software Platform

PowWow is an open-source hardware and software platform designed to handle wireless sensor network (WSN) protocols and related applications. Based on an optimized preamble sampling medium access (MAC) protocol, geographical routing and `protothread` library, PowWow requires a lighter hardware system than Zigbee [72] to be processed (memory usage including application is less than 10kb). Therefore, network lifetime is increased and price per node is significantly decreased.

CAIRN's hardware platform (see Figure 3) is composed of:

- The motherboard, designed to reduce power consumption of sensor nodes, embeds an MSP430 microcontroller and all needed components to process PowWow protocol except radio chip. JTAG, RS232, and I2C interfaces are available on this board.
- The radio chip daughter board is currently based on a TI CC2420.
- The coprocessing daughter board includes a low-power FPGA which allows for hardware acceleration for some PowWow features and also includes dynamic voltage scaling features to increase power efficiency. The current version of PowWow integrates an Actel IGLOO AGL250 FPGA and a programmable DC-DC converter. We have shown that gains in energy of up to 700 can be obtained by using FPGA acceleration on functions like CRC-32 or error detection with regards to a software implementation on the MSP430.
- Finally, a last daughter board is dedicated to energy harvesting techniques. Based on the energy management component LTC3108 from Linear Technologies, the board can be configured with several types of stored energy (batteries, micro-batteries, super-capacitors) and several types of energy sources (a small solar panel to recover photovoltaic energy, a piezoelectric sensor for mechanical energy and a Peltier thermal energy sensor).

PowWow distribution also includes a generic software architecture using event-driven programming and organized into protocol layers. The software is based on Contiki [84], and more precisely on the `Protothread` library which provides a sequential control flow without complex state machines or full multi-threading.

To optimize the network regarding a particular application and to define a global strategy to reduce energy, PowWow offers the following extra tools: over-the-air reprogramming, analytical power estimation based on software profiling and power measurements, a dedicated network analyzer to probe and fix transmissions errors in the network. More information can be found at http://powwow.gforge.inria.fr.

6.5. Ziggie: a Platform for Wireless Body Sensor Networks

Participants: Olivier Sentieys [corresponding author], Arnaud Carer.

Figure 3. CAIRN*'s PowWow motherboard with radio and energy-harvesting boards connected*

Keywords: Wireless Body Sensor Networks, Low Power, Gesture Recognition, Localization, Hardware and Software Platform

The Zyggie sensor node has been developed in the team to create an autonomous Wireless Body Sensor Network (WBSN) with the capabilities of monitoring body movements. The Zyggie platform is part of the BoWI project funded by CominLabs. Zyggie is composed of: an ATMEGA128RFA1 microcontroller, an MPU9150 Inertial Measurement Unit (IMU), an RF AS193 switch with two antennas, an LSP331AP barometer, a DC/DC voltage regulator with a battery charge controller, a wireless inductive battery charge controller, and some switches and control LEDs.

Figure 4. CAIRN*'s Ziggie platform for WBSN*

The IMU is composed of a 3-axis accelerometer, a 3-axis gyrometer and a 3-axis magnetometer. The IMU is communicating its data to the embedded microcontroller via an I2C protocol. We also developed our own MAC protocol for synchronization and data exchanges between nodes.

CELTIQUE Project-Team

5. New Software and Platforms

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

5.2. Jacal

JAvaCard AnaLyseur
KEYWORDS: JavaCard - Certification - Static program analysis - AFSCM
FUNCTIONAL DESCRIPTION

Jacal is a JAvaCard AnaLyseur developed on top of the SAWJA platform. This 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: Delphine Demange, David Pichardie, Thomas Jensen and Frédéric Besson
- Contact: Thomas Jensen

5.3. Javalib

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: Frédéric Besson, David Pichardie and Laurent Guillo
- Contact: David Pichardie
- URL: http://sawja.inria.fr/

5.4. SAWJA

Static Analysis Workshop for Java
KEYWORDS: Security - Software - Code review
FUNCTIONAL DESCRIPTION

Sawja is a library written in OCaml, relying on Javalib to provide a high level representation of Java bytecode programs. It name comes from Static Analysis Workshop for JAva. Whereas Javalib is dedicated to isolated classes, Sawja handles bytecode programs with their class hierarchy and with control flow algorithms.

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

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

5.5. Timbuk

KEYWORDS: Demonstration - Ocaml - Vérification de programmes - Tree Automata
FUNCTIONAL DESCRIPTION

Timbuk is a collection of tools for achieving proofs of reachability over Term Rewriting Systems and for manipulating Tree Automata (bottom-up non-deterministic finite tree automata)

- Participant: Thomas Genet
- Contact: Thomas Genet
- URL: http://www.irisa.fr/celtique/genet/timbuk/

5.6. CompCertSSA

KEYWORDS: Verified compilation - Single Static Assignment form - Optimization - Coq - OCaml
FUNCTIONAL DESCRIPTION

CompCertSSA is built on top of the C CompCert verified compiler, by adding a SSA-based middle-end (conversion to SSA, SSA-based optimizations, destruction of SSA). It is verified in the Coq proof assistant.

- Participant: Delphine Demange, David Pichardie, Yon Fernandez de Retana, Leo Stefanesco
- Contact: Delphine Demange
- URL: http://compcertssa.gforge.inria.fr/

DECENTRALISE Team

5. New Software and Platforms

5.1. GNUnet

GNUnet
KEYWORD: Privacy
FUNCTIONAL DESCRIPTION

GNUnet is a framework for secure peer-to-peer networking that does not use any centralized or otherwise trusted services. Our high-level goal is to provide a strong free software foundation for a global network that provides security and in particular respects privacy.

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

- Participants: Hans Grothoff, Florian Dold, Jeffrey Paul Burdges and Gabor Toth
- Partner: The GNU Project
- Contact: Hans Grothoff
- URL: https://gnunet.org/

5.2. MHD

GNU libmicrohttpd
KEYWORDS: Embedded - Web 2.0
FUNCTIONAL DESCRIPTION

GNU libmicrohttpd is a small C library that is supposed to make it easy to run an HTTP server as part of another application.

- Author: Hans Grothoff
- Contact: Hans Grothoff
- URL: http://www.gnu.org/software/libmicrohttpd/

5.3. Taler

GNU Taler
KEYWORD: Privacy
FUNCTIONAL DESCRIPTION

Taler is a new electronic payment system.

- Partner: The GNU Project
- Contact: Hans Grothoff
- URL: http://taler.net/

ESTASYS Team

5. New Software and Platforms

5.1. PLASMA Lab

Platform for Learning and Advanced Statistical Model checking Algorithms
KEYWORDS: Model Checking - Statistical - Model Checker - Runtime Analysis - Statistics
SCIENTIFIC DESCRIPTION

Statistical model checking (SMC) is a fast emerging technology for industrial scale verification and optimisation problems. Plasma was conceived to have high performance and be extensible, using a proprietary virtual machine. Since SMC requires only an executable semantics and is not constrained by decidability, we can easily implement different modelling languages and logics.
FUNCTIONAL DESCRIPTION

Plasma-Lab is a formal verification tool for complex embeded systems. It uses statistical model checking, and applies to complex problems coming from the area of security, cyber physical systems, or privacy.

- Participants: Axel Legay, Sean Sedwards, Louis-Marie Traonouez, Jean Quilbeuf
- Contact: Axel Legay
- URL: https://project.inria.fr/plasma-lab

5.2. PyECDAR

KEYWORDS: Timed input - Output automata
SCIENTIFIC DESCRIPTION

The tool has been originally developed to analyze the robustness of timed specifications, in extension of the tool Ecdar. As Ecdar , it allows to compose components specifications based on Timed I/O Automata (TIOA), and it implements timed game algorithms for checking consistency and compatibility. Additionally, it features original methods for checking the robustness of these specifications.

The tool has been later extended to analyse adaptive systems. It therefore implements original algorithms for checking featured timed games against requirements expressed in the timed AdaCTL logic.

The tool is written in Python with around 3’000 lines of code. It uses a Python console as user interface, from which it can load TIOA components from XML files written in the UPPAAL format, and design complex systems by combining the components using a simple algebra. Then, it can analyze these systems, transform them and save them in a new XML file.
FUNCTIONAL DESCRIPTION

PyEcdar is a free software that analyses timed games and timed specifications. The goal of the tool is to allow a fast prototyping of new analysis techniques. It currently allows to solve timed games based on timed automata models. These can be extended with adaptive features to represent dynamicity and to model software product lines.

- Participants: Louis-Marie Traonouez and Axel Legay
- Contact: Louis-Marie Traonouez
- URL: https://project.inria.fr/pyecdar/

5.3. Quail

FUNCTIONAL DESCRIPTION

Privacy is a central issue for Systems of Systems and interconnected objects. We propose QUAIL, a tool that can be used to quantify privacy of components. QUAIL is the only tool able to perform an arbitrary-precision quantitative analysis of the security of a system depending on private information. Thanks to its Markovian semantics model, QUAIL computes the correlation between the system's observable output and the private information, obtaining the amount of bits of the secret that the attacker will infer by observing the output.

- Participants: Fabrizio Biondi, Axel Legay, Louis-Marie Traonouez and Andrzej Wasowski
- Contact: Axel Legay
- URL: https://project.inria.fr/quail/

HYCOMES Team

5. New Software and Platforms

5.1. Flipflop

Test & Flip Net Synthesis Tool for the Inference of Technical Procedure Models
FUNCTIONAL DESCRIPTION

Flipflop is a Test and Flip net 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.

- Contact: Benoît Caillaud
- URL: http://tinyurl.com/oql6f3y

5.2. MICA

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

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

Thanks to the Inter module and the mica interactive environment, users can define complex systems and interfaces using Ocaml syntax. It is even possible to define parameterized components as Ocaml functions.
FUNCTIONAL DESCRIPTION

Mica is an Ocaml library implementing the Modal Interface algebra. The purpose of Modal Interfaces is to provide a formal support to contract based design methods in the field of system engineering. Modal Interfaces enable compositional reasoning methods on I/O reactive systems.

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

5.3. TnF-C++

FUNCTIONAL DESCRIPTION

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

- Contact: Benoît Caillaud
- URL: https://bitbucket.org/cpenet/tnf_cpp

SUMO Project-Team

6. New Software and Platforms

6.1. SIMSTORS

SIMSTORS is a simulator for regulated stochastic timed Petri nets. These Petri nets are a variant of stochastic and timed nets, which execution is controlled by a regulation policy an a predetermined theoretical schedule. The role of the regulation policy is to control the system to realize the schedule with the best possible precision. This software allows not only for step by step simulation, but also for performance analysis of systems such as production cells or train systems.

SIMSTORS was used successfully during a collaboration with Alstom transport to model existing urban railway systems and their regulation schemes. Alstom transport is willing to transfer this software and use it during early design phase of regulation algorithms in their metro lines.

Future extensions of the software will deal with verification of several new properties such as the robustness of proposed schedules.

- Participants: Loïc Hélouët and Abd El Karim Kecir
- Contact: Loïc Hélouët

6.2. Sigali

FUNCTIONAL DESCRIPTION

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

- Contact: Hervé Marchand

6.3. Tipex

TImed Properties Enforcement during eXecution

FUNCTIONAL DESCRIPTION

We are implementing a prototype tool named Tipex (TImed Properties Enforcement during eXecution) for the enforcement of timed properties. Tipex is based on the theory and algorithms that we develop for the synthesis of enforcement monitors for properties specified by timed automata (TA). The prototype is developped in python, and uses the PyUPPAAL and DBMpyuppaal libraries of the UPPAAL tool . It is currently restricted to safety and co-safety timed property. The property provided as input to the tool is a TA that can be specified using the UPPAAL tool, and is stored in XML format. The tool synthesizes an enforcement monitor from this TA, which can then be used to enforce a sequence of timed events to satisfy the property. Experiments have been conducted on a set of case studies. This allowed to validate the architecture and feasibility of enforcement monitoring in a timed setting and to have a first assessment of performance (and to what extent the overhead induced by monitoring is negligible).

- Contact: Thierry Jéron, Hervé Marchand
- URL: http://srinivaspinisetty.github.io/Timed-Enforcement-Tools/

6.4. ReaX

ReaX is a tool developed by Nicolas Berthier that investigates the control of safety properties for infnite reactive synchronous systems modeled by arithmetic symbolic transition systems. It provides effective algorithms allowing to solve the safety control problem (including the dead-lock free case), and report some experiments. Its aim is to replace Sigali, which is limited to finite state systems described by boolean variables.

- Contact : Nicolas Berthier, Hervé Marchand
- URL : http://reatk.gforge.inria.fr/

6.5. Open Agora Core

Christophe Morvan participates to the implementation of a sophisticated voting system: Open Agora Core. It currently implements several voting methods among which *Condorcet* (Schulze method) or *instant runoff*. It is integrated into a Slack [0] polling plugin. This development serves as a basic building block in the process of elaborating Open Agora, a startup that should be created during 2016.

- Contact : Christophe Morvan
- URL : http://www.open-agora.com

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[0] Slack, `http://slack.com`, is an industrial team communication tool.

TASC Project-Team

6. New Software and Platforms

6.1. AIUR

(Artificial Intelligence Using Randomness)
FUNCTIONAL DESCRIPTION

The main idea is to be unpredictable by making some stochastic choices. The AI starts a game with a "mood" randomly picked up among 5 moods, dictating some behaviours (aggressive, fast expand, macro-game, ...). In addition, some other choices (productions, timing attacks, early aggressions, ...) are also taken under random conditions.

Learning is an essential part of AIUR . For this, it uses persistent I/O files system to record which moods are efficient against a given opponent, in order to modify the probability distribution for the mood selection. The current system allows both on-line and off-line learning.

- Contact: Florian Richoux
- URL: https://github.com/AIUR-group/AIUR

6.2. CHOCO

SCIENTIFIC DESCRIPTION

For fourth consecutive year, CHOCO has participated at the MiniZinc Challenge , an annual competition of constraint programming solvers. Since then, in concurrency with 16 other solvers, CHOCO has won two silver medals and four bronze medals in three out of four categories (Free search, Parallel search and Open class). Five versions have been released all year long, the last one (v3.3.3, Dec. 22th) has the particularity to be promoted on Maven Central Repository. The major modifications were related to an improvement of the overall solver (efficiency, stability and robustness) but also a simplification of the API. As an example, more flexibility has been injected to the search loop, a central concept of the solver.
FUNCTIONAL DESCRIPTION

CHOCO is a Free and Open-Source Software dedicated to Constraint Programming. It is a Java library written under BSD 4-clause license (700 classes, 134K lines of code). It aims at describing hard combinatorial problems in the form of Constraint Satisfaction Problems and solving them with Constraint Programming techniques. The user models its problem in a declarative way by stating the set of constraints that need to be satisfied in every solution. Then, CHOCO solves the problem by alternating constraint filtering algorithms with a search mechanism. In addition to native explanations system, soft constraints and global constraints, the library is, in practice, open, easy to integrate and to tweak. A User Guide is now available: 164 pages describing how to use CHOCO, together with responsive online support (forums and mailing-lists).

- Participants: Charles Prud'homme, Nicolas Beldiceanu, Jean-Guillaume Fages, Xavier Lorca, Thierry Petit and Rémi Douence
- Partner: Ecole des Mines de Nantes
- Contact: Charles Prud'homme
- URL: http://www.choco-solver.org/

6.3. GCCat

Global Constraint Catalog
KEYWORDS: Constraint Programming - Global constraint - Catalogue - Graph - Automaton - Transducer - First order formula - meta-data - ontology - symmetry - counting -

FUNCTIONAL DESCRIPTION

This global constraint catalog presents a catalogue of global constraints where each constraint is explicitly described in terms of graph properties and/or automata and/or first order logical formulae with arithmetic. When available, it also presents some typical usage as well as some pointers to existing filtering algorithms. This year we were preparing a second volume of the catalog focused on time-series constraints. It presents a restricted set of finite transducers used to synthesise structural time-series constraints described by means of a multi-layered functions composition scheme. Second it provides the corresponding synthesised catalogue of structural time-series constraints where each constraint is explicitly described in terms of automata with accumulators.

- Participants: Nicolas Beldiceanu, Mats Carlsson, Sophie Demassey and Helmut Simonis
- Contact: Nicolas Beldiceanu
- URL: http://sofdem.github.io/gccat/gccat/index.html

6.4. GHOST

General meta-Heuristic Optimization Solving Tool

FUNCTIONAL DESCRIPTION

GHOST, i.e. General meta-Heuristic Optimization Solving Tool, is a template C++ library designed for StarCraft:BroodWartm. GHOST implements a meta-heuristic solver aiming to solve any kind of combinatorial and optimization RTS-related problems represented by a csp /cop. The solver handles dedicated geometric and assignment constraints in a way that is compatible with very strong real time requirements.

- Contact: Florian Richoux
- URL: http://github.com/richoux/GHOST

6.5. IBEX

pour le calcul ensembliste (calcul numérique garanti avec propagation rigoureuse d'incertitudes)

KEYWORD: Constraint Programming

SCIENTIFIC DESCRIPTION

In 2014 the development on IBEX has focused on the following points:

Rejection test based on first-order conditions (see First Order Rejection Tests For Multiple-Objective Optimization, A. Goldsztejn et al. [42]).

Q-intersection (see Q-intersection Algorithms for Constraint-Based Robust Parameter Estimation, C. Carbonnel et al., AAAI 2014)

FUNCTIONAL DESCRIPTION

IBEX is a C++ library for solving nonlinear constraints over real numbers. The main feature of Ibex is its ability to build solver/paver strategies declaratively through the contractor programming paradigm. It also comes with a black-box solver and a global optimizer.

- Participants: Ignacio Araya, Gilles Chabert, Bertrand Neveu, Ignacio Salas Donoso and Gilles Trombettoni
- Partners: ENSTA - Ecole des Ponts ParisTech
- Contact: Gilles Chabert
- URL: http://www.ibex-lib.org/

TEA Project-Team

6. New Software and Platforms

6.1. The Eclipse project POP

Participants: Loïc Besnard, Thierry Gautier, Paul Le Guernic, Jean-Pierre Talpin.

The distribution of project POP [0] is 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. Project-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.

Technically, project POP is composed of the Polychrony toolset, under GPL license, and its Eclipse framework, under EPL license. SSME (Syntactic Signal-Meta under Eclipse), is the metamodel of the Signal language implemented with Eclipse/Ecore. It describes all syntactic elements specified in Signal Reference Manual [0]: all Signal operators (e.g. arithmetic, clock synchronization), model (e.g. process frame, module), and construction (e.g. iteration, type declaration).

The metamodel 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 toolchain. 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 toolchain.

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.

6.2. The Polychrony toolset

Participants: Loïc Besnard, Thierry Gautier, Paul Le Guernic, Jean-Pierre Talpin.

The Polychrony toolset is an Open Source development environment for critical/embedded systems. It is based on Signal, a real-time polychronous dataflow 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 toolset 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,
- assemble heterogeneous predefined components (bottom-up with COTS),
- generate executable code for various architectures.

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[0] *Polychrony on POLARSYS (POP)*, an Eclipse project in the POLARSYS Industry Working Group, 2013. https://www.POLARSYS.org/projects/POLARSYS.pop

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

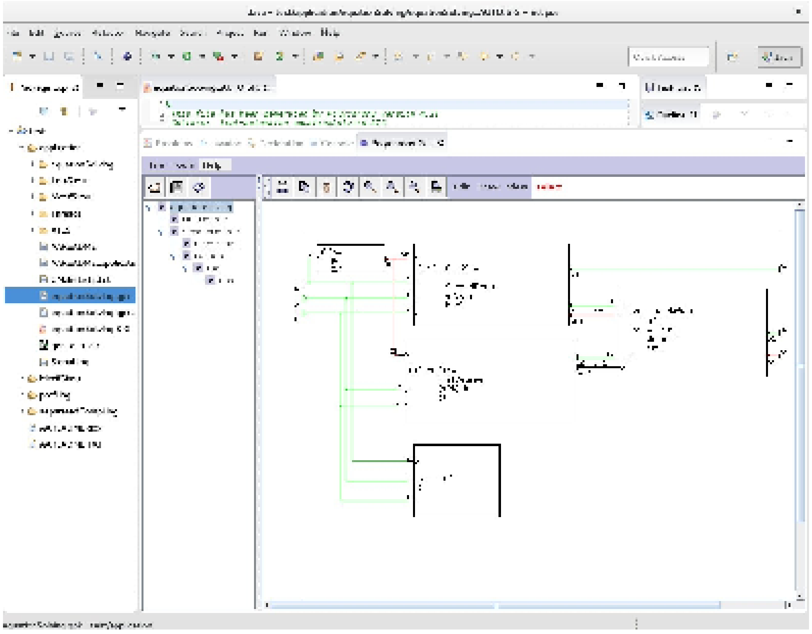

Figure 1. The Eclipse POP Environment

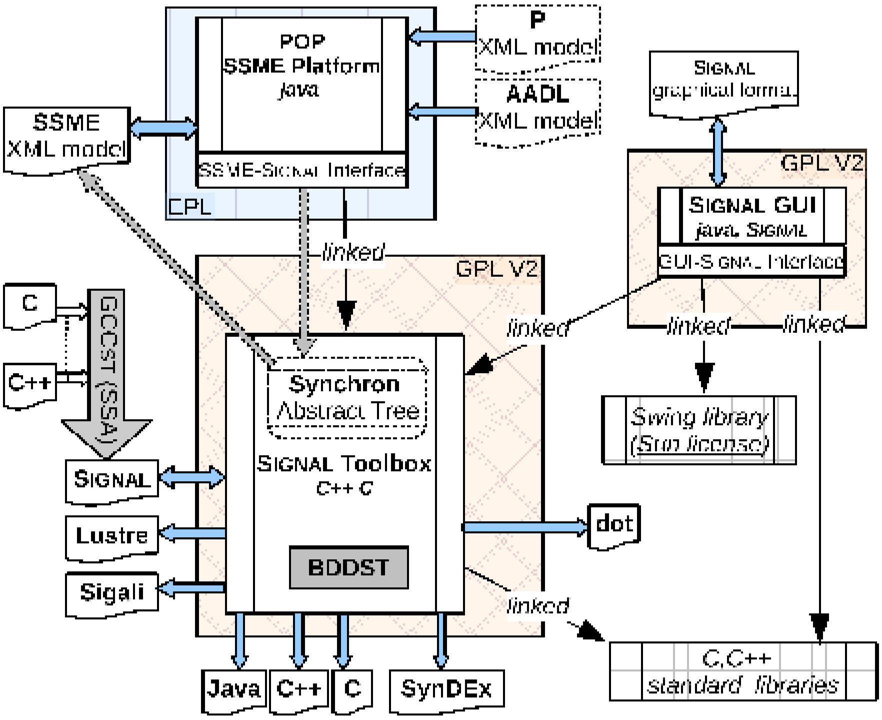

Figure 2. The Polychrony toolset high-level architecture

The Polychrony toolset contains three main components and an experimental interface to GNU Compiler Collection (GCC):

- The Signal toolbox, a batch compiler for the Signal language, and a structured API that provides a set of program transformations. Itcan be installed without other components and is distributed under GPL V2 license.
- The Signal GUI, a Graphical User Interface to the Signal toolbox (editor + interactive access to compiling functionalities). It can be used either as a specific tool or as a graphical view under Eclipse. In 2015, 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 SSME platform, a front-end to the Signal toolbox in the Eclipse environment. It is distributed under EPL license.
- GCCst, a back-end to GCC that generates Signal programs (not yet available for download).

The Polychrony toolset also provides a large library of Signal programs and examples, user documentations and developer-oriented implementation documents, and facilities to generate new versions.

The Polychrony toolset can be freely downloaded on the following web sites:

- The Polychrony toolset public web site: http://polychrony.inria.fr/. This site, intended for users and for developers, contains downloadable executable and source versions of the software for differents platforms, user documentation, examples, libraries, scientific publications and implementation documentation. In particular, this is the site for the open-source distribution of Polychrony.
- The Inria GForge: https://gforge.inria.fr. This site, intended for internal developers, contains the whole sources of the environment and their documentation.

As part of its open-source release, the Polychrony toolset not only comprises source code libraries but also an important corpus of structured documentation, whose aim is not only to document each functionality and service, but also to help a potential developer to package a subset of these functionalities and services, and adapt them to developing a new application-specific tool: a new language front-end, a new back-end compiler. This multi-scale, multi-purpose documentation aims to provide different views of the software, from a high-level structural view to low-level descriptions of basic modules. It supports a distribution of the software "by apartment" (a functionality or a set of functionalities) intended for developers who would only be interested by part of the services of the toolset.

6.3. SigCert: translation validation from Signal to C

Participants: Van-Chan Ngo, Jean-Pierre Talpin, Thierry Gautier, Paul Le Guernic, Loïc Besnard.

Translation validation [00] is a technique that attempts to verify that program transformations preserve the program semantics. It is obvious to prove globally that the source program and its final compiled program have the same semantics. However, we believe that a better approach is to separate concerns and prove each analysis and transformation stage separately with respect to ad-hoc data-structures to carry the semantic information relevant to that phase.

In the case of the Signal compiler [1], [7], the preservation of the semantics can be decomposed into the preservation of clock semantics at the *clock calculation* phase [15] and that of data dependencies at the *static scheduling* phase[16], and, finally, value-equivalence of variables at the *code generation* phase[14].

