Activity Report 2015

Section Software

ATEAMS Project-Team

5. New Software and Platforms

5.1. MicroMachinations

FUNCTIONAL DESCRIPTION

Objective: To create an integrated, live environment for modelling and evolving game economies. This will allow game designers to experiment with different strategies to realise game mechanics. The environment integrates with the SPIN model checker to prove properties (reachability, liveness). A runtime system for executing game economies allows MicroMachinations models to be embedded in actual games.

Impact: One of the important problems in game software development is the distance between game design and implementation in software. MicroMachinations has the potential to bridge this gap by providing live design tools that directly modify or create the desired software behaviours.

- Participants: Paul Klint and Riemer Van Rozen
- Contact: Riemer Van Rozen
- URL: https://github.com/vrozen/MM-Lib

5.2. OSSMETER

KEYWORDS: Software Quality, Metrics, Open-source SCIENTIFIC DESCRIPTION: OSSMETER meets the challenge of software project quality assessment via fact-based business intelligence. The goal of the project was to design and evaluate a platform for incremental analysis of long lasting open-source projects to support decision making on the corporate level. FUNCTIONAL DESCRIPTION: OSSMETER is a platform which integrates metrics of open-source projects: their source code quality, the contents of their social interactions and their activity in issue tracking systems. It includes a fully programmable user-defined quality model utility and configurable dash-board user-interface. The basic metrics of the platform and their aggregation to the project level are carefully considered and rationalised.

- Participants: Paul Klint, Jurgen Vinju, Tijs Van Der Storm, Ashim Shahi, Bas Basten.
- Contact: Jurgen Vinju
- URL: http://www.ossmeter.org/

5.3. Rascal

KEYWORDS: Metaprogramming - Language
SCIENTIFIC DESCRIPTION

Rascal primitives include immutable data, context-free grammars and algebraic data-types, relations, relational calculus operators, advanced patterns matching, generic type-safe traversal, comprehensions, concrete syntax for objects, lexically scoped backtracking, and string templates for code generation. It has libraries for integrating language front-ends, for reusing analysis algorithms, for getting typed meta-data out of version management systems, for interactive visualization, etc.
FUNCTIONAL DESCRIPTION

Rascal is a programming language, such that meta programs can be created by, understood by, and debugged by programmers.

You want to use the best tool for the job when analyzing, transforming or generating source code, so normally you will end up with many different tools, possibly even written in different languages. Now the problem is to integrate these tools again. Rascal solves this problem by integrating source code analysis, transformation, and generation primitives on the language level. Use it for any kind of metaprogramming task: to construct parsers for programming languages, to analyze and transform source code, or to define new DSLs with full IDE support.

- Participants: Paul Klint, Jurgen Vinju, Tijs Van Der Storm, Davy Landman, Bert Lisser, Atze Van Der Ploeg, Vadim Zaytsev, Anastasia Izmaylova, Michael Steindorfer, Jouke Stoel, Ali Afroozeh and Ashim Shahi
- Contact: Paul Klint
- URL: http://www.rascal-mpl.org/

5.4. Meerkat

FUNCTIONAL DESCRIPTION

Objective: To enable fully context-free general parsing using a parser combinator library (including allowing left recursion and arbitrary context-sensitive disambiguation).

Impact: Meerkat explores algorithmic advances in context-free general parsing (based on the GLL parsing algorithm and memoized continuations) in the context of a scala parsing combinator library. This library uniquely combines the worst-case execution time guarantees of GLL with the flexibility of parsing combinators. [47]

- Participants: Anastasia Izmaylova, Ali Afroozeh and Tijs van der Storm.
- Contact: Anastasia Izmaylova, Ali Afroozeh
- URL: http://meerkat-parser.github.io/

5.5. Iguana

FUNCTIONAL DESCRIPTION

Objective: To provide a data-dependent context-free general parsing infra-structure for parsing programming languages and other formal data, program and modeling notations.

Impact: Iguana is a fast implementation of data-dependent grammars based on the GLL context-free parsing algorithm with data-dependent non-terminals and constraints on top. It comes with a number of high-level disambiguation constructs which are translated to the intermediate layer of data-dependent (E)BNF before being loaded into an object-oriented implementation of GLL based on abstract transition network. Using Iguana parsers for languages which are considered to be hard to parse (such as Haskell and OCAML) are within reach of being generated from simple declarative specifications [25].

