Activity Report 2016

Section Software

<p style="text-align:center; color:red;">**CAIRN Project-Team**</p>

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 designed an extensible source-to-source compiler infrastructure that takes advantage of leading edge model-driven object-oriented software engineering principles and technologies.
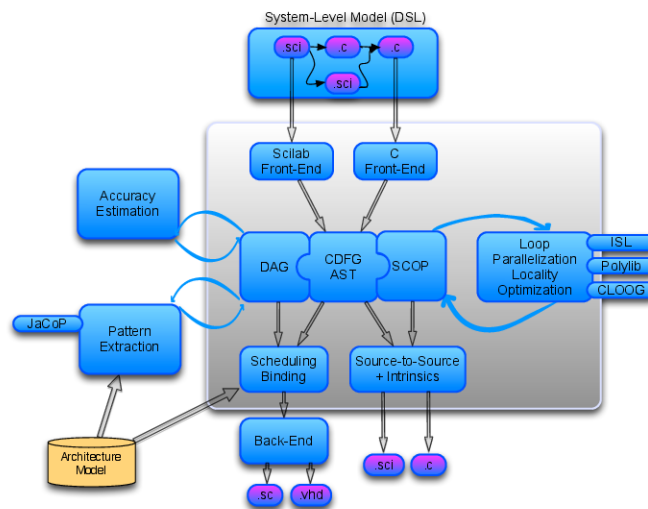
Figure 2. CAIRN*'s general software development framework.*

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 ASIC/FPGA 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.

- A polyhedral-based loop transformation and parallelization engine (mostly targeted at HLS).

- A custom instruction extraction flow (for ASIP and dynamically reconfigurable architectures). **Durase** is developed for the compilation and the synthesis targeting reconfigurable platforms and the automatic synthesis of application specific processor extensions. It uses advanced technologies, such as graph matching 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).

Gecos, ID.Fix or Durase have been demonstrated during "University Booths" in various conference such as IEEE/ACM DAC or DATE.

6.2. Gecos

KEYWORDS: Source-to-source compiler - Model-driven software engineering - Retargetable compilation
SCIENTIFIC DESCRIPTION

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

Gecos is 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 between 2012 and 2015 it was used in the context of the FP7 ALMA European project. The Gecos infrastructure will also be used by the EMMTRIX start-up, a spin-off from the ALMA project which aims at commercializing the results of the project and in the context of the H2020 ARGO European project.

FUNCTIONAL DESCRIPTION

Gecos provides a program transformation toolbox facilitating parallelisation of applications for heterogeneous multiprocessor embedded platforms. This includes a polyhedral loop transformation toolbox, efficient SIMD code generation for fixed point arithmetic data-types, coarse-grain parallelization engine targeting the data-flow actor model, and a Matlab/Scilab front-end. In addition to targeting programmable processors, Gecos can regenerate optimized code for High Level Synthesis tools.

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- Partner: Université de Rennes 1

- Contact: Steven Derrien

- URL: http://gecos.gforge.inria.fr/doku/doku.php

6.3. ID-Fix

KEYWORDS: Energy efficiency - Embedded systems - Analytical accuracy evaluation - Fixed-point arithmetic - Accuracy optimization - Dynamic range evaluation - Code optimisation

SCIENTIFIC DESCRIPTION

The different techniques proposed by the team for fixed-point conversion are implemented on the ID.Fix infrastructure. The application is described with a C code using floating-point data types and different pragmas, used to specify parameters (dynamic, input/output word-length, delay operations) for the fixed-point conversion. This tool determines and optimizes the fixed-point specification and then, generates a C code using different fixed-point data types. The infrastructure is made-up of two main modules corresponding to the fixed-point conversion (ID.Fix-Conv) and the accuracy evaluation (ID.Fix-Eval).

FUNCTIONAL DESCRIPTION

ID.Fix focuses on computational accuracy and can provide an optimised specification using fixed point arithmetic from a C source code with floating point data types. Fixed point arithmetic is very widely used in embedded systems as it provides better performance and is much more energy efficient. ID.Fix used an analytical model of the software code, which means it can explore more solutions and thereby produce much more efficient code than classical simulation-based tools.

- Participants: Olivier Sentieys, Benjamin Barrois and Nicolas Simon
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- URL: http://idfix.gforge.inria.fr/doku.php

6.4. Zyggie

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

SCIENTIFIC DESCRIPTION

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

FUNCTIONAL DESCRIPTION

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

The Zyggie V2 prototype includes new features: a 32-bit microcontroller to manage a custom MAC layer and processe quaternions based on IMU measures, and an UWB radio from DecaWave to measure distances between nodes with Time of Flight (ToF).

- Participants: Arnaud Carer and Olivier Sentieys
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- URL: http://www.bowi.cominlabs.ueb.eu/fr/zyggie-wbsn-platform

Figure 3. CAIRN*'s Ziggie platform for WBSN*

CELTIQUE Project-Team

3. New Software and Platforms

3.1. JSCert

Certified JavaScript
FUNCTIONAL DESCRIPTION

The JSCert project aims to develop a formal understanding of the JavaScript programming language. 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/

3.2. 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: Frederic Besson, David Pichardie, Pierre Vittet, Laurent Guillo, Laurent Hubert, Tiphaine Turpin and Nicolas Barre
- Contact: Frederic Besson
- URL: http://sawja.inria.fr/

3.3. SAWJA

Static Analysis Workshop for Java
KEYWORDS: Security - Software - Code review - Smart card
SCIENTIFIC DESCRIPTION

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

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

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

Version: 1.5

Programming language: Ocaml
FUNCTIONAL DESCRIPTION

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

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

3.4. Timbuk

KEYWORDS: Proof - Ocaml - Program verification - 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
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- URL: http://www.irisa.fr/celtique/genet/timbuk/

3.5. 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).

Notably, the middle-end features:

- new important optimizations (Sparse Conditional Constant Propagation, and a coalescing phase on Conventional SSA)
- a generic dominance-based proof framework that rationalizes the proof process
- improved performance regarding compilation time

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/

HYCOMES Project-Team

6. New Software and Platforms

6.1. SunDAE

Structural analysis tool for multimode DAE systems

FUNCTIONAL DESCRIPTION

SunDAE is a multimode DAE (mDAE) structural analysis tool. Structural differentiation index is determined, impulsion analysis is performed and a BTF scheduling of the equations is performed, for each mode of a mDAE system. The input language consists in guarded equations. The output is a state-machine where states define continuous-time dynamics and transitions define resets. Both are defined by scheduled blocks of equations. SunDAE has been developed since 2016 by the Hycomes team and is distributed as an open-source software, under the CeCCIL Free Software Licensing Agreement.

- Contact: Benoit Caillaud

6.2. 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: Benoit Caillaud
- URL: http://tinyurl.com/oql6f3y

6.3. 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: Benoit Caillaud
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- URL: http://www.irisa.fr/s4/tools/mica/

<h1 style="text-align:center; color:red;">PACAP Project-Team</h1>

6. New Software and Platforms

6.1. ATMI

KEYWORDS: Analytic model - Chip design - Temperature
SCIENTIFIC DESCRIPTION

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

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.

FUNCTIONAL DESCRIPTION

ATMI is a library for modelling steady-state and time-varying temperature in microprocessors. ATMI uses a simplified representation of microprocessor packaging.

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

6.2. Heptane

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

WCET estimation

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.

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.

For more information, please contact Damien Hardy or Isabelle Puaut.

FUNCTIONAL DESCRIPTION

In a hard real-time system, it is essential to comply with timing constraints, and Worst Case Execution Time (WCET) in particular. Timing analysis is performed at two levels: analysis of the WCET for each task in isolation taking account of the hardware architecture, and schedulability analysis of all the tasks in the system. Heptane is a static WCET analyser designed to address the first issue.

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- Contact: Isabelle Puaut
- URL: https://team.inria.fr/pacap/software/heptane/

6.3. Tiptop

KEYWORDS: HPC - Performance - CPU - Cache - Cycles - Instructions - Branch predictor
SCIENTIFIC DESCRIPTION

Tiptop is written in C. It can take advantage of libncurses when available for pseudo-graphic display.

Performance, hardware counters, analysis tool.

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 July 2015.

Tiptop has been integrated in major Linux distributions, such as Fedora, Debian, Ubuntu.

Tiptop is a new simple and flexible user-level tool that collects hardware counter data on Linux platforms (version 2.6.31+). 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
FUNCTIONAL DESCRIPTION

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

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

6.4. 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/pacap/software/atc/

6.5. 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
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- URL: http://barra.gforge.inria.fr/

6.6. 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

6.7. 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.2015.000.10800.

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/pacap/software/Padrone/

6.8. 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
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6.9. 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
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- URL: https://team.inria.fr/pacap/software/tpcalc/

6.10. Parasuite

Participants: Sylvain Collange, Imane Lasri, 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/

6.11. Simty

Participant: Sylvain Collange.

Simty: A Synthesizable General-Purpose SIMT Processor.

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

Visit: http://team.inria.fr/pacap/simty

SUMO Project-Team

6. New Software and Platforms

6.1. Active Workspaces

KEYWORDS: Guarded attribute grammar - Active workspace - Artifact centric workflow system
SCIENTIFIC DESCRIPTION

Tool for computer supported cooperative work where a user's workspace is given by an active structured repository containing the pending tasks together with information needed to perform the tasks. Communication between active workspaces is asynchronous using message passing. The tool is based on the model of guarded attribute grammars [44]. Late in 2015 Éric Badouel produced in Haskell a software prototype implementing active workspaces based on Guarded Attribute Grammars (GAGs).

Concurrently, Christophe Morvan was beginning a startup project consisting in making on-line collective decision making tools: *Open Agora*. This project included collaboration workspaces for people participating in constructing possible decisions. There was a natural connection between the prototype, and the startup project.

In order to make industrial use of the GAG prototype, Olivier Bache (already involved in the Open agora project) applied to a 6 month InriaHub program (between April and September 2016). During these 6 months he bundeled the prototype into an API (also programmed in Haskell) and developed a web infrastructure, based on the PHP framework, to allow the interaction with Active Workspaces in a browser. This developpement will be licenced to Open Agora SAS after its creation expected in January 2017.
FUNCTIONAL DESCRIPTION

Prototype in Haskell of user's active workspaces based on Guarded Attribute Grammars.

- Author: Eric Badouel
- Contact: Eric Badouel
- URL: http://people.rennes.inria.fr/Eric.Badouel/Research/ActiveWorkspaces.html

6.2. SIMSTORS

SIMSTORS is a simulator for regulated stochastic timed Petri nets. These Petri nets are a variant of stochastic and timed nets, whose 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. This year, the software has been extended to consider headway management.

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

<p style="text-align:center">**TAMIS Team**</p>

6. New Software and Platforms

6.1. MHD

GNU libmicrohttpd
KEYWORDS: Embedded - Web 2.0
SCIENTIFIC DESCRIPTION

We are providing a standards compliant and complete implementation of the HTTP server protocol that allows developers to easily write correct HTTP servers. Key challenges include code size minimization (for IoT devices), performance (zero copy, scalability to 100k concurrent connections), portability and security. MHD is already widely used in production by both academic and industrial users. Ongoing research challenges include formal verification.

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.

- Participants: Evgeny Grin, Christian Grothoff and Sree Hrsha Totakura
- Partner: The GNU Project
- Contact: Christian Grothoff
- URL: http://www.gnu.org/software/libmicrohttpd/

6.2. PLASMA Lab

KEYWORDS: Model Checking - Statistical - Model Checker - Runtime Analysis - Security - Code analysis - Statistics - Energy - Aeronautics
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 compact, efficient and flexible platform for statistical model checking of stochastic models. PLASMA Lab demonstrates the following advances: -Use your own simulator and checker via our plugin system. -Build your software around Plasma Lab using our API. -Prism (Reactives Modules Language-RML) and Biological languages supported. -Matlab and SytemC plugins. -Distributed architecture. Whether you plan to use several computers on a local area network or a grid, you can run PLASMA Lab in an easy way. -Fast algorithms. -Efficient data structure, low memory consumption. -Developed with Java for compatibility.

- Participants: Axel Legay, Sean Sedwards, Benoit Boyer, Louis-Marie Traonouez, Kevin Corre and Matthieu Simonin
- Contact: Axel Legay
- URL: http://plasma-lab.gforge.inria.fr/plasma_lab_doc/1.4.0/html/introduction.html#

6.3. Quail

FUNCTIONAL DESCRIPTION

Privacy is a central concern 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/

6.4. GNUnet

SCIENTIFIC DESCRIPTION

The GNUnet project seeks to answer the question what a modern Internet architecture should look like for a society that care about security and privacy. We are considering all layers of the existing well-known Internet, but are also providing new and higher-level abstractions (such as voting protocols, Byzantine consensus, etc.) that are today solved in application-specific ways. Research questions include the desired functionality of the overall stack, protocol design for the various layers as well as implementation considerations, i.e. how to implement the design securely.

FUNCTIONAL DESCRIPTION

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

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

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

6.5. Taler

GNU Taler
KEYWORD: Privacy
SCIENTIFIC DESCRIPTION

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

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

We argue that Taler provides a secure digital currency for modern liberal societies as it is a flexible, *libre* and efficient protocol and adequately balances the state's need for monetary control with the citizen's needs for private economic activity.

Taler is a new electronic payment system. It includes an electronic wallet for customers, a payment backend for merchants and the main payment service provider logic called the exchange. Taler offers Chaum-style anonymous payments for citizens, and income-transparency for taxability.

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

6.6. VITRAIL - Visualisation Tool

Real-Time, Advanced, Immersive Visualization of Software / Visualizer
KEYWORD: Visualization of software
SCIENTIFIC DESCRIPTION

It is difficult for developers to explore and understand the source code of large programs, for example in objet-oriented languages programs featuring thousands of classes. Visualization methods based on daily life metaphors have thus been proposed. The VITRAIL Visualization tool (or VITRAIL Vizualizer) makes it possible to display, visualize and explore Java programs in a metaphorical way, using the city metaphor. An execution trace of the Java (byte)code provided by VITRAIL JBInstrace tool, is provided as input to VITRAIL Visualizer which displays a city-like metaphorical world showing the static structure of the code as well as some dynamic elements (calls).
This program may be used in Tamis as a basis for tools for the visualization of security events in programs.

FUNCTIONAL DESCRIPTION

This program makes it possible to displays, visualizes and explores Java programs in a metaphorical way (using the city metaphore). Useful for complex application developers/architects.

- Participants: Damien Bodenes, Olivier Zendra and Olivier Demengeon
- Contact: Olivier Zendra

6.7. VITRAIL 6 JBInsTrace

Real-Time, Advanced, Immersive Visualization of Software / Java Bytecode Instrumenter and Tracer
KEYWORDS: Java - Bytecode - Instrumentation - Profiling - Execution trace - Basic block
SCIENTIFIC DESCRIPTION

VITRAIL JBInsTrace is a program to instrument Java bytecode to trace its execution. The trace contains both static and dynamic information (calls). It is produced by intercepting the JVM class loader and replacing it by ours. Thus Java bytecode file are not modified, since instrumentation is performed on the fly, in memory. This makes it possible to instrument the whole program code, including libraries. Java source code is not needed. The trace which is then fed into our program VITRAIL Visualizer is an XML-like file.
This program may be used in Tamis as a basis for tools to instrument Java bytecode for security.

FUNCTIONAL DESCRIPTION

VITRAIL JBInsTrace is a program to instrument Java bytecode files to trace their execution. The trace is then fed into our VITRAIL Visualizer tool.

- Participants: Pierre Caserta and Olivier Zendra
- Contact: Olivier Zendra

6.8. Platforms

6.8.1. *Malware'o'Matic*

This LHS platform is dedicated to the collect, the categorization and the analyze of malware. We are currently interested in a specific kind of malware the ransomware. The platform grabs periodically samples of public data bases, executes the ransomware without virtualization on a victim PC and evaluate the implemented detection mechanisms. Once a ransomware has been executed the image of the OS is automatically restored and a new sample is evaluated. The platform is fully automatic and target Windows platforms (seven, W10) in both 32 bits and 64 bits versions.

6.8.2. *Faustine*

This LHS platform is dedicated to the EM fault injection experiments. It is composed of a motion table (XY), a pulse generator, an amplifier and a control PC. It injects EM pulses in a controlled way on a targeted device using an EM probe. It controls with a high precision the timing and the edges of the pulse. A recent development consists in adding a FPGA board to control the trigger in a more convenient and precise way. Then, the pulse can be triggered while a specific information is sent to the board under attack.

6.8.3. *EMA*

This last LHS platform is dedicated to side channel analysis (SCA) for evaluating the capabilities of dynamic countermeasure developed in the ANR Cogito. This platform uses a low cost oscilloscope, an EM probe and a set of software developed to perform the analysis. An additional oscilloscope, more performant has been added to the platform to target faster devices. We use the Julia language platform and custom developments to control the target and to analyze the EM traces.

<h2 style="text-align:center;color:red;">TASC Project-Team</h2>

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 behaviors (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

KEYWORDS: Constraint Programming - Scheduling - Optimisation - Operational research - Financial analysis - Planning
SCIENTIFIC DESCRIPTION

or second consecutive year, CHOCO has participated at the MiniZinc Challenge , an annual competition of constraint programming solvers. In concurrency with 16 other solvers, CHOCO has won three 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 (v3.3.0, Dec. 17th) has the particularity to be promoted on Maven Central Repository. The major modifications were related to a simplification of the API but also improvement of the overall solver.