Translation Validation for Clock Transformations in a Synchronous Compiler. The clock semantics of the source and transformed programs are formally represented as *clock models*. A clock model is a first-order logic formula that characterizes the presence/absence status of all signals in a Signal program at a given instant. Given two clock models, a *clock refinement* between them is defined which expresses the semantic preservation of clock semantics[15]. A method to check the existence of clock refinement is defined as a satisfiability problem which can be automatically and efficiently proved by a SMT solver [0].

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[0] *Translation validation.* Pnueli A., Siegel M., and Singerman E. In Proceedings of TACAS'98, 1998.

[0] *Translation validation: From signal to c.* M. Siegel A. Pnueli and E. Singeman. In Correct Sytem Design Recent Insights and Advances, 2000.

[0] *Satisfiability modulo theories: An appetizer.* L. de Moura and N. Bjorner. In Brazilian Symposium on Formal Methods, 2009.

Precise Deadlock Detection for Polychronous Data-flow Specifications. Dependency graphs are a commonly used data structure to encode the streams of values in data-flow programs and play a central role in scheduling instructions during automated code generation from such specifications. We propose a precise and effective method that combines a structure of dependency graph and first order logic formulas to check whether multi-clocked data-flow specifications are deadlock-free before generating code from them. We represent the flow of values in the source programs by means of a dependency graph and attach first-order logic formulas to condition these dependencies. We use an SMT solver to effectively reason about the implied formulas and check deadlock freedom [16].

Implementation and Experiments. At a high level, our prototype tool *SigCert* ([14]) developed in OCaml could check the correctness of the compilation of Signal compiler w.r.t clock semantics, data dependence, and value-equivalence as given in Figure 3 . The individual modules designed in the context of this work are now being implemented and integrated in the open-source Polychrony toolset.

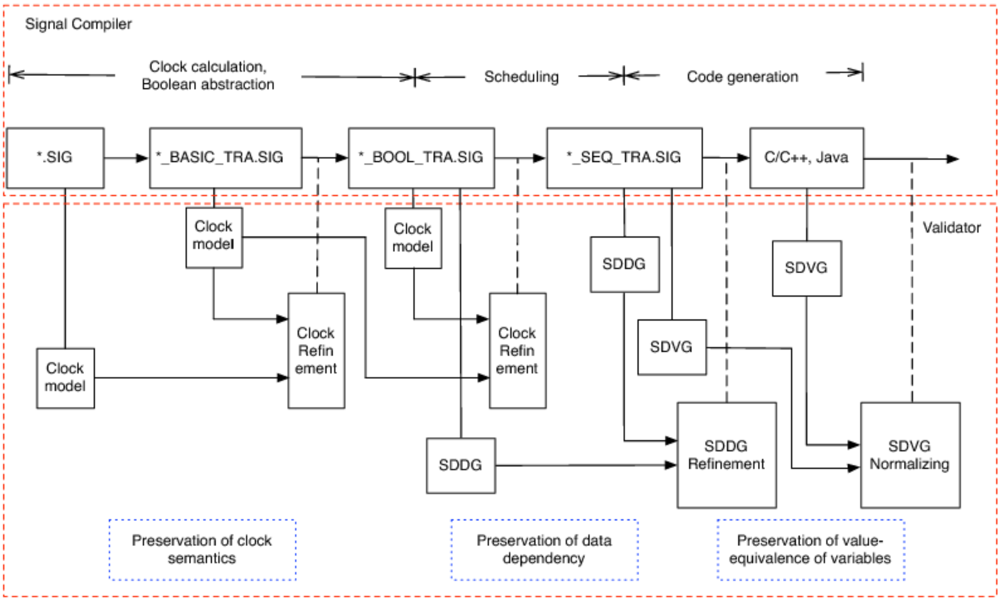

Figure 3. Our Integration within Polychrony Toolset

6.4. ADFG: Affine data-flow graphs scheduler synthesis under Eclipse

Participants: Alexandre Honorat, Jean-Pierre Talpin, Thierry Gautier, Loïc Besnard.

We have proposed a dataflow design model [2] of SCJ/L1 applications [0] in which handlers (periodic and aperiodic actors) communicate only through lock-free channels. Hence, each mission is modeled as a dataflow graph. The presented dataflow design model comes with a development tool integrated in the Eclipse IDE for easing the development of SCJ/L1 applications and enforcing the restrictions imposed by the design model. It consists of a GMF editor where applications are designed graphically and timing and buffering parameters can be synthesized. Indeed, abstract affine scheduling is first applied on the dataflow subgraph, 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 fixed-priority schedulability analysis (i.e., synthesis of timing and scheduling parameters of actors) considers both periodic and aperiodic actors.

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[0] *Safety critical Java technology specification*. JSR-302, Year = 2010

Through a model-to-text transformation, using Acceleo, the SCJ code for missions, interfaces of handlers, and the mission sequencer is automatically generated in addition to the annotations needed by the memory checker. Channels are implemented as cyclic arrays or cyclical asynchronous buffers; and a fixed amount of memory is hence reused to store the infinite streams of tokens. The user must provide the SCJ code of all the `handleAsyncEvent()` methods. We have integrated the SCJ memory checker [0] in our tool so that potential dangling pointers can be highlighted at compile-time. To enhance functional determinism, we would like to develop an ownership type system to ensure that actors are strongly isolated and communicate only through buffers.

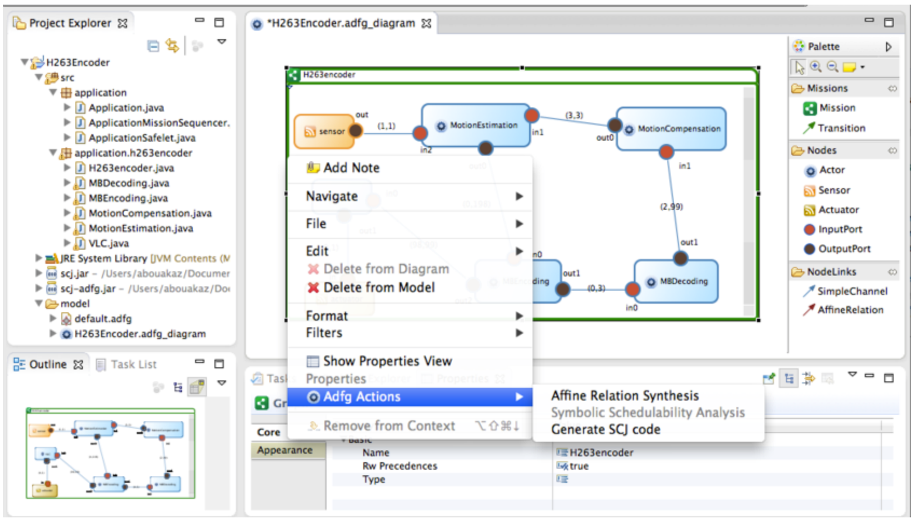

Figure 4. The ADFG Tool

The ADFG tool is being further developed in the context of the ADT "La vie d'AADL" in order to serve both as scheduler synthesis tool from AADL specifications and SCJ tasksets. We plan to further the front end analysis tools from Java task sets in order to build the input CSDF graphs from program analysis, in the context of a future PhD.

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[0] *Static checking of safety critical Java annotations*. Tang, D. Plsek, A. and Vitek, J. International Workshop on Java Technologies for Real-Time and Embedded Systems, 2010

ASPI Project-Team (section vide)

I4S Project-Team

6. New Software and Platforms

6.1. Platform: PEGASE

Plate-forme Experte Générique pour Applications Sans-fil Embarquées
Keyword: SHM (Structural Health Monitoring)
Scientific Description

I4S is actually finalizing the setup of a new platform named PEGASE 2.0 as the technological successor of the previous PEGASE platform developed by IFSTTAR.

The new version of PEGASE keeps the best of its previous version in its main vocation, to be a generic high level Wireless Sensor Platofrm.

What does not change between PEGASE 1 and 2.0: Based on various feedback from application fields, results from real structures monitored by PEGASE, and due to the rapid obsolescence of electronic devices, the design of the new PEGASE platform has been launched in 2013. Some of the main functions of PEGASE does not change but are reinforced.

Software genericity: use of a Linux embedded OS to make any application developed independently from the hardware, to make the user able to manage the system without ant physical and heavy operations.

Hardware genericity: with a principle of daughter and mother boards, each redundant need is embedded (processing, memory, timing, GPS, energy, etc) which each pluggable daughter board implements a specific function (sensing, 3G, Ethernet, communication, signal processing and relay control).

Accurate time synchronization: based on an original GPS and PPS algorithm, PEGASE platform is one of the only board able to time-stamp data from sensors or any event with an accuracy of some micro-seconds Universal Time.

What's new on PEGASE 2 platform ?

Previous principles are maintained or extended. Full electronic design from scratch occurred in 2014 to maximise its capacities in terms efficiency, cost, energy consumption, etc. Its main characteristics are

Important software evolutions: the platform embedded a real Linux kernel (not
Functional Description

I4S is actually finalizing the setup of a new platform named PEGASE 2.0 as the technological successor of the previous PEGASE platform developed by IFSTTAR.

The new version of PEGASE keeps the best of its previous version in its main vocation, to be a generic high level Wireless Sensor Platofrm.

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Accurate time synchronization: based on an original GPS and PPS algorithm, PEGASE platform is one of the only board able to time-stamp data from sensors or any event with an accuracy of some micro-seconds Universal Time.

- Participants: Vincent Le Cam, Mathieu Le Pen, Laurent Mevel and Michael Doehler
- Contact: Michael Doehler
- URL: http://www.a3ip.com/joomla/index.php?option=com_content&view=article&id=12&Itemid=8

6.2. TDISTL

Time domain inverse scattering for transmission lines
KEYWORDS: Transmission lines - Problem inverse - Fault diagnosis
SCIENTIFIC DESCRIPTION

TDISTL is a time domain variant of the previously developed frequency domain software ISTL for numerical computations of the inverse scattering transform applied to electrical transmission lines. It provides an efficient solution to experimentally determining the distributed characteristic impedance of electrical transmission line from the time domain reflectogram (impulse response) measured at one end of the line. Its current applications are in the fields of electrical cable fault diagnosis. It is registered at Agence pour la Protection des Programmes (APP) under the number IDDN.FR.001.250014.000.S.P.2015.000.30705.

FUNCTIONAL DESCRIPTION

Computation of the distributed characteristic impedance of a transmission line from time domain reflectometry measurement

- Participants: Qinghua Zhang and Michel Sorine
- Contact: Qinghua Zhang

6.3. Cloud2SM

Cloud architecture design for Structural Monitoring with in-line Sensors and Models tasking
KEYWORDS: SHM, online physical models, Data Management, Multi-physics Sensing, GPGPU acceleration
SCIENTIFIC DESCRIPTION

From the past decades the monitoring of civil engineering structure became a major field of research and development process in the domains of modelling and integrated instrumentation. This increasing of interest can be attributed in part to the need of controlling the aging of such structures and on the other hand to the need to optimize maintenance costs. From this standpoint the project Cloud2SM (inria ADT) has been launched to develop a robust information system able to assess the long term monitoring of civil engineering structures as well as interfacing various sensors and data. The specificity of such architecture is to be based on the notion of data processing through physical or statistical models. Thus the data processing, whether material or mathematical, can be seen here as a resource of the main architecture. The project can be divided in various items:

- The sensors and their measurement process: Those items provide data to the main architecture and can embed storage or computational resources. Dependent of onboard capacity and the amount of data generated it can be distinguished heavy and light sensors.
- The storage resources: Based on the cloud concept this resource can store at least two types of data, raw data and processed ones.
- The computational resources: This item includes embedded “pseudo real time” resources as the dedicated computer cluster or computational resources.
- The models: Used for the conversion of raw data to meaningful data. Those types of resources inform the system of their needs they can be seen as independents blocks of the system.
- The user interface: This item can be divided in various HMI to assess maintaining operation on the sensors or pop-up some information to the user.
- The demonstrators: The structures themselves.

Beside those objective, the I4S ADT campaign has allowed the development of the first block of the architecture: the data acquisition system. Called Cloud2IR, this prototype implementation of generic sensor interface has been specialized for the long term thermal monitoring of civil engineering structure and opened the way to the development of a whole ecosystem of sensors

6.3.1. Cloud2IR

Cloud 2IR is a software dedicated to the structural health monitoring of civil engineering structures thanks to long term thermal imaging. Its particularity lies in the fact that it is based on a generic approach of the acquisition system concept and the format of the data. That allow it to apply to other types of sensor. Information can be obtained on the inria bil, https://bil.inria.fr/fr/software/view/2536/tab.

IPSO Project-Team (section vide)

DYLISS Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: Bioinformatics - Linked data - Networks - Semantic Web - Omics
FUNCTIONAL DESCRIPTION

This tool was designed in 2015 in the framework of the MIRNadapt project. Biological studies and bioinformatical analysis produce numerous heterogeneous data, calling for their integration. AskOmics is an integration and interrogation software relying on an RDF model and the SPARQL query language. Its purpose is to obtain quick answers to biological questions demanding currently hours of manual search in several spreadsheet results files. New study perpectives will arise from these answers and from this integration work. Using AskOmics, we integrated an omic dataset borrowed from the MiRNAdapt ANR project that aims to describe the networks of the genes involved in aphids adaptation to seasons. AskOmics allows biologists to integrate and interrogate themselves their data without needing any knowledge about RDF and SPARQL. The query process consists in linking sets of biological entities as nodes in a graphical interface, optionaly specifying biological attributes for these nodes. The graph is then converted inton a SPARQL query to provide the user an answer to his biological questions. The answers are the elements of the sets that match the query contraints.

- Participants: Charles Bettembourg, Anthony Bretaudeau, Olivier Dameron, Aurélie Evrard, Yvanne Chaussin, Anne Siegel, Fabrice Legeai
- Partners: INRA IGEPP
- Contact: Fabrice Legeai
- URL: http://bipaa.genouest.org/askomics_aphid/

6.2. VIRALpro

FUNCTIONAL DESCRIPTION

VIRALpro is a predictor capable of identifying capsid and tail protein sequences using support vector machines (SVM) with an estimated accuracy between 90% and 97%. Predictions are based on the protein amino acid composition, on the protein predicted secondary structure, as predicted by SSpro, and on a boosted linear combination of HMM e-values obtained from 3,380 HMMs built from multiple sequence alignments of specific fragments - called contact fragments - of both capsid and tail sequences. This tool was designed in the context of a 2015 Explorer Program visit at University of California, Irvine

- Participants: Clovis Galiez, François Coste
- Partner: Pierre Baldi, University of California, Irvine
- Contact: Clovis Galiez

6.3. Shogen

KEYWORDS: Systems Biology - Bioinformatics - Genomics
FUNCTIONAL DESCRIPTION

This ASP-based software aims at identifying every segments of consecutive genes in a bacterial genome with a maximum number of genes that participates in a given metabolic pathway. Through this selection, the shogen tool deciphers putative sets of genes that (1) take an active part in metabolic pathways while being closely connected via metabolic networks and (2) are consecutive on each of the genomes involved. In practice, our approach connects genomic and metabolic knowledge by considering the genome organization and the biochemical reactions catalyzed by enzymes encoded by its genes. The underline parsimonious principle assumes that genes must be jointly regulated to activate a metabolic reaction cascade, and should be close enough in the genome organization. In 2015, the tool was simplified to handle standardized data formats, enabling its application to the modelling of a bacterial community [17]

- Participants: Philippe Bordron, Damien Eveillard, Alejandro Maass and Anne Siegel
- Partners: LINA - University of Chile
- Contact: Anne Siegel
- URL: http://aspforbiology.genouest.org/wiki.php/Software%20&%20Biological%20applications

6.4. Caspo

Cell ASP Optimizer
FUNCTIONAL DESCRIPTION

Cell ASP Optimizer (caspo) is a pipeline for automated reasoning on logical signaling networks. The main underlying issue is that inherent experimental noise is considered, so that many different logical networks can be compatible with a set of experimental observations. Caspo-learn performs an automated inference of logical networks from experimental data. It identifies admissible large-scale families of logic models without any a priori bias, thus saving a lot of efforts. Next, once a family a logical networks has been identified, caspo-design can suggest or design new experiments in order to reduce the uncertainty associated to this family. Finally, caspo-control computes intervention strategies (i.e. inclusion minimal sets of knock-ins and knock-outs) that force a set of target species or compounds into a desired steady state. In 2015, the tool was extended to compute experimental design proposition [23], and to handle time-series datasets [31].

- Participants: Santiago Videla, Carito Guziolowski, Sven Thiele, Thomas Cokelaer, Torsten Schaub, Anne Siegel, Loic Paulevé and Max Ostrowski
- Partners: Ecole Centrale de Nantes - University of Potsdam - EMBL - LRI - Laboratoire de Recherche en Informatique
- Contact: Anne Siegel
- URL: http://bioasp.github.io/caspo/

6.5. Platforms and toolboxes

Among others, a goal of the team is to facilitate interplays between tools for biological data analysis and integration. Our tools are based on formal systems. They aim at guiding the user to progressively reduce the space of models (families of sequences of genes or proteins, families of keys actors involved in a system response, dynamical models) which are compatible with both knowledge and experimental observations.

Most of our tools are available both as stand-alone software and through portals such as Mobyle or Galaxy interfaces. Tools are developed in collaboration with the GenOuest resource and data center hosted in the IRISA laboratory, including their computer facilities [more info].

We present here three toolboxes which each contains complementary tools with respect to their targeted sub-domain of bioinformatics.

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

The goal is to offer a toolbox for the reconstruction of networks from genome, literature and large-scale observation data (expression data, metabolomics...) in order to elucidate the main regulators of an observed phenotype. Most of the optimization issues are addressed with Answer Set Programming.

MeMap and MeMerge. We develop a workflow for the **Au**tomatic **Re**construction of **Me**tabolic networks (AuReMe). In this workflow, we use heterogeneous sources of data with identifiers from different namespaces. MeMap (**Me**tabolic network **Map**ping) consists in mapping identifiers from different namespaces to a unified namespace. Then, MeMerge (**Me**tabolic network **Merge**) merges two metabolic networks previously mapped on the same namespace. [web server].

meneco [*input*: draft metabolic network & metabolic profiles. *output*: metabolic network]. It is a qualitative approach to elaborate the biosynthetic capacities of metabolic networks and solve incompleteness of large-scale metabolic networks. Since November 2015, a new version of Meneco has been available with Python 3, and a new functionality of topological producibility checking has been set up. [82] [60] [python package][web server].

shogen [*input*: genome & metabolic network. *output* : functional regulatory modules]. This software is able to identify genome portions which contain a large density of genes coding for enzymes that regulate successive reactions of metabolic pathways. See section 6.3 for details. [55][python package].

lombarde [*input*: genome, modules & several gene-expression datasets. *output*: oriented regulation network]. This tool is useful to enhance key causalities within a regulatory transcriptional network when it is challenged by several environmental perturbations. In 2015, the tool was simplified to handle standardized data formats. [41] [web server].

ingranalysis [*input*: signed regulation network & one gene-expression dataset. *output*: network repair gene-expression prediction] This tool is an extension to the bioquali tool. It proposes a range of different operations for altering experimental data and/or a biological network in order to re-establish their mutual consistency, an indispensable prerequisite for automated prediction. For accomplishing repair and prediction, we take advantage of the distinguished modeling and reasoning capacities of Answer Set Programming. The tool has evolved to the *iggy* tool recently [5] [21] [Python package][web server].

6.5.2. Dynamics and invariant-based prediction

We develop tools predicting some characteristics of a biological system behavior from incomplete sets of parameters or observations.

cadbiom. Based on Guarded transition semantic, this software provides a formal framework to help the modeling of biological systems such as cell signaling network. It allows investigating synchronization events in biological networks. [software][web server].

caspo: Cell ASP Optimizer This soft provides an easy to use software for learning Boolean logic models describing the immediate-early response of protein signaling networks. See Sec. 6.4 for details. The tool is included in the cellNopt package [0]. [python package][web server].

nutritionAnalyzer. This tool is dedicated to the computation of allocation for an extremal flux distribution. It allows quantifying the precursor composition of each system output (AIO) and to discuss the biological relevance of a set of flux in a given metabolic network by computing the extremal values of AIO coefficients. This approach enables to discriminate diets without making any assumption on the internal behaviour of the system [40][webserver][software and doc].

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

6.5.3. Sequence annotation

We develop tools for discovery and search of complex signatures within biological sequences.

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[0] http://www.cellnopt.org/

Logol Logol is a swiss-army-knife for pattern matching on DNA/RNA/Protein sequences, using a high-level grammar to permit a large expressivity [48]. In 2015, the efficiency of the tool was improved by slight evolutions of the underlying grammar. Possible fields of application are the detection of mutated binding sites or stem-loop identification (e.g. in CRISPR [0] [10]) [software].

Protomata learner Protomata software suite provides a grammatical inference framework for learning the specific signature of a functional protein family from unaligned sequences by partial and local multiple alignment and automata modeling. In 2015, motivated by the characterization of viral protein sequences during the internship of Maud Jusot [38], we have begun a refactoring of the parsing part of Protomata and we implemented a new mode returning the sum of the scores over all paths (Forward score), besides the classical score on best path (Viterbi score), to improve parsing's sensitivity on divergent but conserved families of sequences. [web server].

6.5.4. Integration of toolboxes and platforms in webservices

Most of our software were designed as "bricks" that can be combined through workflow application such as Mobyle. It worths considering them into larger dedicated environments to benefit from the expertise of other research groups.

Plateform for data storage, expertise sharing and application inventory In collaboration with the GenOuest ressource center, the BII plateform (Bio Investigation Index) is a good way to enhance knowledge and expertise sharing, improve the visibility on the team's work in progress and record the History of the team's discoveries and main results. It enables experiment reproducibility, reporting on experiment process details, storing all scripts and softwares (in the corresponding versions) and linking all input files, results and not reproducible intermediate data. [web access].

Web servers In collaboration with the GenOuest ressource center, most our tools are made available through several web portals.

- The **mobyle@GenOuest portal** is the generic web server of our ressource center. It hosts the ingranalysis, meneco, caspo, lombarde and shogun tools [website].
- The **Mobyle@Biotempo server** is a mobyle portal for system biology with formal approaches. It hosts the memap, memerge, meneco, ingranalysis, cadbiom and pogg tools [website].
- The **GenOuest galaxy portal** now provides access to most tools for integrative biology and sequence annotation (access on demand).

Dr Motif This resource aims at the integration of different software commonly used in pattern discovery and matching. This resource also integrates Dyliss pattern search and discovery software.

ASP4biology and BioASP It is a meta-package to create a powerful environment of biological data integration and analysis in system biology, based on knowledge representation and combinatorial optimization technologies (ASP). It provides a collection of python applications which encapsulates ASP tools and several encodings making them easy to use by non-expert users out-of-the-box. [Python package][website].

ASP encodings repository This suite comprises projects related to applications of Answer Set Programming using Potassco systems (the Potsdam Answer Set Solving Collection, bundles tools for Answer Set Programming developed at the University of Potsdam). These are usually a set of encodings possibly including auxiliary software and scripts [respository].

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[0] http://crispi.genouest.org/

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: Etienne Mémin
- Contact: Etienne 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 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: Etienne 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. The different variants of this code correspond to research studies that have been published in IEEE transaction on Pattern Analysis and machine Intelligence, Experiments in Fluids, IEEE transaction on Image Processing, IEEE transaction on Geo-Science end Remote Sensing. The binary of this code can be freely downloaded on the FLUID web site http://fluid.irisa.fr.

- Participants: Étienne Mémin and Thomas Corpetti
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.4. Low-Order-Motion - Estimation of low order representation of fluid motion

Low order description and estimation of 2D dense motion fields

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: Étienne Mémin and Anne Cuzol
- Contact: Étienne Mémin
- URL: http://fluid.irisa.fr

5.5. TYPHOON

GPU implementation of wavelet based motion estimator for Lidar data. This code is developped in coproperty between Inria and Chico.

FUNCTIONAL DESCRIPTION Typhoon is a motion estimation software specialized in fluid motion estimation. It is based on a dense optical flow technique associated to a multiscale wavelet representation of the estimated motion.

- Participants: Pierre Dérian, Christopher Mauzey and Étienne Mémin
- Contact: Étienne Mémin

GENSCALE Project-Team

6. New Software and Platforms

6.1. HTS data processing

6.1.1. GATB: Genome Assembly & Analysis Tool Box

The GATB software toolbox aims to lighten the design of NGS algorithms. It offers a panel of high-level optimized building blocks to speed-up the development of NGS tools related to genome assembly and/or genome analysis. The underlying data structure is the de Bruijn graph, and the general parallelism model is multithreading. The GATB library targets standard computing resources such as current multicore processors (laptop computer, small server) with a few GB of memory. From high-level API, NGS programming designers can rapidly elaborate their own software based on domain state-of-the-art algorithms and data structures. The GATB library is written in C++.