- Participants: Anastasia Izmaylova, Ali Afroozeh.
- Contact: Anastasia Izmaylova, Ali Afroozeh
- URL: http://iguana-parser.github.io/

5.6. Capsule

FUNCTIONAL DESCRIPTION

Objective: A generic and highly optimised product-family of immutable collection data-structures.

Impact: Capsule is a library for immutable sets, maps and tables. The code is generated using high-level descriptions of the requirements and internal trade-offs of hash-trie map based implementations. We are using this code generator to experiment with the fastest and leanest representations of these persistent data-types to satisfy the requirements of Rascal meta-programming applications in static analysis, empirical research in software engineering and software analytics [37].

- Participants: Michael Steindorfer, Jurgen Vinju
- Contact: Michael Steindorfer
- URL: http://usethesource.io/projects/capsule/

BONSAI Project-Team

6. New Software and Platforms

6.1. Iedera

Iedera : subset seed design tool
KEYWORDS: Computational biology - Sequence alignment - Spaced seeds
SCIENTIFIC DESCRIPTION

Iedera is a tool based on a weighted automata framework that enables to compute spaced seeds, associated probability distributions, scores/costs, counts, and even polynomials on a classical semi-ring framework. Seed design is computed by full enumeration or hill-climbing optimization.
FUNCTIONAL DESCRIPTION

Iedera is a tool to select and design subset seed and vectorized subset seed patterns. Spaced seeds and transition-constrained spaced seeds can be perfectly represented in the subset seed model.

- Participants: Laurent Noé, Grégory Kucherov and Mikhail Roytberg
- Partners: CNRS - Université de Nancy - Université de Lille
- Contact: Laurent Noé
- URL: http://bioinfo.lifl.fr/yass/iedera.php

6.2. NORINE

Nonribosomal peptides resource
KEYWORDS: Bioinformatics - Biotechnology - Biology - Genomics - Graph algorithmics - Chemistry - Knowledge database - Drug development - Computational biology
FUNCTIONAL DESCRIPTION

Norine is a public computational resource with a web interface and REST access to a knowledge-base of nonribosomal peptides. It also contains dedicated tools : 2D graph viewer and editor, comparison of NRPs, MyNorine, a tool allowing anybody to easily submit new nonribosomal peptides, Smiles2monomers (s2m), a tool that deciphers the monomeric structure of polymers from their chemical structure.

- Participants: Maude Pupin, Areski Flissi, Valerie Leclère, Laurent Noé, Yoann Dufresne, Juraj Michalik and Stéphane Janot
- Partners: CNRS - Université Lille 1 - Institut Charles Viollette
- Contact: Maude Pupin
- URL: http://bioinfo.lille.inria.fr/NRP

6.3. ProCARs

PROgressive Contiguous Ancestral RegionS
KEYWORDS: Bioinformatics - Evolution - Metagenomics
SCIENTIFIC DESCRIPTION

ProCars is a program used to reconstruct ancestral gene orders as CARs (Contiguous Ancestral Regions) with a progressive homology-based method. The method runs from a phylogeny tree (without branch lengths needed) with a marked ancestor and a block file. This homology-based method is based on iteratively detecting and assembling ancestral adjacencies, while allowing some micro-rearrangements of synteny blocks at the extremities of the progressively assembled CARs. The method starts with a set of blocks as initial set of CARs, and detects iteratively the potential ancestral adjacencies between extremities of CARs, while building up the CARs progressively by adding, at each step, new non-conflicting adjacencies that induce the less homoplasy phenomenon. The species tree is used, in some additional internal steps, to compute a score for the remaining conflicting adjacencies, and to detect other reliable adjacencies, in order to reach completely assembled ancestral genomes.

FUNCTIONAL DESCRIPTION

ProCARs is a program used to reconstruct ancestral gene orders as CARs (Contiguous Ancestral Regions) with a progressive homology-based method. The method runs from a phylogeny tree with a marked ancestor and a block file.

- Participants: Aïda Ouangraoua, Samuel Blanquart, Jean-Stéphane Varré and Amandine Perrin
- Partners: CNRS - Université de Lille
- Contact: Jean-Stéphane Varré
- URL: http://bioinfo.lifl.fr/procars

6.4. SortMeRNA

KEYWORDS: Bioinformatics - NGS - Genomic sequence

SCIENTIFIC DESCRIPTION

SortMeRNA is a biological sequence analysis tool for metatranscriptomic and metagenomic data filtering, mapping and OTU-picking. The main application of SortMeRNA is filtering and mapping ribosomal RNA from NGS reads.