Within the context of the PhD thesis of Charles Prud'homme, a domain specific language that allows prototyping propagation engines was integrated within CHOCO, A paper appears at Constraints.

Within the context of the PhD thesis of Charles Prud'homme, a generic strategy based on explanations for large neighborhood search was designed and integrated within CHOCO. A corresponding paper appears at Constraints.

Within the context of the PhD thesis of Jean-Guillaume Fages, a documented package for graph variables was designed and integrated within CHOCO .
FUNCTIONAL DESCRIPTION

CHOCO is a Java discrete constraints library for describing hard combinatorial problems in the form of Constraint Satisfaction Problems and solving them with Constraint Programming techniques. Choco can be used to solve a broad range of real combinatorial problems. It is easy to use and offers excellent performance. This technique enables non-specialists to tackle strategic or operational problems, for instance, problems related to planning, scheduling, logistics, financial analysis and bio-informatics.

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

6.3. GCCat

Global Constraint Catalog
KEYWORDS: Constraint Programming - Graph - Global constraint
FUNCTIONAL DESCRIPTION

The global constraint catalog presents and classifies global constraints and describes different aspects with meta data.

- Participants: Nicolas Beldiceanu and Sophie Demassey
- Contact: Nicolas Beldiceanu
- URL: http://sofdem.github.io/gccat/gccat/index.html

6.4. GCCat on time series

Global Constraint Catalog, Volume II, time-series constraints
KEYWORDS: Constraint Programming - Sequence - Transducer - Global constraint
FUNCTIONAL DESCRIPTION

The second volume of the Global Constraint Catalogue is devoted to time-series constraints. Within the context of Constraint Programming, time-series constraints go back to the work of Goldin and Kanellakis. This volume contains 626 constraints, which are explicitly described in terms of automata with accumulators. Checkers and propagators for all these constraints were synthesised from 22 transducers.

As in the first volume, the global constraints described in this second volume are not only accessible to humans, who can read the catalogue when searching for some information. It is also available to machines, which can read and interpret it. This is why there also exists an electronic version of this catalogue where one can get, for all time-series constraints, a complete description in terms of meta-data used in the first volume. In fact, unlike the first volume, *all the meta-data* of the electronic version as well as *all text and figures* of this second volume were automatically generated. While this second volume is by no means supposed to contain all possible time-series constraints, it contributes in the context of time-series constraints to the *systematic reconstruction* of the Global Constraint Catalogue that we have previously advocated. This reconstruction is based on the following methodology:

- First reuse, adapt or come up with abstractions, which allow to concisely represent structures and properties of time series as abstract combinatorial objects. In our context these abstractions essentially correspond to:
  1. Transducers where letters of the output alphabet are interpreted as semantic letters indicating how to recognise pattern occurrences.
  2. Transducers glue matrices expressing the relationship between the prefix, the suffix and the full sequence passed to a transducer.
  3. Properties associated to regular expressions corresponding to fragments of the input language of our transducers.
- Second, create from these abstract combinatorial objects a data base of concrete combinatorial objects.
- Third, synthesise concrete code for various technologies, languages, tasks from this data base of concrete combinatorial objects. In this context, correctness and efficiency of the synthesised code are essentially side product of:
  - The correctness of the formulae of our data base which is itself based on the wellformedness of our abstractions.
  - The generality behind our abstract combinatorial objects.

The time-series catalogue is done in the following way:

- All time-series constraints are now defined in a *compositional way* from a few basic constituents, i.e., patterns, features, aggregators, and predicates, which completely define the meaning of a constraint, where patterns are defined using regular expressions.

- Constraint names are now constructed in a systematic way as the *concatenation* of pattern name, feature name, and aggregation or predicate name.

- Given a pattern p, checkers and constraints are now *systematically synthesised* from a transducer that, given an input sequence over the input alphabet $\{<, =, >\}$, compares two adjacent values of a time-series and determines an output sequence over a output semantic alphabet describing how to recognise the occurrences of p.

- For each time-series constraint associated with a pattern p, the generation of an automaton with accumulators is completely driven by the transducer associated with pattern p as well as by *decoration tables* describing for each semantic letter of the output alphabet of the transducers how to generate accumulator updates. Code optimisation is ensured by using decoration tables that depend on properties of the pattern, of the feature, and of the aggregator associated with the time-series constraint.

- Lower and upper bounds of characteristics of time-series that appear in the restriction slot of a time-series constraint are synthesised from a *few parameterised formulae* that only depend on a restricted set of characteristics of the regular expression associated with the pattern.

- Parametrised glue matrices are provided for each transducer that corresponds to reversible time-series constraints. A concrete glue matrix is given for each reversible time-series constraint.

- Linear invariants are systematically obtained by applying the Farkas Lemma to the automata with accumulators that were synthesised. They consist of *linear constraints typically linking consecutive accumulator values*, e.g., see the legend of the second automaton of the constraints, which are generated even with non-linear accumulator updates. Missing linear invariants will be completed later on.

- Last but not least, time-series constraints were used for generating time-series verifying a conjunction of constraints both in the context of Constraint Programming and in the context of Linear Programming.

- In the context of sequential pattern mining, time-series constraint checkers can be used to identify and extract patterns from fixed sequences. While the time-series catalogue may need to be extended in order to capture more patterns, having a possibly large set of fixed time-series constraints is a natural safeguard to prevent overfitting when dealing with few sequences, at a price of not finding patterns that are not covered by the catalogue.

- Finally, both SICStus and MiniZinc code are synthesised. The later allows using time series constraints on many plate forms such as Choco, Gecode, ORtools, Cplex or Gurobi and is available Electronic Constraint Catalogue.

- Participants: Ekaterina Arafailova, Nicolas Beldiceanu, Rémi Douence, Mats Carlsson, Pierre Flener, Maria Andreina Francisco Rodriguez, Justin Pearson, Helmut Simonis

- Contact: Nicolas Beldiceanu

- URL: https://arxiv.org/abs/1609.08925

6.5. GHOST

General meta-Heuristic Optimization Solving Tool
FUNCTIONAL DESCRIPTION

GHOST 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

6.6. TorchCraft

Machine learning framework for games
FUNCTIONAL DESCRIPTION

TorchCraft is a library that enables deep learning research on Real-Time Strategy (RTS) games such as StarCraft: Brood War, by making it easier to control these games from a machine learning framework, here Torch. This white paper argues for using RTS games as a benchmark for AI research, and describes the design and components of TorchCraft.

- Participants: Gabriel Synnaeve, Nantas Nardelli, Alex Auvolat, Soumith Chintala, Timothe´e Lacroix, Zeming Lin, Florian Richoux, Nicolas Usunier
- Contact: Florian Richoux
- URL: https://arxiv.org/abs/1611.00625

6. New Software and Platforms

6.1. ADFG: Affine data-flow graphs scheduler synthesis

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

We proposed [2], and implemented [0], a new data-flow design model: ADFG, initially to synthesize schedulers for SCJ/L1 applications. The principle of ADFG is to perform a linear abstraction of complex cyclo-static scheduling problems followed by the exploration of a concrete solution extracted from the abstract solution space, hence the name: abstract affine data-flow scheduling. ADFG guarantees schedules that ordinary (e.g. RTJ, SCJ) task-sets do not cause overflows or underflows. ADFG objectives are to maximize the throughput (the processors utilization) while minimizing buffering storage space needed between actors. ADFG supports EDF and fixed-priority scheduling policies for uni-, multi-processors and distributed systems.

The data-flow design model of ADFG 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. Abstract affine scheduling is first applied on the data-flow 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.

In the case of safety-critical Java, and through a model-to-text transformations using Acceleo, 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.

6.2. The Eclipse project POP

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

The distribution of project POP 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 finalized 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.

Project POP is composed of the Polychrony tool set, under GPL license, and its Eclipse framework, under EPL license. SSME (Syntactic Signal-Meta under Eclipse), is the meta-model of the Signal language implemented with Eclipse/Ecore. It describes all syntactic elements specified in Signal Reference Manual [0]: all Signal operators (e.g. arithmetic, clock synchronization), model (e.g. process frame, module), and construction (e.g. iteration, type declaration). The meta-model primarily aims at making the language and services of the Polychrony environment available to inter-operation and composition with other components (e.g. AADL, Simulink, GeneAuto, P) within an Eclipse-based development tool-chain. Polychrony now comprises the

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[0]*The ADFG tool*, Adnan Bouakaz, http://people.irisa.fr/Adnan.Bouakaz/software.htm
[0]
SIGNAL V4-Inria version: Reference Manual. Besnard, L., Gautier, T. and Le Guernic, P. http://www.irisa.fr/espresso/Polychrony, 2010
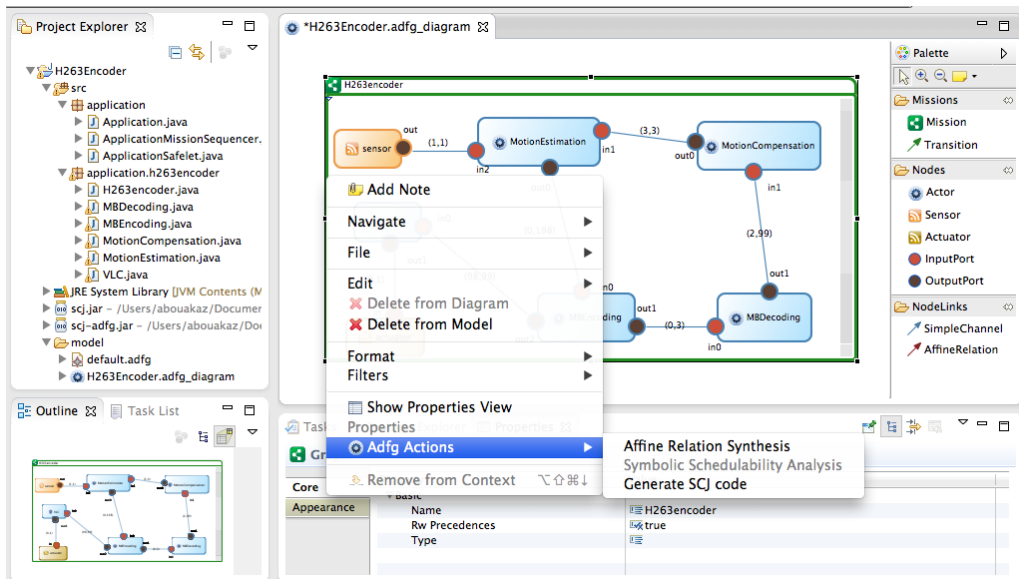
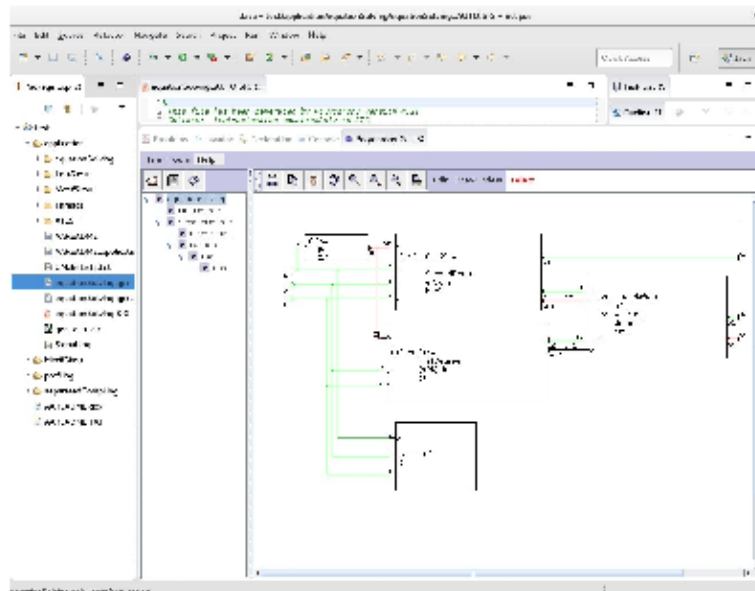*Figure 1. The ADFG tool*

Figure 2. The Eclipse POP Environment

capability to directly import and export Ecore models instead of textual Signal programs, in order to facilitate interaction between components within such a tool-chain. The download site for project POP has opened in 2015 at https://www.polarsys.org/projects/polarsys.pop. It should be noted that the Eclipse Foundation does not host code under GPL license. So, the Signal toolbox useful to compile Signal code from Eclipse is hosted on our web server.

6.3. The Polychrony toolset

Participants: Loïc Besnard, Thierry Gautier, 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 data-flow language. It provides a unified model-driven environment to perform design exploration by using top-down and bottom-up design methodologies formally supported by design model transformations from specification to implementation and from synchrony to asynchrony. It can be included in heterogeneous design systems with various input formalisms and output languages. The Polychrony tool-set provides a formal framework to: validate a design at different levels, by the way of formal verification and/or simulation; refine descriptions in a top-down approach; abstract properties needed for black-box composition; compose heterogeneous components (bottom-up with COTS); generate executable code for various architectures. The Polychrony tool-set contains three main components and an experimental interface to GNU Compiler Collection (GCC):

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

- The Signal GUI, a Graphical User Interface to the Signal toolbox (editor + interactive access to compiling functionalities). It can be used either as a specific tool or as a graphical view under Eclipse. 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.

As part of its open-source release, the Polychrony tool-set 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 tool-set. The Polychrony tool-set 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 tool-set can be freely downloaded from http://polychrony.inria.fr/. This site, intended for users and for developers, contains executable and source versions of the software for different 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 contains the whole source of the environment and its documentation. It is intended for developers.
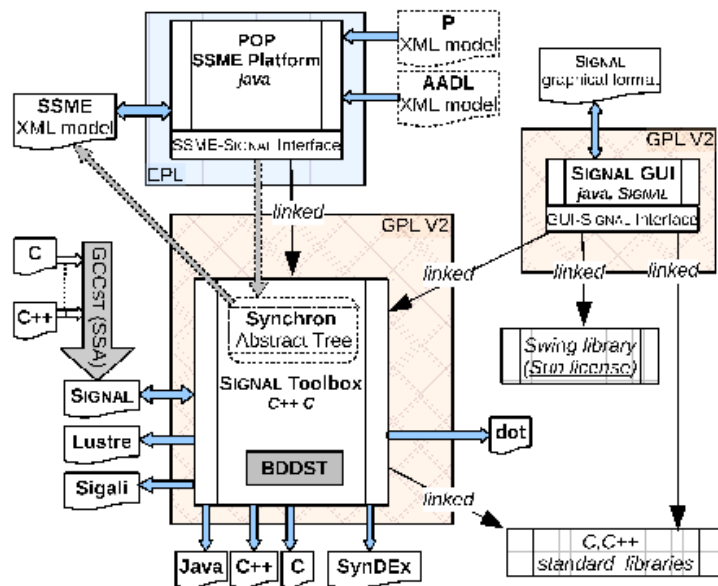
Figure 3. The Polychrony toolset high-level architecture

<p style="text-align:center; color:red;">**ANJA Team**</p>

5. New Software and Platforms

5.1. New Software

5.1.1. Law

In order for our research to become used in a non-technological domain as is law, we make special efforts to develop user-friendly software tools. We have already made available an iOS application for computing the amount of child support. Another application is currently being developed for spousal support.

Future user-friendly software we intend to propose will be concerned with the areas of personal injury and intellectual property.

5.1.2. Economy and finance

The software toolbox FracLab (http://fraclab.saclay.inria.fr) contains a number of tools related to multistable processes, including their simulation and calibration. We intend to pursue these developments in particular by proposing methods dealing with self-stabilizing processes.

We also hope to be able to collaborate with financial institutions, in view of advancing the idea that current regulations, because they are model-based, perform the economy in a way that needs to be carefully scrutinized.

5.1.3. Archaeology

Our software ChronoModel provides a set of Bayesian statistical tools for constructing chronologies using measurement coming from different dating methods (e.g. 14C, TL/OSL, AM, typo-chronology). Chronomodel is a free and open-source cross-platform software that can be downloaded at http://www.chronomodel.fr

It offers a user-friendly interface for entering both data and archaeological facts : stratigraphy, temporal order constraints, contemporaneous events.

ChronoModel is currently used by researchers in laboratories of archaeology and earth science, and also by archaeologists working in the organizations of rescue archaeology.

ASPI Project-Team (section vide)

<p style="text-align:center; color:red; font-weight:bold">I4S Project-Team</p>

6. New Software and Platforms

6.1. Cloud2IR

KEYWORDS: Sensors - SHM (Structural Health Monitoring) - Sensors network - Open Geospatial Consortium - OGC

SCIENTIFIC DESCRIPTION

Cloud2IR is an helpful tool to build physicals models for the SHM of civil engineering structures.

In this context the software is deployed in the SenseCity-EQUIPEX driven by IFSTTAR (http://sense-city.ifsttar.fr/)

FUNCTIONAL DESCRIPTION

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.

- Partner: IFSTTAR
- Contact: Jean Dumoulin

This work has been developed during the ADT of Antoine Crinière, Cloud2SM.