Contact: Dominique Lavenier

URL: https://gatb.inria.fr/

6.1.2. LEON: Genomic Data Compression

Leon is a lossless compression software that achieves compression of DNA sequences of high throughput sequencing data, without the need of a reference genome. Techniques are derived from assembly principles that better exploit NGS data redundancy. A reference is built de novo from the set of reads as a probabilistic de-Bruijn graph stored in a Bloom filter. Each read is encoded as a path in this graph, storing only an anchoring kmer and a list of bifurcations indicating which path to follow in the graph. This new method will allow to have compressed read files containing its underlying de-Bruijn Graph, thus directly re-usable by many tools relying on this structure. Leon achieved the encoding of a *C. elegans* reads set with 0.7 bits per base, outperforming state of the art reference-free methods.

Contact: Claire Lemaitre

URL: https://gatb.inria.fr/software/leon/

6.1.3. BLOOCOO: Genomic Data Correction

Bloocoo is a k-mer spectrum-based read error corrector, designed to correct large datasets with a very low memory footprint. It uses the disk streaming k-mer counting algorithm included in the GATB library, and inserts solid k-mers in a bloom-filter. The correction procedure is similar to the Musket multistage approach. Bloocoo yields similar results while requiring far less memory: as an example, it can correct whole human genome re-sequencing reads at 70 x coverage with less than 4GB of memory.

Contact: Claire Lemaitre

URL: https://gatb.inria.fr/bloocoo-read-corrector/

6.1.4. DiscoSnp++: DISCOvering Single Nucleotide Polymorphism

DiscoSnp++ is designed for discovering Single Nucleotide Polymorphism (SNP) and insertions/deletions (indels) from raw set(s) of reads obtained with Next Generation Sequencers (NGS). The number of input read sets is not constrained, it can be one, two, or more. No other data as reference genome or annotations are needed. The software is composed of three modules: (1) kissnp2, that detects SNPs and indels from read sets; (2) kissreads2, that enhances the kissnp2 results by providing for each variant a read coverage mean and a (phred) quality; (3) VCF_creator, that provides a file in the Variant Calling Format (VCF). A VCF file using or not a reference genome is also created.

Contact: Pierre Peterlongo

URL: http://colibread.inria.fr/software/discosnp/

6.1.5. MindTheGap: Detection of insertion

MindTheGap is a software that performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It takes as input a set of reads and a reference genome. It outputs two sets of FASTA sequences: one is the set of breakpoints of detected insertion sites, the other is the set of assembled insertions for each breakpoint. For each breakpoint, MindTheGap either returns a single insertion sequence (when there is no assembly ambiguity), or a set of candidate insertion sequences (due to ambiguities) or nothing at all (when the insertion is too complex to be assembled). MindTheGap performs de novo assembly using the de Bruijn Graph implementation of GATB. Hence, the computational resources required to run MindTheGap are significantly lower than that of other assemblers.

Contact: Claire Lemaitre

URL: http://mindthegap.genouest.org/

6.1.6. TakeABreak: Detection of inversion breakpoints

TakeABreak is a tool that can detect inversion breakpoints directly from raw NGS reads, without the need of any reference genome and without de novo assembling the genomes. Its implementation is based on the Genome Assembly Tool Box (GATB) library, and has a very limited memory impact allowing its usage on common desktop computers and acceptable runtime (Illumina reads simulated at 80x coverage from human chromosome 22 can be treated in less than two hours, with less than 1GB of memory).

Contact: Claire Lemaitre

URL: http://colibread.inria.fr/software/takeabreak/

6.2. Sequence comparison

6.2.1. PLAST: Parallel Local Alignment Search Tool

PLAST is a fast, accurate and NGS scalable bank-to-bank sequence similarity search tool providing significant accelerations of seeds-based heuristic comparison methods, such as the Blast suite. PLAST is fully designed to compare query and subject comprised of large sets of DNA, RNA and protein sequences. It is significantly faster than BLAST, while providing comparable sensitivity. PLAST contains a fully integrated data-filtering engine capable of selecting relevant hits with user-defined criteria (E-Value, identity, coverage, alignment length, etc.).

Contact: Dominique Lavenier

URL: https://plast.inria.fr

6.2.2. SIMKA: Comparison of metagenomic datasets

Simka rapidly compares a large number of metagenomics datasets using efficient kmer-based method. Datasets may contains hundreds of millions of NGS sequences. Kmers of each datasets are rapidly counted and identified to estimate the pairwise similarities between datasets. The output of Simka can be used for clustering purpose or for checking correlation between metadata.

Contact: Gaëtan Benoit

URL: https://gatb.inria.fr/software/simka/

6.2.3. BGREAT: read mapper on de-Bruijn graph

BGREAT maps reads on a de-Bruijn Graph, usually used for genome assembly. Mapping reads on graphs offers the possibility to conserve all the pieces of information lost during the assembly process and to avoid multi-mapping problems due to genomic repeats. BGREAT rewrites a read sequence as a succession of unitigs sequences. It can map millions of reads per CPU hour on a de-Bruijn graph built from a large set of human genomic reads.

Contact: Antoine Limasset

URL: http://github.com/Malfoy/BGREAT/

SAGE Project-Team

6. New Software and Platforms

6.1. GENFIELD

FUNCTIONAL DESCRIPTION

GENFIELD allows the generation of log-normal correlated fields. It is based on a spectral method and uses the FFTW library. Parallelism is implemented using MPI communications. GENFIELD is used in hydrogeology to model natural fields, like hydraulic conductivity or porosity fields.

- Authors: Grégoire Lecourt, Jocelyne Erhel, Jean-Raynald De Dreuzy and Géraldine Pichot
- Contact: Jocelyne Erhel

6.2. GLiMuH

Grains with Liquid Meniscus under Heating
FUNCTIONAL DESCRIPTION

The GLiMuH code is devoted to the understanding of how heat diffuses in an assembly of solid grains separated by air and water. In the pendular regime, the quantity of water is very small, leading to liquid bridges between the grains. In the current approximation, the grains are spherical in shape, and the numerical simulation is done in a 3D axisymmetric coordinate system. The shape of the liquid/gas interface is computed by integrating a differential algebraic system of equations, with a given quantity of water per unit volume of the porous medium, and under the constraint of a given contact angle between the liquid/gas interface and the solid boundaries. The numerical results allow us to estimate the effective thermal conductivity of a real wet granular medium, which is required to establish more realistic models for the HeMaTiS code.

- Authors: Édouard Canot, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.3. GRT3D

KEYWORDS: Advection - Simulation - Scientific calculation - Dispersion - Geochemistry
APP: version 2.0, April 2014, registered

Programming language: C

Current work: refactoring

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.

- Authors: Yvan Crenner, Caroline De Dieuleveult, Jocelyne Erhel, Souhila Sabit, Nadir Soualem
- Partner: ANDRA
- Contact: Jocelyne Erhel

6.4. HeMaTiS

Heat and Mass Transfer in Soils
FUNCTIONAL DESCRIPTION

HeMaTiS is a set of Finite Volume programs (variants concern different geometrical configurations: 1D, 1D-radial, 2D, 3D-axisymmetric) for computing the transient heat diffusion in soils when there is a phase change of water. Currently, the soil is modelled by a heterogeneous porous medium having constant thermo-physical properties, and the porous medium is saturated with water. The phase change is treated by means of the Apparent Heat Capacity method. In the near future, we plan to use an unsaturated model (but limited to small water content), and an effective thermal conductivity which depends on the local humidity (this latter law may reveal hysteresis behaviour). The software is written in Fortran 95 and is based on the Muesli library. A Computer Algebra System (Maple or Maxima) is used to compute the Jacobian matrix.

- Authors: Édouard Canot, Mohamad Muhieddine, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.5. PALMTREE

FUNCTIONAL DESCRIPTION PALMTREE is an easy-to-use library for the parallelization of Lagrangian methods for partial differential equations and general Monte Carlo methods. The code aims at satisfying three properties:

1. Reduction of computation time by using parallel architecture,
2. Simplicity as the user just has to add the algorithm governing the behaviour of the particles,
3. Portability since one has the possibility to use the package with any compiler and OS,
4. Action-Replay which provides the ability of the package to replay a selected batch of particles.

The software also now possesses a beta version which allows to run in parallel hybrid solvers, that is solvers which use both deterministic methods (FEM, FDM, etc...) and probabilistic methods. Moreover, the engineering being this software was published in MCQMC 2014 [32].

- Authors: Lionel Lenôtre, Géraldine Pichot.
- Contact: Lionel Lenôtre.
- URL: http://people.irisa.fr/Lionel.Lenotre/software.html

6.6. SBM

Skew Brownian Motion
FUNCTIONAL DESCRIPTION

SBM is a code allowing exact or approximated simulations of the Skew Brownian Motion. This code is used for the simulation, with a Monte-Carlo approach, of a 1D diffusion process with a discontinuous diffusion coefficient. Several benchmark tests are also implemented.

- Authors: Antoine Lejay and Géraldine Pichot
- Contact: Géraldine Pichot

6.7. TPIP

Thermal Properties by Inverse Problem
FUNCTIONAL DESCRIPTION

TPIP is a program which aims at estimating the thermo-physical of a saturated porous medium after a strong heating which leads to the phase change of the water contained in the pores, knowing the experimental heating curves history at few selected points. The least-square criterion is used, in which sensitivity coefficients are the solution of a huge, complex PDE system in order to take into account the phase change of water. These equations for the sensitivity coefficients are therefore obtained via a Computer Algebra System (Maple or Maxima). In many aspects, the forward problem is similar to the HeMaTiS code, and like it, is based on Muesli. Two different minimization algorithms may be used, Damped Gauss-Newton or Levenberg-Marquardt. A special procedure has been applied in order to obtain a robust convergence, by changing some parameters of the forward problem during the iterations.

- Authors: Édouard Canot, Mohamad Muhieddine, Salwa Mansour and Renaud Delannay
- Contact: Édouard Canot

6.8. Zohour

FUNCTIONAL DESCRIPTION

Zohour is a node-based adaptive 2D mesh algorithm, written in Fortran 2003. A basic rectangular, regular set of nodes is recursively refined. Then the cells come from the Voronoi tessellation. While the domain is currently limited to a rectangular shape, its strength is three-fold:first, computing the flux via a Finite Element or Finite Volume method is both simple and accurate because each cell-side of cells is the bisection of two nodes,

second, the transition between zones of different levels of refinement is more progressive than other methods, leading to a smaller number of nodes for the whole mesh,

third, during successive refinements when dealing with a transient problem, interpolation is needed only by the new nodes, limiting the numerical errors.

- Author: Édouard Canot
- Contact: Édouard Canot
- URL: http://people.irisa.fr/Edouard.Canot/zohour/

SERPICO Project-Team

6. New Software and Platforms

6.1. C-CRAFT

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The C-CRAFT software enables to jointly segment small particles and estimate background in 2D or 3D fluorescence microscopy image sequences. The vesicle segmentation and background estimation problem is formulated as a global energy minimization problem in the Conditional Random Field framework. A patch-based image representation is used to detect spatial irregularity in the image. An iterative scheme based on graph-cut algorithm is proposed for energy minimization.

- **Participants**: Thierry Pécot, Charles Kervrann, Patrick Bouthemy, Jean Salamero.
- **Contact:** Thierry Pécot, Charles Kervrann.
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::C-CRAFT
- **Languages:** C/C++ and JAVA (plug-in ICY: http://icy.bioimageanalysis.org/plugin/C-CRAFT)
- **Reference:** [26]

6.2. ATLAS

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The ATLAS software enables to detect spots in 2D fluoresence images. The spot size is automatically selected and the detection threshold adapts to the local image dynamics. ATLAS relies on the Laplacian of Gaussian (LoG) filter, which both reduces noise and enhances spots. A multiscale representation of the image is built to automatically select the optimal LoG variance. Local statistics of the LoG image are estimated in a Gaussian window, and the detection threshold is pointwise inferred from a probability of false alarm (PFA). The user only has to specify: i/ standard deviation of the Gaussian window; ii/ PFA value. The Gaussian window must be about the size of the background structures; increasing the PFA increases the number of detections.

- **Participants**: Antoine Basset, Patrick Bouthemy, Thierry Pécot, Charles Kervrann.
- **Contact:** Thierry Pécot, Patrick Bouthemy, Charles Kervrann.
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::ATLAS
- **Language:** C/C++
- **Reference:** [12]

6.3. Hullkground

KEYWORDS: Bioinformatics - Biomedical imaging

FUNCTIONAL DESCRIPTION: The HULLKGROUND software decomposes a fluorescence microscopy image sequence into two dynamic components: i/ an image sequence showing mobile objects, ii/ an image sequence showing the slightly moving background. Each temporal signal of the sequence is processed individually and analyzed with computational geometry tools. The convex hull is estimated automatically for each pixel and subtracted to the original signal. The method is unsupervised, requires no parameter tuning and is a simplified version of the shapes-based scale-space method.

- **Participants:** Anatole Chessel, Jean Salamero, Charles Kervrann.
- **Contact:** Charles Kervrann.
- **APP deposit number:** IDDN.FR.001.400005.000.S.P.2009.000.21000
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Hullkground
- **Free distribution:** http://serpico.rennes.inria.fr/doku.php?id=software:hullkground:hullkground
- **Language:** JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.4. Motion2D

KEYWORDS: Image sequence - Motion model - 2D
FUNCTIONAL DESCRIPTION: The MOTION2D software is a multi-platform object-oriented library to estimate 2D parametric motion models in an image sequence. It can handle several types of motion models, namely, constant (translation), affine, and quadratic models. Moreover, it includes the possibility of accounting for a global variation of illumination and more recently for temporal image intensity decay (e.g. due to photobleaching decay in fluorescence microscopy). The use of such motion models has been proved adequate and efficient for solving problems such as optic flow computation, motion segmentation, detection of independent moving objects, object tracking, or camera motion estimation, and in numerous application domains (video surveillance, visual servoing for robots, video coding, video indexing), including biological imaging (image stack registration, motion compensation in videomicroscopy). Motion2D is an extended and optimized implementation of the robust, multi-resolution and incremental estimation method (exploiting only the spatio-temporal derivatives of the image intensity function). Real-time processing is achievable for motion models involving up to six parameters. Motion2D can be applied to the entire image or to any pre-defined window or region in the image.

- **Participants:** Patrick Bouthemy, Jean-Marc Odobez, Fabien Spindler.
- **Contact:** Patrick Bouthemy, Fabien Spindler.
- **APP deposit number:** FR.001.520021.001.S.A.1998.000.21000 / release 1.3.11, January 2005)
- **Free academic software distribution:** http://www.irisa.fr/vista/Motion2D
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::Motion2D
- **Languages:** C/C++ and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.5. ND-SAFIR

KEYWORDS: Biology - Health - Image analysis - Photonic imaging - Fluorescence microscopy - Biomedical imaging
SCIENTIFIC DESCRIPTION: The ND-SAFIR software removes additive Gaussian and non-Gaussian noise in still 2D or 3D images or in 2D or 3D image sequences (without any motion computation) [4]. The method is unsupervised and is based on a pointwise selection of small image patches of fixed size (a data-driven adapted way) in spatial or space-time neighbourhood of each pixel (or voxel). The main idea is to modify each pixel (or voxel) using the weighted sum of intensities within an adaptive 2D or 3D (or 2D or 3D + time) neighbourhood and to use image patches to take into account complex spatial interactions. The neighbourhood size is selected at each spatial or space-time position according to a bias-variance criterion. The algorithm requires no tuning of control parameters (already calibrated with statistical arguments) and no library of image patches. The method has been applied to real noisy images (old photographs, JPEG-coded images, videos, ...) and is exploited in different biomedical application domains (time-lapse fluorescence microscopy, video-microscopy, MRI imagery, X-ray imagery, ultrasound imagery, ...).

- **Participants:** Jérôme Boulanger, Charles Kervrann, Patrick Bouthemy, Jean Salamero.
- **Partners:** INRA, PiCT - CNRS - Institut Curie.
- **APP deposit number:** IDDN.FR.001.190033.002.S.A.2007.000.21000 / new release 3.0 in 2013)
- **Free academic software distribution:** Binaries of the software ND-SAFIR are freely and electronically distributed (http://serpico.rennes.inria.fr/doku.php?id=software:nd-safir:index).
- **On-line demo:** http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#forms::NDSafir
- **Languages:** C/C++, MATLAB and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/). The C/C++ software has been developed under Linux using the CImg library and has been tested over several platforms such as Linux/Unix, Windows XP and Mac OS.
- **Commercial licence agreements:** Innopsys, Roper Scientfic, Photmetrics, Nikon Europe BV (2016).
- **Reference:** [4]

6.6. F2D-SAFIR

KEYWORD: Biomedical imaging
FUNCTIONAL DESCRIPTION: The F2D -SAFIR software removes mixed Gaussian-Poisson noise in large 2D images, typically $10^3 \times 10^3$ pixels, in a few seconds. The method is unsupervised and is a simplified version of the method related to the ND-SAFIR software. The software dedicated to microarrays image denoising, was licensed to the INNOPSYS company which develops scanners for disease diagnosis and multiple applications (gene expression, genotyping, aCGH, ChIP-chip, microRNA, ...).

- **Participant**: Charles Kervrann.
- **Partner:** INRA.
- **Contact:** Charles Kervrann.
- **APP deposit number:** IDDN.FR.001.190033.001.S.A.2007.000.21000
- **Language:** C/C++

6.7. TubuleJ

KEYWORDS: Bioinformatics - Biomedical imaging
FUNCTIONAL DESCRIPTION: The TUBULEJ software written in java (plug-in ImageJ) is devoted to the analysis of microtubules and helical structures in 2D cryo-electron microscope images. The software straightens curved microtubule images by estimating automatically point locations on the microtubule axis. The estimation of microtubule principal axis relies on microtubule cylindrical shape analyzed in the Fourier domain. A user-friendly interface enables to filter straight fiber images by selecting manually the layer lines of interest in the Fourier domain. This software can be used to generate a set of 2D projection views from a single microtubule projection view and a few parameters of this microtubule structure.

- **Contact:** Denis Chrétien.
- **Partners:** University of Rennes 1, CNRS.
- **APP deposit number:** IDDN.FR.001.240023.000.S.P.2011.000.21000
- **On-line demo:** http://equipes.igdr.univ-rennes1.fr/en/tips/Software/TubuleJ/
- **Language:** JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

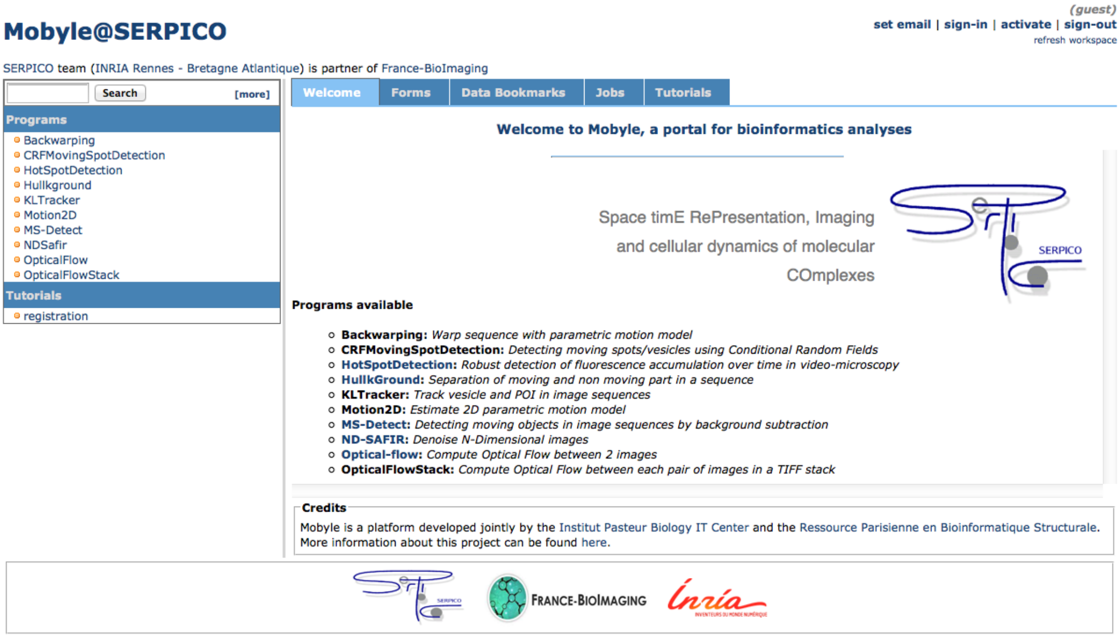
6.8. Cryo-Seg

KEYWORDS: Bioinformatics - Biomedical imaging
FUNCTIONAL DESCRIPTION: The CRYO-SEG software has been developed to detect microtubule structures and helical structures in 2D cryo-electron microscope images. Cryo-electron tomography allows 3D observation of biological specimens in their hydrated state. Segmentation is formulated as Maximum A Posteriori estimation problem and exploits image patches to take into account spatial contexts (Markov Random Fields). Because of the contrast anisotropy in the specimen thickness direction, the whole tomogram is segmented section by section, with an automatic update of reference patches. This algorithm has been evaluated on synthetic data and on cryo-electron tomograms of in vitro microtubules. On real data, this segmentation method extracts the most contrasted regions of microtubules, and 3D visualization is improved.

- **Participants:** Denis Chrétien, Charles Kervrann, Sophie Blestel.
- **Contact:** Denis Chrétien.
- **Partners:** University of Rennes 1, CNRS.
- **Languages:** C/C++ and JAVA (plug-in IMAGEJ: http://rsbweb.nih.gov/ij/)

6.9. Platforms

6.9.1. Mobyle@Serpico plateform and software distribution



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

Welcome to Mobyle, a portal for bioinformatics analyses

Space timE RePresentation, Imaging
and cellular dynamics of molecular
COmplexes

Programs available

- **Backwarping:** *Warp sequence with parametric motion model*
- **CRFMovingSpotDetection:** *Detecting moving spots/vesicles using Conditional Random Fields*
- **HotSpotDetection:** *Robust detection of fluorescence accumulation over time in video-microscopy*
- **HullkGround:** *Separation of moving and non moving part in a sequence*
- **KLTracker:** *Track vesicle and POI in image sequences*
- **Motion2D:** *Estimate 2D parametric motion model*
- **MS-Detect:** *Detecting moving objects in image sequences by background subtraction*
- **ND-SAFIR:** *Denoise N-Dimensional images*
- **Optical-flow:** *Compute Optical Flow between 2 images*
- **OpticalFlowStack:** *Compute Optical Flow between each pair of images in a TIFF stack*

Credits

Mobyle is a platform developed jointly by the Institut Pasteur Biology IT Center and the Ressource Parisienne en Bioinformatique Structurale. More information about this project can be found here.

*Figure 2. Mobyle@*SERPICO *web portal.*

The objective is to disseminate the distribution of SERPICO image processing software for biologist users:
Free binaries: software packages have been compiled for the main operating systems (Linux, MacOS, Windows) using CMake (see http://www.cmake.org/). They are freely available on the team website under a proprietary license (e.g. ND-SAFIR and HULLKGROUND are distributed this way at http://serpico.rennes.inria.fr/doku.php?id=software:index).

*Mobyle@*SERPICO *web portal*: An on-line version of the image processing algorithms has been developped using the Mobyle framework (Institut Pasteur, see http://mobyle.pasteur.fr/). The main role of this web portal (see Fig. 2) is to demonstrate the performance of the programs developed by the team: C-CRAFT[26], ATLAS[12], HOTSPOTDETECTION[57], HULLKGROUND[43], KLTRACKER[55], MOTION2D[54], MS-DETECT[45], ND-SAFIR[4], OPTICALFLOW and FLUX ESTIMATION [26]. The web interface makes our image processing methods available for biologist users at Mobyle@SERPICO (http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#welcome) without any installation or configuration on their own. The size of submitted images is limited to 200 MegaBytes per user and all the results are kept 15 days. The web portal and calculations run on a server with 2 CPU x 8 cores, 64 GigaBytes of RAM (500 MegaBytes for each user / Data is saved for 3 months).

IMAGEJ *plug-ins*: IMAGEJ (see http://rsb.info.nih.gov/ij/) is a widely used image visualization and analysis software for biologist users. We have developed IMAGEJ plug-in JAVA versions of the following software: ND-SAFIR [4], HULLKGROUND [43], MOTION2D [54], HOTSPOTDETECTION [57], STLAS [12]. The C-CRAFT algorithm [26] has been developped for the image processing ICY platform (http://icy.bioimageanalysis.org/).

Institut Curie CID iManage database: The microscopy facility of Institut Curie has co-developped a commercial database system (CID iManage/Strand Avadis company). The database can be searched via meta-data and includes menu selections that enable to run remote processing from a cluster. We have integrated ND-SAFIR and HULLKGROUND in the interface environment to allow the database users to process their images easily, and store associated results and parameters used.

- **Participants:** Thierry Pécot, Charles Kervrann, Charles Deltel (Inria Rennes SED).
- **Contact:** Thierry Pécot, Charles Kervrann.

6.9.2. IGRIDA-Serpico cluster

The IGRIDA-Serpico cluster of 200 nodes is opened for end-users for large scale computing and data sets processing (200 TeraBytes).

- **Batch Scheduler:** OAR
- **File management:** Puppet / Git / Capistrano
- **OS:** Linux Debian 7
- **User connexion:** public ssh key
- **Contact:** Thierry Pécot, Charles Kervrann, Charles Deltel (Inria Rennes SED).