FUNCTIONAL DESCRIPTION The core algorithm is based on approximate seeds as well as an optimized text index data structure. It allows for fast and sensitive analyses of nucleotide sequences.

SortMeRNA takes as input a file of reads (fasta or fastq format) and one or multiple rRNA database file(s), and sorts apart rRNA and rejected reads into two files specified by the user. Optionally, it can provide high quality local alignments of rRNA reads against the rRNA database. SortMeRNA works with Illumina, 454, Ion Torrent and PacBio data, and can produce SAM and BLAST-like alignments. It is implemented in C++.

- Participants: Hélène Touzet, Laurent Noé and Evguenia Kopylova
- Contact: Hélène Touzet
- URL: http://bioinfo.lille.inria.fr/RNA/sortmerna/

6.5. Vidjil

High-Throughput Analysis of V(D)J Immune Repertoire

KEYWORDS: Bioinformatics - NGS - Indexation - Cancer - Drug development

SCIENTIFIC DESCRIPTION

Vidjil is made of three components: an algorithm, a visualisation browser and a server that allow an analysis of lymphocyte populations containing V(D)J recombinations.

Vidjil high-throughput algorithm extracts V(D)J junctions and gather them into clones. This analysis is based on a spaced seed heuristics and is fast and scalable, as, in the first phase, no alignment is performed with database germline sequences. Each sequence is put in a cluster depending on its V(D)J junction. Then a representative sequence of each cluster is computed in time linear in the size of the cluster. Finally, we perform a full alignment using dynamic programming of that representative sequence againt the germline sequences.

Vidjil also contains a dynamic browser (with D3JS) for visualization and analysis of clones and their tracking along the time in a MRD setup or in a immunological study.

FUNCTIONAL DESCRIPTION

Vidjil is an open-source platform for the analysis of high-throughput sequencing data from lymphocytes. V(D)J recombinations in lymphocytes are essential for immunological diversity. They are also useful markers of pathologies, and in leukemia, are used to quantify the minimal residual disease during patient follow-up. High-throughput sequencing (NGS/HTS) now enables the deep sequencing of a lymphoid population with dedicated Rep-Seq methods and software.

- Participants: Mathieu Giraud, Mikaël Salson, Marc Duez, Ryan Herbert, Tatiana Rocher and Florian Thonier
- Partners: CNRS - Inria - Université de Lille
- Contact: Mathieu Giraud
- URL: http://www.vidjil.org

6.6. Yass

KEYWORDS: Bioinformatics - Genomic sequence - Computational biology - Sequence alignment

SCIENTIFIC DESCRIPTION

As most of the heuristic DNA local alignment softwares (BLAST, FASTA, PATTERNHUNTER, BLASTZ, LAST...) YASS uses seeds to detect potential similarity regions, and then tries to extend them to actual alignments.

This genomic search tool uses multiple transition-constrained spaced seeds (most of the design of these seeds is provided by the Iedera tool) to search for more fuzzy repeats, such as non-coding DNA/RNA.

Main features of YASS are: (i) multiple, possibly overlapping seeds and a new hit criterion to ensure a good sensitivity/selectivity trade-off (ii) transition-constrained spaced seeds to improve sensitivity (transition mutations are purine to purine [AG] or pyrimidine to pyrimidine [CT]) (iii) using different scoring schemes with bit-score and E-value evaluated according to the sequence background frequencies (iv) parameterizable output filter for low complexity repeats (v) reporting of various alignment statistical parameters (mutation bias along triplets, transition/transversion), and (vi) post-processing step to group gapped alignments.

FUNCTIONAL DESCRIPTION

YASS is a genomic similarity search tool, for nucleic (DNA/RNA) sequences in fasta or plain text format : it produces local pairwise alignments.

- Participants: Laurent Noé and Grégory Kucherov
- Partners: CNRS - Université de Nancy - Université de Lille
- Contact: Laurent Noé
- URL: http://bioinfo.lifl.fr/yass

6.7. miRkwood

KEYWORDS: Bioinformatics - Genomics

SCIENTIFIC DESCRIPTION

miRkwood is a bioinformatic pipeline that allows for the fast and easy identification of microRNAs in plant genomes. It is both available as a webserver and a stand-alone software. It offers an user-friendly interface to navigate in the data, as well as many export options to allow the user to conduct further analyses on a local computer.