6.2. PEGASE

KEYWORD: Sensors - SHM (Structural Health Monitoring)

SCIENTIFIC DESCRIPTION

PEGASE (Plate-forme Experte Générique pour Applications Sans-fil Embarquées) is a generic and high level wireless sensor platform. Currently, the setup of the new PEGASE 2 platform is finalized as the technological successor of the previous PEGASE platform developed by IFSTTAR. This PEGASE 1 platform is licensed and disseminated by the third party company A3IP since 2008 and has been sold in thousands of units.

Based on various feedback from monitoring applications of PEGASE, and due to the fast obsolescence of electronic devices, the design of the new PEGASE 2 platform has been launched in 2013. Some of the main functions of PEGASE are reinforced:

- Software genericity: use of a Linux embedded OS to make application development independent from the hardware, and to enable the user to manage the system without any 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) where each pluggable daughter board implements a specific function (sensing, 3G, Ethernet, communication, signal processing and relay control).
- Accurate time synchronization principle: based on an original GPS and PPS algorithm, PEGASE platform is one of the only boards able to time-stamp data from sensors or any event with high accuracy and in a deterministic way.

On PEGASE 2 platform, previous principles are maintained or extended. A full electronic design from scratch has been decided by the team in 2014 to maximize its capacities in terms efficiency, cost, energy consumption, etc. The main new characteristics of PEGASE 2 are:

- A "real" Linux kernel is now flashed inside the board based on a professional Debian 4.0 (or higher version) of Linux. This Linux branch is the only one validated by IEEE to suit embedded applications
- Previous SDK in C language has been ported and improved in C++ with a generalization of the signal/slot principle to offer end-users a full programing context based on "event driven developments".
- Extended hardware capacities: GigaBytes of memory, multiple USB port, etc...
- PEGASE 2 board implements new hardware such as a on-board Battery Management System (BMS) to be able to manage an energy efficiency based on a battery and a solar cell; PEGASE 2 mother board integrates a MEMS Mpu9150 from Invenses company wich is a MEMS that provides Acceleration, Temperature and Gyroscope in 3D,...

In 2015 and 2016 various functional daughter boards have been designed to complete the PEGASE 2 panoply:

- 8 analog and 8 digital daughter boards
- LORA protocol Daughter Board
- 3G Daughter Board

Figure 6. PEGASE and PEGASE daughter board

In 2016, based on an industrial contract with the company SDEL-CC (subsidiary company of Vinci group) an important algorithm has been implemented in PEGASE 2 board to make it able to time stamp any physical event up to 10 nanoseconds (independently from the wireless protocol or the distances between the platform that could be some tens of kilometers). This time stamping ability is unique and makes PEGASE 2 the only wireless device in the world with such a time accuracy in a deterministic way and in universal time (based on its GSP/PPS principle).

The most significant development in the PEGASE 2 context is the development of a Generic Cloud Server Application:

- manage multiple instrumentation projects
- various sensors (based on PEGASE 1 or 2 or others) can be set up
- collect big data based on Mongo DB database
- visualize the graphs of data from sensors in f(t) on dynamic charts
- export data to files, through specific API, or to third-party software (Matlab, QT C++...)

In the last two years the Generic Supervisor became a professional software product that is transfered under industrial Licensing, e.g. to the companies Power Lan and Stimio. By the end of 2016, at least these 2 companies will be officially licensed by IFSTTAR to disseminate the Supervisor.

- 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

Figure 7. Supervisor

6.3. TrackingMecaSys

KEYWORDS: Bayesian estimation - Monte-Carlo - GPGPU - Kalman filter - Particular filter - Vibrating system
FUNCTIONAL DESCRIPTION

Implementation of a method based on the use of Bayesian modal parameter recursive estimation based on a particular Kalman filter algorithm with decoupled distributions for mass and stiffness. Algorithm optimized for a GPGPU implementation. This work has been done during ADT of Antoine Crinière and will be updated during the postdoc of S. Sen.

- Contact: Laurent Mevel

IPSO Project-Team (section vide)

DYLISS Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: RDF - SPARQL - Querying - Graph
FUNCTIONAL DESCRIPTION

AskOmics allows to load heterogeneous bioinformatics data (formatted as tabular files or directly in RDF) into a Triple Store system using a user-friendly web interface. AskOmics also provides an intuitive graph-based user interface supporting the creation of complex queries that currently require hours of manual searches across tens of spreadsheet files. The elements of interest selected in the graph are then automatically converted into a SPARQL query that is executed on the users' data.

- Authors: Charles Bettembourg, Yvanne Chaussin, Anthony Bretaudeau, Olivier Filangi, Fabrice Legeai and Olivier Dameron
- Partners: CNRS - INRA - Université de Rennes 1
- Contact: Fabrice Legeai
- https://github.com/askomics/askomics

6.2. PADMet

PortAble Database for Metabolism
KEYWORDS: Bioinformatics - Toolbox - Metabolic networks - Standardization
FUNCTIONAL DESCRIPTION

The PADMet package allows conciliating genomics and metabolic network information used to produce a genome-scale constraint-based metabolic model within a database that traces all the reconstruction process steps. It allows representing the metabolic model in the form of a Wiki containing all the used/traced information. Other standard outputs are made available with the package. The main concept underlying PADMet-Package is to provide solutions that ensure the consistency, the internal standardization and the reconciliation of the information used within any workflow that combines several tools involving metabolic networks reconstruction or analysis. The PADMet package is at the core of the AuReMe workflow, dedicated to the primary reconstruction of genome-scale metabolic networks from raw data. It allows the study of organisms for which few experimental data are available. Its main feature is to undergo the reconstruction of the metabolic network by combining several heterogeneous knowledge and data sources, including the information reported by several scaffold metabolic networks for cousin species.

- Partners: CNRS - Inria - Université de Rennes 1 - University of Chile.
- Contact: Meziane Aite
- https://gitlab.inria.fr/DYLISS/padmet-toolbox

6.3. PowerGrASP

Power Graph compression in ASP
KEYWORDS: Bioinformatics - Constraint-based Programming - Data visualization - Optimization - Decomposition - Graph - Graph visualization - Pattern extraction - Answer Set Programming - Formal concept analysis
FUNCTIONAL DESCRIPTION

Implementation of graph compression methods oriented toward visualization, and based on power graph analysis. The method relies of formal concept analysis and is implemented in the declarative langage Answer Set Programming. It is applied to regulatory networks currently produced in the domain of bioinformatics.

- Participants: Lucas Bourneuf, Jacques Nicolas
- Partners: Inria - Université de Rennes 1 - INRA.
- Contact: Lucas Bourneuf
- URL: http://github.com/aluriak/powergrasp

6.4. Platforms and toolboxes

A goal of the team is to facilitate interplays between tools for biological data analysis and integration. Our tools 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 developed in collaboration with the GenOuest resource and data center hosted in the IRISA laboratory, including their computer facilities [more info]. It worths considering them into larger dedicated environments to benefit from the expertise of other research groups.

- The **BioShadock** repository allows one to share the different docker containers that we are developing [website].
- The **Inria chile Mobyle portal** gathers some of the tools that were developed in collaboration with Dyliss, such as meneco, shogen and lombarde [website].
- The **bioASP portal** gather most of ASP-based python packages that we are developping in collaboration with Potsdam university [website]
- The **GenOuest galaxy portal** now provides access to most tools for integrative biology and sequence annotation (access on demand).

6.4.1. AuReMe - Tracable reconstruction of metabolic networks

The toolbox **AuReMe** allows for the **Au**tomatic **Re**construction of **Me**tabolic networks based on the combination of multiple heteregeneous data and knowledge sources. Since 2016, the workflow has been made available as a Docker image to facilitate its distribution among the scientific community [web page].

- The **Model-management PADmet module** allows conciliating genomics and metabolic network information used to produce the metabolic model within a local database that traces all the reconstruction process steps and to connect software in the pipeline. This toolbox was completly redesigned in 2016. [package]
- The **meneco python package** allows filling the gaps of a metabolic network by using a qualitative approach to elaborate the biosynthetic capacities; the problem is viewed as a combinatorial optimization problem encoded in a Answer Set Programming Problem [87] [64]. [python package].
- The **shogen python package** allows aligning genome and metabolic network to identify genome units which contain a large density of genes coding for enzymes that regulate successive reactions of metabolic pathways; the problem is also encoded with an ASP program. [62]. [python package].
- The **Manual curation assistance PADmet module** allows for curating the reported metabolic networks and modify metadata [package].
- The **Wiki-export PADmet module** enables the export of the metabolic network and its functional genomic unit as a local wiki platform allowing the user-friendly investigation of the network together with the main steps used to reconstruct it. It was developed in 2016. [package].

6.4.2. *Filtering interaction networks with graph-based optimization criteria*

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.

- The **lombarde package** enables the filtering of transcription-factor/binding-site regulatory networks with mutual information reported by the response to environmental perturbations. The high level of false-positive interactions is filters according to graph-based criteria. Knowledge about regulatory modules such as operons or the output of the shogen package can be taken into account [48][13] [web server].

- The **KeyRegulatorFinder package** allows searching key regulators of lists of molecules (like metabolites, enzymes or genes) by taking advantage of knowledge databases in cell metabolism and signaling. The complete information is transcribed into a large-scale interaction graph which is filtered to report the most significant upstream regulators of the considered list of molecules [61] [package].

- The **powerGrasp python package** provides an implementation of graph compression methods oriented toward visualization, and based on power graph analysis. [package].

- The **iggy package** enables the repairing of an interaction graph with respect to expression data. 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. [5] [93] [Python package][web server].

6.4.3. *Caspo - Studying synchronous boolean networks*

The **caspo** pipeline is dedicated to 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.

Software provides an easy to use software for the study of synchronous logical (boolean) networks. In 2016, the tool was redesigned to enhance its functionalities and integrated in a docker container to facilitate its use on any platform [86] [28] [python package and docker container].

- The **caspo-learn module** performs an automated inference of logical networks from the observed response to different perturbations (phosphoproteomics datasets). It allows for identifying admissible large-scale logic models saving a lot of efforts and without any a priori bias. It is also included in the cellNopt package [0] [7] [94].

- The **caspo-classify, predict and visualize modules** allows for classifying a family of boolean networks with respect to their input–out- put predictions [7].

- The **caspo-design module** designs experimental perturbations which would allow for an optimal discrimination of rival models in a family of boolean networks [95].

- The **caspo-control module** identifies key-players of a family of networks: it computes robust 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 [73].

- **caspo-timeseries module** have been designed by our colleagues from LRI as an extension of the caspo pipeline to take into account time-series observation datasets in the learning procedure [23] [python package and docker container].

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

6.4.4. cadbiom - Building and analyzing the asynchronous dynamics of enriched logical networks

Based on Guarded transition semantic, the **cadbiom** 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. In 2016, the tool was integrated in a docker container in order to facilitate its use on any platform [49] [docker container][web server].

- **The cadbiom graphical interface** is useful to build and study moderate size models. It provides means for model exploration, simulation and checking. For large-scale models, the graphical interface allows to focus on specific nodes of interest.
- **The cadbiom API** allows to load a model (including large-scale ones), perform static analysis (exploration, frontier computation, statistics, and dependence graph computation) and check temporal properties on a finite horizon in the future or in the past.
- **Exploring large-scale knowledge repositories** A main feature of cadbiom is that automatic translation of the large-scale PID repository (about 10,000 curated interactions) have been automatically translated into the cadbiom formalism. Therefore, the API allows for computing the upstream regulators of any set of genes based on this large-scale repository.

6.4.5. Protomata - Expressive pattern discovery on protein sequences

Protomata is a machine learning suite for the inference of *automata* characterizing (functional) families of proteins from available sequences. Based on a new kind of alignment said partial and local, it learns precise characterizations of the families – beyond the scope of classical sequence patterns such as PSSM, Profile HMM, or Prosite Patterns – allowing to predict new family members with a high specificity.

Protomata gives access to the three main modules as stand-alone programs, which are also integrated in a single workflow *protomata-learner*:

- **Paloma** builds partial local multiple alignments;
- **Protobuild** infers automata from these alignements;
- **Protomatch and Protoalign** scan, parse and align new sequences based on the automata infered previously. This module was improved in 2016 by embedding new options to score the sequences with respect to all accepting paths (Forward score) in addition to the scoring module based on the best path (Viterbi score). More generally, we have worked on the efficiency of the automata's weighting scheme based on the state-of-the-art schemes used for profile HMMs.

The suite is completed by many tools to handle or visualize data and can be used online via a [web interface].

6.4.6. Logol - Complex pattern modelling and matching

The **Logol** toolbox is a swiss-army-knife for pattern matching on DNA/RNA/Protein sequences, using a high-level grammatical formalism to permit a large expressivity for patterns [54]. A Logol pattern consists in a complex combination of motifs (such as degenerated strings) and structures (such as imperfect stem-loop ou repeats). Compared to other specialized pattern matching tools, some of the Logol key features are the possibilities to divide a pattern description into several sub-patterns, to enable the use of ambiguous models or to permit the inclusion of negative conditions in a pattern definition. Possible fields of application are the detection of mutated binding sites [32] or stem-loop identification (e.g. in CRISPR [0] [10]) [web page].

- The **Graphical designer** allows a user to iteratively build a complex pattern based on basic graphical patterns. The associated grammar file is an export of the graphical designer. In 2015, the efficiency of the tool was improved by slight evolutions of the underlying grammar.
- The **LogolMatch** parser takes as input a biological (nucleic or amino acid) sequence and a grammar file (i.e. a pattern). It combines a grammar analyzer, a sequence analyzer and a prolog Library. It returns a file containing all the occurrences of the pattern in the sequence with their parsing details.
- Full genome analysis, and connection to biological databases have been made available recently.

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

<p align="center" style="color:red">FLUMINANCE Project-Team</p>

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 Memin
- Contact: Etienne Memin
- URL: http://fluid.irisa.fr/index.html

5.2. 3DLayeredMotion

Estimation of 3D interconnected layered atmospheric motion fields

FUNCTIONAL DESCRIPTION

This software extends the previous 2D version. It allows (for the first time to our knowledge) the recovery of 3D wind fields from satellite image sequences. As with the previous techniques, the atmosphere is decomposed into a stack of pressure layers. The estimation relies also on pressure data and classification clouds maps and top of clouds pressure maps. In order to recover the 3D missing velocity information, physical knowledge on 3D mass exchanges between layers has been introduced in the data model. The corresponding data model appears to be a generalization of the previous data model constructed from a vertical integration of the continuity equation.

- Contact: Etienne Memin
- URL: http://fluid.irisa.fr

5.3. DenseMotion

Estimation of 2D dense motion fields

FUNCTIONAL DESCRIPTION

This code allows the computation from two consecutive images of a dense motion field. The estimator is expressed as a global energy function minimization. The code enables the choice of different data models and different regularization functionals depending on the targeted application. Generic motion estimators for video sequences or fluid flows dedicated estimators can be set up. This software allows in addition the users to specify additional correlation based matching measurements. It enables also the inclusion of a temporal smoothing prior relying on a velocity vorticity formulation of the Navier-Stoke equation for Fluid motion analysis applications.

- Participant: Etienne Memin
- Contact: Etienne Memin
- URL: http://fluid.irisa.fr/index.html

5.4. Low-Order-Motion

Estimation of low order representation of fluid motion
FUNCTIONAL DESCRIPTION

This code enables the estimation of a low order representation of a fluid motion field from two consecutive images.The fluid motion representation is obtained using a discretization of the vorticity and divergence maps through regularized Dirac measure. The irrotational and solenoidal components of the motion fields are expressed as linear combinations of basis functions obtained through the Biot-Savart law. The coefficient values and the basis function parameters are formalized as the minimizer of a functional relying on an intensity variation model obtained from an integrated version of the mass conservation principle of fluid mechanics.

- Participants: Etienne Memin and Anne Cuzol
- Contact: Etienne Memin
- URL: http://fluid.irisa.fr

5.5. TYPHOON

GPU implementation of wavelet based motion estimator for Lidar data. This code is developed 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 Derian, Christopher Mauzey and Etienne Memin
- Partner: CSU Chico
- Contact: Etienne Memin
- URL: http://phys.csuchico.edu/lidar/typhoon/

5.6. GRT3D

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.

- Participants: Yvan Crenner, Jocelyne Erhel
- Partner: ANDRA
- Contact: Jocelyne Erhel
- URL: http://www.irisa.fr/sage/recherche/chemistry.html

5.7. H2OLab

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

The software platform contains a database which is interfaced through the web portal H2OWeb. It contains also software modules which can be used through the interface H2OGuilde. The platform H2OLab is an essential tool for the dissemination of scientific results. Currently, software and database are shared by the partners of the h2mno4 project.
FUNCTIONAL DESCRIPTION

The software platform H2OLab is devoted to stochastic simulations of groundwater flow and contaminant transport in highly heterogeneous porous and fractured geological media.

-Modeling and numerical simulation of aquifers -Porous and fractured heterogeneous media -Flow with mixed finite elements -Solute transport with a Lagrangian method -Stochastic modeling for data uncertainty.