VISAGES Project-Team

6. New Software and Platforms

6.1. Anima

KEYWORDS: Filtering - Medical imaging - Diffusion imaging - Registration - Relaxometry
SCIENTIFIC DESCRIPTION Anima is a set of libraries and tools developed by the team as a common repository of research algorithms. As of now, it contains tools for image registration, statistical analysis (group comparison, patient to group comparison), diffusion imaging (model estimation, tractography, etc.), quantitative MRI processing (quantitative relaxation times estimation, MR simulation), image denoising and filtering, and segmentation tools. All of these tools are based on stable libraries (ITK, VTK), making it simple to maintain.

- Participants: Laurence Catanese, Olivier Commowick, René-Paul Debroize, Florent Leray, Renaud Hédouin and Guillaume Pasquier
- Contact: Olivier Commowick
- URL: https://github.com/Inria-Visages/Anima-Public/wiki
- APP number: IDDN.FR.001.460020.000.S.P.2015.000.31230

6.2. MedInria

KEYWORDS: Segmentation - Health - DWI - Visualization - Medical imaging
SCIENTIFIC DESCRIPTION It aims at creating an easily extensible platform for the distribution of research algorithms developed at Inria for medical image processing. This project has been funded by the D2T (ADT MedInria-NT) in 2010 and renewed in 2012. The Visages team leads this Inria national project and participates in the development of the common core architecture and features of the software as well as in the development of specific plugins for the team's algorithm.
FUNCTIONAL DESCRIPTION MedInria is a free software platform dedicated to medical data visualization and processing as illustrated in figure 2 .

- Participants: Olivier Commowick, René-Paul Debroize, Guillaume Pasquier, Laurence Catanese
- Partners: HARVARD Medical School - IHU - LIRYC - IHU - Strasbourg - NIH
- Inria structures involved : ASCLEPIOS, ATHENA, PARIETAL, VISAGES
- Contact: Olivier Commowick
- URL: http://med.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230

6.3. autoMRI

KEYWORDS: Magnetic Resonance Imaging (MRI) - functional MRI (fMRI) - Arterial Spin Labeling (ASL) - functional ASL (fASL) - Statistical Parametric Mapping (SPM) - Automation
SCIENTIFIC DESCRIPTION This software is highly configurable in order to fit to a wide range of needs. Pre-processing includes segmentation of anatomical data, as well as co-registration, spatial normalization and atlas building of all data types. The analysis pipelines perform either within-group analysis or between-group or one subject-versus-group comparison and produce statistical maps of regions with significant differences. These pipelines can be applied to structural data to exhibit patterns of atrophy or lesions, to ASL (both pulsed or pseudo-continuous sequences) or PET data to detect perfusion or metabolic abnormalities (see figure 3 , left), to relaxometry data to detect deviations from a template (see figure 3 , right), to functional data - either BOLD or ASL - to outline brain activations related to block or event-related paradigms. In addition to the standard General Linear Model approach, the ASL pipelines implement an a contrario approach and, for patient-specific perfusion study, an heteroscedastic variance model. Besides, the vascular pipeline processes 4D MRA data and enables accurate assessment of hemodynamic patterns.

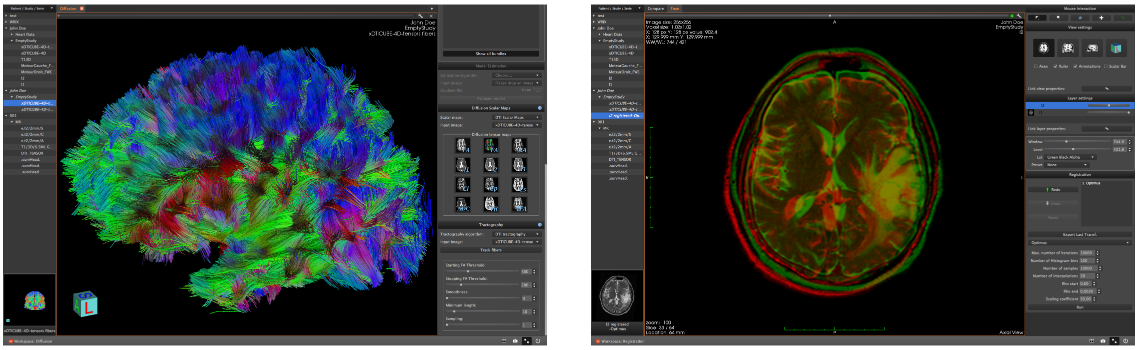


Figure 2. The medInria software platform: Tractography overlapped with 3D image (left), and Fused view of registered images (right)

FUNCTIONAL DESCRIPTION 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). A new version of the ASL post-processing part was developed in Python and Nipype, therefore not requiring the disponibility of Matlab licences.

- Participants: Isabelle Corouge, Cédric Meurée, Pierre Maurel and Elise Bannier
- Contact: Isabelle Corouge
- URL: http://www.irisa.fr/visages/

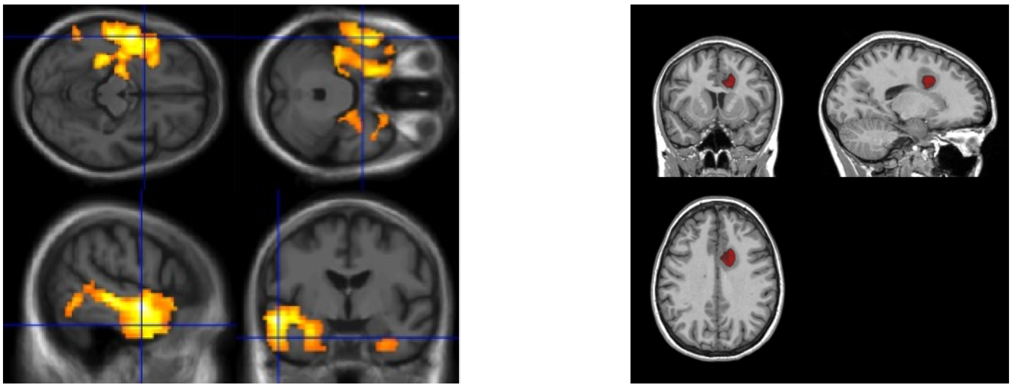


Figure 3. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (left) and detection of relaxometry defect in an MS patient (right).

6.4. Shanoir

KEYWORDS: Shanoir - Webservices - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS - Nifti

FUNCTIONAL DESCRIPTION SHAring NeurOImaging Resources (Shanoir, Previously InriaNeuroTk) is an open source software platform designed to structure, manage, archive, visualize and share neuroimaging data with an emphasis on multi-centric collaborative research projects. It provides common features of neuroimaging data management systems along with research-oriented data organization and enhanced accessibility (see figure 4).

Shanoir is a secured J2EE application running on a JBoss server, reachable via graphical interfaces in a browser or by third party programs via web services. It behaves as a repository of neuroimaging files coupled with a relational database hoding meta-data. The data model, based on OntoNeurolog, an ontology devoted to the neuroimaging field, is structured around the concept of "research study". A research study includes patients who themselves have examinations that either produce image acquisitions or clinical scores. Each image acquisition is composed of datasets represented by their acquisition parameters and image files. The system only keeps anonymous data.

Image file imports are possible from various sources (DICOM CDs, PACs, image files in NIfTI / Analyze format) using either online wizards, with completions of related meta-data, or commande line tools. Once de-identified during the import phase, DICOM header's customizable feature. Shanoir can also record any executed processing allowing to retrieve workflows applied to a particular dataset along with the intermediate data.

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 to be downloaded. Client side applications have as well been developed to illustrate how to locally access and exploit data through the available web services. With regards to security, the system requires authentication and user rights are tunable for each hosted studies. A study responsible can thereby define the users allowed to see, download or import data into his study or simply make it public.

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.

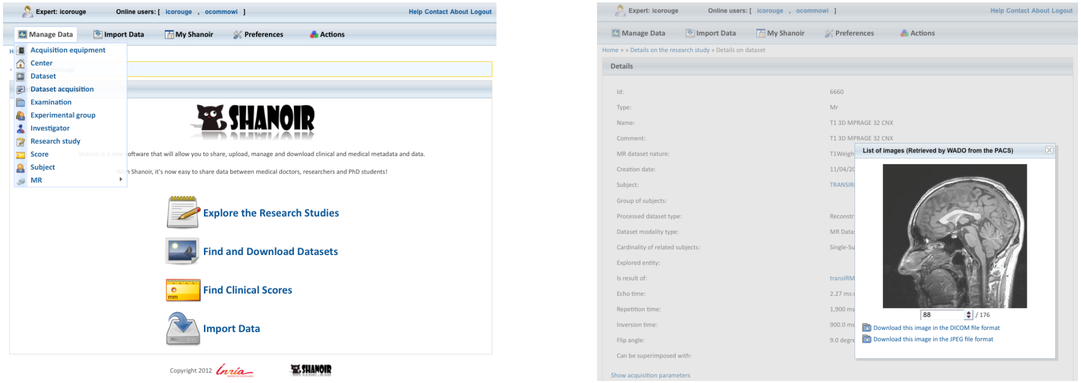
Shanoir integrates the enterprise search platform, Apache Solr, to provide the users a vast array of advanced features such as near real-time indexing and queries, full-text search, faceted navigation, autosuggestion and autocomplete.

- Participants: Michael Kain, Justine Guillaumont, Christian Barillot, Anthony Baire and Yao Yao
- Partners: Université de Rennes 1 - CNRS - INSERM
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.520021.003.S.A.2008.000.31230 (2014/08/20)

6.5. QtShanoir

KEYWORDS: Shanoir - Qt - Webservices - Soap - C++ - Health - DICOM - Plug-in - Medical imaging - Nifti

SCIENTIFIC DESCRIPTION QtShanoir is based on Qt/C++ librairie. It interacts with the Shanoir server using SOAP web services provided. This application queries the server and displays hierarchical data extracted in tree view. Data could also be easily downloaded or uploaded on the server. In order to extend the Shanoir environment, QtShanoir is developed to contain two shared libraries: - « GUI » that represents all user interfaces. - « DAO » that takes in charge the data model. This library assures the connection to the server and provides all QtShanoir services : research, download and upload of Processed Dataset (NIfTI). QtShanoir dynamic libraries are already reused and integrated in other projects: in the software medInria and in an under development command line program.



oftware that will allow you to share, upload, manage and download clinical and medical metadata and data.

h Shanoir, it's now easy to share data between medical doctors, researchers and PhD students!

Id: 6660
Type: Mr
Name: T1 3D MPRAGE 32 CNX
Comment: T1 3D MPRAGE 32 CNX
MR dataset nature: T1Weigh
Creation date: 11/04/20
Subject: TRANSIR
Group of subjects:
Processed dataset type: Reconstr
Dataset modality type: MR Data
Cardinality of related subjects: Single-Su
Explored entity:
Is result of: transIRM
Echo time: 2.27 ms
Repetition time: 1,900 ms
Inversion time: 900.0 ms
Flip angle: 9.0 degre
Can be superimposed with:

Figure 4. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

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: Olivier Commowick, Justine Guillaumont, Florent Leray, and Wefa Hakem
- Contact: Olivier Commowick
- URL: http://qtshanoir.gforge.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230 (2012/02/08)

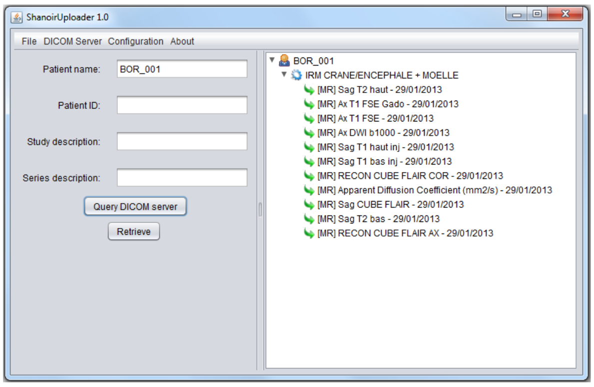
6.6. ShanoirUploader

KEYWORDS: Shanoir - Webservices - Java - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS

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 as illustrated in figure 5 . 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: Justine Guillaumont, Michael Kain, Christian Barillot, Yao Yao, Inès Fakhfakh
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.380026.000.S.P.2015.000.31230 (2015/09/11)



Patient name: BOR_001
Patient ID:
Study description:
Series description:

- BOR_001
  - IRM CRANE/ENCEPHALE + MOELLE
    - [MR] Sag T2 haut - 29/01/2013
    - [MR] Ax T1 FSE Gado - 29/01/2013
    - [MR] Ax T1 FSE - 29/01/2013
    - [MR] Ax DWI b1000 - 29/01/2013
    - [MR] Sag T1 haut inj - 29/01/2013
    - [MR] Sag T1 bas inj - 29/01/2013
    - [MR] RECON CUBE FLAIR COR - 29/01/2013
    - [MR] Apparent Diffusion Coefficient (mm2/s) - 29/01/2013
    - [MR] Sag CUBE FLAIR - 29/01/2013
    - [MR] Sag T2 bas - 29/01/2013
    - [MR] RECON CUBE FLAIR AX - 29/01/2013

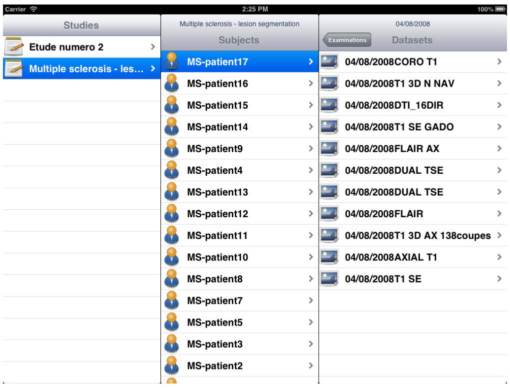
Figure 5. The ShanoirUploader software is a desktop application designed to interact with a PACS to query and retrieve the data stored on any PACS.

6.7. iShanoir

KEYWORDS: Shanoir - Biology - Health - Neuroimaging - Mobile application - Medical imaging - Biomedical imaging

FUNCTIONAL DESCRIPTION iShanoir is an iOS application, designed for iPhone and iPad. On base of this application a Shanoir server can be accessed. For this the Shanoir SOAP web-services are called. As shown in figure 6 , iShanoir can be used to access and navigate in the data tree structure, stored on a Shanoir server. iShanoir displays as well additional meta data corresponding to the data entities in the tree structure. On base of these informations image files (NIfTI and DICOM) can be selected and downloaded on a local iPhone/iPad in a temporary cache. From this cache the files can be opened and displayed with a viewer that the user has already installed on his device.

- Participants: Michael Kain, Christian Barillot
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr



Etude numero 2
Multiple sclerosis - les...

MS-patient17
MS-patient16
MS-patient15
MS-patient14
MS-patient9
MS-patient4
MS-patient13
MS-patient12
MS-patient11
MS-patient10
MS-patient8
MS-patient7
MS-patient5
MS-patient3
MS-patient2

04/08/2008CORO T1
04/08/2008T1 3D N NAV
04/08/2008DTI_16DIR
04/08/2008T1 SE GADO
04/08/2008FLAIR AX
04/08/2008DUAL TSE
04/08/2008DUAL TSE
04/08/2008FLAIR
04/08/2008T1 3D AX 138coupes
04/08/2008AXIAL T1
04/08/2008T1 SE

Figure 6. The iShanoir software is a desktop application designed to...

6.8. Integration of EEG and fMRI

Participants: Marsel Mano, Lorraine Perronnet.

Related to the project Hemisfer there have been development of new functions, scripts and demos for the acquisition and processing of the EEG and fMRI data in Real-time. These include:

- Functions for fMRI header info reader, volume reader, motion correction, slice time correction nifty output conversion, real time fMRI initialization, real time fMRI processing, z-score calculation, volume smoother, alignment, etc., functions for real time EEG data acquisition, filtering, power calculation and display.
- Scripts for various protocols used in offline fMRI experiments, real time processing loop for EEG and fMRI.
- Demo for real time acquisition of the EEG and fMRI data, demo for real time processing efficiency of the fMRI data, demo for the real time processing of EEG data, real time z-Score for fMRI data.
- Several small aux functions for I/O interfaces (e.g. com, serial)

In the current stage the prototype also relies on various other free toolboxes (e.g. SPM, pnet)

- Keywords: medical imaging, EEG, fMRI
- Software benefit: integration of EEG and fMRI processing
- Type of human computer interaction: C++ API, shell scripts
- OS/Middleware: Windows, Mac and Linux.
- Required library or software : SPM, pnet.
- Programming language: C++, shell scripts

6.9. Platforms

6.9.1. The Neurinfo Platform

VISAGES is the founding actor of an experimental research platform which was installed in August 2009 at the University Hospital of Rennes. The University of Rennes 1, Inria, Inserm for the academic side, and the University Hospital of Rennes and the Cancer Institute “Eugene Marquis“ for the clinical side, are partners of this neuroinformatics platform called Neurinfo (http://www.neurinfo.org). This platform has been supported under the “Contrat de Projets Etat-Région” (C. Barillot is the PI) and has received a total amount of 4.01 M€ for the period 2007–2014. European (FEDER), National (through Ministry of research, Inria, Inserm and ANR) and local councils (Brittany Region, Ille et Vilaine, and Rennes Metropole) have joined their effort to support this operation for a total amount of 4010 k€ (600 k€ for the infrastructures, 2850 k€ for the equipments and 560 k€ for the functioning). This application was set up through the Regional PIMATGI initiative coordinated by INSERM in Brittany (C. Roux). The overall PIMATGI initiative served for the financing of three distinct, but complementary, platforms: Neurinfo, TheraFONC as a technical platform dedicated to therapy guided by functional imaging especially in the oncology domain (Inserm U 650 - LaTIM, Dir. Ch. Roux, Brest), and TherA-Image as a platform dedicated to image guided mini-invasive surgery and therapy especially in the domain of cardio-vascular diseases (U642 -LTSI, Dir. L. Senhadji, Rennes).

Concerning the Neurinfo Platform, the activity domain is a continuum between methodological and technological research built around specific clinical research projects. The ambition is to do innovation in science, technology and medical technology transfer for the implementation on the clinical field. On the medical field, the translational research domain mainly concerns medical imaging and more specifically the clinical neurosciences. Among them are multiple sclerosis, epilepsy, neurodegenerative, neurodevelopmental and psychiatric diseases, surgical procedures of brain lesions, neuro-oncology and radiotherapy planning. Beyond these CNS applications, the platform is also open to alternative applications. Neurinfo ambitions to support the emergence of research projects based on their level of innovation, their pluri-disciplinarity and their ability to foster collaborations between different actors (public and private research entities, different medical specialties, different scientific profiles).

In this context, a new research 3T MRI system (Siemens Verio system) was acquired in summer 2009 in order to develop the clinical research in the domain of morphological, functional, structural and cellular in-vivo imaging. In 2014 a new equipment for simultaneous recording of EEG and MRI images has been acquired from Brain Product. In 2015, a mock scanner for experimental set-up has been acquired as well as a new High Performance Computing environment made of one large computing cluster and a data center that is shared and operated by the Inria center at IRISA (UMR CNRS 6074). The computation cluster (240 cores) and the data center (up to 50 TB) are dedicated to host and process imaging data produced by the Neurinfo platform, but also by other research partners that share their protocols on the Neurinfo neuroinformatics system (currently more than 30 sites).

Visages and its partners in the Neurinfo project are committed to use this new research platform for developing new regional, national and international collaborations around fundamental and applied clinical research projects dealing with in-vivo medical imaging.

ASAP Project-Team

5. New Software and Platforms

5.1. Brow2Brow

Browser-to-browser serverless toolboxes
FUNCTIONAL DESCRIPTION

Brow2Brow is an “Action de Development Technologique”, i.e. a collaborative development project that aims at providing a middleware and software library for browser-to-browser applications. Brow2Brow involves the ASAP team as well as the DICE Team from Inria Grenoble (Antenne de Lyon). The project seeks to provide an alternative to the current model followed by Web2.0 applications by exploiting the recently introduced WebRTC standard. Existing Web 2.0 applications collect data on browsers and send it to servers that store and process it. The goal of Brow2Brow is to provide an alternative approach where browsers can themselves proceed to collaborative data processing. This will make it possible avoid data concentration at a single server. The project has resulted so far in the development of WebGC, a library for gossip-based applications on browsers.

- Participants: Anne-Marie Kermarrec, Davide Frey and Raziel Carvajal Gomez
- Contact: Davide Frey

5.2. Dashboard

MediEgo Dashboard: A personalized news dashboard
KEYWORDS: Recommender system - Personalized stream of news - Dashboard
FUNCTIONAL DESCRIPTION

This work has led to the development of MEDIEGO Dashboard, a personalized news recommendation system. In MEDIEGO Dashboard, users benefit from a personalized stream of news matching their interests. Additionally, users can use explicit subscriptions as well as post content and navigate through tags. MEDIEGO Dashboard is available through a web interface and a mobile-based Android application. To provide personalization, MEDIEGO Dashboard exploits the users’ opinions regarding their received news to identify users with similar interests. MEDIEGO Dashboard is centralized and it allows us to test and evaluate different recommendation schemes. In collaboration with EIT/ICT Lab, an experiment has been conducted with a set of users at Trento (Italie). This experiment allowed us to collect traces and to perform a user survey to assess and improve our solution. This solution will soon be interconnected to AllYours-P2P.

- Participants: Anne-Marie Kermarrec, Antoine Boutet, Yuri Barssi and Jean-Francois Verdonck
- Contact: Anne-Marie Kermarrec
- URL: http://www.mediego.com

5.3. GossipLib

KEYWORDS: Nat traversal - Epidemic protocols - Gossip protocols - Overlay maintenance - Peer-to-peer - Dissemination
FUNCTIONAL DESCRIPTION

GossipLib is a library consisting of a set of Java classes aimed to facilitate the development of gossip-based application in a large-scale setting. It provides developers with a set of support classes that constitute a solid starting point for building any gossip-based application. GossipLib is designed to facilitate code reuse and testing of distributed application and as thus also provides the implementation of a number of standard gossip protocols that may be used out of the box or extended to build more complex protocols and applications. These include for example the peer-sampling protocols for overlay management.

GossipLib also provides facility for the configuration and deployment of applications as final-product but also as research prototype in environments like PlanetLab, clusters, network emulators, and even as event-based simulation. The code developed with GossipLib can be run both as a real application and in simulation simply by changing one line in a configuration file.

- Participants: Davide Frey, Ribeiro Heverson, Anne Marie Kermarrec, Imane Al Ifdal, and Ilham Ikbal
- Contact: Davide Frey
- URL: http://gossiplib.gforge.inria.fr/

5.4. MediEgo

KEYWORDS: Widget web - Social network - Recommendation
FUNCTIONAL DESCRIPTION

MediEgo is a solution for content recommendation based on the users navigation history. The solution 1) collects the usages of the Web users and store them in a profile, 2) uses this profile to associate to each user her most similar users, 3) leverages this implicit network of close users in order to infer their preferences and recommend advertisements and recommendations. MediEgo achieves scalability using a sampling method, which provides very good results at a drastically reduced cost.

- Participants: Antoine Boutet, Jacques Falcou, Jean-Francois Verdonck, Anne Marie Kermarrec, Sébastien Campion, Rachid Guerraoui, Davide Frey and Arnaud Jegou
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Sébastien Campion
- URL: http://www.mediego.com

5.5. WebGC

Web-based Gossip Communication
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 is a library for gossip-based communication between web-browsers. It has been developed in collaboration with Mathieu Simonin in the context of the Brow2Brow ADT project. WebGC builds on the recent WebRTC standard as well as on PeerJS, an open-source project that provides primitives for data transfer on top of WebRTC.

- Participants: Raziel Carvajal Gomez, Davide Frey and Anne-Marie Kermarrec
- Contact: Davide Frey

5.6. WhatsUp

KEYWORD: Recommender system
FUNCTIONAL DESCRIPTION

WhatsUp is a distributed recommendation system aimed to distribute instant news in a large scale dynamic system. WhatsUp has two parts, an embedded application server in order to exchange with others peers in the system and a fully dynamic web interface for displaying news and collecting opinions about what the user reads. Underlying this web-based application lies Beep, a biased epidemic dissemination protocol that delivers news to interested users in a fast manner while limiting spam. Beep is parametrized on the fly to manage the orientation and the amplification of news dissemination. Every user forwards the news of interest to a randomly selected set of users with a preference towards those that have similar interests (orientation). The notion of interest does not rely on any explicit social network or subscription scheme, but rather on an implicit and dynamic overlay capturing the commonalities between users with respect to they are interested in. The size of the set of users to which a news is forwarded depends on the interest of the news (amplification). A centralized version of WhatsUp is already up and running and the decentralized one is still in beta version.

- Participants: Davide Frey, Ribeiro Heverson, Antoine Boutet, Anne Marie Kermarrec, Arnaud Jegou, Rachid Guerraoui and Jean-Francois Verdonck
- Contact: Davide Frey

5.7. 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.

This year's new work consisted in adding support for Non-Blocking I/O. It was carried out during the internship of Nominoe Kervadec.

- Participants: Davide Frey, Maxime Monod, Heverson Borba Ribeiro, Anne Marie Kermarrec and Arnaud Jegou, and Nominoe Kervadec
- Contact: Davide Frey
- URL: http://yalps.gforge.inria.fr/

5.8. p2p-allyours

Peer-to-Peer AllYours

FUNCTIONAL DESCRIPTION

P2P AllYours is customization of WhatsUp developed in the context of the EIT/ICT-Labs AllYours project. In addition to WhatsUp (the distributed recommender engine), p2p-AllYours comprises the following features: - a new web interface, which users can access through a local web-server integrated in P2PAllYours, - a set of automatic nodes (BOTs) that can extract news items from RSS feeds and insert them into the recommender system - a content-bootstrap that solves the issues related to bootstrapping the recommender system when a user connects for the first time. - An experiment management server that allows users to register for the application in the context of the testing program.

- Participants: Davide Frey, Heverson Borba Ribeiro, Raziel Carvajal Gomez, Arnaud Jegou and Anne-Marie Kermarrec
- Contact: Davide Frey

ASCOLA Project-Team

5. New Software and Platforms

5.1. CSLA

Cloud Service Level Agreement language
KEYWORDS: Cloud computing - Service-level agreement - Elasticity
FUNCTIONAL DESCRIPTION

CSLA, the Cloud Service Level Agreement language, allows the definition of SLA properties for arbitrary Cloud services (XaaS). CSLA addresses QoS uncertainty in unpredictable and dynamic environment and provides a cost model of Cloud computing. Besides the standard formal definition of contracts – comprising validity, parties, services definition and guarantees/violations – CSLA is enriched with features, such as QoS degradation and an advanced penalty model, thus introducing fine-grained language support for Cloud elasticity management.

- Participants: Thomas Ledoux and Md Sabbir Hasan
- Contact: Thomas Ledoux
- URL: http://www.emn.fr/z-info/csla/

5.2. JEScala

FUNCTIONAL DESCRIPTION

JEScala is a Scala library which implements a seamless programming model combining object-oriented, aspect-oriented, event-based and concurrent programming. Events are object members. They can be explicitly triggered as in standard event-based programming but also implicitly triggered, as join points in aspect-oriented programming. Event expressions make it possible to compose events, filter them, and alter their content. Event handlers can be registered, and unregistered, dynamically.

Concurrency can be handled without any explicit thread manipulation. By default, primitive events are synchronous but they can also be declared as asynchronous. This creates concurrency between the source of the event and its handlers. This concurrency can then be handled by composing events with the join operator and creating disjunctions of the resulting events.

- Participants: Jurgen Van Ham, Guido Salvaneschi, Mira Mezini and Jacques Noyé
- Partners: *Technische Universität Darmstadt*
- Contact: Jacques Noyé
- URL: http://www.stg.tu-darmstadt.de/research/jescala_menu/index.en.jsp

5.3. SimGrid

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

Scientific Instrument for the study of Large-Scale Distributed Systems. SimGrid is a toolkit that provides core functionalities for the simulation of distributed applications in heterogeneous distributed environments.

The contributions by the ASCOLA team are related to the virtualization abstractions in particular the different models to simulate VM manipulations (*e.g.*, the live migration model).

- Participants: Jonathan Rouzaud-Cornabas, Frédéric Suter, Martin Quinson, Arnaud Legrand, Adrien Lebre, Jonathan Pastor, Mario Südholt, Luka Stanisic, Augustin Degomme, Jean-Marc Vincent and Florence Perronnin
- Partners: CNRS - Université de Nancy - University of Hawaii - Université de Reims Champagne-Ardenne - Femto-st
- Contact: Arnaud Legrand
- URL: http://simgrid.gforge.inria.fr/

5.4. VMPlaces

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 Lebre, Jonathan Pastor, and Mario Südholt
- Contact: Adrien Lebre
- URL: http://beyondtheclouds.github.io/VMPlaceS/

5.5. btrCloud

KEYWORDS: Cloud computing - Virtualization - Grid - Energy - Orchestration - Autonomic system - Placement - Cluster - Data center - Scheduler

FUNCTIONAL DESCRIPTION

Orchestration, virtualization, energy, autonomic system, placement, cloud computing, cluster, data center, scheduler, grid

btrCloud is a virtual machine manager for clusters and provides a complete solution for the management and optimization of virtualized data centers. btrCloud (acronym of better cloud) is composed of three parts.

The analysis function enables operatives and people in charge to monitor and analyze how a data-center works - be it on a daily basis, on the long run, or in order to predict future trends. This feature includes boards for performance evaluation and analysis as well as trends estimation.

btrCloud, by the integration of btrScript, provides (semi-)automated VM lifecycle management, including provisioning, resource pool management, VM tracking, cost accounting, and scheduled deprovisioning. Key features include a thin client interface, template-based provisioning, approval workflows, and policy-based VM placement.

Finally, several kinds of optimizations are currently available, such as energy and load balancing. The former can help save up to around 20% of the data-center energy consumption. The latter provides optimized quality of service properties for applications that are hosted in the virtualized datacenters.

- Participants: Guillaume Le Louët, Frédéric Dumont and Jean-Marc Menaud
- Contact: Guillaume Le Louët
- URL: http://www.btrcloud.org/btrCloud/index_EN.html

ATLANMODELS Team

6. New Software and Platforms

6.1. AM3

AtlanMod MegaModel Management
KEYWORDS: Modeling artifact - MDA - MDE - Megamodeling
FUNCTIONAL DESCRIPTION

AM3 (AtlanMod MegaModel Management) is a generic and extensible tool/framework dedicated to global model management, i.e., the management of different modeling artifacts as well as their interrelationships.

- Participant: Hugo Brunelière
- Partner: Ecole des Mines de Nantes
- Contact: Hugo Brunelière
- URL: http://wiki.eclipse.org/AM3

6.2. AMW

Atlas Model Weaver
KEYWORDS: MDA - MDE - Weaving - Link - Model element
FUNCTIONAL DESCRIPTION

AMW is a generic and extensible tool dedicated to the creation and handling of weavings between models, these weavings representing sets of links existing between elements potentially coming from different models. Language

- Participant: Frédéric Jouault
- Contact: Hugo Brunelière
- URL: http://wiki.eclipse.org/AMW

6.3. ATL

Atlanmod Transformation Language
KEYWORDS: MDA - MDE - ATL - QVT - Model - Transformation
FUNCTIONAL DESCRIPTION

ATL is a tool dedicated to model transformation, complete, integrated into Eclipse and including its own development and execution environment, concrete examples as well as the corresponding associated documentation.

- Participants: Jean Bézivin, Frédéric Jouault and Patrick Valduriez
- Partner: Ecole des Mines de Nantes
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/m2m/atl/

6.4. ATL-MR

ATL-MapReduce
KEYWORDS: Transformation - Distributed
SCIENTIFIC DESCRIPTION

ATL-MapReduce

ATL-MapReduce (ATL-MR) is a prototype tool for running complex ATL transformation in the cloud using Hadoop MapReduce. ATL-MapReduce is implemented on top of an extended ATL VM that can be found on (https://github.com/atlanmod/org.eclipse.atl.atlMR/tree/master). Coupling ATL-MR with the [the extended VM](https://github.com/atlanmod/org.eclipse.atl.atlMR/tree/master) has proved a good performance, especially in terms of execution time. [In our experiments](http://www.emn.fr/z-info/atlanmod/index.php/Image:Atlmr-experiments-raw-data.zip), ATL-MR runs up to 6x faster compared to the regular VM while distributing it over 8 machines.

- Participants: Amine Benelallam, Abel Gomez Llana and Massimo Tisi
- Contact: Amine Benelallam
- URL: https://github.com/atlanmod/ATL_MR

6.5. ATLAS model weaver

ATLAS Model Weaver
KEYWORDS: Model - Metamodel - Weaving model
SCIENTIFIC DESCRIPTION

AMW is a component-based platform for model weaving that can be used to establish and manage abstract correspondences between models. The platform is generic and based on the Eclipse contribution mechanism: components are defined in separate plugins. The plugins are further interconnected to create the model weaver workbench. Components for user interface, matching algorithms and serialization of models may be plugged as necessary. We extended the Eclipse EMF architecture for model manipulation to coordinate the weaving actions. We use the EMF reflective API to obtain a standard weaving editor which adapts its interface according to metamodels modifications. The ATL transformation engine is plugged as the standard transformation platform.

FUNCTIONAL DESCRIPTION

The AMW is a tool for establishing relationships (i.e., links) between models. The links are stored in a model, called weaving model. It is created conforming to a weaving metamodel.

- Participants: Jean Bézivin, Erwan Breton, Marcos Didonet Del Fabro, Guillaume Gueltas, Frédéric Jouault and Patrick Valduriez
- Contact: Frédéric Jouault
- URL: http://www.eclipse.org/gmt/amw/

6.6. AmmA

Atlas Model Management Architecture
FUNCTIONAL DESCRIPTION

The AMMA platform is a model management platform. It is composed of several elements. Three of them: AM3, AMW, and MoDisco are available as GMT components. ATL is a component of M2M project.

- Participants: Mikaël Barbero and Frédéric Jouault
- Contact: Frédéric Jouault
- URL: https://wiki.eclipse.org/AMMA

6.7. Collaboro

SCIENTIFIC DESCRIPTION

Collaboro is an approach to make language development processes more participative, meaning that both developers and users of the language can collaborate together to create and evolve it. Collaboro supports both the collaborative definition of the abstract (i.e., metamodel) and concrete (i.e., notation) syntaxes for your DSL by providing a collaborative enviroment enabling the discussion.

Anyone has the chance to request changes, propose solutions and give an opinion (and vote) about those from others. This discussion enrichs the language definition signicantly and ensures that the end result satisfies as much as possible the expectations of the end-users.

- Participants: Jordi Cabot, Robin Boncorps and Javier Canovas Izquierdo
- Contact: Hugo Brunelière
- URL: http://atlanmod.github.io/collaboro/#/

6.8. EMF Facet

KEYWORDS: MDE - Model - Metamodel - Extension - Dynamicity - Querying
FUNCTIONAL DESCRIPTION

EMF Facet is a tool/framework dedicated to the non-intrusive and dynamic extension of metamodels (adding of new types, attributes, references, etc), based on a model query generic mechanism

- Partners: Ecole des Mines de Nantes - Mia-Software
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/modeling/emft/facet/

6.9. EMF Views

Eclipse Modeling Framework Views
FUNCTIONAL DESCRIPTION

Some users only need to see some parts of a model, others have to get the full model extended with data from another model, and others simply access to a combination of information coming from different models. Based on the unquestionable success/usefulness of database views to solve similar problems in databases, EMF Views aims to bring the same concept to the modeling world.

- Contact: Hugo Brunelière
- URL: https://github.com/atlanmod/emfviews

6.10. EMF-REST

Eclipse Modeling Framework Rest
FUNCTIONAL DESCRIPTION

EMF is the modeling framework of the Eclipse community. While EMF is able to automatically generate Java APIs from Ecore models, it is still missing support to deal with Web APIs such as RESTful ones that could boost the use of modeling techniques in the Web. However, the creation of RESTful APIs requires from developers not only an investment in implementation but also a good understanding of the REST Principles to apply them correctly. We therefore created EMF-REST, a tool that empowers EMF to get Truly RESTFul APIs from Ecore models, thus allowing web developers to generate JSON-based Web APIs for their applications. It generates both a JavaScript API to work with models as Javascript Objects in the client-side (without any EMF dependency) and REST services in the server-side based on the Java JAX-RS specification.

- Contact: Gerson Sunyé
- URL: http://emf-rest.com/

6.11. EMFtoCSP

SCIENTIFIC DESCRIPTION

Essentially, the EMFtoCSP is a sophisticated bounded model finder that yields instances of the model that conform not only to the structural definition of the model (e.g. the multiplicity constraints), but also to the OCL constraints. Based on this core, several correctness properties can be verified:

Satisfiability – is the model able to express our domain? For this check, the minimal number of instances and links can be specified to ensure non-trivial instances.

Unsatisfiability – is the model unable to express undesirable states? To verify this, we add further constraints to the model that state undesired conditions. Then we can check if is it impossible to instantiate the amended model.

Constraint subsumption – is one constraint already implied by others (and could therefore be removed)?

Constraint redundancy – do different constraints express the same fact (and could therefore be removed)?

FUNCTIONAL DESCRIPTION

EMFtoCSP is a tool for the verification of precisely defined conceptual models and metamodels. For these models, the definition of the general model structure (using UML or EMF) is supplemented by OCL constraints. The Eclipse Modeling Development Tools (MDT) provides mature tool support for such OCL-annotated models with respect to model definition, transformation, and validation.

- Contact: Hugo Brunelière
- URL: https://github.com/SOM-Research/EMFtoCSP

6.12. GiLA

GitHub Label Analyzer

FUNCTIONAL DESCRIPTION

Reporting bugs, asking for new features and in general giving any kind of feedback is the easiest way to contribute to an Open-Source Software (OSS) project. In GitHub, the largest code hosting service for OSS, this feedback is typically expressed as new issues for the project managed by an issue-tracking system available in each new project repository. Among other features, the issue tracker allows creating and assigning labels to issues with the goal of helping the project community to better classify and manage those issues (e.g., facilitating the identification of issues for top priority components or candidate developers that could solve them). Nevertheless, as the project grows a manual browsing of the project issues is no longer feasible.

- Contact: Gerson Sunyé

6.13. JSON Discoverer

FUNCTIONAL DESCRIPTION

The JSON discoverer allows you to discover the implicit schema of your JSON documents. Any JSON document includes both metadata (i.e., the schema) and data (i.e., the objects/values conforming to the schema). Given a (set of) JSON documents our discoverer analyzes the JSON definitions and generates for you a class diagram showing graphically the implicit JSON schema of your documents plus an object diagram representing their data.

- Participants: Jordi Cabot and Javier Canovas Izquierdo
- Contact: Hugo Brunelière
- URL: http://atlanmod.github.io/json-discoverer/#/

6.14. MODISCO

analyser, refactorer et comprendre le legacy

KEYWORDS: MDA - MDE - Model - Modernisation - Discoverer

SCIENTIFIC DESCRIPTION

MoDisco is an open source Eclipse project that provides a generic and extensible framework dedicated to the elaboration of Model Driven Reverse Engineering (MDRE) solutions. Gathering contributions from both academics and industrials, the goal of the project is to federate common efforts in the model-based transformation of legacy software systems implemented using different technologies (e.g. Java, COBOL, C). The first principle is to discover models out of legacy artifacts, representing appropriately all the relevant information, to be then used as part of reverse engineering processes for software understanding, evolution or modernization. Targeted scenarios include software (technical or architectural) migration of large legacy systems, but also retro-documentation, refactoring, quality assurance, etc. Within this context, MoDisco has collaborations with the OMG Architecture Driven Modernization (ADM) Task Force, for which the project provides several reference implementations of its standards: Knowledge Discovery Metamodel (KDM), Software Measurement Metamodel (SMM) and Abstract Syntax Tree Metamodel (ASTM).

The MoDisco framework is composed of a set of Eclipse plugins, and relies on the de-facto standard Eclipse Modeling Framework (EMF) for model handling. Thanks to its modular architecture, it allows completely covering the three steps of a standard MDRE approach: 1) Discovery (i.e. extracting a complete model of the source code), 2) Understanding (i.e. browsing and providing views on this model for a given purpose) and 3) Transformation (evolving the model towards a new technology, architecture, etc). More specifically, as part of its Infrastructure layer, MoDisco offers the set of generic (i.e., legacy technology-independent) reusable components really useful to build the core of MDRE solutions: Discovery Manager and Workflow for MDRE task orchestration, Model Browser for advanced navigation in complex models, model extension and customization capabilities for understanding (e.g. views definition), etc. As part of its Technologies layer, it provides an advanced support for the Java, JEE and XML technologies, including complete metamodels, corresponding model discoverers, transformations, code generators, customizations, query libraries, etc.

MoDisco (or some of its components) is being used by different partners including other academics, industrials (e.g. Sodifrance on several of their real modernization projects for their customers) or Eclipse projects (e.g. Eclipse-MDT Papyrus as developed by CEA). Moreover, the Eclipse-EMFT EMF Facet project has been initiated as a MoDisco spin-off, in order to externalize some features which are not actually specific to reverse engineering problems and thus may be reused in many different contexts (cf. corresponding EMF Facet section).

The initiative continues to be developed within the context of the European FP7-ICT project named ARTIST (http://www.artist-project.eu/), and also to a lower extent within the context of the French FUI 13 project named TEAP.

FUNCTIONAL DESCRIPTION

MoDisco is an Eclipse generic and extensible tool/framework providing to developers a set of reusable base components and dedicated to the elaboration of model driven reverse engineering (MDRE) solutions.

- Participant: Hugo Brunelière
- Partners: Ecole des Mines de Nantes - Mia-Software
- Contact: Hugo Brunelière
- URL: http://www.eclipse.org/MoDisco/

6.15. NeoEMF

FUNCTIONAL DESCRIPTION

NeoEMF is an open source software distributed under the terms of the Eclipse Public License that provides a backend-agnostic persistence solution for big, complex and highly interconnected EMF models. NeoEMF is a model repository and persistence framework allowing on-demand loading, storage, and unloading of large-scale EMF models.

- Partner: Mia-Software
- Contact: Gerson Sunyé
- URL: http://www.neoemf.com/

6.16. Reactive-ATL

KEYWORDS: Transformation - Reactive

SCIENTIFIC DESCRIPTION

Reactive engine for the ATL transformation language. In a model-driven application environment it works by activating only the strictly needed computation in response to updates or requests of model elements. Computation is updated when necessary, in an autonomous and optimized way by using incrementality and lazy evaluation.

- Participants: Salvador Martinez Perez and Massimo Tisi
- Contact: Salvador Martinez Perez
- URL: http://atlanmod.github.io/org.eclipse.atl.reactive

CIDRE Project-Team

6. New Software and Platforms

6.1. 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 at the OS level for a single node and a set of nodes.
FUNCTIONAL DESCRIPTION

Blare IDS is a set of tools that implements our approach to illegal information flow detection at the OS level for a single node and a set of nodes.

- Partner: CentraleSupélec
- Contact: Frédéric Tronel
- URL: http://blare-ids.org

6.2. ELVIS

Extensible Log VISualization
KEYWORDS: Visualization - Cybersecurity - Intrusion Detection Systems (IDS) - Cyber attack - Forensics
SCIENTIFIC DESCRIPTION

The studies that were performed last year clearly showed that there was an important need for technologies that would allow analysts to handle in a consistent way the various types of log files that they have to study in order to detect intrusion or to perform forensic analysis. Consequently, we proposed this year ELVis, a security-oriented log visualization system that allows the analyst to import its log files and to obtain automatically a relevant representation of their content based on the type of the fields they are made of. First, a summary view is proposed. This summary displays in an adequate manner each field according to its type (i.e. categorical, ordinal, geographical, etc.). Then, the analyst can select one or more fields to obtain some details about it. A relevant representation is then automatically selected by the tool according to the types of the fields that were selected.

ELVis [35] has been presented in VizSec 2013 (part of Vis 2013) in October in Atlanta. A working prototype is currently being tuned in order to perform field trials with our partners in DGA-MI. Next year, we are planing to perform research on how various log files can be combined in the same representation. In the PANOPTESEC project, we will also perform some research on visualization for security monitoring in the context of SCADA systems.
FUNCTIONAL DESCRIPTION

ELVIS is a log visualization tool that allows analyst-friendly log explorations through automated selection of adequate representations. Many log formats can be used and it is quite simple to add new ones. ELVis has been presented in VizSec 2013 (part of Vis 2013) in October in Atlanta.

- Participant: Nicolas Prigent
- Partner: CentraleSupélec
- Contact: Nicolas Prigent

6.3. GEPETO

GEoPrivacy-Enhancing TOolkit

KEYWORDS: Privacy - Mobility
SCIENTIFIC DESCRIPTION

(GEoPrivacy-Enhancing TOolkit) is an open source software for managing location data (currently in development in cooperation with LAAS). GEPETO can be used to visualize, sanitize, perform inference attacks and measure the utility of a particular geolocated dataset. For each of these actions, a set of different techniques and algorithms can be applied. The global objective of GEPETO is to enable a user to design, tune, experiment and evaluate various sanitization algorithms and inference attacks as well as visualizing the following results and evaluating the resulting trade-off between privacy and utility. An engineer (Izabela Moïse) has contributed to the development of a distributed version of GEPETO based on the MapReduce paradigm and the Hadoop framework that is able to analyze datasets composed of millions of mobility traces in a few minutes [30] .
FUNCTIONAL DESCRIPTION

GEPETO is an open source software for managing location data. GEPETO can be used to visualize, sanitize, perform inference attacks, and measures the utility of a particular geolocated dataset.

- Partners: Université de Rennes 1 - CNRS
- Contact: Sébastien Gambs
- URL: https://gforge.inria.fr/projects/gepeto/

6.4. GNG

Security Supervision by Alert Correlation
KEYWORDS: Intrusion Detection Systems (IDS) - SIEM
SCIENTIFIC DESCRIPTION

GNG is an intrusion detection system that correlates different sources (such as different logs) in order to identify attacks against the system. The attack scenarios are defined using the Attack Description Langage (ADeLe) proposed by our team, and are internally translated to attack recognition automatons. GNG intends to define time efficient algorithms based on these automatons to recognize complex attack scenarios.

- Partner: CentraleSupélec
- Contact: Eric Totel
- URL: http://www.rennes.supelec.fr/ren/perso/etotel/GNG/index.html

6.5. JBlare

FUNCTIONAL DESCRIPTION

JBlare is a Java Virtual Machine (JVM) hypervisor, able to track information flows inside Java programs. Being a modified JVM, it runs vanilla java applications. A cooperation mode with KBlare affords both IDS more precision. JBlare can use hybrid analysis combining dynamic analysis with static analysis using Soot.

- Contact: Guillaume Hiet
- URL: https://www.blare-ids.org/flavors/jblare/

6.6. Netzob

FUNCTIONAL DESCRIPTION

Netzob is an opensource tool for reverse engineering, traffic generation and fuzzing of communication protocols. This tool allows to infer the message format (vocabulary) and the state machine (grammar) of a protocol through passive and active processes. Its objective is to bring state of art academic researches to the operational field, by leveraging bio-informatic and grammatical inferring algorithms in a semi-automatic manner.

- Participant: Georges Bossert
- Contact: Ludovic Mé
- URL: http://www.netzob.org/

6.7. GroddDroid

Automatic Triggering of Android Malware
KEYWORDS: Malware analysis
SCIENTIFIC DESCRIPTION GroddDroid is a tool dedicated to the automatic triggering of suspicious code in Android applications. GroddDroid copes with a classical problem in dynamic analysis which is the triggering of malicious actions. To avoid dynamic analysis, malware authors develop some protections that delay the malicious executions. GroddDroid overrides these protections by modifying the bytecode of the infected applications and reconstructing the application. The modified application can thus be executed and monitored.

- Partner: CentraleSupélec
- Contact: Valérie Viet Triem Tong
- URL: http://kharon.gforge.inria.fr/grodddroid.html

DIONYSOS Project-Team

5. New Software and Platforms

5.1. 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: Cesar Pascal Viho
- Contact: Cesar Pascal Viho
- URL: http://www.irisa.fr/tipi

5.2. Passive Test Tool

- Participants: Cesar Pascal Viho
- Contact: Cesar Pascal Viho
- URL: http://www.irisa.fr/tipi

5.3. T3DevKit

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
- built-in scripts for the generation of executable test suites, which are tool-independent and facilitate the distribution of test suite sources
- Participants: Cesar Pascal Viho
- Contact: Cesar Pascal Viho

5.4. Interoperability Assessment

Participant: César Viho.

Our experience in interoperability assessment (since 1996) and in using the TTCN-3 standard allowed us to develop a tool (called `ttproto`) that helps in: (i) experimenting new concepts for long term evolution of the TTCN-3 standard and (ii) facilitating new approaches and methods for interoperability assessment. For instance, new passive approaches that we developed have been implemented and validated using `ttproto`. This tool `ttproto` has been used to develop test suites for 6LoWPAN-ND (IPv6 for Low Power Networks) and CoAP (Constrained Application Protocol). The CoAP test suites have been successfully used for two Plugtest interoperability events organized by ETSI, IPSO Alliance and the FP7 PROBE-IT project. The tool `ttproto` and the test suites indicated above are freely available at http://www.irisa.fr/tipi.

5.5. Performance and dependability evaluation

Participants: Gerardo Rubino, Bruno Sericola, Bruno Tuffin.

We develop software tools for the evaluation of two classes of models: Markov models and reliability networks. The main objective is to quantify dependability aspects of the behaviors of the modeled systems, but other aspects of the systems can be handled (performance, performability, vulnerability). The tools are specialized libraries implementing numerical, Monte Carlo and Quasi-Monte Carlo algorithms.

One of these libraries has been developed for the Celar (DGA), and its goal is the evaluation of dependability and vulnerability metrics of wide area communication networks (WANs). The algorithms in this library can also evaluate the sensitivities of the implemented dependability measures with respect to the parameters characterizing the behavior of the components of the networks (nodes, lines).