- Participants: Jean-Raynald De Dreuzy, Jocelyne Erhel
- Partners: Université de Rennes 1 - CNRS - Université de Lyon - Université de Poitiers
- Contact: Jocelyne Erhel
- URL: http://h2olab.inria.fr/

5.8. PALMTREE

FUNCTIONAL DESCRIPTION

We present an easy-to-use package for the parallelization of Lagrangian methods for partial differential equations. In addition to the reduction of computation time, the code aims at satisfying three properties:

simplicity: the user just has to add the algorithm governing the behaviour of the particles. portability: the possibility to use the package with any compiler and OS. action-replay: the ability of the package to replay a selected batch of particles.

The last property allows the user to replay and capture the whole sample path for selected particles of a batch. This feature is very useful for debugging and catching some relevant information.

- Participants: Lionel Lenotre
- Contact: Jocelyne Erhel

GENSCALE Project-Team

6. New Software and Platforms

6.1. AskOmics

KEYWORDS: RDF - SPARQL - Querying - Graph
FUNCTIONAL DESCRIPTION

AskOmics allows to load heterogeneous bioinformatics data (formatted as tabular files) into a Triple Store system using a user-friendly web interface. AskOmics also provides an intuitive graph-based user interface supporting the creation of complex queries that currently require hours of manual searches across tens of spreadsheet files. The elements of interest selected in the graph are then automatically converted into a SPARQL query that is executed on the users' data.

- Authors: Charles Bettembourg, Yvanne Chaussin, Anthony Bretaudeau, Olivier Filangi, Fabrice Legeai and Olivier Dameron
- Partners: CNRS - INRA - Université de Rennes 1
- Contact: Fabrice Legeai
- URL: https://github.com/askomics/askomics

6.2. BBhash

Basic binary representation of successive hash
KEYWORDS: C++ - Indexation - Data structures
FUNCTIONAL DESCRIPTION

BBHash is a simple library for building minimal perfect hash function. Given a set of N input keys, it will compute a bijective function that will associate to each key an integer between 1 and N. This then allows to create an indexed array that will hold some data for each key. It is designed to handle large scale datasets (hundred billion and more elements). The function itself is just a little bit larger than other state-of-the-art libraries, it takes approximately 3 bits / elements (compared to 2.62 bits/elem for the emphf lib), but construction is faster and does not require additional memory.

- Participants: Guillaume Rizk, Pierre Peterlongo, Rayan Chikhi and Antoine Limasset
- Contact: Guillaume Rizk
- URL: https://github.com/rizkg/BBHash

6.3. BCALM 2

KEYWORDS: Bioinformatics - NGS - Genomics - Metagenomics - De Bruijn graphs
SCIENTIFIC DESCRIPTION

BCALM 2 is a bioinformatics tool for constructing the compacted de Bruijn graph from sequencing data. It is a parallel algorithm that distributes the input based on a minimizer hashing technique, allowing for good balance of memory usage throughout its execution. It is able to compact very large datasets, such as spruce or pine genome raw reads in less than 2 days and 40 GB of memory on a single machine.
FUNCTIONAL DESCRIPTION

BCALM 2 is an open-source tool for dealing with DNA sequencing data. It constructs a compacted representation of the de Bruijn graph. Such a graph is useful for many types of analyses, i.e. de novo assembly, de novo variant detection, transcriptomics, etc. The software is written in C++ and makes extensive use of the GATB library.

- Participants: Rayan Chikhi, Antoine Limasset and Paul Medvedev
- Contact: Rayan Chikhi
- URL: https://github.com/GATB/bcalm

6.4. BGREAT

De bruijn graph read alignment tool
KEYWORDS: Short reads - Genome assembling
FUNCTIONAL DESCRIPTION

Mapping genomic extracts (reads) on genomic references is a central and necessary task in most genomic studies. But reference sequences are mainly extracted from assembly graphs through an inexact process that both creates chimeras and losses biological pieces of information. This motivates the need of mapping sequences on references represented by graphs. BGREAT is conceived to map reads on de Bruijn graph, a widely used graph in genome assembly.

- Participants: Pierre Peterlongo and Antoine Limasset
- Contact: Pierre Peterlongo
- URL: https://github.com/Malfoy/BGREAT

6.5. GATB-Core

Genome Assembly and Analysis Tool Box
KEYWORDS: Bioinformatics - NGS - Genomics - Genome assembling
FUNCTIONAL DESCRIPTION

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

- Participants: Dominique Lavenier, Guillaume Rizk, Pierre Peterlongo, Charles Deltel, Patrick Durand and Claire Lemaitre
- Contact: Dominique Lavenier
- URL: http://gatb.inria.fr/

6.6. GATB-Core Tutorial

Online GATB-Core tutorial
KEYWORD: Bioinformatics
FUNCTIONAL DESCRIPTION

"GATB-Core tutorial" is an interactive learning tool that aims at learning software development relying on the bioinformatics toolkit GATB-Core without the need of installing it, its dependencies and a C++ compiler. The tutorial relies on a client-server system. The client is simply a web browser running a full-featured C++ code editor. In turns, it is embedded in templates for the purpose of displaying various lessons. The server side is a Linux-based VM capable of compiling and running "online" any C++ code snippets using GATB-Core. That VM is deployed on Inria's AllGo SaaS platform.

- Participant: Patrick Durand
- Contact: Patrick Durand
- URL: http://gatb-core.gforge.inria.fr/training/

6.7. MindTheGap

KEYWORDS: Bioinformatics - NGS - Genome assembling
FUNCTIONAL DESCRIPTION

MindTheGap performs detection and assembly of DNA insertion variants in NGS read datasets with respect to a reference genome. It is designed to call insertions of any size, whether they are novel or duplicated, homozygous or heterozygous in the donor genome. The main algorithmic improvement of version 2.0.0 is to detect additionnal variants, such as SNPs and deletions. This feature improves the sensitivity of the insertion detection algorithm for insertions that are located near these other variants. Additionnally, 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.

- Participants: Claire Lemaitre and Guillaume Rizk
- Contact: Claire Lemaitre
- URL: https://gatb.inria.fr/software/mind-the-gap/

6.8. PLAST

Local alignment tool
KEYWORDS: Bioinformatics - Genomic sequence - Genomics
FUNCTIONAL DESCRIPTION

PLAST is a parallel alignment search tool for comparing large protein banks.

Sequence similarity searching is an important and challenging task in molecular biology and next-generation sequencing should further strengthen the need for faster algorithms to process such huge amount of data. At the same time, the internal architecture of current microprocessors is tending towards more parallelism, leading to the use of chips with two, four and more cores integrated on the same die. The main purpose of this work was to design an effective algorithm to fit with the parallel capabilities of modern microprocessors. A parallel algorithm for comparing large genomic banks and targeting middle-range computers has been developed and implemented in PLAST software. The algorithm exploits two key parallel features of existing and future microprocessors: the SIMD programming model (SSE instruction set) and the multithreading concept (multicore). Compared to multithreaded BLAST software, tests performed on an 8-processor server have shown speedup ranging from 3 to 6 with a similar level of accuracy.

- Participants: Dominique Lavenier, Erwan Drezen and Van Hoa Nguyen
- Contact: Dominique Lavenier
- URL: https://team.inria.fr/genscale/high-throughput-sequence-analysis/plast-intensive-sequence-comparison/

6.9. Simka

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

Simka is a comparative metagenomics method dedicated to NGS datasets. It computes a large collection of distances classically used in ecology to compare communities by approximating species counts by k-mer counts. The method scales to a large number of datasets thanks to an efficient and parallel kmer-counting strategy that processes all datasets simultaneoulsy.

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

6.10. short read connector

KEYWORDS: Bioinformatics - Genomics - Metagenomics
SCIENTIFIC DESCRIPTION

Short read connector enables the comparisons of two read sets B and Q. For each read from Q it provides either:

The number of occurrences of each k-mers of the read in the set B (SRC_counter) or A list of reads from B that share enough k-mers with the tested read from B (SRC_linker)
FUNCTIONAL DESCRIPTION

This tool uses a data structure (BBHASH) adapted to the indexing of big data. Short Read Connector works on reads, which are sequencing data from high-throughput sequencers. Once the data is indexed, short read connector makes it possible either to find the similar reads in a dataset or to simply retrieve the approximate number of these similar reads.

- Participants: Pierre Peterlongo, Camille Marchet and Antoine Limasset
- Partner: UPMC
- Contact: Pierre Peterlongo
- URL: https://github.com/pierrepeterlongo/short_read_connector

SERPICO Project-Team

6. New Software and Platforms

6.1. TMA-Lib

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The TMA-LIB enables to jointly detect (adaptive wavelet transform), segment (parametric active contours) and restore (artifact correction and deconvolution) TMA (Tissue MicroArrays) images.

- **Participants**: Hoai Nam Nguyen, Charles Kervrann.
- **Partner:** INNOPSYS Company.
- **Contact:** Charles Kervrann.
- **Languages:** C/C++, Matlab.

6.2. QuantEv

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The QUANTEv software is dedicated to the analysis of the spatial distribution of intracellular events represented by any static or dynamical descriptor (e.g. detected points, segmented regions, trajectories...), provided that the descriptors are associated with spatial coordinates. QuantEv first computes 3D histograms of descriptors in a cylindrical coordinate system with computational cell shape normalization, enabling comparisons between cells of different shape. Densities are obtained via adaptive kernel density estimation, and we use the Circular Earth Mover's Distance to measure the dissimilarity between densities associated to different experimental conditions. A statistical analysis on these distances reliably takes into account the biological variability over replicated experiments.

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

6.3. 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:** [12]

6.4. ATLAS

KEYWORD: Biomedical imaging

FUNCTIONAL DESCRIPTION: The ATLAS software enables to detect spots in 2D fluorescence images. The spot size is automatically selected and the detection threshold adapts to the local image 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:** [1]

6.5. 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 shape-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/).

6.6. Motion2D

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

- **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/).

6.7. 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) [5]. 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:** [5]

6.8. 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++.

6.9. 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.

- **Participants:** Denis Chrétien, Charles Kervrann, Sophie Blestel.
- **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/).

6.10. 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/).

6.11. Platforms

6.11.1. Mobyle@Serpico plateform and software distribution

The objective is to disseminate the distribution of SERPICO image processing software for biologists:

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: QUANTEV, C-CRAFT[12], ATLAS[1], HOTSPOTDETECTION[56], HULLKGROUND[45], KLTRACKER[55], MOTION2D[54], MS-DETECT[47], ND-SAFIR[5], OPTICALFLOW and FLUX ESTIMATION [12]. The web interface makes our image processing methods available for biologists at Mobyle@SERPICO (http://mobyle-serpico.rennes.inria.fr/cgi-bin/portal.py#welcome) without any installation or configuration on their own. The size of submitted images is limited to 200 MegaBytes per user and all the results are kept 15 days. The web portal and calculations run on a server with 2 CPU x 8 cores, 64 GigaBytes of RAM (500 MegaBytes for each user / Data is saved for 3 months).

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

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 [5], HULLKGROUND [45], MOTION2D [54], HOTSPOTDETECTION [56], STLAS [1]. The C-CRAFT algorithm [12] 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-developed a commercial database system (CID iManage/Strand Avadis company). The database can be searched via metadata 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.

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

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.
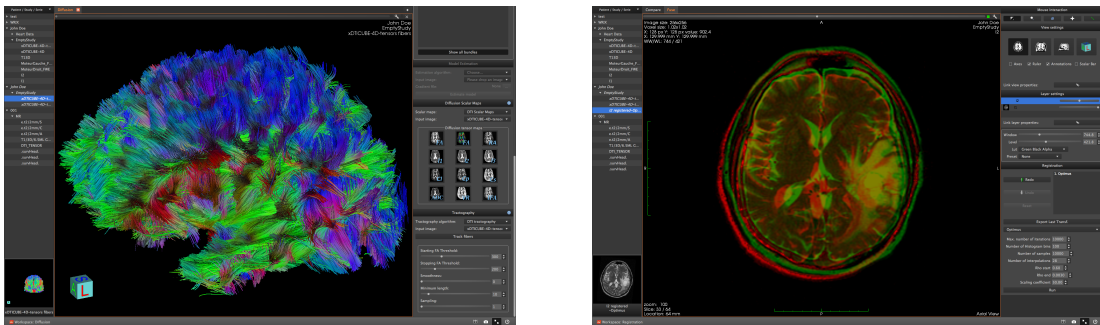

Figure 2. The medInria software platform: Tractography overlapped with 3D image (left), and Fused view of registered images (right).

FUNCTIONAL DESCRIPTION: MedInria is a free software platform dedicated to medical data visualization and processing as illustrated in Fig. 2 .

- Participants: Olivier Commowick and Rene-Paul Debroize

- 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. Shanoir

SHAring NeurOImaging Resources

KEYWORDS: Shanoir - Webservices - Data base - Biology - Health - DICOM - Neuroimaging - Medical imaging - PACS - Nifti - Data Sharing - Web Application

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 Fig. 3).

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 research studies where of involved patients have examinations which 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 files 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 an new measures can be added in order to meet specific project needs, by use of intuitive graphical interfaces.

Using cross-data navigation and advanced search criteria, the users can quickly point to a subset of data 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.
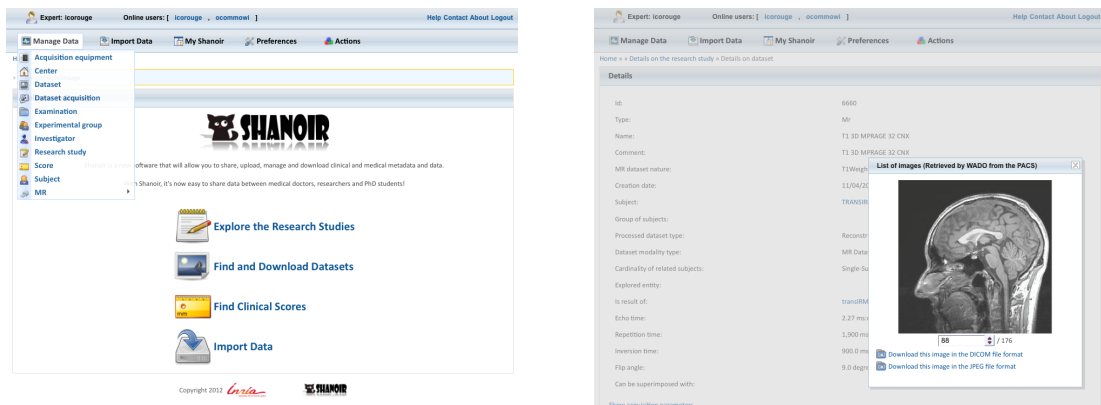
Figure 3. The SHANOIR software is a web application to share, archive, search and visualize neuroimaging data.

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, Christian Barillot, Anthony Baire, Mathieu Simon, Julien Louis, Isabelle Corouge, Élise Bannier, Aneta Morawin and Yao Chi
- Partners: CNRS - INSERM - Université de Rennes 1
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.520021.003.S.A.2008.000.31230 (2014/08/20)

6.4. 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.
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 and Florent Leray
- Contact: Christian Barillot
- URL: http://qtshanoir.gforge.inria.fr
- APP number: IDDN.FR.001.130017.000.S.A.2012.000.31230 (2012/02/08)

6.5. 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 Fig. 4 . 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.
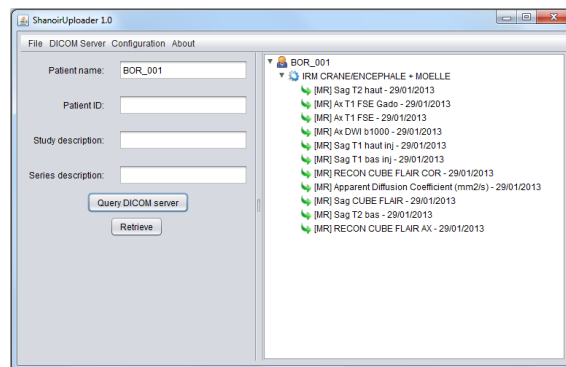

Figure 4. The ShanoirUploader software is a desktop application designed to interact with a PACS to query and retrieve the data stored on any PACS.

- Participants: Michael Kain, Inès Fakhfakh and Christian Barillot
- Contact: Christian Barillot
- URL: http://shanoir.gforge.inria.fr
- APP number: IDDN.FR.001.380026.000.S.P.2015.000.31230 (2015/09/11)

6.6. 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 as illustrated in Fig. 5 . For this the Shanoir SOAP web-services are called. 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 corresponding viewer, the user already has to have installed on his device.
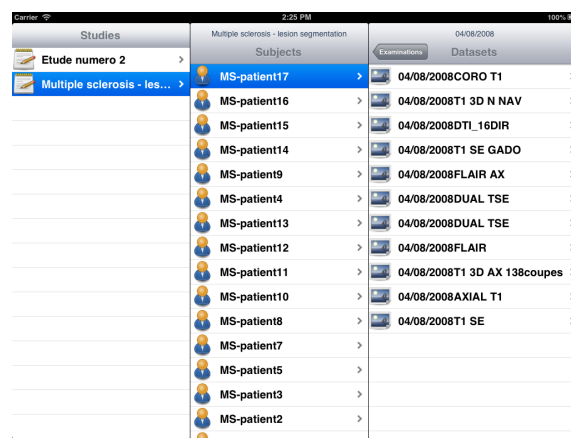

Figure 5. The iShanoir interface, showing the browsing tabs within the research studies stored in the Shanoir database.