We are also developing tools with the objective of building Markovian models and to compute bounds of asymptotic metrics such as the asymptotic availability of standard metrics of models in equilibrium, loss probabilities, blocking probabilities, mean backlogs, etc. A set of functions designed for dependability analysis is being built under the name `DependLib`.

We contribute to the development of SPNP (*Stochastic Petri Net Package*). SPNP is used by more than 200 companies and universities. The main designer is Duke University. Our contributions are on Monte Carlo methods. We plan to increase our participation in the development of this tool.

Pierre L'Ecuyer is also developing in Montreal a library, *Stochastic Simulation in Java* (SSJ), providing facilities for generating uniform and nonuniform random variates, computing different measures related to probability distributions, performing goodness-of-fit tests, applying quasi-Monte Carlo methods, collecting (elementary) statistics, and programming discrete-event simulations with both events and processes.

DIVERSE Project-Team

6. New Software and Platforms

6.1. FAMILIAR

FeAture Model scrIpt Language for manIpulation and Automatic Reasoning
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.

- Participants: Mathieu Acher, Guillaume Bécan, Sana Ben Nasr, Jose Galindo, Olivier Barais
- Contact: Mathieu Acher
- URL: http://familiar-project.github.com

6.2. OpenCompare

OpenCompare.org
KEYWORDS: product comparison matrix - tabular data - comparison
SCIENTIFIC DESCRIPTION

Product comparison matrices (PCMs) are tabular data: supported and unsupported features are documented for both describing the product itself and for discriminating one product compared to another. PCMs abound and constitute a rich source of knowledge for easily comparing and choosing product. Yet the current practice is suboptimal both for humans and computers, mainly due to unclear semantics, heterogeneous forms of data, and lack of dedicated support.

OpenCompare.org is a project for the collaborative edition, the sharing, the standardisation, and the open exploitation of PCMs. The goal of OpenCompare.org is to provide an integrated set of tools (e.g., APIs, visualizations, configurators, editors) for democratizing their creation, import, maintenance, and exploitation.

MatrixMiner is also part of opencompare. It is a tool for automatically synthesizing PCMs from a set of product descriptions written in natural language. MatrixMiner is capable of identifying and organizing features and values in a PCM despite the informality and absence of structure in the textual descriptions of products. More information here: https://matrix-miner.variability.io/

- Participants: Guillaume Bécan, Mathieu Acher, Sana Ben Nasr
- Contact: Mathieu Acher
- URL: http://opencompare.org

6.3. Kermeta

KEYWORDS: Eclipse - Model-driven engineering
SCIENTIFIC DESCRIPTION

Kermeta is used in several cases:

to give a precise semantic of the behavior of a metamodel, which then can be simulated,

to act as a model transformation language,

to act as a constraint language.

FUNCTIONAL DESCRIPTION

The Kermeta workbench is a powerful meta-programming environment based on an object-oriented DSL (Domain Specific Language) optimized for metamodel engineering. Kermeta is now integrated into Melange (see next tool), and will continue to be supported and developed under this new project with a broader scope.

- Participants: Zoé Drey, Cyril Faucher, Franck Fleurey, Jean Marc Jezequel, Pierre Alain Muller, Jim Steel, François Tanguy, Didier Vojtisek, Benoît Combemale, Olivier Barais, Arnaud Blouin, Benoit Baudry, Thomas Degueule, David Mendez Acuna, Erwan Bousse and Fabien Coulon
- Partners: Université de Rennes 1 - UHA
- Contact: Benoît Combemale
- URL: http://www.kermeta.org

6.4. Melange

KEYWORDS: Language workbench, Domain-Specific (Modeling) Language, Model-Driven Engineering, Model execution and debugging, Execution trace management

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 type system that statically ensures the structural correctness of the produced DSMLs, and specific subtyping relationships between DSMLs to reason about their substitutability. 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 a language workbench that support a modular and reusable approach for domain-specific language design and implementation.

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. The language workbench embeds a 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 DSMLs. Melange also provides a dedicated meta-language where models are first-class citizens and languages are used to instantiate and manipulate them. By analogy with the class-based, object-oriented paradigm, Melange can be classified as a language-based, model-oriented programming language. 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 DSMLs. Executable meta-modeling is supported by weaving operational semantics defined with Kermeta (defined on top of Xtend). Melange is bundled as a set of Eclipse plug-ins.

- Participants: Thomas Degueule, Erwan Bousse, Fabien Coulon, Dorian Leroy, Didier Vojtisek, Olivier Barais, Arnaud Blouin, Benoit Combemale, Jean-Marc Jézéquel
- Partners: Université de Rennes 1
- Contact: Benoît Combemale
- URL: http://melange-lang.org

6.5. Kevoree

Kevoree Core C++

KEYWORDS: Embedded - Software Components - Software component - Dynamic adaptation

SCIENTIFIC DESCRIPTION

Kevoree is an open-source models@runtime platform (http://www.kevoree.org) to properly support the dynamic adaptation of distributed systems. Models@runtime basically pushes the idea of reflection [132] one step further by considering the reflection layer as a real model that can be uncoupled from the running architecture (e.g. for reasoning, validation, and simulation purposes) and later automatically resynchronized with its running instance.

Kevoree has been influenced by previous work that we carried out in the DiVA project [132] and the Entimid project [135] . With Kevoree we push our vision of models@runtime [131] farther. In particular, Kevoree provides a proper support for distributed models@runtime. To this aim we introduced the Node concept to model the infrastructure topology and the Group concept to model semantics of inter node communication during synchronization of the reflection model among nodes. Kevoree includes a Channel concept to allow for multiple communication semantics between remoteComponents deployed on heterogeneous nodes. All Kevoree concepts (Component, Channel, Node, Group) obey the object type design pattern to separate deployment artifacts from running artifacts. Kevoree supports multiple kinds of very different execution node technology (e.g. Java, Android, MiniCloud, FreeBSD, Arduino, ...).

Kevoree is distributed under the terms of the LGPL open source license.

Main competitors:

- the Fractal/Frascati eco-system (http://frascati.ow2.org).
- SpringSource Dynamic Module (http://spring.io/)
- GCM-Proactive (http://proactive.inria.fr/)
- OSGi (http://www.osgi.org)
- Chef
- Vagran (http://vagrantup.com/)

Main innovative features:

- distributed models@runtime platform (with a distributed reflection model and an extensible models@runtime dissemination set of strategies).
- Support for heterogeneous node type (from Cyber Physical System with few resources until cloud computing infrastructure).
- Fully automated provisioning model to correctly deploy software modules and their dependencies.
- Communication and concurrency access between software modules expressed at the model level (not in the module implementation).

Impact:

Several tutorials and courses have been performed this year at EJCP for French PhD student, at ECNU summer school for 82 chineese PhD students. See also the web page http://www.kevoree.org .

In 2015, we mainly created a new implementation in C# and we created an implementation for system containers for driving resources using Kevoree. We also use Kevoree in the context of Mohammed's PhD to create testing infrastructure on-demand.

Version: 5.3.1

Programming language: Java, Scala, Kermeta, Kotlin, Javascript, c#

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: Olivier Barais, Johann Bourcier, Noël Plouzeau, Benoit Baudry, Maxime Tricoire, Jacky Bourgeois, Inti Gonzalez Herrera, Ivan Paez Anaya, Manuel Leduc, Francisco-Javier Acosta Padilla and Mohamed Boussaa
- Partner: Université de Rennes 1
- Contact: Olivier Barais
- URL: http://kevoree.org/

6.6. amiunique

KEYWORDS: Privacy - Browser fingerprinting

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).

SCIENTIFIC DESCRIPTION

The amiunique web site has been deployed in the context of the DiverSE's research activities on browser fingerprinting and how software diversity can be leveraged in order to mitigate the impact of fingerprinting on the privacy of users. The construction of a dataset of genuine fingerprints is essential to understand in details how browser fingerprints can serve as unique identifiers and hence what should be modified in order to mitigate its impact privacy. This dataset also supports the large-scale investigation of the impact of web technology advances on fingerprinting. For example, we can analyze in details the impact of the HTML5 canvas element or the behavior of fingerprinting on mobile devices.

The whole source code of amiunique is open source and is distributed under the terms of the MIT license.

Similar sites:

- Panopticlick https://panopticlick.eff.org/
- BrowserSpy http://browserspy.dk/
- http://noc.to/

Main innovative features:

- canvas fingerprinting
- WebGL fingerprinting
- advanced JS features (platform, DNT, etc.)

Impact:

The website has been showcased in several professional forums in 2014 and 2015 (Open World Forum 2015, FOSSA'14, FIC'15, ICT'15) and it has been visited by more than 100000 unique visitors in one year.

Programming language: Java, JavaScript, Scala

- Participants: Pierre Laperdrix, Benoit Baudry
- Partner: INSA Rennes
- Contact: Benoit Baudry
- URL: https://amiunique.org/
- URL source code: https://github.com/DIVERSIFY-project/amiunique

KERDATA Project-Team

6. New Software and Platforms

6.1. Major Software

6.1.1. BlobSeer

Participants: Alexandru Costan, Gabriel Antoniu, Luc Bougé, Loïc Cloatre.

Contact: Gabriel Antoniu.

Presentation: BlobSeer is the core software platform for many current cloud-oriented projects of the KerData team. It is a data storage service specifically designed to deal with the requirements of large-scale, data-intensive distributed applications that abstract data as huge sequences of bytes, called BLOBs (Binary Large OBjects). It provides a versatile versioning interface for manipulating BLOBs that enables reading, writing and appending to them.

BlobSeer offers both scalability and performance with respect to a series of issues typically associated with the data-intensive context: *scalable aggregation of storage space* from the participating nodes with minimal overhead, ability to store *huge data objects*, *efficient fine-grain access* to data subsets, *high throughput in spite of heavy access concurrency*, as well as *fault-tolerance*. This year we have mainly focused on the deployment in production of the BlobSeer software on IBM's cluster at Montpellier, in the context of the ANR MapReduce project. To this end, several bugs were solved, and several optimizations were brought to the communication layer of BlobSeer. To showcase the benefits of BlobSeer on this platform we focused on the Terasort benchmark. Currently, preliminary tests on Grid5000 with this benchmark show that BlobSeer performs better than HDFS for block sizes lower than 2 MB. We have also improved the continuous integration process of BlobSeer by deploying daily builds and automatic tests on Grid5000.

Users: Work is currently in progress in several formalized projects (see previous section) to integrate and leverage BlobSeer as a data storage back-end in the reference cloud environments: a) Microsoft Azure; b) the Nimbus cloud toolkit developed at Argonne National Lab (USA); and c) the OpenNebula IaaS cloud toolkit developed at UCM (Madrid).

URL: http://blobseer.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: This software is available on Inria's forge. Version 1.0 (released late 2010) registered with APP: IDDN.FR.001.310009.000.S.P.000.10700.

A *Technology Research Action* (ADT, *Action de recherche technologique*) was active for two years until January 2015, aiming to robustify the BlobSeer software and to make it a safely distributable product. This project is funded by Inria *Technological Development Office* (D2T, *Direction du Développement Technologique*).

6.1.2. Damaris

Participants: Matthieu Dorier, Gabriel Antoniu, Orçun Yildiz, Lokman Rahmani, Shadi Ibrahim.

Contact: Gabriel Antoniu.

Presentation: Damaris is a middleware for multicore SMP nodes enabling them to handle data transfers for storage and visualization efficiently. The key idea is to dedicate one or a few cores of each SMP node to the application I/O. It is developed within the framework of a collaboration between KerData and the *Joint Laboratory for Petascale Computing* (JLPC). Damaris enables efficient asynchronous I/O, hiding all I/O related overheads such as data compression and post-processing, as well as direct (*in-situ*) interactive visualization of the generated data. Version 1.0 was released in November 2014 and enables other approaches such as the use of dedicated nodes instead of dedicated cores.

Users: Damaris has been preliminarily evaluated at NCSA/UIUC (Urbana-Champaign, IL, USA) with the CM1 tornado simulation code. CM1 is one of the target applications of the Blue Waters supercomputer in production at, in the framework of the Inria-UIUC-ANL Joint Lab (JLPC). Damaris now has external users, including (to our knowledge) visualization specialists from NCSA and researchers from the France/Brazil Associated research team on Parallel Computing (joint team between Inria/LIG Grenoble and the UFRGS in Brazil). Damaris has been successfully integrated into four large-scale simulations (CM1, OLAM, Nek5000, GTC).

URL: http://damaris.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: This software is available on Inria's forge and registered with APP. Registration of the latest version with APP is in progress.

6.2. Other Software

6.2.1. Omnisc'IO

Participants: Matthieu Dorier, Shadi Ibrahim, Gabriel Antoniu.

Contact: Matthieu Dorier

Presentation: Omnisc'IO is a middleware integrated in the POSIX and MPI-I/O stacks to observe, model and predict the I/O behavior of any HPC application transparently. It is based on formal grammars, implementing a modified version of the Sequitur algorithm. Omnisc'IO has been used on Grid'5000 with the CM1 atmospheric simulation, the LAMMPS molecular dynamics simulation, the GTC fusion simulation and the Nek5000 CFD simulation. Omnisc'IO was subject to a publication at SC14.

Users: Omnisc'IO is currently used only within the KerData team and at Argonne National Lab.

URL: http://omniscio.gforge.inria.fr/

License: GNU Lesser General Public License (LGPL) version 3.

Status: Currently unavailable for distribution (subject to major changes). Version 1.0 (released in November 2015) registered with APP: IDDN.FR.001.540003.000.S.P.2015.000.10000.

6.2.2. JetStream

Participants: Radu Tudoran, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan

Presentation: JetStream is a middleware solution for batch-based, high-performance streaming across cloud data centers. JetStream implements a set of context-aware strategies for optimizing batch-based streaming, being able to self-adapt to changing conditions. Additionally, the system provides multi-route streaming across cloud data centers for aggregating bandwidth by leveraging the network parallelism. It enables easy deployment across .Net frameworks and seamless binding with event processing engines such as StreamInsight.

Users: JetStream is currently used at Microsoft Research ATLE Munich for the management of the Azure cloud infrastructure.

License: Microsoft Public License.

Status: Prototype and demo available.

6.2.3. OverFlow

Participants: Radu Tudoran, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan.

Presentation: 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. In 2015, OverFlow was extended with support for efficient metadata operations: the newly implemented strategies leverage workflow semantics in a 2-level metadata partitioning hierarchy that combines distribution and replication.

Users: 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.

License: GNU Lesser General Public License (LGPL) version 3.

Status: Registration of the latest version with APP is in progress

6.2.4. iHadoop

Participants: Tien Dat Phan, Shadi Ibrahim.

Contact: Shadi Ibrahim

Presentation: *iHadoop* is a Hadoop simulator developed in Java on top of SimGrid to simulate the behavior of Hadoop and therefore accurately predict the performance of Hadoop in normal scenarios and under failures. In 2015, iHadoop was extended to simulate the execution and predict the performance of multiple Map-Reduce applications, sharing the same Hadoop cluster. Two schedulers (Fifo, Fair) are now available in iHadoop.

Users: iHadoop is an internal software prototype, which was initially developed to validate our idea for exploring the behavior of Hadoop under failures. iHadoop has preliminarily evaluated within our group and it has shown very high accuracy when predicating the execution time of a Map-Reduce application. iHadoop was discussed with the SimGrid community during the SimGrid user days in Lyon (June 2015). We intend to add iHadoop to the contributions site of the SimGrid project and make it available to the SimGrid community.

License: GNU Lesser General Public License (LGPL) version 3.

Status: Available on Inria’s forge. Registration of the latest version with APP is in progress.

MYRIADS Project-Team

6. New Software and Platforms

6.1. ConPaaS

Hosting complex applications in the cloud

Contact: Guillaume Pierre, `Guillaume.Pierre@irisa.fr`

URL: http://www.conpaas.eu/

Status: Version 1.5.1

License: BSD

Presentation: ConPaaS [55] is a runtime environment for hosting applications in the cloud. It aims at offering the full power of the cloud to application developers while shielding them from the associated complexity of the cloud. ConPaaS is designed to host both high-performance scientific applications and online Web applications. It automates the entire life-cycle of an application, including collaborative development, deployment, performance monitoring, and automatic scaling. This allows developers to focus their attention on application-specific concerns rather than on cloud-specific details.

New features developed in 2015 include: a “Generic” service which allows the easy deployment and execution of arbitrary applications in ConPaaS; the “ConPaaS Nutshell edition” which allows users to deploy a fully-functional ConPaaS installation within a single VirtualBox VM; and the “ConPaaS Raspberry Pi edition” which allows users to deploy ConPaaS on a set of Raspberry Pi devices, paving the way toward the development of a fully-featured mobile edge cloud.

Active contributors (from the Myriads team): Ancuta Iordache, Genc Tato, Teodor Crivat, Guillaume Pierre.

Impact: ConPaaS is recognized as one of the major open-source PaaS environments. It is being developed by teams in Rennes, Amsterdam, Berlin and Ljubljana. Technology transfer of ConPaaS technology is ongoing in the context of the MC-DATA EIT Digital project.

6.2. GinFlow

Contact: Cédric Tedeschi, `Cedric.Tedeschi@irisa.fr`

Status: Version 1.0 released in open source, and registered at APP.

License: LGPL-3

Presentation: GinFlow is a decentralized workflow engine. It relies on a set of processes deployed over a cluster. Every task of the workflow is basically encapsulated into a GinFlow worker, workers being able to coordinate with others through read and write operations of a shared space containing the status of the workflow. GinFlow provides the ability to change the workflow logic on-the-fly upon the detection of a non-desired behavior within the execution of some of the tasks of the workflow.

Users typically submit a workflow through its JSON representation (both the by-default workflow and its alternate version if adaptation is needed). It can also use the API to describe its workflow in a more *programmatic* fashion.

Active contributors (from Myriads project-team): Matthieu Simonin, Cédric Tedeschi, Javier Rojas Balderrama.

Impact: GinFlow is a tool meant to provide support for workflow-based applications needing adaptation at run time. It is also targeted at offering a platform for future development and researches around the decentralized execution of workflows. It has been used in the framework of the DALHIS [0] associate team, as a workflow template executor, integrated with the TIGRES workflow manager developed at the Lawrence Berkeley National Lab. It has been supported by the GinFlow ADT funded by Inria since 2014 (see Section 9.2.1).

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[0] http://project.inria.fr/dalhis

6.3. Merkat

Contact: Nikolaos Parlavantzas, `Nikolaos.Parlavantzas@irisa.fr`

URL: http://www.irisa.fr/myriads/software/Merkat/

Status: Version 1.0

Presentation: Merkat is a market-based private PaaS (Platform-as-a-Service) system, supporting dynamic, fine-grained resource allocation and automatic application management [47], [46] [3]. Merkat implements a proportional-share auction that ensures maximum resource utilization while providing incentives to applications to regulate their resource usage. Merkat includes generic mechanisms for application deployment and automatic scaling. These mechanisms can be adapted to support diverse performance goals and application types, such as master-worker, MPI, or MapReduce applications. Merkat is implemented in Python and uses OpenNebula for virtual machine management. Experimental results on the Grid'5000 testbed show that using Merkat increases resource utilization and improves application performance. The development was initiated in the framework of Stefania Costache PhD's thesis.

Active contributors (from the Myriads team): Christine Morin, Nikolaos Parlavantzas.

Other contributors: Stefania Costache.

Impact: Merkat has been integrated in EDF R&D portal providing access to internal computing resources and is currently used on a testbed at EDF R&D.

6.4. Meryn

Contact: Nikolaos Parlavantzas, `Nikolaos.Parlavantzas@irisa.fr`

URL: http://www.irisa.fr/myriads/software/Meryn/

Status: Version 1.0

Presentation: Meryn is an open, SLA-driven PaaS architecture that supports cloud bursting and allows hosting an extensible set of application types. Meryn relies on a decentralized optimization policy that aims at maximizing the overall provider profit, taking into account the penalties incurred when quality guarantees are unsatisfied [49]. The current Meryn prototype was implemented using shell scripts, builds upon the Snooze VM manager software, and supports batch and MapReduce applications using respectively the Oracle Grid Engine OGE 6.2u7 and Hadoop 0.20.2 frameworks.

Active contributors (from the Myriads team): Christine Morin, Nikolaos Parlavantzas.

Other contributors: Djawida Dib.

Impact: Meryn is not yet distributed as an open source software.

6.5. Snooze

Contact: Christine Morin, `Christine.Morin@inria.fr`

URL: http://snooze.inria.fr

Status: Version 2.1.5

License: GPLv2

Presentation: Snooze [51], [50], [52] [4] is a novel Infrastructure-as-a-Service (IaaS) cloud-management system, which is designed to scale across many thousands of servers and virtual machines (VMs) while being easy to configure, highly available, and energy efficient. For scalability, Snooze performs distributed VM management based on a hierarchical architecture. To support ease of configuration and high availability Snooze implements self-configuring and self-healing features. Finally, for energy efficiency, Snooze integrates a holistic energy management approach via VM resource (i.e. CPU, memory, network) utilization monitoring, underload/overload detection and mitigation, VM consolidation (by implementing a modified version of the Sercon algorithm [54]), and power management to transition idle servers into a power saving mode. Snooze is a highly modular piece of software. It has been extensively evaluated on the Grid'5000 testbed using realistic applications.

Snooze is fully implemented from scratch in Java and currently comprises approximately 15.000 lines of maintainable abstractions-based code. In order to provide a uniform interface to the underlying hypervisors and support transparent VM monitoring and management, Snooze integrates the *libvirt* virtualization library. Cassandra (since 2.0.0) can be used as base backend, providing reliability and scalability to the database management system. At a higher level Snooze provides its own REST API as well as an EC2 compatible API (since 2.1.0). It can thus be controlled from the command line (using the legacy client or an EC2 compatible tool), or from different language libraries (libcloud, jcloud ...). Snooze also provides a web interface to control the system. In collaboration with the Northeastern University of Bostonwe built the *Checkpoint as a Service* system on top of Snooze. The service allows users to execute their computations in a cloud environment in a reliable way. Periodic checkpoints are saved making it possible to restore the computation from a previous state in the event of failures. This work is described in [16].

Active contributors (from Myriads team): Yvon Jégou, David Margery, Christine Morin, Matthieu Simonin.

Other contributors: Jiajun Cao, Gene Cooperman, Eugen Feller.

Impact: Snooze has been used by students at LIFL, IRIT in France and LBNL in the US in the framework of internships. It has also been deployed and experimented at EDF R&D. Snooze entry won the 2nd prize of the scalability challenge at CCGrid 2013. Finally, we know that it was used by external users from academia and industry as we received feed-back from them. Snooze development was supported by the Snooze ADT funded by Inria from October 2012 to September 2014.

6.6. SimGrid

Scientific Instrument for the study of Large-Scale Distributed Systems.

Contact: Martin Quinson, `Martin.Quinson@ens-rennes.fr`

URL: http://simgrid.gforge.inria.fr/

Status: Version 3.12

License: LGPL 2.1

Presentation: SimGrid is a toolkit providing core features 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.

Active contributors from Myriads project-team: Martin Quinson and Anne-Cécile Orgerie.

Other active contributors: Arnaud Legrand (Mescal project-team, CNRS & Inria Rhone-Alpes), Frédéric Suter (Avalon project-team, CNRS & Inria Rhone-Alpes).

Impact: SimGrid has an active user community of more than one hundred members, mainly composed of researchers and students. In the last decade only, it grounded the experiments of 6 PhDs works, 25 journal papers, and over 100 conference papers. The community gathers every year during the SimGrid User's Days workshop.

SimGrid is also used to run the regression and performance tests and tuning of two large applications: BigDFT (a massively parallel code computing the electronic structure of chemical elements developed by the CEA) and StarPU (a Unified Runtime System for Heterogeneous Multicore Architectures developed by Inria Bordeaux). Both of these programs enjoy large user communities themselves.

TACOMA Team

5. New Software and Platforms

5.1. THEGAME: data fusion for Smart Home and Smart Building

KEYWORDS: Smart home - Smart building

- Participants: Aurélien Richez
- Partner: Université de Rennes 1
- Contact: Frédéric Weis
- URL: https://github.com/bpietropaoli/THEGAME/

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. It is maintained and experimented within a sensor network platform developed by TACOMA since June 2013.

5.2. Platforms

5.2.1. Platform Pervasive_RFID

KEYWORDS: Composite objects - RFID

- Participants: Paul Couderc and Nebil Ben Mabrouck
- Partner: Université de Rennes 1 (IETR)
- Contact: Paul Couderc

SCIENTIFIC DESCRIPTION

In 2015 we completed the RFID experiment testbed realized in 2014 in collaboration with IETR (see Figure 1).

This system allows both interactive testing as well as long running experiments of RFID reading protocols. It comprises a software platform (see Figure 2) 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). This testbed supports the reproduction of most situations found in real applications. We achieved the following improvements on the testbed in 2015:

- The implementation of a software controllable smart antenna, with dynamic radiating pattern, was completed along with its the hardware interface. This is an important feature when experimenting pervasive application, in particular to determine the radio performance improvements expectable from antenna diversity.