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

6.7. autoMRI

KEYWORDS: FMRI - MRI - ASL - FASL - SPM - Automation

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

FUNCTIONAL DESCRIPTION: 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).
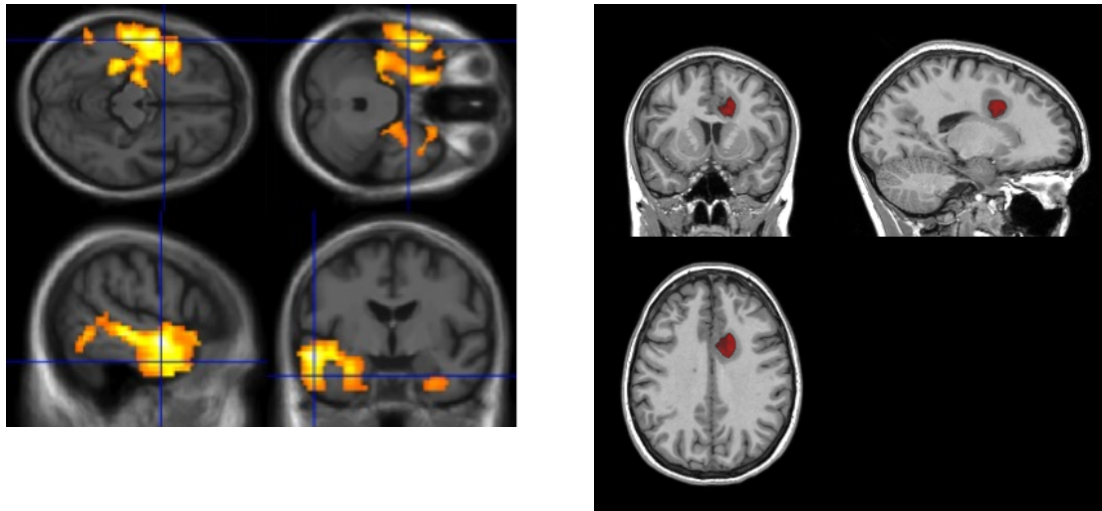

Figure 6. Illustrations of results obtained with autoMRI: Conjunction map showing areas of hypoperfusion and hypometabolism in semantic dementia (left) and detection of relaxometry defect in an MS patient (right).

- Participants: Isabelle Corouge, Quentin Duché, Cédric Meurée, Pierre Maurel and Élise Bannier.
- Contact: Isabelle Corouge
- URL: http://www.irisa.fr/visages/
- APP number: Part in IDDN.FR.001.130017.000.S.A.2012.000.31230

6.8. Integration of EEG and fMRI

KEYWORDS: medical imaging - EEG - fMRI

FUNCTIONAL DESCRIPTION: 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).

- Participants: Marsel Mano, Lorraine Perronnet, Anatole Lecyuer, Christian Barillot.
- Contact: Marsel Mano
- International Patent Number: PCT/EP2016/1652279

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 [0]. This platform has been supported under the "Contrat de Projets Etat-Région" (Christian Barillot is the PI) and has received a total amount of 4.01 M€ for the period 2007–2014. European (FEDER), National (through Ministry of research, Inria, Inserm and ANR) and local councils (Brittany Region, Ille et Vilaine, and Rennes Metropole) have joined their effort to support this operation for a total amount of 4 010 k€ (600 k€ for the infrastructures, 2 850 k€ for the equipments and 560 k€ for the functioning). This application was set up through the Regional PIMATGI initiative coordinated by INSERM in Brittany (C. Roux). The 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 U650 - LaTIM, Dir. Ch. Roux, Brest), and TherA-Image as a platform dedicated to image guided mini-invasive surgery and therapy especially in the domain of cardio-vascular diseases (U642 -LTSI, Dir. L. Senhadji, Rennes).

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

In this context, a 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.

In 2016, VisAGeS has been awarded by IBISA as a "Plateforme d'excellence".

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

<p style="text-align: center; color: red;">**ASAP Project-Team**</p>

5. New Software and Platforms

5.1. Asapknn (MediEgo)

KEYWORDS: Widget web - Social network - Recommendation
FUNCTIONAL DESCRIPTION

Asapknn (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, Sebastien Campion, Rachid Guerraoui, Davide Frey and Arnaud Jegou
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Sebastien Campion

5.2. 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: Raziel Carvajal Gomez

5.3. 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 P2P-AllYours.

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

5.4. 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/

5.5. HEAP

Heterogeneity-aware gossip protocol

FUNCTIONAL DESCRIPTION

A video streaming platform based on HEAP. The platform is particularly suited for environment characterized by heterogeneous bandwidth capabilities such as those comprising ADSL edge nodes. HEAP is, in fact, able to dynamically leverage the most capable nodes and increase their contribution to the protocol, while decreasing by the same proportion that of less capable nodes. During the last few months, we have integrated HEAP with the ability to dynamically measure the available bandwidth of nodes, thereby making it independent of the input of the user.

- Participants: Davide Frey, Arnaud Jegou, Anne-Marie Kermarrec, Vivien Quema, Maxime Monod and Rachid Guerraoui
- Contact: Davide Frey

5.6. HyRec

Hybrid Recommender System

FUNCTIONAL DESCRIPTION

The motivation of this work is to explore solutions that could in some sense democratize personalization by making it accessible to any content provider company without generating huge investments. HyRec implements a user-based collaborative filtering scheme and offloads CPU-intensive recommendation tasks to front-end client browsers, while retaining storage and orchestration tasks within back-end servers. HyRec seeks to provide the scalability of p2p approaches without forcing content providers to give up the control of the system.

- Participants: Antoine Boutet, Davide Frey, Anne Marie Kermarrec, Arnaud Jegou and Rachid Guerraoui
- Contact: Davide Frey

5.7. WebGC

Web-based Gossip Communication

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

5.8. 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

5.9. 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, P2P-AllYours, and Behave.

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

5.10. 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 P2P-AllYours.

- 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

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ASCOLA Project-Team

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6. New Software and Platforms

6.1. 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 Yousri Kouki
- Contact: Thomas Ledoux
- URL: http://www.emn.fr/z-info/csla/

6.2. CSQL

Cryptographic Composition for Query Language

SCIENTIFIC DESCRIPTION

C2QL is a compositional language of security techniques for information privacy in the cloud. A cloud service can use security techniques to ensure information privacy. These techniques protect privacy by converting the client's personal data into unintelligible text. But they also cause the loss of some functionalities of the service. As a solution, CSQL permits to compose security techniques to ensure information privacy without the loss of functionalities. But, the composition makes the writing of programs more intricate. To help the programmer, C2QL defines a query language for the definition of cloud services that enforces information privacy with the composition of security techniques. This language comes with a set of algebraic laws to, systematically, transform a local service without protection into its cloud equivalent that is protected by composition.

FUNCTIONAL DESCRIPTION

C2QL is implemented in Idris, a functional language of the Haskell family. The implementation harnesses the Idris dependant type system to ensure the correct composition of security mechanisms and provides a transformation of the implementation into a π-calculus. This transformation serves two purposes. First, it makes the distribution explicit, showing how a computation is distributed over SaaS, PaaS and client applications. Then, it helps defining an encoding into ProVerif to check that the service preserves the privacy of its clients.

- Participants: Ronan-Alexandre Cherrueau, Rémi Douence, Mario Südholt
- Contact: Ronan-Alexandre Cherrueau
- URL: https://github.com/rcherrueau/C2QL

6.3. EScala

SCIENTIFIC DESCRIPTION

EScala extends the idea of events as object members, as realized by C# events, with the possibility to define events declaratively by expressions over other events. The occurrences of an event can be defined by various set operations, such as union, intersection and difference, applied on the occurrences of other events. Events can be filtered by arbitrary conditions, the data attached to the events can be transformed by arbitrary functions. Event expressions make it possible to define events in terms of other events, at the lowest level relying on primitive events.

FUNCTIONAL DESCRIPTION

EScala is an extension of Scala programming language with support for events as attributes of objects. The support for events in EScala, combine the ideas of event-driven, aspect-oriented and functional-reactive programming.

- Participants: Jacques Noyé and Jurgen Van Ham
- Contact: Jurgen Van Ham
- URL: http://www.stg.tu-darmstadt.de/research/escala/index.en.jsp

6.4. JEScala

FUNCTIONAL DESCRIPTION

JEScala extends EScala with support for concurrent programming. Events can be declared as asynchronous so that their handling takes place concurrently. A new composition operator, the join operator, inspired by the join calculus, can also be used to synchronize the concurrent activities created by asynchronous events and communicate between them.

- Participants: Jurgen Van Ham and Jacques Noyé
- Contact: Jurgen Van Ham
- URL: http://www.stg.tu-darmstadt.de/research/jescala_menu/index.en.jsp

6.5. SimGrid

Scientific Instrument for the study of Large-Scale Distributed Systems
KEYWORDS: Large-scale Emulators - Grid Computing - Distributed Applications
FUNCTIONAL DESCRIPTION

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

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

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

- Participants: Frederic Suter, Martin Quinson, Arnaud Legrand, Takahiro Hirofuchi, Adrien Lebre, Jonathan Pastor, Mario Sudholt, Luka Stanisic, Augustin Degomme, Jean Marc Vincent, Florence Perronnin and Jonathan Rouzaud-Cornabas
- Partners: CNRS - ENS Rennes - Université de Nancy
- Contact: Martin Quinson
- URL: http://simgrid.gforge.inria.fr/

6.6. 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: Takahiro Hirofuchi, Adrien Lebre, Jonathan Pastor, Flavien Quesnel and Mario Sudholt
- Contact: Adrien Lebre
- URL: http://beyondtheclouds.github.io/VMPlaceS/

6.7. 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 Louet, Frederic Dumont and Jean-Marc Menaud
- Contact: Jean-Marc Menaud
- URL: http://www.btrcloud.org/btrCloud/index_EN.html

<p style="text-align:center;color:red;font-weight:bold">CIDRE Project-Team</p>

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 for a single node (Android and Linux kernel, JVM) and a set of nodes (monitoring of flows between linux machines).

FUNCTIONAL DESCRIPTION

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

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

6.2. ELVIS

Extensible Log VISualization

KEYWORDS: Visualization - Cybersecurity - Intrusion Detection Systems (IDS) - SIEM - Cyber attack - Forensics

SCIENTIFIC DESCRIPTION

The studies that were performed since 2012 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 2013 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.

FUNCTIONAL DESCRIPTION

ELVIS is a visualisation tool geared to system security which enables analysts to visually explore log files using relevant representations. The tool accepts many different types of log file and can easily be extended to accept new ones opportunistically. Thanks to its data typing mechanisms, it can automatically choose relevant representations depending on the type of data that the analyst wants to observe.

- Participant: Nicolas Prigent
- Partner: SUPELEC
- Contact: Nicolas Prigent
- URL: https://hal.inria.fr/hal-00875668

6.3. GEPETO

GEoPrivacy-Enhancing TOolkit
KEYWORDS: Cyber attack - 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: CNRS - Université de Rennes 1
- 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: SUPELEC
- Contact: Eric Totel
- URL: http://www.rennes.supelec.fr/ren/perso/etotel/GNG/index.html

6.5. GroddDroid

KEYWORDS: Android - Detection - Malware
FUNCTIONAL DESCRIPTION

GroddDroid

1- locates suspicious code in Android application

2-computes execution paths towards suspicious code

3- forces executions of suspicious code

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

6.6. Kharon platform

KEYWORDS: Android - Malware - Dynamic Analysis
FUNCTIONAL DESCRIPTION

This platform executes Android applications and computes a graph representing all the information flows that occurred in the operating system due to a malicious execution. It can then classify observed behavior as benign or malicious. Access to this platform is currently in physically controlled at the high security laboratory (LHS) of Rennes.

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

6.7. 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/

6.8. VEGAS

Visualizing, Exploring and Grouping AlertS
KEYWORDS: Security - Visualization - Cybersecurity - Intrusion Detection Systems (IDS) - SIEM
SCIENTIFIC DESCRIPTION

VEGAS explore the hypothesis that is is possible to offer to front-line security operators a visualization tool that allows the to perform a first informed triage of the alerts that were received from IDSes so as to group them and transmit them to security analysts in a relevant way.
FUNCTIONAL DESCRIPTION

VEGAS is a visualization tool that allows to easily identify, explore and group alerts generated by an IDS. This tool allows security operators to easily dispatch similar alerts to security analyst to help them study them more efficiently.

- Participants: Damien Cremilleux, Frédéric Majorczyk and Nicolas Prigent
- Partner: SUPELEC
- Contact: Damien Crémilleux

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DIONYSOS Project-Team

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6. New Software and Platforms

6.1. The Passive Test Tool (ttproto) and CoAP Testing Tool

`ttproto` is an experimental tool for implementing testing tools, for conformance and interoperability testing. It was first implemented to explore interesting features and concepts for the TTCN-3 standard. It was also used to implement a passive interoperability test suite we provided for the CoAP (Constrained Application Protocol) interoperability event held in Paris in March 2012. It is currently used for the purpose of developing testing tools (for interoperability and conformance testing) for the F-interop european project (see http://www.f-interop.eu/). This tool is implemented in `python3` and its design was influenced mainly by TTCN-3 (abstract model, templates, snapshots, behavior trees, communication ports, logging) and by Scapy (syntax, flexibility, customizability) Its purpose is to facilitate rapid prototyping and experimentation (rather than production use). We chose to maximize its modularity and readability rather than performances and real-time considerations.

- Participants: César Viho, Federico Sismondi
- Contact: César Viho, Federico Sismondi
- http://www.irisa.fr/tipi

6.2. T3DevKit and IPv6 testing tools

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).

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) provides an object oriented framework to manipulate TTCN-3 entities (values, ports, timers, external functions). T3DevKit offers an implementation of the TRI and TCI standard interfaces a default implementations for the system adapter (SA), platform adapter (PA), test management (TM), test logging (TL) and component handling (CH) modules and a default codec. Built-in scripts for the generation of executable test suite, which are tool-independent facilitate the distribution of test suite sources.

IPv6 test suites have been developed using the TTCN-3 environment. The full Abstract Test Suites are written in TTCN-3 and the source files for building the codecs and adapters with the help of T3DevKit.

- Participants: César Viho, Federico Sismondi
- Contact: Federico Sismondi

6.3. 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 internal 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

KEYWORDS: Software line product - Configators - Customisation
SCIENTIFIC DESCRIPTION

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

FUNCTIONAL DESCRIPTION

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

- Participants: Mathieu Acher, Guillaume Becan, Olivier Barais

- Contact: Mathieu Acher

- URL: http://familiar-project.github.com

6.2. GEMOC Studio

KEYWORDS: Model-driven engineering - Meta model - MDE - DSL - Model-driven software engineering - Dedicated langage - Language workbench - Meta-modelisation - Modeling language - Meta-modeling
SCIENTIFIC DESCRIPTION

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

- Melange, a tool-supported meta-language to modularly define executable modeling languages with execution functions and data, and to extend (EMF-based) existing modeling languages.

- MoCCML, a tool-supported meta-language dedicated to the specification of a Model of Concurrency and Communication (MoCC) and its mapping to a specific abstract syntax and associated execution functions of a modeling language.

- GEL, a tool-supported meta-language dedicated to the specification of the protocol between the execution functions and the MoCC to support the feedback of the data as well as the callback of other expected execution functions.

- BCOoL, a tool-supported meta-language dedicated to the specification of language coordination patterns to automatically coordinates the execution of, possibly heterogeneous, models.

- Sirius Animator, an extension to the model editor designer Sirius to create graphical animators for executable modeling languages.

FUNCTIONAL DESCRIPTION

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

- Participants: Benoit Combemale, Dorian Leroy, Thomas Degueule, Erwan Bousse, Fabien Coulon and Didier Vojtisek
- Contact: Benoit Combemale
- URL: http://gemoc.org

6.3. Kevoree

Kevoree Core

KEYWORDS: Cloud - Deployment - Embedded - Domotique - Heterogeneity - Software Components - Architecture - Software component - Dynamic adaptation - M2M - Dynamic deployment

SCIENTIFIC DESCRIPTION

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

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

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

Main competitors:

the Fractal/Frascati eco-system (http://frascati.ow2.org).

SpringSource Dynamic Module (http://spring.io/)

GCM-Proactive (http://proactive.inria.fr/)

OSGi (http://www.osgi.org)

Chef

Vagran (http://vagrantup.com/)

Main innovative features:

distributed models@runtime platform (with a distributed reflection model and an extensible models@runtime dissemination set of strategies).

Support for heterogeneous node type (from Cyber Physical System with few resources until cloud computing infrastructure).

Fully automated provisioning model to correctly deploy software modules and their dependencies.

Communication and concurrency access between software modules expressed at the model level (not in the module implementation).