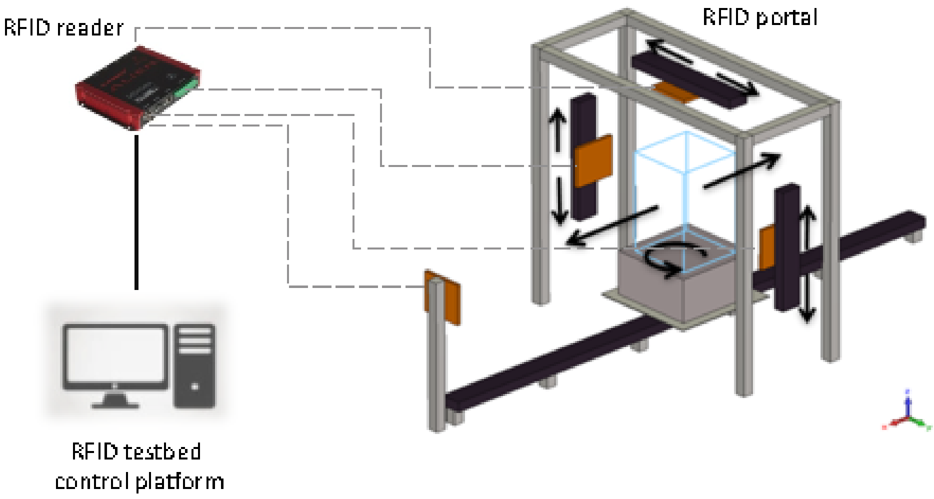

Figure 1. RFID testbed

- A particular effort was put on improving the operational performance and robustness of the system: the initial implementation was completed in 2014 in a context tightly coupled with our on-going RFID research, and with an important dependency on the technical expertise of short term positions staff-member. In order to widen the testbed?s perspectives as a research tool, two aspects were improved:
  1. a high-level scripting interface was added to offer easy automatized experimentation campaign. Iterative RFID experiments with fine-tuning parameters can be specified using a variety of script languages, and further executed in a remote fashion via the added interface.
  2. A virtualization of RFID readers and motion drives was also developed to simulate the behavior of critical experiments or new software updates before executing them on the real testbed.
  3. Functional tests were developed to ascertain that crucial functions of the testbed would work correctly after future software updates, thus ensuring the maintainability and sustainability of the system.

5.2.2. On-demand room

KEYWORDS: Smart Home - Metamorphic House

- Partner: Université de Rennes 1
- Partner: Université de Rennes 1 (Fondation Rennes 1)
- Contact: Michele Dominici and Frédéric Weis

DESCRIPTION

As part of the demonstration activities, we realized a prototype of the on-demand room as an immersive interactive virtual-reality application, leveraging the Immersia platform. Two iterations were achieved so far.

For the first iteration of the demonstrator, we realized a three-dimensional model of the on-demand room and two adjacent apartments, using the software SketchUp. This model was then imported in Unity3D and MiddleVR, which allow to display and navigate inside the model using the virtual reality platform Immersia [0].

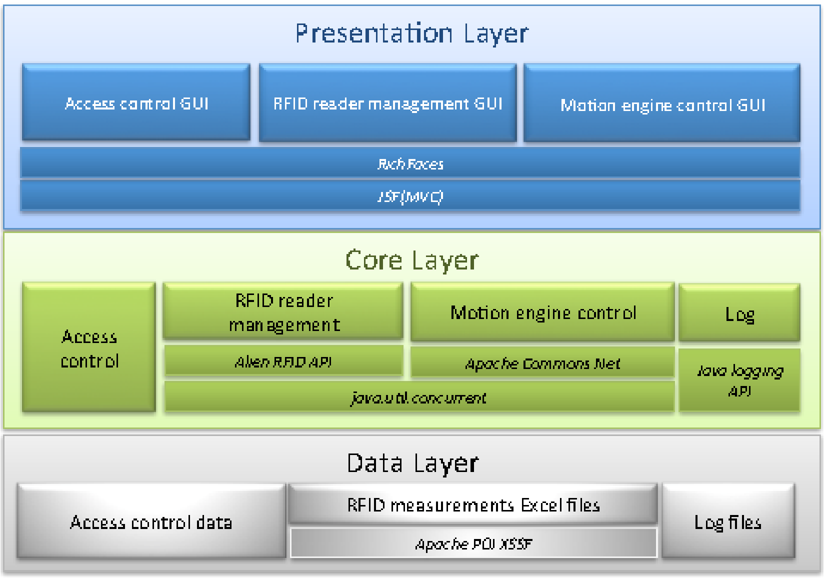

Figure 2. Software architecture of the RFID testbed

We then implemented the application logic of the on-demand room using Unity scripting facilities. By wearing 3D glasses and a marker on their hand, users can literally walk inside the apartments, open doors and observe how the configuration of the room changes to become a part of one dwelling or another, as shown in Figure 3 .

Figure 3. 3D model in the Immersia platform

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[0] http://www.irisa.fr/immersia/

The second (and current) iteration of the demonstrator introduced a major feature: the real/virtual integration. Actual domestic appliances can now be connected to Immersia and participate to the on-demand room demonstration. In this phase we showed that a real light switch, located in the virtual on-demand room, can change its behavior and alternatively control one of the two real lamps, each located in one of the aparments, as shown in Figure 4 .

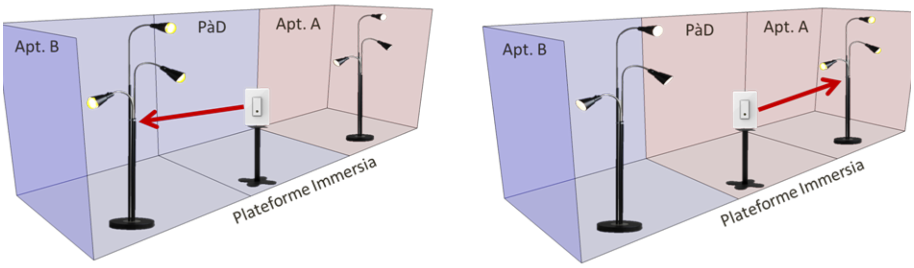

Figure 4. Integration of real devices

To develop the real/virtual integration feature, we used home automation controllers and devices implementing the KNX standard. After wiring and programming the domotic network, we developed an application that leverages the Falcon library, provided by the KNX association, to dynamically change the behavior of the real light switch.

DREAM Project-Team

6. New Software and Platforms

6.1. Platforms

The Dream project-team, in collaboration with their applicative partners, has proposed and maintains several important software platforms for its main research topics.

6.1.1. Platform: Environmental decision-support systems

Participants: Marie-Odile Cordier, Christine Largouët, Véronique Masson.

6.1.1.1. SACADEAU

Système d'Acquisition des Connaissances pour l'Aide à la Décision sur la qualité de l'EAU

FUNCTIONAL DESCRIPTION

the Sacadeau system is an environmental decision software that implements the Sacadeau transfer model. The Sacadeau simulation model couples two qualitative models, a transfer model describing the pesticide transfer through the catchment and a management model describing the farmer decisions. Giving as inputs a climate file, a topological description of a catchment, and a cadastral repartition of the plots, the Sacadeau model simulates the application of herbicides by the farmers on the maize plots, and the transfer of these pollutants through the catchment until the river. The two main simulated processes are the runoff and the leaching. The output of the model simulation is the quantity of herbicides arriving daily to the stream and its concentration at the outlets. The originality of the model is the representation of water and pesticide runoffs with tree structures where leaves and roots are respectively up-streams and down-streams of the catchment.

- Contact: Véronique Masson
- URL: http://www.irisa.fr/dream/SACADEAU/

6.1.1.2. EcoMata

FUNCTIONAL DESCRIPTION

The EcoMata tool-box provides means for qualitative modeling and exploring ecosystems and for aiding to design environmental guidelines.We have proposed a new qualitative approach for ecosystem modeling based on timed automata (TA) formalism combined to a high-level query language for exploring scenarios.

- Participants: Marie-Odile Cordier, Yulong Zhao, Christine Largouët and Thomas Guyet
- Contact: Christine Largouët
- URL: https://team.inria.fr/dream/fr/ecomata/

6.1.1.3. PaturMata

KEYWORDS: Bioinformatics - Biology

SCIENTIFIC DESCRIPTION

In the PaturMata software, users can create a pasture system description by entering herds and plots information. For each herd, the only parameter is the number of animals. For each plot, users should enter the surface, the density, the herb height, the distance to the milking shed, a herb growth profile and an accessibility degree.

Users then specify pasturing and fertilization strategies. Finally, users can launch a pasture execution. PaturMata displays the results and a detailed trace of pasture. Users can launch a batch of different strategies and compare the results in order to find the best pasture strategy.

PaturMata is developed in Java (Swing for the GUI) and the model-checker that is called for the timed properties verification is UPPAAL .

FUNCTIONAL DESCRIPTION

The Paturmata tool-box provides means for qualitative modeling and exploring agrosystems, specifically management of herd based on pasture. The system is modelled using a hierarchical hybrid model described in timed automata formalism.

- Contact: Christine Largouët

6.1.2. Platform: Pattern Mining

Participants: Thomas Guyet, René Quiniou.

6.1.2.1. QTempIntMiner

Temporal pattern mining in sequences
SCIENTIFIC DESCRIPTION

The QTempIntMiner data mining software implements several algorithms (QTIAPRIORI and QTIPREFIXSPAN). The software is mainly implemented in Matlab. It uses the Mixmod toolbox to compute multi-dimensional Gaussian distributions. The main features of QTEMPINTMINER are:

- a tool for generating synthetic noisy sequences of temporal events,
- an implementation of the QTEMPINTMINER, QTIAPRIORI and QTIPREFIXSPAN algorithms,
- a graphical interface that enables the user to generate or import data set and to define the parameters of the algorithm and that displays the extracted temporal patterns.
- a sequence transformer to process long sequences of temporal events. Long sequences are transformed into a database of short temporal sequences that are used as input instances for the available algorithms.

The software includes one new algorithm based on the separation of the set of interval to extract more efficiently but less accurately the time interval in temporal patterns. This new algorithm version is still under evaluation on simulated and real datasets.

This year, an APP deposit of the early version (in Matlab) of this framework has been done. In parallel, we started the developement of a C++ version of the framework.

- Participants: Thomas Guyet and René Quiniou
- Partner: AGROCAMPUS
- Contact: Thomas Guyet
- URL: http://www.irisa.fr/dream/QTempIntMiner/

6.1.3. Platform: Diagnostic and Monitoring Systems

Participants: Marie-Odile Cordier, René Quiniou, Sophie Robin, Laurence Rozé.

6.1.3.1. ManageYourself

FUNCTIONAL DESCRIPTION

The ManageYourself software comes from a collaborative project between Dream and the Telelogos company aiming at monitoring smartphones from a stream of observations made on the smartphone state.

Today's smartphones are able to perform calls, as well as to realize much more complex activities. They are small computers. But as in computers, the set of applications embedded on the smartphone can lead to problems. The aim of the project ManageYourself is to monitor smartphones in order to avoid problems or to detect problems and to repair them. To this end, a model of the martphone system is learned and updated incrementally.

- Contact: Laurence Rozé

6.1.3.2. Odisseptale

KEYWORDS: Biology - Health
FUNCTIONAL DESCRIPTION

The Odisseptale software implements disease detectors using monitoring of data provided by sensors placed on calves or cows. Sensors record streams of data such as body temperature, physical activity, feeding behavior, etc. These data are transmitted regularly to a monitoring software that aims to detect if a noticeable change has occurred on the data streams. Several detectors can be simultaneously active and each contribute to the final decision (detection of a disease). Two kinds of detectors have been implemented: a generic detector based on adaptive CUSUM and a symbolic pattern-based detector. Odisseptale provides also facilities for parameter setting and performance evaluation.

- Contact: René Quiniou

6.2. TraceSquiz

FUNCTIONAL DESCRIPTION

TraceSquiz is a software developped in collaboration with STMicroelectronics. Its goal is to reduce the volume of execution trace captured during endurance tests of multimedia applications. It uses anomaly detection techniques to "learn" regular parts of the trace and only capture the irregular ones. The software is written in C++.

- Participants: Alexandre Termier, Serge Vladimir Emteu Tchagou, René Quiniou
- Contact: Serge Vladimir Emteu Tchagou

HYBRID Project-Team

6. New Software and Platforms

6.1. OpenViBE

KEYWORDS: Brain-Computer Interface, EEG, Neuroscience, Interaction, Health, Neurofeedback

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 40000 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: Anatole Lécuyer, Jussi Tapio Lindgren, Jérôme Chabrol, Charles Garraud, and Marsel Mano
- Partners: Inria teams POTIOC, ATHENA and NEUROSYS
- Contact: Anatole Lécuyer
- URL: http://openvibe.inria.fr

6.2. Statefinder

KEYWORDS: Brain-Computer Interface, EEG, Neuroscience, Interaction, Health, Neurofeedback, Welfare

FUNCTIONAL DESCRIPTION Statefinder is a software for determining the mental state of a user based on EEG signals analysis. It notably enables to classify between different different mental states on-line, using a preliminary training phase during which the EEG signals corresponding to these different mental states were recorded. This software was designed and used during the PhD of Mr. Laurent George, in Hybrid team. It has been transferred to Mensia Technologies startup company.

- Participants: Anatole Lécuyer
- Contact: Anatole Lécuyer

6.3. Pseudohaptik

KEYWORDS: User Interfaces, 3D web, Pseudo-Haptic, Deph Perception

FUNCTIONAL DESCRIPTION

PSEUDOHAPTIK is a software which enables to simulate pseudo-haptic effects notably for web applications. Pseudo-haptic feedback enables to simulate haptic properties such as feeling the texture or relief of an image using visual effects synchronized with the motion of the user. This software has been notably transferred to MBA Multimédia and Polymorph companies.

- Participants: Anatole Lécuyer, Ferran Argelaguet Sanz and Maud Marchal
- Contact: Anatole Lécuyer
- URL: https://team.inria.fr/hybrid/w3d-project/

6.4. Elastic_Images

KEYWORDS: User Interfaces, Depth Perception, 3D web, Pseudo-Haptic
FUNCTIONAL DESCRIPTION

Elastic_Images is a software which enables to simulate pseudo-haptic effects related to the elasticity or stiffness of 2D images, notably for web application purpose. This software has been transferred to MBA Multimédia and Polymorph companies.

- Participants: Anatole Lécuyer, Ferran Argelaguet Sanz and Maud Marchal
- Contact: Anatole Lécuyer
- URL: https://team.inria.fr/hybrid/w3d-project/

6.5. #FIVE

KEYWORDS: Virtual Reality, Collaboration, 3D Interaction
FUNCTIONAL DESCRIPTION

#FIVE is a set of software modules for the design of interactive and collaborative virtual environments. The user can focus on domain-specific aspects of his/her application (e.g., industry, medicine, etc). The #FIVE modules can then be used in a vast range of domains based on virtual reality and requiring interactive environments and collaboration - such as in training simulators for example when connected to the #SEVEN engine (see section 6.6).

- Participants: Thomas Boggini, Valérie Gouranton, Bruno Arnaldi, Florian Nouviale
- Contact: Florian Nouviale
- URL: https://hal.archives-ouvertes.fr/IRISA/hal-01147734v1

6.6. #SEVEN

KEYWORDS: Virtual Reality, Training, Scenario, Petri Net
FUNCTIONAL DESCRIPTION

#SEVEN is a scenario engines that enables the execution of complex scenarios for driving Virtual Reality training applications. #SEVEN's scenarios are based on an enhanced Petri net model that can describe and solve intricate event sequence. #SEVEN comes with an editor capable of creating, editing and remotely controlling and running such scenarios. #SEVEN is implemented in C# and can be used as a standalone application or as a library. An integration with the Unity3D engine, compatible with MiddleVR, also exists.

- Participants: Guillaume Claude, Valérie Gouranton, Bruno Arnaldi, Florian Nouviale
- Contact: Florian Nouviale
- URL: https://hal.archives-ouvertes.fr/hal-01086237

LAGADIC Project-Team

6. New Software and Platforms

6.1. DESlam

Dense Egocentric SLAM
KEYWORDS: Deph Perception - Robotics - Localisation
FUNCTIONAL DESCRIPTION

This software proposes a full and self content solution to the dense Slam problem. Based on a generic RGB-D representation valid for various type of sensors (stereovision, multi-cameras, RGB-D sensors...), it provides a 3D textured representation of complex large indoor and outdoor environments and it allows localizing in real time (45Hz) a robot or a person carrying out a mobile camera.

- Participants: Maxime Meilland, Andrew Ian Comport and Patrick Rives
- Contact: Patrick Rives
- URL: http://team.inria.fr/lagadic

6.2. HandiViz

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
- Contact: Marie Babel
- URL: https://team.inria.fr/lagadic/

6.3. Perception360

Robot vision and 3D mapping with omnidirectional RGB-D sensors.
KEYWORDS: Depth Perception - 3D rendering - Computer vision - Robotics - Image registration - Sensors - Realistic rendering - 3D reconstruction - Localization
FUNCTIONAL DESCRIPTION

This software is a collection of libraries and applications for robot vision and 3D mapping with omnidirectional RGB-D sensors or standard perspective cameras. This project provides the functionality to do image acquisition, semantic annotation, dense registration, localization and 3D mapping. The omnidirectional RGB-D sensors used within this project have been developed in Inria Sophia-Antipolis by the team LAGADIC.

- Contact: Patrick Rives
- URL: https://team.inria.fr/lagadic/software-eng.html

6.4. Sinatrack

KEYWORDS: Computer vision - Robotics
FUNCTIONAL DESCRIPTION

Sinatrack is a tracking software that allows the 3D localization (translation and rotation) of an object with respect to a monocular camera. It allows to consider object with complex shape. The underlying approach is a model-based tracking techniques. It has been developed for satellite localization and on-orbit service applications but is also suitable for augmented reality purpose.

- Participants: Antoine Guillaume Petit, Éric Marchand and François Chaumette
- Contact: Éric Marchand
- URL: http://team.inria.fr/lagadic

6.5. UsTk

Ultrasound Toolkit
KEYWORDS: Echographic imagery - Image reconstruction - Active contours - Medical robotics
FUNCTIONAL DESCRIPTION

UsTk, standing for Ultrasound Toolkit, is a cross-platform library for two- and three-dimensional ultrasound image processing. Written in C++, UsTk provides tools for ultrasound image acquisition, processing and display of these images. Combined with the UsSimulator software that simulates a virtual ultrasound probe interacting with a 3D ultrasound volume and the UsGraphCut library that allows real-time segmentation of ultrasound images, it can serve as an useful framework for developing and testing new visual servoing approaches based on ultrasound images.

- Participants: Alexandre Krupa, Pierre Chatelain and Christophe Collewet
- Partners: Université de Rennes 1 - IRSTEA
- Contact: Alexandre Krupa
- URL: https://team.inria.fr/lagadic/

6.6. ViSP

KEYWORDS: Augmented reality - Computer vision - Robotics - Visual servoing (VS)
SCIENTIFIC DESCRIPTION

Since 2005, we develop and release ViSP [5] , an open source library available from http://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 Lagadic research. ViSP was designed to be independent from the hardware, to be simple to use, expandable and cross-platform. ViSP allows to design vision-based tasks for eye-in-hand and eye-to-hand visual servoing that contains the most classical visual features that are used in practice. It involves a large set of elementary positioning tasks with respect to various visual features (points, segments, straight lines, circles, spheres, cylinders, image moments, pose...) that can be combined together, and image processing algorithms that allow tracking of visual cues (dots, segments, ellipses...) or 3D model-based tracking of known objects or template tracking. Simulation capabilities are also available.

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, Windows and Linux. ViSP online documentation allows to ease learning. More than 250 fully documented classes organized in 16 different modules, with more than 200 examples and 35 tutorials are proposed to the user. ViSP is released under a dual licensing model. It is open-source with a GNU GPLv2 license. A professional edition license that replaces GNU GPLv2 is also available.

- Participants: François Chaumette, Éric Marchand, Fabien Spindler, Aurélien Yol and Souriya Trinh
- Partners: Université de Rennes 1 - CNRS
- Contact: Fabien Spindler
- URL: http://visp.inria.fr

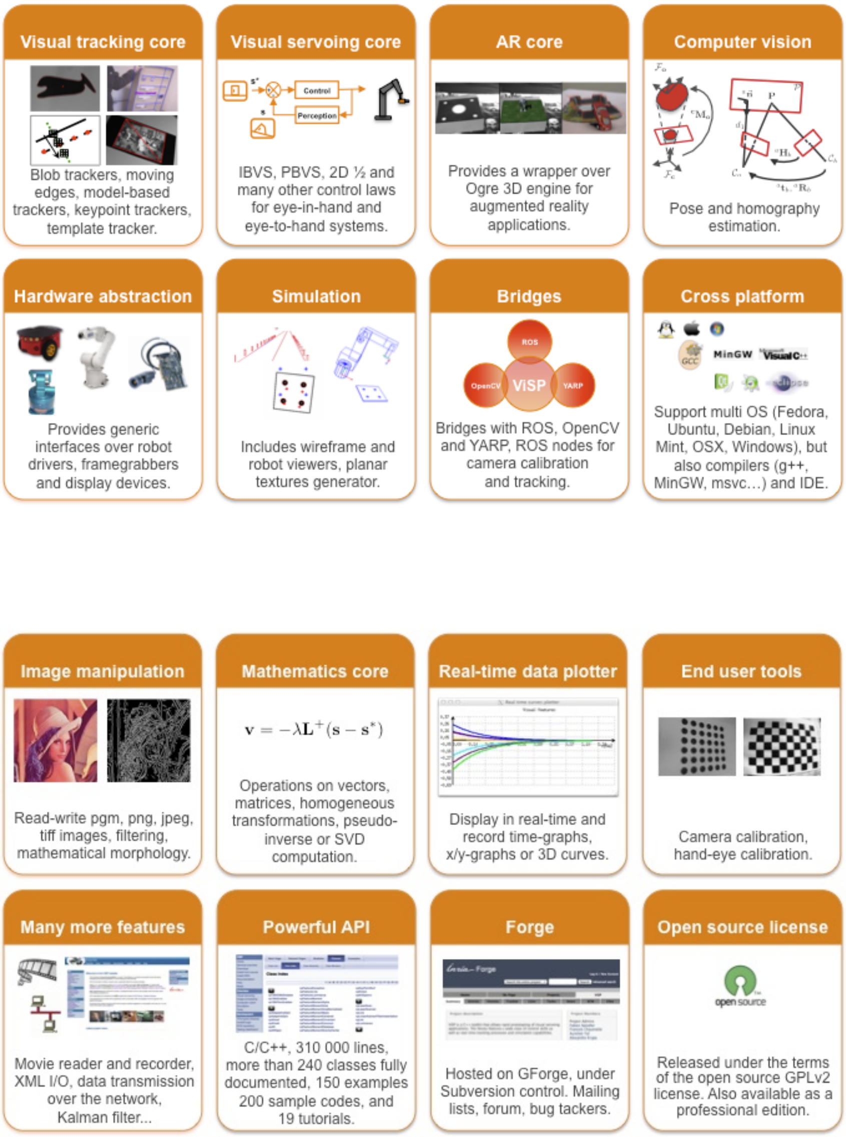

Figure 1. This figure highlights ViSP main capabilities for visual tracking, visual servoing, and augmented reality that may benefit from computer vision algorithms. ViSP allows controlling specific platforms through hardware abstraction or in simulation. ViSP provides also bridges over other frameworks such as OpenCV and ROS. All these capabilities are cross-platform. Moreover, for easing the prototyping of applications, ViSP provides tools for image manipulation, mathematics, data plotting, camera calibration, and many other features. ViSP powerful API is fully documented and available on Inria's forge as an open source software under GPLv2 license.

This year, a new ViSP 2.10 release was produced in February. The corresponding source code tarball was downloaded 1290 times. With the help of the community, this release was packaged for Debian and Ubuntu 14.04. We also designed a new modular software architecture where ViSP capabilities are grouped in several modules (core, io, gui, vision...). As a result, the user will find several shared or static libraries, one for each module. In the mean time we continued our efforts to improve the software by ensuring the compatibility with third-party libraries that continue also to evolve like CMake and OpenCV. We also fixed some issues, allowed the markerless 3D model-based hybrid tracker to consider cylinders and introduce a new algorithm to determine face visibility. Moreover, we improve the object detection algorithm based on keypoints that is able to return the pose of a learned object. We improved the documentation by providing new tutorials and by updating the existing ones. ViSP 3.0.0 will be released these days.

Concerning ROS community, all the existing packages in "`vision_visp`" ROS stack (see http://wiki.ros.org/vision_visp) were updated and ported to jade build system. To ease ViSP usage in the ROS framework, the releases of the year were packaged for ROS.

ViSP is used in research labs in France, USA, Japan, Korea, India, China, Lebanon, Italy, Spain, Portugal, Hungary, Canada. For instance, it is used as a support in graduate courses at IFMA Clermont-Ferrand, University of Picardie in Amiens, Télécom Physique in Strasbourg and ESIR in Rennes.

6.7. bib2html

FUNCTIONAL DESCRIPTION

The purpose of this software is to automatically produce html pages from BibTEX files, and to provide access to the BibTEX entries by several criteria: year of publication, category of publication, keywords, author name. Moreover cross-linking is generating between pages to provide an easy navigation through the pages without going back to the index.

- Contact: Éric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html

6.8. Robot vision platform

Participant: Fabien Spindler [correspondant].

We exploit two industrial robotic systems built by Afma Robots in the nineties to validate our researches in visual servoing and active vision. The first one is a Gantry robot with six degrees of freedom, the other one is a cylindrical robot with four degrees of freedom (see Fig. 2). These robots are equipped with cameras. The Gantry robot allows also to embed grippers on its end-effector.

Five papers published by Lagadic in 2015 enclose results validated on this platform [30][53][29][31][50].

6.9. Mobile robotics platforms

Participants: Fabien Spindler [correspondant], Marie Babel, Patrick Rives.

6.9.1. Indoor mobile robots

For fast prototyping of algorithms in perception, control and autonomous navigation, the team uses Hannibal in Sophia Antipolis, a cart-like platform built by Neobotix (see Fig. 3 .a), and, in Rennes, a Robotino from Festo (see Fig. 3 .b) and a Pioneer 3DX from Adept (see Fig. 3 .c). These platforms are equipped with various sensors needed for Slam purposes, autonomous navigation and sensor-based control.

Moreover, to validate the researches in personally assisted living topic (see 7.3.3), we have in Rennes a six wheel electric wheelchair from Penny and Giles Drives Technology (see Fig. 3 .d) and a five wheel electric wheelchair from You-Q (see Fig. 3 .e). The control of the wheelchair is performed using a plug and play system between the joystick and the low level control of the wheelchair. Such a system lets us acquire the user intention through the joystick position and control the wheelchair by applying corrections to its motion. The wheelchairs have been fitted with cameras and eleven ultrasound sensors to perform the required servoing for assisting handicapped people.

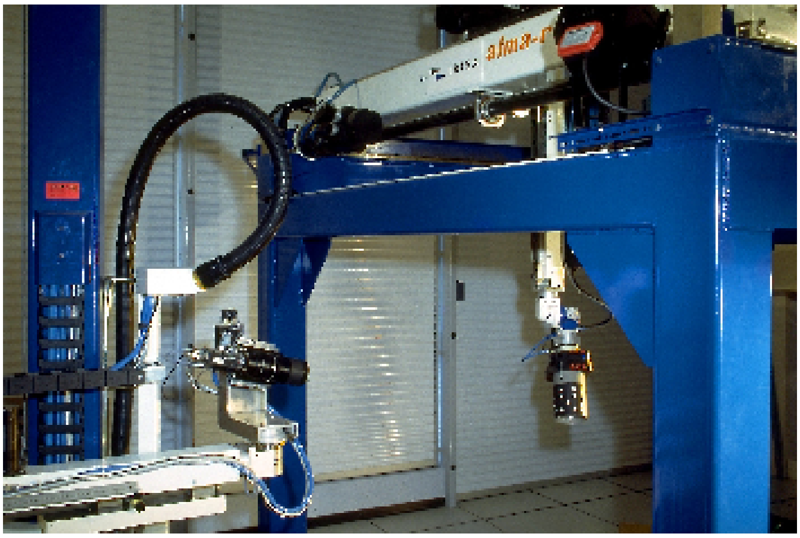

Figure 2. Lagadic robotics platform for vision-based manipulation

Note that 5 papers exploiting the indoors mobile robots were published this year [14][22][28][56][27].

6.9.2. Outdoor vehicles

The team exploits also Cycab urban electrical cars (see Figs. 3 .f and 3 .g). Two vehicles in Sophia Antipolis and one in Rennes are instrumented with cameras and range finders to validate researches in the domain of intelligent urban vehicle. Cycabs were used as experimental testbeds in several national projects in the past. This year we decided to donate the Cycab in Rennes to the INSA engineer school were it started a second live.

The camera rig can also be fixed to a standard car (see Fig. 4), which is driven at a variable speed depending on the road/traffic conditions, with an average of 30 km/h and a maximum speed of 80 km/h. The sequences are recorded at a frame rate of 20 Hz, where the six global shutter cameras of the stereo system are synchronized, producing spherical images with a resolution of 2048x665 (see fig. 4). Such sequences are fused offline to obtain maps that can be used later for localization or for scene rendering. (in a similar fashion to Google Street View) as we show in the accompanying video [0].

Four papers published by Lagadic in 2015 enclose experimental results obtained with these outdoor vehicles [20][37][10][42].

6.10. Medical robotics platform

Participants: Fabien Spindler [correspondant], Alexandre Krupa.

This testbed is of primary interest for researches and experiments concerning ultrasound visual servoing applied to probe positioning, soft tissue tracking or robotic needle insertion tasks described in Section 7.6 .

This platform is composed by two Adept Viper six degrees of freedom arms (see Fig. 5 .a). Ultrasound probes connected either to a SonoSite 180 Plus or an Ultrasonix SonixTouch imaging system can be mounted on a force torque sensor attached to each robot end-effector.

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[0] video url:(www-sop.inria.fr/members/Renato-Jose.Martins/iros15.html)

(a) (b) (c)

(d) (e)

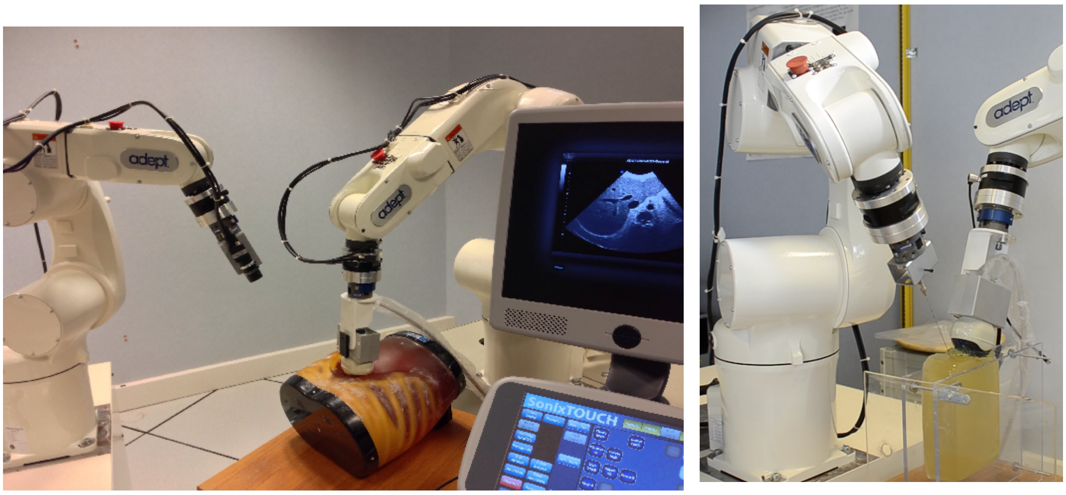
(f) (g)

Figure 3. a) Hannibal platform, b) Robotino, c) Pioneer P3-DX robot, d) wheelchair from Penny and Giles Drives Technology, e) wheelchair from You-Q , f) Cycab available in Rennes, g) one of the Cycabs available in Sophia Antipolis.

Figure 4. Globeye stereo sensor and acquisition system.

We designed an experimental setup to test an autonomous robotic needle insertion method based on visual servoing 7.6.2 . The experimental setup is composed with a gelatin phantom simulating soft tissues, a flexible biopsy needle actuated by an Adept Viper arm and a 3D ultrasound probe held by the second Adept Viper arm (see Fig. 5 .b).

This year, 5 papers enclose experimental results obtained with this platform [49][48][47][33][32].



(a) (b)

Figure 5. a) Lagadic medical robotics platforms. On the right Viper S850 robot arm equipped with a SonixTouch 3D ultrasound probe. On the left Viper S650 equipped with a tool changer that allows to attach a classical camera or biopsy needles. b) Robotic setup for autonomous needle insertion by visual servoing.

6.11. Humanoid robot platform

Participants: Giovanni Claudio, Fabien Spindler [correspondant].

Romeo is a humanoid robot from Aldebaran Robotics which is intended to be a genuine personal assistant and companion. For the moment only the upper part of the body (trunk, arms, neck, head, eyes) is working. This research platform is used to validate our researches in visual servoing and visual tracking. We continue to improve the work initiated last year to grasp a box and deliver it to a human introducing especially joint limits avoidance (see Fig. 6). We started also to work on a visual servoing framework able to control both arms to manipulate an object using only vision.

This year one paper encloses experimental results obtained with this platform [54].

6.12. Unmanned Aerial Vehicles (UAVs) platform

Participants: Thomas Bellavoir, Paolo Robuffo Giordano [correspondant].

From 2014, the team also started some activities involving perception and control for single and multiple quadrotor UAVs, especially thanks to a grant from “Rennes Métropole” (see Section 9.1.5) and the ANR project “SenseFly” (see Section 9.2.4). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (Fig. 7 .a), and one quadrotor from 3DRobotics, USA (Fig. 7 .b). The Mikrokopter quadrotors have been heavily customized by: (i) reprogramming from scratch the low-level attitude controller onboard the microcontroller of the quadrotors, (ii) equipping each quadrotor with an Odroid XU4 board (Fig. 7 .d)

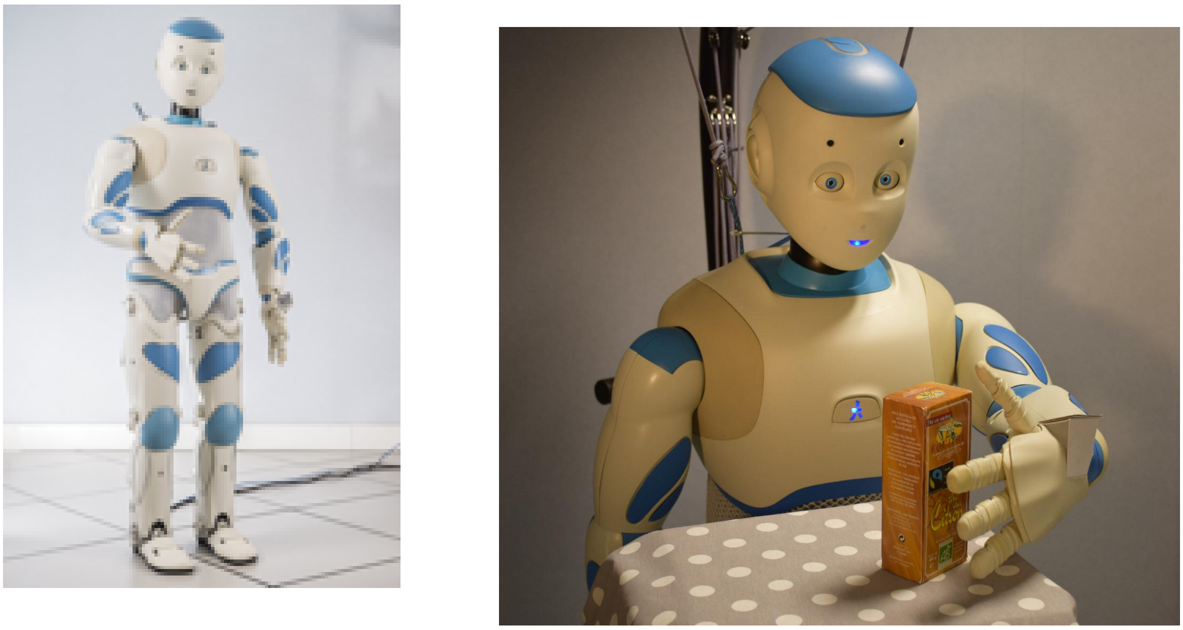
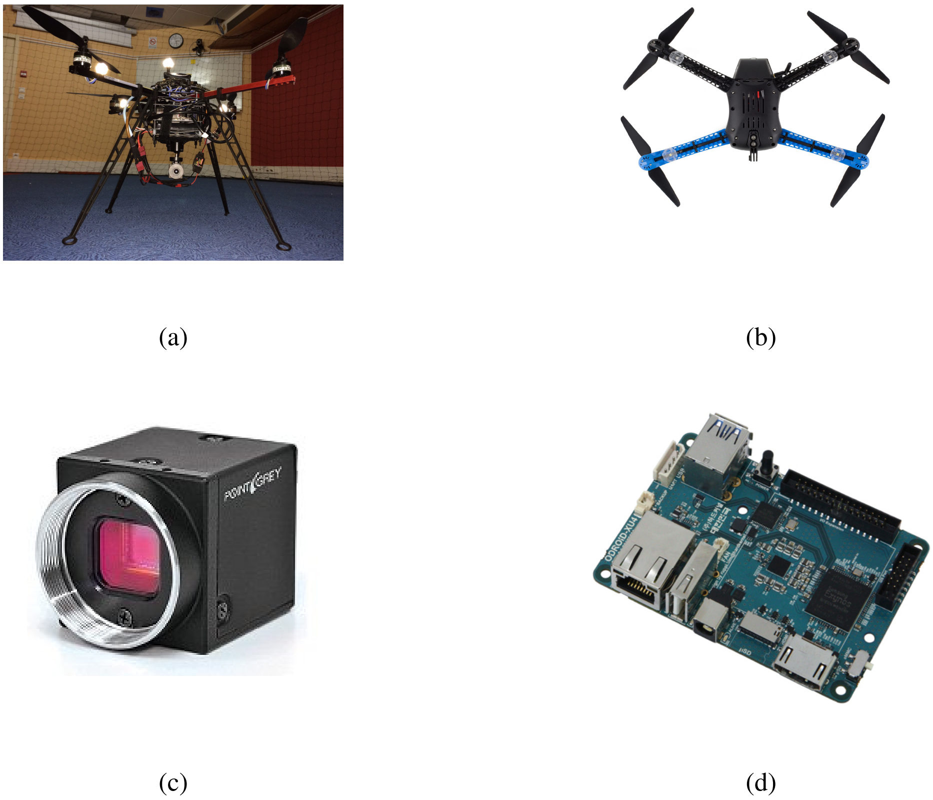


Figure 6. Romeo experimental platform.

running Linux Ubuntu and the TeleKyb software (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 (Fig. 7 .c). The quadrotor group will be 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.



(a) (b)

(c) (d)

Figure 7. a) Quadrotor XL1 from Mikrokopter, b) Quadrotor Iris from 3DRobotics, c) Flea Color USB3 camera, d) Odroid XU4 board

LINKMEDIA Project-Team

5. New Software and Platforms

5.1. TermEx

Participant: Vincent Claveau [correspondent].

TermEx is a domain-independent terminology extraction system based on natural language processing and information retrieval concepts. This year, a new version (2.0) has been implemented that corresponds to a major rewriting in Python3 with support for English (in addition to French) and faster processing of documents in batch.

In 2015, TermEx has been licensed to a large company as a key component of the archiving process.

5.2. Experimental platform

Participant: Laurent Amsaleg [correspondent].

The experimental multimedia indexing platform (PIM) consists of dedicated equipments to experiment on very large collections of multimedia data. In 2015, no major evolution of PIM occurred and activities on the platform mainly consisted on maintenance. Due to the departure of Sébastien Campion, our former PIM manager, we have also initiated a reorganization of the responsibilities, in collaboration with SED.

5.3. A||GO multimedia web services

Participant: Guillaume Gravier [correspondent].

Available at http://allgo.irisa.fr, the A||GO platform allows for the easy deployment of the technology developed in the team as web services. The engineer hired by SED in October 2013 developed several new features that enable software providers to deploy autonomously their algorithm. In 2015, the team hired a development engineer to revamp the web service offer, making services interoperable and broadening the scope of services made available.

MIMETIC Project-Team

6. New Software and Platforms

6.1. AsymGait

Asymmetry index for clinical gait analysis based on depth images
KEYWORDS: Motion analysis - Kinect - Clinical analysis
SCIENTIFIC DESCRIPTION

The system uses depth images delivered by the Microsoft Kinect to retrieve the gait cycles first. To this end it is based on a analyzing the knees trajectories instead of the feet to obtain more robust gait event detection. Based on these cycles, the system computes a mean gait cycle model to decrease the effect of noise of the system. Asymmetry is then computed at each frame of the gait cycle as the spatial difference between the left and right parts of the body. This information is computed for each frame of the cycle.

FUNCTIONAL DESCRIPTION

AsymGait is a software package that works with Microsoft Kinect data, especially depth images, in order to carry-out clinical gait analysis. First is 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: Franck Multon and Edouard Auvinet
- Contact: Franck Multon

6.2. Cinematic Viewpoint Generator

KEYWORDS: Virtual Cinematography - Intelligent Gallery
FUNCTIONAL DESCRIPTION

The software, developed as an API, provides a mean to automatically compute a collection of viewpoints over one or two specified geometric entities, in a given 3D scene, at a given time. These viewpoints satisfy classical cinematographic framing conventions and guidelines including different shot scales (from extreme long shot to extreme close-up), different shot angles (internal, external, parallel, apex), and different screen compositions (thirds,fifths, symmetric of di-symmetric). The viewpoints allow to cover the range of possible framings for the specified entities. The computation of such viewpoints relies on a database of framings that are dynamically adapted to the 3D scene by using a manifold parametric representation and guarantee the visibility of the specified entities. The set of viewpoints is also automatically annotated with cinematographic tags such as shot scales, angles, compositions, relative placement of entities, line of interest.

- Participants: Emmanuel Badier, Christophe Lino and Marc Christie
- Partners: Université d'Udine - Université de Nantes - William Bares
- Contact: Marc Christie

6.3. Directors Lens Motion Builder

KEYWORDS: Previzualisation - Virtual cinematography - 3D animation
FUNCTIONAL DESCRIPTION

Directors Lens Motion Builder is a software plugin for Autodesk's Motion Builder animation tool. This plugin features a novel workflow to rapidly prototype cinematographic sequences in a 3D scene, and is dedicated to the 3D animation and movie previsualization industries. The workflow integrates the automated computation of viewpoints (using the Cinematic Viewpoint Generator) to interactively explore different framings of the scene, proposes means to interactively control framings in the image space, and proposes a technique to automatically retarget a camera trajectory from one scene to another while enforcing visual properties. The tool also proposes to edit the cinematographic sequence and export the animation. The software can be linked to different virtual camera systems available on the market.

- Participants: Emmanuel Badier, Christophe Lino and Marc Christie
- Partner: Université de Rennes 1
- Contact: Marc Christie

6.4. Kimea

Kinect IMprovement for Egronomics Assessment
KEYWORDS: Biomechanics - Motion analysis - Kinect
SCIENTIFIC DESCRIPTION

Kimea consists in correcting skeleton data delivered by a Microsoft Kinect in an ergonomics purpose. Kimea is able to manage most of the occlultations that can occur in real working situation, on workstations. To this end, Kimea relies on a database of examples/poses organized as a graph, in order to replace unreliable body segments reconstruction by poses that have already been measured on real subject. The potential pose candidates are used in an optimization framework.

FUNCTIONAL DESCRIPTION

Kimea gets Kinect data as input data (skeleton data) and correct most of measurement errors to carry-out ergonomic assessment at workstation.

- Participants: Franck Multon, Pierre Plantard and Hubert Shum
- Partner: Faurecia
- Contact: Franck Multon

6.5. Populate

SCIENTIFIC 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 fulfilment are identified and locations where tasks should be performed are automatically selected.

FUNCTIONAL 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.

- Participants: Fabrice Lamarche and Carl-Johan Jorgensen
- Contact: Fabrice Lamarche

6.6. The Theater

SCIENTIFIC DESCRIPTION

The Theater is a software framework to develop interactive scenarios in virtual 3D environements. The framework provides means to author and orchestrate 3D character behaviors and simulate them in real-time. The tools provides a basis to build a range of 3D applications, from simple simulations with reactive behaviors, to complex storytelling applications including narrative mechanisms such as flashbacks.

FUNCTIONAL DESCRIPTION

The Theater is Unity 3D application. XML descriptions are used to specify characters behaviors.

- Contact: Marc Christie

PANAMA Project-Team

6. New Software and Platforms

6.1. FASST2

Flexible Audio Source Separation Toolbox
KEYWORDS: Audio - Source Separation
SCIENTIFIC DESCRIPTION

Only source separation software publicly availble allowing to use both spacial and spectral source properties with a generalised EM algorithm (expectation - maximisation). Fast specification of each use case by the choice of suitable constraints in constraint libraries.

FUNCTIONAL DESCRIPTION

Toolbox for the fast design of audio source separation adapted to any use case.

- Participants: Emmanuel Vincent and Yann Salaun
- Contact: Emmanuel Vincent
- URL: http://fasst.gforge.inria.fr

6.2. 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).

- Authors: Emmanuel Vincent, Charles Blandin, Alexey Ozerov, Ewen Camberlein, Romain Lebarbenchon, Frédéric Bimbot and Nancy Bertin
- Contact: Emmanuel Vincent
- URL: http://bass-db.gforge.inria.fr/bss_locate/

6.3. SPADE

Sparse Audio Declipper
KEYWORDS: Audio - Sparse regularization - Declipping
FUNCTIONAL DESCRIPTION

Matlab routines to reproduce audio declipping experiments from the papers:

- Srdan Kitic, Nancy Bertin, Remi Gribonval. Audio Declipping by Cosparse Hard Thresholding. iTwist - 2nd international - Traveling Workshop on Interactions between Sparse models and Technology, Aug 2014, Namur, Belgium. [95]
- Srdan Kitic, Nancy Bertin, Remi Gribonval. Sparsity and cosparsity for audio declipping: a flexible non-convex approach. LVA/ICA 2015 - The 12th International Conference on Latent Variable Analysis and Signal Separation, Aug 2015, Liberec, Czech Republic. pp.8. [31]
- Participants: Srdan Kitic, Nancy Bertin and Rémi Gribonval
- Contact: Rémi Gribonval
- URL: http://xspaad.gforge.inria.fr/

SIROCCO Project-Team

6. New Software and Platforms

6.1. Fixation Analysis

FUNCTIONAL DESCRIPTION

From a set of fixation data and a picture, the software called Visual Fixation Analysis extracts from the input data a number of features (fixation duration, saccade length, orientation of saccade...) and computes a human saliency map. The software can also be used to assess the degree of similarity between a ground truth (eye fixation data) and a predicted saliency map. This software is dedicated to people working in cognitive science and computer vision.

- Participants: Olivier Le Meur and Thierry Baccino
- Contact: Olivier Le Meur

6.2. Salient object extraction

FUNCTIONAL DESCRIPTION

This software detects salient object in an input picture in an automatic manner. The detection is based on super-pixel segmentation and contrast of histogram. This software is dedicated to people working in image processing and post production.

- Participants: Zhi Liu and Olivier Le Meur
- Contact: Olivier Le Meur

6.3. Saccadic model

The software called Scanpath Prediction aims at predicting the visual scanpath of an observer. The visual scanpath is a set of fixation points. The computational model is based on bottom-up saliency maps, viewing tendencies (that have been learned from eye tracking datasets) and inhibition-of-return. This study is based on the following paper [20]. This software is dedicated to people working in computer science, computer vision and cognitive science. This software is being registered at the APP (Agence de Protection des Programmes).

- Participants: Olivier Le Meur
- Contact: Olivier Le Meur

6.4. Hierarchical super-resolution based inpainting

From an input binary mask and a source picture, the software performs an examplar-based inpainting. The method is based on the combination of multiple inpainting applied on a low resolution of the input picture. Once the combination has been done, a single-image super-resolution method is applied to recover the details and the high frequency in the inpainted areas. The developments have been pursued in 2014, in particular by introducing a Poisson blending step in order to improve the visual quality of the inpainted video. This software is dedicated to people working in image processing and post production. This software is being registered at the APP (Agence de Protection des Programmes).

- Participants: Olivier Le Meur
- Contact: Olivier Le Meur

6.5. Video Inpainting for Loss Concealment

KEYWORDS: Video Inpainting - Motion informations - Loss concealment - BMFI (Bilinear Motion Field Interpolation)

FUNCTIONAL DESCRIPTION

From an input binary mask and a source video, the software performs an examplar-based inpainting. The motion information of the impaired areas is first recovered with a Bilinear Motion Field Interpolation (BMFI). The texture information is then recovered using a spatio-temporal examplar-based inpainting algorithm. The method to recover the texture proceeds in two steps: it first inpaints a low resolution version using an examplar-based method. Details of the inpainted corrupted areas of the input video are then retrieved using a nearest neighbor field (NNF) based super-resolution technique. A NNF is computed between an interpolated version of the concealed LR video and the known part of the received video at native resolution. In the same vein as in single-image super-resolution, the NNF is used to recover the high frequencies of the inpainted areas of the video.

- Participants: Ronan Le Boulch
- Contact: Olivier Le Meur

6.6. Video Inpainting for Editing

KEYWORDS: Video Inpainting - Editing

FUNCTIONAL DESCRIPTION

This software performs video inpainting for both static or free-moving camera videos. The method can be used for object removal, error concealment, and background reconstruction applications. To inpaint a frame, the method starts by aligning all the frames of a group of pictures (GOP). This is achieved by a region-based homography computation method which allows us to strengthen the spatial consistency of aligned frames. Then, from the stack of aligned frames, an energy function based on both spatial and temporal coherency terms is globally minimized. This energy function is efficient enough to provide high quality results even when the number of pictures in the GoP is rather small, e.g. 20 neighboring frames. This reduces the algorithm complexity and makes the approach well suited for near real-time video editing applications as well as for loss concealment applications.

- Participants: Mounira Ebdelli
- Contact: Olivier Le Meur