Impact:

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

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

FUNCTIONAL DESCRIPTION

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

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

6.4. Melange

KEYWORDS: Model-driven engineering - Meta model - MDE - DSL - Model-driven software engineering - Dedicated langage - Language workbench - Meta-modelisation - Modeling language - Meta-modeling
SCIENTIFIC DESCRIPTION

Melange is a follow-up of the executable metamodeling language Kermeta, which provides a tool-supported dedicated meta-language to safely assemble language modules, customize them and produce new DSMLs. Melange provides specific constructs to assemble together various abstract syntax and operational semantics artifacts into a DSML. DSMLs can then be used as first class entities to be reused, extended, restricted or adapted into other DSMLs. Melange relies on a particular model-oriented type system that provides model polymorphism and language substitutability, i.e. the possibility to manipulate a model through different interfaces and to define generic transformations that can be invoked on models written using different DSLs. Newly produced DSMLs are correct by construction, ready for production (i.e., the result can be deployed and used as-is), and reusable in a new assembly.

Melange is tightly integrated with the Eclipse Modeling Framework ecosystem and relies on the meta-language Ecore for the definition of the abstract syntax of DSLs. Executable meta-modeling is supported by weaving operational semantics defined with Xtend. Designers can thus easily design an interpreter for their DSL in a non-intrusive way. Melange is bundled as a set of Eclipse plug-ins.
FUNCTIONAL DESCRIPTION

Melange is a language workbench which helps language engineers to mashup their various language concerns as language design choices, to manage their variability, and support their reuse. It provides a modular and reusable approach for customizing, assembling and integrating DSMLs specifications and implementations.

- Participants: Thomas Degueule, Benoit Combemale, Dorian Leroy, Erwan Bousse, Didier Vojtisek, Fabien Coulon, Jean-Marc Jezequel, Arnaud Blouin, Olivier Barais and David Mendez Acuna
- Contact: Benoit Combemale
- URL: http://melange-lang.org

6.5. Opencompare

KEYWORD: Software Product Line, Variability, MDE, Meta model, Configuration
FUNCTIONAL DESCRIPTION

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

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

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

6.6. amiunique

KEYWORDS: Privacy - Browser fingerprinting
SCIENTIFIC DESCRIPTION

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

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

Similar sites: Panopticlick https://panopticlick.eff.org/ BrowserSpy http://browserspy.dk/http://noc.to/ Main innovative features: canvas fingerprinting WebGL fingerprinting advanced JS features (platform, DNT, etc.)

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

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

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

<p style="text-align:center">**KERDATA Project-Team**</p>

6. New Software and Platforms

6.1. Týr

Title: Týr: Blob Storage Meets Built-In Transactions.

Keywords: Big Data; Transactions; Tyr; BlobSeer.

Scientific Description: Týr [25] is the first blob storage system to provide built-in, multi-blob transactions, while retaining sequential consistency and high throughput under heavy access concurrency.

Functional Description: Týr offers fine-grained random write access to data and in-place atomic operations. Large-scale experiments on Microsoft Azure with a production application from CERN LHC show Týr throughput outperforms state-of-the-art solutions by more than 75%. Týr leverages the approaches developed within BlobSeer, the reference data management system for large distributed blobs, developed over the past years in KerData.

Contact data:

Participants: Pierre Matri, Alexandru Costan and Gabriel Antoniu.

Partners: INSA Rennes, Universidad Politécnica de Madrid.

Contact: Gabriel Antoniu.

URL: http://tyr.io/.

6.2. Damaris

Title: Damaris: I/O and data management for large-scale, MPI-based HPC simulations.

Keywords: I/O; HPC; Data management; Visualization; Big Data; Exascale.

Scientific Description: Damaris is a middleware for multicore SMP nodes enabling them to efficiently handle data transfers for storage and visualization. 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 JLESC. The current version 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.

Damaris has been preliminarily evaluated at NCSA (Urbana-Champaign) with the CM1 tornado simulation code. CM1 is one of the target applications of the Blue Waters supercomputer in production at NCSA/UIUC (USA), in the framework of the JLESC. Damaris now has external users, including (to our knowledge) visualization specialists from NCSA, Big Data experts from the HDF group, 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, CROCO). Works are in progress to evaluate it in the context of several other simulation codes including HACC (cosmology) and GTC (fusion).

Damaris is the object of a *Technical Development Action* (ADT) supported by Inria.

Functional Description: Damaris targets large-scale HPC simulations: in situ data analysis by some dedicated cores of the simulation platform; asynchronous and fast data transfer from HPC simulations to Damaris; semantic-aware dataset processing through Damaris plug-ins.

Contact data:

Participants: Matthieu Dorier (ANL), Lokman Rahmani, Gabriel Antoniu, Orçun Yildiz, Hadi Salimi and Luc Bougé.

Partners: ENS Rennes, Argonne National Laboratory.

Contact: Gabriel Antoniu.

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

6.3. Other software

6.3.1. JetStream

Title: JetStream: Enabling High-Performance Event Streaming across Cloud Data-Centers.

Keywords: Big Data, streaming, data transfer, multisite cloud.

Scientific Description.   JetStream is a middleware solution for batch-based, high-performance streaming across cloud data centers. JetStream implements a set of context-aware strategies to optimize batch-based streaming, being able to self-adapt to changing conditions.

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

Participants: Ovidiu-Cristian Marcu, Alexandru Costan, Gabriel Antoniu.

Contact: Alexandru Costan.

6.3.2. Omnisc'IO

Title: Omnisc'IO: a Grammar-Based Approach to Spatial and Temporal I/O Patterns Prediction.

Keywords: HPC, Input-Output, Prediction, Grammar.

Scientific Description.   Omnisc'IO is a library that aims to be integrated into I/O middleware.

Functional Description.   It traces I/O operations, models the stream of such operations using grammar-inference techniques, and predicts when new I/O operations will be performed, as well as where and how much data will be written.

Participants: Matthieu Dorier (ANL), Gabriel Antoniu, Shadi Ibrahim.

Contact: Gabriel Antoniu.

6.3.3. OverFlow

Title: OverFlow: Workflow Data Management as a Service for Multi-Site Applications.

Keywords: Small data; workflow; multi-site cloud.

Scientific Description.   OverFlow is a uniform data management system for scientific workflows running across geographically distributed sites, aiming to reap economic benefits from this geo-diversity. The software is environment-aware, as it monitors and models the global cloud infrastructure, offering high and predictable performance for transfer cost and time, within and across sites.

Functional Description.   OverFlow proposes a set of pluggable services, grouped in a data-scientist cloud kit. They provide the applications with the possibility to monitor the underlying infrastructure, to exploit smart data compression, deduplication and geo-replication, to evaluate data management costs, to set a tradeoff between money and time, and optimize the transfer strategy accordingly. Currently, OverFlow is used for data transfers by the Microsoft Research ATLE Munich team as well as for synthetic benchmarks at the Politehnica University of Bucharest.

Participants: Paul Le Noac'h, Ovidiu-Cristian Marcu, Alexandru Costan and Gabriel Antoniu.

Contact: Alexandru Costan.

6.3.4. iHadoop

Title: iHadoop: A Hadoop Simulator Developed In Java on Top of SimGrid.

Keywords: Simulation, Map-Reduce, Hadoop, SimGrid.

Scientific Description.   iHadoop is a Hadoop simulator developed in Java on top of SimGrid. It simulates the behavior of Hadoop and therefore accurately predicts the performance of Hadoop in normal scenarios and under failures. iHadoop is extended to (1) simulate the execution and predict the performance of multiple Map-Reduce applications; (2) simulate the execution of Map-Reduce applications under various data distributions and data skew models.

Functional Description.   iHadoop is an internal software prototype, which was initially developed to validate our idea regarding the behavior of Hadoop under failures. iHadoop has preliminarily evaluated within our group and it has shown very high accuracy to predict the execution time of a Map-Reduce applications. We intend to integrate iHadoop within the SimGrid distribution and make it available to the SimGrid community.

Participants: Shadi Ibrahim and Tien-Dat Phan.

Contact: Shadi Ibrahim.

MYRIADS Project-Team

6. New Software and Platforms

6.1. ConPaaS

KEYWORDS: Cloud computing - PaaS

SCIENTIFIC DESCRIPTION ConPaaS [60] 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.

FUNCTIONAL DESCRIPTION

ConPaaS 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.

- Participants: Guillaume Pierre, Eliya Buyukkaya, Ancuta Iordache, Morteza Neishaboori, Dzenan Softic, Genc Tato and Teodor Crivat
- Contact: Guillaume Pierre
- URL: http://www.conpaas.eu/

6.2. GinFlow

KEYWORDS: Workflow - Distributed computing - Distributed - Distributed Applications - Framework

FUNCTIONAL DESCRIPTION GinFlow decentralizes the coordination of the execution of workflow-based applications. GinFlow relyies on an architecture where multiple service agents (SA) coordinate each others through a shared space containing the workflow description and current status. GinFlow allows the user to define several variants of a workflow and to switch from one to the other during run time.

- Participants: Matthieu Simonin, Cédric Tedeschi, Hector Fernandez, Javier Rojas Balderrama and Thierry Priol
- Partner: Université de Rennes 1
- Contact: Cédric Tedeschi
- URL: http://ginflow.inria.fr

6.3. Merkat

KEYWORDS: Resource management - Cloud - Elastic scaling - Market mechanisms - Service Level Objectives - HPC

FUNCTIONAL DESCRIPTION

Merkat is a platform that allows users of an organization to automatically manage and scale their applications while maximizing the infrastructure's utilization [12]. Merkat is generic and extensible, allowing users to automate the application deployment and management process. Users have the flexibility to control how many resources are allocated to their applications and to define their own resource demand adaptation policies. Merkat applies an unique approach to multiplex the infrastructure capacity between the applications, by implementing a proportional-share market and allowing applications to adapt autonomously to resource price and their given performance objectives. The price of the acquired resources acts as a control mechanism to ensure that resources are distributed to applications according to the user's value for them. Merkat was evaluated on Grid'5000 with several scientific applications.

- Participants: Stefania Costache, Christine Morin and Nikos Parlavantzas
- Contact: Nikos Parlavantzas
- URL: http://www.irisa.fr/myriads/software/Merkat/

6.4. Meryn

KEYWORDS: Resource management - PaaS - Cloud - Market mechanisms - Service Level Agreements
FUNCTIONAL DESCRIPTION

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. Meryn builds on the Snooze VM manager, and currently supports batch and MapReduce applications.

- Participants: Nikos Parlavantzas, Djawida Dib and Christine Morin
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- URL: http://www.irisa.fr/myriads/software/Meryn/

6.5. PaaSage Adapter

KEYWORDS: Cloud computing - Dynamic adaptation - Cloud applications management
FUNCTIONAL DESCRIPTION

The purpose of the Adapter is to transform the current configuration of a cloud application into a target configuration in an efficient and safe way. The Adapter is part of PaaSage, an open-source platform for modeling, deploying and executing applications on different clouds in an optimal manner. The Adapter has the following responsibilities: (1) validating reconfiguration plans, (2) applying the plans to the running system, and (3) maintaining an up-to-date representation of the current system state.

- Participants: Nikos Parlavantzas, Arnab Sinha, Manh Linh Pham, and Christine Morin
- Contact: Nikos Parlavantzas
- URL: https://team.inria.fr/myriads/software-and-platforms/paasage-adapter/

6.6. Resilin

KEYWORDS: Map Reduce - Parallel processing - Hadoop - Cloud - PaaS
FUNCTIONAL DESCRIPTION

Resilin is an open-source system for creating and managing MapReduce execution platforms over clouds. Resilin is compatible with the Amazon Elastic MapReduce (EMR) API, but it goes beyond Amazon's proprietary EMR solution in allowing users (e.g. companies, scientists) to leverage resources from one or more public and/or private clouds. This enables performing MapReduce computations over a large number of geographically-distributed and diverse resources. Resilin can be deployed across most of the open-source and commercial IaaS cloud management systems (e.g., OpenStack, OpenNebula, Amazon EC2). Once deployed, Resilin takes care of provisioning Hadoop clusters and submitting MapReduce jobs, allowing users to focus on writing their MapReduce applications rather than managing cloud resources. Resilin is implemented in the Python language and uses the Apache Libcloud library to interact with IaaS clouds. Resilin has been evaluated on multiple clusters of the Grid'5000 experimentation testbed. The results show that Resilin enables the use of geographically distributed resources with a limited impact on MapReduce job execution time.

- Participants: Ancuta Iodache, Christine Morin, Pierre Riteau, Nikos Parlavantzas and Matthieu Simonin

- Contact: Christine Morin

- URL: http://resilin.inria.fr

6.7. SAIDS

KEYWORDS: Cloud - Security

FUNCTIONAL DESCRIPTION SAIDS is a self-adaptable intrusion detection system for IaaS clouds. To maintain an effective level of intrusion detection, SAIDS monitors changes in the virtual infrastructure of a Cloud environment and reconfigures its components (security probes) accordingly. SAIDS can also reconfigure probes in the case of a change in the list of running services.

- Participants: Anna Giannakou, Jean-Léon Cusinato, Christine Morin, Jean-Louis Pazat, Louis Rilling and Fergal Martin-Tricot,

- Contact: Christine Morin

- URL: https://bil.inria.fr

6.8. SimGrid

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

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

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

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

- Participants: Martin Quinson,

- Partners: Frédéric Suter, Arnaud Legrand, Adrien Lèbre, Luka Stanisic, Augustin Degomme.

- Contact: Martin Quinson

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

6.9. Snooze

KEYWORDS: Energy management - Fault-tolerance - Self-organization - Self-healing - Cloud computing - Consolidation - Virtualization

SCIENTIFIC DESCRIPTION

Snooze is a scalable, resilient and energy-aware virtual machine management framework for clouds. It is the result of Eugen Feller's PhD thesis which has been funded by the ANR EcoGrappe project (2008 - 2012).

The objectives of the Snooze ADT are threefold: (i) to distribute Snooze system as an open source software and to provide support to the user community (ii) to implement additional features to make it more user-friendly (iii) to integrate it with other open source software stacks and in public testbeds to favour its dissemination.

Snooze is a highly modular system for IaaS clouds. For the scientific community, it constitutes a unique framework for the experimentation of resource management policies in a real system. More generally, it allows any organization to operate a large-scale cluster as a resilient and energy-aware computing infrastructure enabling on demand provisioning of virtual clusters.

FUNCTIONAL DESCRIPTION

Snooze is a self-organizing and energy aware Cloud management framework.

Snooze 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 [59]), 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.

- Participants: Eugen Feller, Christine Morin, Jiajun Cao, Gene Cooperman, Yvon Jégou, David Margery and Matthieu Simonin
- Contact: Christine Morin
- URL: http://snooze.inria.fr/

6.10. VEP

KEYWORDS: Cloud - Security - Computing - IaaS - Standards - OVF - CIMI - SLA

SCIENTIFIC DESCRIPTION

Virtual Execution Platform (VEP) is a Contrail service that sits just above IaaS layer at the service provider end of the Contrail cloud federation. The VEP service provides a uniform interface for managing the whole lifecycle of elastic applications on the cloud and hides the details of the IaaS layer to the user. VEP applications are described in OVF (Open Virtualization Format) standard format. Resource usage is controlled by CEE (Constrained Execution Environment) rules which can be derived from SLAs (Service Level Agreement). The VEP service integrates a monitoring system where the major events about the application, mainly resource usage, are made available to the user.

The VEP service provides a RESTful interface and can be exploited directly by users on top of the provider IaaS. OpenNebula and OpenStack IaaS frameworks were initially supported. During the VEP-S EIT ICT Labs activity in 2014, VEP was extended with a new OCCI IaaS driver which allows to control any IaaS framework providing a standard OCCI API. Support for the new OCCI SLA proposition from OGF has also been added and allows to represent the VEP CEEs in a standard format. Finally, during this activity, the Zabbix open source distributed monitoring system was integrated to VEP.

FUNCTIONAL DESCRIPTION VEP is a management tool for IaaS clouds with a REST interface and simple GUI for administrator. It is an extensible and reusable software for easy deployment of distributed applications. It provides advance reservation, pro-active fault tolerance. It is SLA aware and manages elasticity.

- Participants: Yvon Jégou, Roberto Gioacchino Cascella, Florian Dudouet, Filippo Gaudenzi, Christine Morin and Arnab Sinha
- Contact: Christine Morin
- URL: https://project.inria.fr/vep/

TACOMA Team

5. New Software and Platforms

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

KEYWORDS: Smart home - Smart building

- Participants: Yoann Maurel and Frédéric Weis
- Partner: Université de Rennes 1
- Contact: Frédéric Weis
- URL: https://github.com/bpietropaoli/THEGAME/ (C-version)
- URL: https://bitbucket.org/TACOMA-irisa/java-bft (Java-version)

SCIENTIFIC DESCRIPTION

Context-aware applications have to sense the environment in order to adapt themselves and provide with contextual services. This is the case of Smart Homes equipped with sensors and augmented appliances. However, sensors can be numerous, heterogeneous and unreliable. Thus the data fusion is complex and requires a solid theory to handle those problems. The aim of the data fusion, in our case, is to compute small pieces of context we call context attributes. Those context attributes are diverse and could be for example the presence in a room, the number of people in a room or even that someone may be sleeping in a room. For this purpose, we developed an implementation of the belief functions theory (BFT). THE GAME (THeory of Evidence in a lanGuage Adapted for Many Embedded systems) is made of a set of 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. Platform Pervasive_RFID

KEYWORDS: Composite objects - RFID

- Participants: Paul Couderc and Anthony Blair
- Partner: Université de Rennes 1 (IETR)
- Contact: Paul Couderc

SCIENTIFIC DESCRIPTION

In 2016 we completed the RFID experiment testbed realized in 2014-2015 in collaboration with IETR (see Figure 2). This system allows both interactive testing as well as long running experiments of RFID reading protocols. It comprises a software platform allowing fine control over all dynamic aspects influencing RFID readings: movements for target and antenna, RFID reader configuration, and smart antenna configuration .(diversity and power control).

5.3. Metamorphic Housing platform and Software

KEYWORDS: Smart Home - Metamorphic House

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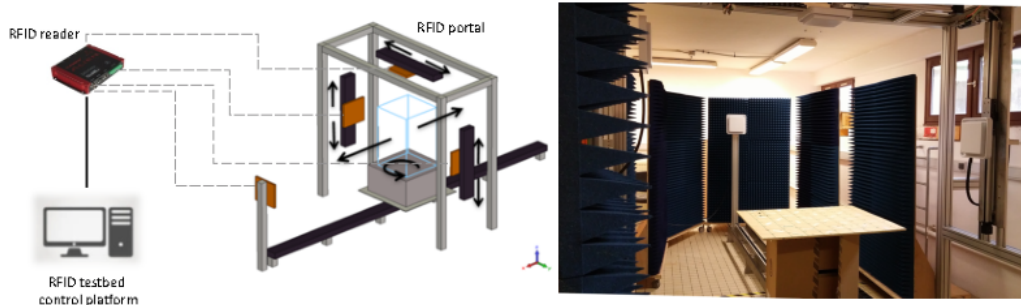
SCIENTIFIC DESCRIPTION- SOFTWARE

Figure 2. RFID testbed

As part of the experimentation of the On-demand room see 6.6 , we have developed a software system that will be used to manage the room and provide functionalities to end users and building managers (access control, electrical and time consumption monitoring and report, room state display...). The software is expected to be deployed in the building that hosts the experimentation. This software is co-developed by Michele Dominici (University of Rennes 1), Guillermo Andrade (SED Inria) and Ghislain Nouvel (MobBI platform). Contributions might be provided by members of the Diverse project-team. Intellectual protection is expected to be applied on such software.

SCIENTIFIC DESCRIPTION- PLATFORM

In 2015, we realized a prototype of the on-demand room as an immersive interactive virtual-reality application, leveraging the Immersia platform (see https://raweb.inria.fr/rapportsactivite/RA2015/tacoma/uid29.html), with real domestic appliances connected to Immersa. In 2016, the experimentation of the On-demand room is organized in the following steps: modification of the original building to create a common, On-demand room between two apartments; deployment of the computer and hardware and software that we are developing; rental of the apartments to two households, for an estimated duration of one year. The building that will host the experimentation is showed in Figure 3 . During the rental of the apartments, data will be collected and stored about the use of the room by households. Data will include time of occupation, mode (private or shared), consumptions, errors etc. The On-demand room will thus constitute an experimentation platform, where real people live and produce data that can be analyzed for statistical purposes. Produced data could also be used in combination with interviews of the occupants to improve the functionalities of the On-demand room, evaluate acceptance and appropriation.

5.4. ISO/IEC 15118-2 Open source Implementation

KEYWORDS: Smart Grid - Intelligent Transport System

- Partner: Telecom Bretagne
- Contact: Jean-Marie Bonnin

SCIENTIFIC DESCRIPTION

The ISO/IEC 15118 standard, named "Road vehicles ? Vehicle-to-Grid Communication Interface", defines how an electric vehicle and a charging station should communicate. It enables the Smart Charging of electric vehicles by allowing them to plan their charging sessions. As we want to be able to manage the charge of electric vehicles in our micro Smart Grid systems, we decided to implement the protocol defined by this standard. The goal is also to participate actively in the design of the new version of this protocol. During a charging session the charging station provides the vehicle with the status of the electric power grid. The vehicle

Figure 3. On-demand room real experimentation

is then able to plan its sharing session accordingly. It sends back its charge plan to the charging station, so that the Smart Grid is aware of it. The protocol also provides security and authentication features.

This software platform was implemented onto small PCs, and was used to control the charge in a small and portable demonstration platform, to demonstrate how it is possible to interconnect this high level decision and communication software with low level components, such as a Battery Management System (BMS), and a battery charger. In 2016, in the context of the Greenfeed project our software has been demonstrated to control the charge of the electric vehicle during the final demonstration of the project. The integration work has been done in collaboration with VeDeCom.

HYBRID Project-Team

6. New Software and Platforms

6.1. #FIVE

KEYWORDS: Virtual reality - Behaviour - 3D interaction

FUNCTIONAL DESCRIPTION

#FIVE (Framework for Interactive Virtual Environments) is a framework for the development of interactive and collaborative virtual environments. #FIVE was developed to answer the need for an easier and a faster design and development of virtual reality applications. #FIVE provides a toolkit that simplifies the declaration of possible actions and behaviours of objects in a VE. It also provides a toolkit that facilitates the setting and the management of collaborative interactions in a VE. It is compliant with a distribution of the VE on different setups. It also proposes guidelines to efficiently create a collaborative and interactive VE. The current implementation is in C# and comes with a Unity3D engine integration, compatible with MiddleVR framework. #FIVE contains software modules that can be interconnected and helps in building interactive and collaborative virtual environments. The user can focus on domain-specific aspects for his/her application thanks to #FIVE's modules. These modules can be used in a vast range of domains using virtual reality applications and requiring interactive environments and collaboration, such as in training for example.

- Participants: Bruno Arnaldi, Valerie Gouranton, Florian Nouviale, Guillaume Claude
- Contact: Valerie Gouranton and Florian Nouviale
- URL: https://bil.inria.fr/fr/software/view/2527/tab

6.2. #SEVEN

KEYWORDS: Virtual reality - Scenario - Training - Petri Net - 3D interaction

FUNCTIONAL DESCRIPTION

#SEVEN (Sensor Effector Based Scenarios Model for Driving Collaborative Virtual Environments) is a sensor effector based scenario engine that enables the execution of complex scenarios for driving Virtual Reality applications. #SEVEN's scenarios are based on an enhanced Petri net model which is able to describe and solve intricate event sequences. #SEVEN comes with an editor for creating, editing and remotely controlling and running scenarios. #SEVEN is implemented in C# and can be used as a stand-alone application or as a library. An integration to the Unity3D engine, compatible with MiddleVR, also exists.

- Participants: Bruno Arnaldi, Valerie Gouranton, Florian Nouviale, Guillaume Claude
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- URL: https://bil.inria.fr/fr/software/view/2528/tab

6.3. OpenViBE

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

FUNCTIONAL DESCRIPTION

OpenViBE is a free and open-source software platform devoted to the design, test and use of Brain-Computer Interfaces (BCI). The platform consists of a set of software modules that can be integrated easily and efficiently to design BCI applications. The key features of OpenViBE software are its modularity, its high-performance, its portability, its multiple-users facilities and its connection with high-end/VR displays. The designer of the platform enables to build complete scenarios based on existing software modules using a dedicated graphical language and a simple Graphical User Interface (GUI). This software is available on the Inria Forge under the terms of the AGPL licence, and it was officially released in June 2009. Since then, the OpenViBE software has already been downloaded more than 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, Jerome Chabrol, Charles Garraud, and Marsel Mano

- Partners: Inria teams POTIOC, ATHENA and NEUROSYS

- Contact: Anatole Lécuyer

- URL: http://openvibe.inria.fr

- URL: https://bil.inria.fr/fr/software/view/1194/tab

6.4. Platform: Immerstar

- Participants : Florian Nouviale, Ronan Gaugne

With the two platforms of virtual reality, Immersia and Immermove, grouped under the name Immerstar, the team has access to high level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform is granted by a Inria CPER funding for 2015-2019 that enables important evolutions of the equipment. In 2016, the first technical evolutions have been decided, with, for Immermove, the addition of a third face to the immersive space, and the extension of the Vicon tracking system, and for Immersia, the installation of WQXGA laser projectors and of a new tracking system.

LACODAM Team

6. New Software and Platforms

6.1. EcoMata

FUNCTIONAL DESCRIPTION

The EcoMata tool-box provides means for qualitative modeling and ecosystem exploration and for assisting the design of 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

6.2. PaturMata

KEYWORDS: Bioinformatics - Biology
SCIENTIFIC 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.
FUNCTIONAL 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 .

- Participants: Christine Largouët, Marie-Odile Cordier, Yulong Zhao
- Contact: Christine Largouët

6.3. QTempIntMiner

KEYWORDS: Data mining - Health - Medical - Physiology - Temporal information
SCIENTIFIC DESCRIPTION

QTempIntMiner: the QTempIntMiner (Quantitative Temporal Interval Miner) data mining software implements several algorithms presented in [46] and [3] (QTIAPriori and QTIPrefixSpan). The software is mainly implemented in Matlab. It uses the Mixmod toolbox [33] 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 intervals 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 (care pathways).

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

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LAGADIC Project-Team

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6. New Software and Platforms

6.1. DESlam

Dense Egocentric SLAM
KEYWORDS: Deph Perception - Robotics - Localization
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 types 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: Francois 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. It provides the functionalities to do image acquisition, semantic annotation, dense registration, localization and 3D mapping. The omnidirectional RGB-D sensors used within this software have been developed at Inria Sophia Antipolis.

- Participants: Eduardo Fernandez Moral, Renato José Martins and Patrick Rives
- Contact: Patrick Rives
- URL: https://team.inria.fr/lagadic

6.4. Sinatrack

KEYWORDS: Computer vision - Robotics
FUNCTIONAL DESCRIPTION

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

- Participants: Antoine Petit, Eric Marchand and Francois Chaumette
- Contact: Eric 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 and visual servoing based on ultrasound images. Written in C++, UsTk provides tools for ultrasound image acquisition, processing, and display, as well as control of ultrasound probe motion by ultrasound visual servoing. This year we started the development of a new version. The objective is first to consolidate existing developments, to improve the quality of the software, to add new state-of-the-art algorithms, and then to disseminate them within the community as an open-source software.

- Participants: Marc Pouliquen, Alexandre Krupa, Pierre Chatelain and Fabien Spindler
- Contact: Alexandre Krupa
- URL: https://team.inria.fr/lagadic/

6.6. ViSP

KEYWORDS: Computer vision - Robotics - Augmented reality - Visual servoing

SCIENTIFIC DESCRIPTION

Since 2005, we have been developing and releasing 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, Eric Marchand, Fabien Spindler, Aurélien Yol and Souriya Trinh
- Partner: Inria, Université de Rennes 1
- Contact: Fabien Spindler
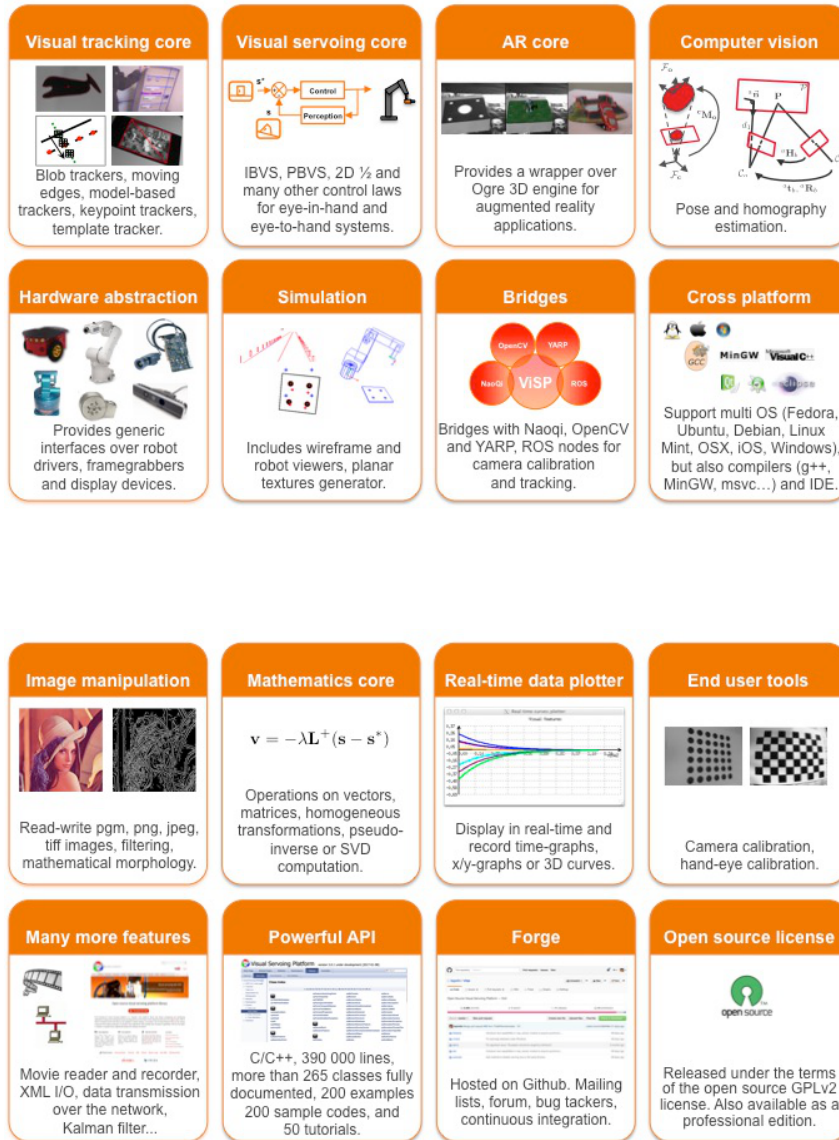- URL: http://visp.inria.fr

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 Github as an open source software under GPLv2 license.

In December 2015, ViSP 3.0.0 new modular architecture was released. The corresponding source code tarball was downloaded 2138 times, much more than the previous 2.10.0 release that was downloaded 1412 times. This confirms that ViSP popularity is increasing and motivates the efforts we are doing since more than 10 years to improve the software. ViSP 3.0.0 last release was packaged for Debian, Ubuntu 16.04 LTS, Arch Linux, OSX and ROS. ViSP 3.0.1 next release is in preparation and should be released at the beginning of 2017. This release will be also packaged for iOS devices. In this new version we introduced new wrapper for USB-3 or GigE PointGrey cameras, Haption haptic device, ATI force/torque sensors, Intel RealSense RGB-D devices. We also make an effort to optimize some critical code sections using SSE and make possible cross-compilation for Raspberry PI and iOS targets, and also Nao, Romeo and Pepper robots from SoftBank Robotics. We also introduce a new version of the 3D model-based tracker dedicated to stereo tracking, fixed some issues, improved the documentation by providing new tutorials and by updating the existing ones.

Concerning ROS community, all the existing packages in "`vision_visp`" ROS stack (see http://wiki.ros.org/vision_visp) were updated and ported to kinetic 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, Canada, Japan, Korea, India, China, Italy, Spain, Portugal, etc. 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. Last August, during the Intel Developer Forum opening keynote, Intel CEO Brian Krzanich introduced the Intel Joule compute module. Using an Intel Joule with glasses from French company PivotHead, Intel demonstrated an augmented reality application that was using ViSP (https://www.youtube.com/watch?v=QRBofzL4MDY).

6.7. WarpDriver

KEYWORDS: Crowd Simulation - Pedestrian Simulation - Collision Avoidance - Reactive Navigation
FUNCTIONAL DESCRIPTION

WarpDriver is a microscopic crowd simulation software, which simulates the collision-free locomotion of many individual agents among the obstacles of a given environment. The originality of the algorithm relies on motion prediction mechanism which allows each agent to predict the probability of colliding other agents with respect to their current motion, their past motion, and the presence of obstacles forcing agents to follow some paths in the environment. Agents then move to their goal whilst they minimize their probability of colliding obstacles.

- Participants: David Wolinski and Julien Pettré
- Contact: Julien Pettré
- URL: http://team.inria.fr/lagadic

6.8. 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: Eric Marchand
- URL: http://www.irisa.fr/lagadic/soft/bib2html/bib2html.html
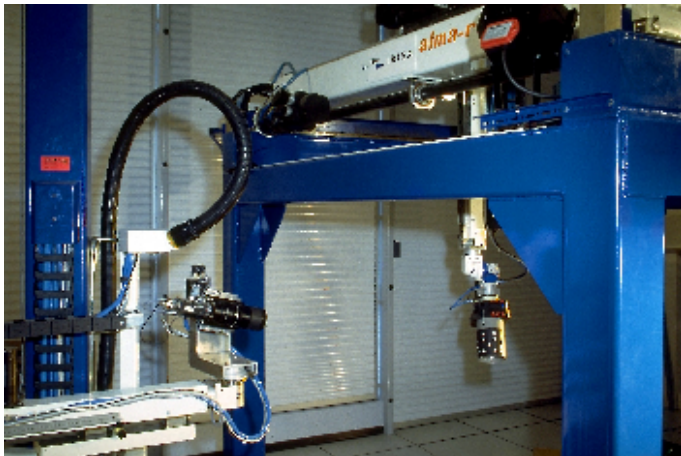
6.9. Platforms

6.9.1. *Robot vision platform*
Participant: Fabien Spindler [contact].

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

This year we completed the platform with a haptic Virtuose 6D device from Haption company (see Fig. 2 .b). This device is used for visual-based shared control (see Section 9.3.1.3).

Note that 3 papers published by Lagadic in 2016 enclose results validated on this platform [21][48][46].

(a)   (b)

Figure 2. a) Lagadic robotics platform for vision-based manipulation, b) Virtuose 6D haptic device

6.9.2. Mobile robots

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

6.9.2.1. 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 Pioneer 3DX from Adept (see Fig. 3 .b). 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 Section 7.4.5), we have three electric wheelchairs in Rennes, one from Permobil, one from Sunrise and the last from YouQ (see Fig. 3 .c). The control of the wheelchair is performed using a plug and play system between the joystick and the low level control of the wheelchair. Such a system lets us acquire the user intention through the joystick position and control the wheelchair by applying corrections to its motion. The wheelchairs have been fitted with cameras and ultrasound sensors to perform the required servoing for assisting handicapped people.

Note that 11 papers exploiting the indoors mobile robots were published this year [67][26][61][37][62][30] [55][38][71][64][66].

6.9.2.2. Outdoor vehicles

A camera rig has been developed in Sophia Antipolis. It can 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 shown in the video http://www-sop.inria.fr/members/Renato-Jose.Martins/iros15.html.

Paper [68] contains experimental results obtained with this camera rig.
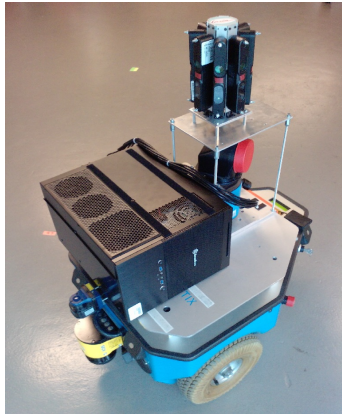
(a)

(b)

(c)

Figure 3. a) Hannibal platform, b) Pioneer P3-DX robot, c) wheelchairs from Permobil, Sunrise and YouQ.

6.9.3. Medical robots

Participants: Fabien Spindler [contact], 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 (see Section 7.3).

Figure 4. Globeye stereo sensor and acquisition system.

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.

This year we replaced the F/T sensor attached to one of the Viper robot in order to use a DAQ acquisition board able to provide measures at a higher frame rate (up to 1 kHz). This feature is especially useful for flexible needle steering by ultrasound visual servoing (see Fig. 5 .b).

Notice that 10 papers published this year include experimental results obtained with this platform [40][31][34][58][57][70][52][59] [50][51].

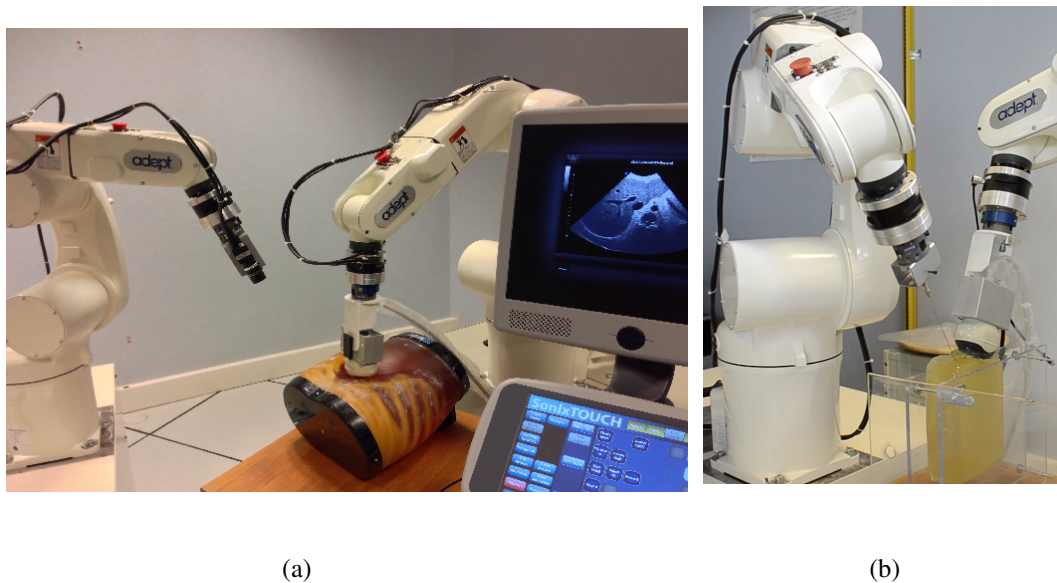(a)   (b)

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.

6.9.4. *Humanoid robots*

Participants: Giovanni Claudio, Fabien Spindler [contact].

Romeo is a humanoid robot from SoftBank 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 for object manipulation (see Fig. 6 .a).

In July, this platform was extended with Pepper, another human-shaped robot designed by SoftBank Robotics to be a genuine day-to-day companion (see Fig. 6 .b). It has 17 degrees of freedom mounted on a wheeled holonomic base and a set of sensors (cameras, laser, ultrasound, inertial) that makes this platform interesting for researches in vision-based manipulation and navigation. Our first developments were devoted to visual servoing for controlling the gaze of the robot exploiting the redundancy of the head and mobile base and adding the capability to follow a person.

Note that 4 papers published this year include experimental results obtained with these platforms [53][81][65][20].

6.9.5. *Unmanned Aerial Vehicles (UAVs)*

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

(a)   (b)
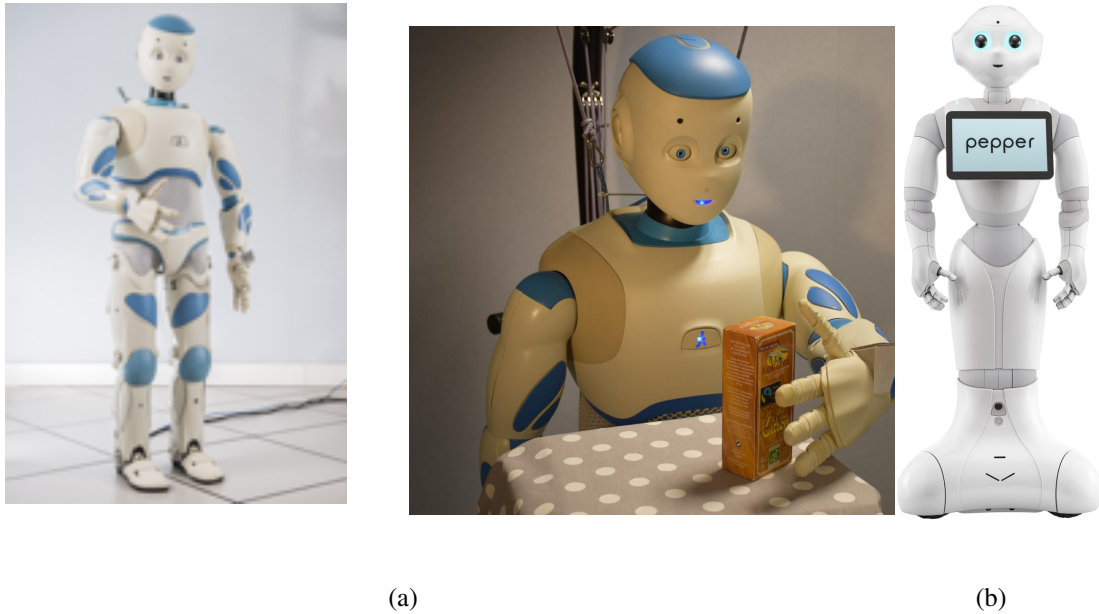
Figure 6. a) Romeo experimental platform, b) Pepper human-shaped robot

From 2014, Lagadic 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 9.2.5). To this end, we purchased four quadrotors from Mikrokopter Gmbh, Germany (see Fig. 7 .a), and one quadrotor from 3DRobotics, USA (see Fig. 7 .b). The Mikrokopter quadrotors have been heavily customized by: (i) reprogramming from scratch the low-level attitude controller onboard the microcontroller of the quadrotors, (ii) equipping each quadrotor with an Odroid XU4 board (see Fig. 7 .d) 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 (see Fig. 7 .c). The quadrotor group is used as robotic platforms for testing a number of single and multiple flight control schemes with a special attention on the use of onboard vision as main sensory modality.

Two papers published this year enclose experimental results obtained with this platform [72][64].

(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

<p style="text-align:center">**LINKMEDIA Project-Team**</p>

6. New Software and Platforms

6.1. A‖GO multimedia web services

Participants: Guillaume Gravier [correspondent], Gabriel Sargent.

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. Based on the A‖GO infrastructure, LINKMEDIA has continued making available a number of web services related to multimedia content analysis. In 2016, we revamped the multimedia-related web service offer, making all serices interoperable and broadening the scope of services made available (silence detection, face detection, text-based fragmentation). We also made available short videos that demonstrate the usefulness of our web services.

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MIMETIC Project-Team

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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 gait cycles. To this end it is based on analyzing the knee 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.

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 for ergonomics purposes. Kimea is able to manage most of the occultations that can occur on workstations (real working situations). To this end, Kimea relies on a database of examples/poses organized as a graph, in order to replace unreliable body segment reconstructions by poses that have already been measured on real subjects. 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

KEYWORDS: Behavioral animation - Virtual cities
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 pedestrians performing different kind of activities implying travels between different locations. However the generic aspect of the algorithm and underlying representations enables 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.

With a good configuration of agents characteristics (based on statistics), we demonstrated that tasks schedules produced by Populate are representative of human ones. In conjunction with TopoPlan, it has been used to populate a district of Paris as well as imaginary cities with several thousands of pedestrians navigating in real time.
FUNCTIONAL DESCRIPTION

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

6.6. The Theater

KEYWORDS: Interactive Scenarios - 3D animation - Storytelling
SCIENTIFIC DESCRIPTION

The Theater is a software framework to develop interactive scenarios in virtual 3D environments. The framework provides means to author and orchestrate 3D character behaviors and simulate them in real-time. The tools provide 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

6.7. Immerstar Platform

Participants: Georges Dumont [contact], Ronan Gaugne, Anthony Sorel, Franck Multon.

With the two platforms of virtual reality, Immersia and Immermove, grouped under the name Immerstar, the team has access to high level scientific facilities. This equipment benefits the research teams of the center and has allowed them to extend their local, national and international collaborations. The Immerstar platform is granted by a Inria CPER funding for 2015-2019 that enables important evolutions of the equipment. In 2016, the first technical evolutions have been decided, with, for Immermove, the addition of a third face to the immersive space, and the extension of the Vicon tracking system, and for Immersia, the installation of WQXGA laser projectors and of a new tracking system.

PANAMA Project-Team

6. New Software and Platforms

6.1. Audio Activity Detector

KEYWORD: Audio activity estimation

- Authors: Frédéric Bimbot, Ewen Camberlein, Romain Lebarbenchon and Vincent Soupe
- Contact: Frédéric Bimbot

6.2. Audio Breath Rhythm Estimator

KEYWORD: Breath rhythm estimation

- Authors: Frédéric Bimbot, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.3. Audio GMM Classifier

- Authors: Frédéric Bimbot, Vincent Soupe, Jérémy Paret, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.4. CSCbox

Compressive Spectral Clustering Toolbox
KEYWORD: Clustering
SCIENTIFIC DESCRIPTION

The Compressive Spectral Clustering Toolbox is a Matlab toolbox implementing routines to reproduce experiments from the paper "Compressive Spectral Clustering", by N. Tremblay, G. Puy, P. Vandergheynst and R. Gribonval.
FUNCTIONAL DESCRIPTION

Matlab toolbox implementing routines to reproduce experiments from the paper "Compressive Spectral Clustering"

- Authors: Nicolas Tremblay, Gilles Puy, Pierre Vandergheynst and Rémi Gribonval
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Rémi Gribonval
- URL: http://www.irisa.fr/panama/software

6.5. 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

6.6. FAuST

KEYWORDS: Learning - Sparsity - Fast transform - Multilayer sparse factorisation
FUNCTIONAL DESCRIPTION

C++ toolbox, designed to decompose a given dense matrix into a product of sparse matrices in order to reduce its computational complexity (both for storage and manipulation).

- Authors: Luc Le Magoarou, Rémi Gribonval, Adrien Leman, Nicolas Bellot and Thomas Gautrais
- Contact: Rémi Gribonval
- URL: http://faust.gforge.inria.fr/

6.7. 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/

6.8. SPADE

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

Matlab routines to reproduce audio declipping experiments from the paper: - 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. <hal-00922497v3> - 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. <hal-01159700v2>

- Participants: Srdan Kitic, Nancy Bertin and Rémi Gribonval
- Contact: Rémi Gribonval
- URL: http://xspaad.gforge.inria.fr/

6.9. SPOD Audio

KEYWORDS: Audio source classification - Speaker verification - Breath rhythm estimation - Audio activity estimation

- Authors: Frédéric Bimbot, Vincent Soupe, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot
- URL: http://www.kerlink.fr/en/

6.10. SPOD Model Generation

KEYWORDS: Machine learning - Audio source classification - Statistical modeling - Speaker verification

- Authors: Frédéric Bimbot, Vincent Soupe, Jérémy Paret, Ewen Camberlein and Romain Lebarbenchon
- Contact: Frédéric Bimbot

6.11. SRP-PHAT

KEYWORD: Source localization

- Authors: Frédéric Bimbot, Nancy Bertin, Ewen Camberlein, Romain Lebarbenchon, Emmanuel Vincent, Charles Blandin and Alexey Ozerov
- Contact: Frédéric Bimbot

6.12. SketchMLBox

KEYWORD: Clustering
SCIENTIFIC DESCRIPTION

The SketchMLbox is a Matlab toolbox for fitting mixture models to large collections of training vectors using sketching techniques. The collection is first compressed into a vector called sketch, then a mixture model (e.g. a Gaussian Mixture Model) is estimated from this sketch using greedy algorithms typical of sparse recovery. The size of the sketch does not depend on the number of elements in the collection, but rather on the complexity of the problem at hand [2,3]. Its computation can be massively parallelized and distributed over several units. It can also be maintained in an online setting at low cost. Mixtures of Diracs ("K-means") and Gaussian Mixture Models with diagonal covariance are currently available, the toolbox is structured so that new mixture models can be easily implemented.

FUNCTIONAL DESCRIPTION

Matlab toolbox for fitting mixture models to large collections of feature vectors using sketching techniques.

- Authors: Nicolas Keriven, Rémi Gribonval and Nicolas Tremblay
- Partner: Université de Rennes 1
- Contact: Rémi Gribonval
- URL: http://sketchml.gforge.inria.fr

6.13. VoiceHome Corpus

KEYWORDS: Audio - Source Separation
FUNCTIONAL DESCRIPTION

This corpus includes reverberated, noisy speech signals spoken by native French talkers in a lounge and recorded by an 8-microphone device at various angles and distances and in various noise conditions. Room impulse responses and noise-only signals recorded in various real rooms and homes and baseline speaker localization and enhancement software are also provided.

- Contact: Nancy Bertin
- URL: http://voice-home.gforge.inria.fr/voiceHome_corpus.html

6.14. graphsamplingbox

- Authors: Nicolas Tremblay, Gilles Puy, Pierre Vandergheynst and Rémi Gribonval
- Partner: EPFL - Ecole Polytechnique Fédérale de Lausanne
- Contact: Rémi Gribonval
- URL: http://www.irisa.fr/panama/software

SIROCCO Project-Team

6. New Software and Platforms

6.1. 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

6.2. VideoInpainting

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

SCIENTIFIC DESCRIPTION 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.

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

6.3. Visual Fixation Analysis

SCIENTIFIC 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
- Partner: Université de Rennes 1
- Contact: Olivier Le Meur

6.4. Saccadic model

SCIENTIFIC DESCRIPTION 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. A presentation of this model is available on the following link: http://fr.slideshare.net/OlivierLeMeur/saccadic-model-of-eye-movements-for-freeviewing-condition. 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) under the number IDDN.FR.001.240029.000.S.P.2016.000.10000.

- Participants: Olivier Le Meur
- Partner: Université de Rennes 1
- Contact: Olivier Le Meur

6.5. ADT-ATep

The scientific and industrial community is nowadays exploring new multimedia applications using 3D data (beyond stereoscopy). In particular, Free Viewpoint Television (FTV) has attracted much attention in the recent years. In those systems, the user can choose in real time the view angle from which he wants to observe the scene. Despite the great interest for FTV, the lack of realistic and ambitious datasets penalizes the research effort. The acquisition of such sequences is very costly in terms of hardware and working effort, which explains why no multi-view videos suitable for FTV has been made available yet.

A project founded by Inriahub has recently started in the SIROCCO team. Called ATeP for "Acquisition, Traitement et Partage" (Acquisition, Processing and Sharing), it targets the acquisition of such dataset. Another interesting aspect of this project is that the acquisition system relies on omnidirectional cameras. The dataset will thus interest all the industries and scientists currently working on the development of efficient processing and coding tools for 360 videos.

- Participants: Cédric Le Cam, Thomas Maugey
- Partner: Inria
- Contact: Thomas Maugey