FUNCTIONAL DESCRIPTION

The method takes as input a set of small reads, that have been previously trimmed and aligned onto the reference genome. It identifies novel microRNAs on the basis of the distributions of reads and the potential of flanking genomic sequence to fold into a stem-loop secondary structure. Then the result is refined through a variety of additional complementary features that bring new evidence to the prediction: duplex stability, thermodynamic stability, phylogenetic conservation, repeats, etc.

- Participants: Hélène Touzet, Mohcen Benmounah, Jean-Frédéric Berthelot, Isabelle Guigon and Sylvain Legrand
- Contact: Hélène Touzet
- URL: http://bioinfo.lille.inria.fr/mirkwood/

DEFROST Team

6. New Software and Platforms

6.1. SOFA

Simulation Open Framework Architecture

KEYWORDS: Physical simulation - Health - Biomechanics - GPU - Computer-assisted surgery

FUNCTIONAL DESCRIPTION

SOFA is an Open Source framework primarily targeted at real-time simulation, with an emphasis on medical simulation. It is mostly intended for the research community to help develop new algorithms, but can also be used as an efficient prototyping tool. Based on an advanced software architecture, it allows : the creation of complex and evolving simulations by combining new algorithms with algorithms already included in SOFA, the modification of most parameters of the simulation (deformable behavior, surface representation, solver, constraints, collision algorithm, etc.) by simply editing an XML file, the building of complex models from simpler ones using a scene-graph description, the efficient simulation of the dynamics of interacting objects using abstract equation solvers, the reuse and easy comparison of a variety of available methods.

- Participants: Stéphane Cotin and Hervé Delingette
- Partner: IGG
- Contact: Stéphane Cotin
- URL: http://www.sofa-framework.org

6.2. Soft robot plugin for sofa

Our contribution consists in a new framework to simulate and control soft robots. This framework is based on a mechanical modeling of the robot elements combined with fast real-time direct/inverse FEM solvers. The keypoint of our approach is that the same modeling is used for interactive simulation of its behavior and interactive control of the fabricated robots. This plugin is being developped in the ADT project SORBET.

KEYWORDS: Simulation - Soft-Robot - Inverse models - Finite Element Method - Quadratic Programmings

- Participants: Eulalie Coevoet, Olivier Goury, Frédéric Largillière, Bruno Carrez, Damien Marchal, Jérémie Dequidt and Christian Duriez
- Contact: Eulalie Coevoet and Christian Duriez
- URL: https://project.inria.fr/softrobot/

6.3. Neurosurgery simulation

Vascular neurosurgery simulation based on SOFA Framework

KEYWORDS: Simulation - Health - Computer-assisted surgery

- Participants: Christian Duriez, Eulalie Coevoet, Laurent Thines and Jérémie Dequidt
- Partners: Université de Lille - CHRU Lille
- Contact: Christian Duriez

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

6. New Software and Platforms

6.1. COCO

COmparing Continuous Optimizers

KEYWORDS: Benchmarking - Numerical optimization - Black-box optimization - Stochastic optimization

6.1.1. *SCIENTIFIC DESCRIPTION*

COmparing Continuous Optimisers (COCO) is a tool for benchmarking algorithms for black-box optimisation. COCO facilitates systematic experimentation in the field of continuous optimization. COCO provides: (1) an experimental framework for testing the algorithms, (2) post-processing facilities for generating publication quality figures and tables, (3) LaTeX templates of articles which present the figures and tables in a single document. The COCO software is composed of two parts: (i) an interface available in different programming languages (C/C++, Java, Matlab/Octave, R, Python) which allows to run and log experiments on multiple test functions testbeds of functions (noisy and noiseless) are provided (ii) a Python tool for generating figures and tables that can be used in the LaTeX templates. In 2015, we extended the software towards multiobjective optimization and will provide a first release in early 2016.

6.1.2. *FUNCTIONAL DESCRIPTION*

The Coco Platform provides the functionality to automatically benchmark optimization algorithms for unbounded, unconstrained optimization problems in continuous domains. Benchmarking is a vital part of algorithm engineering and a necessary path to recommend algorithms for practical applications. The Coco platform releases algorithm developers and practitioners alike from (re-)writing test functions, logging, and plotting facilities by providing an easy-to-handle interface in several programming languages. The Coco platform has been developed since 2007 and has been used extensively within the "Blackbox Optimization Benchmarking (BBOB)" workshop series since 2009. Overall, 151 algorithms and algorithm variants by contributors from all over the world have been benchmarked with the platform so far and all data is publicly available for the research community. For 2016, a new suite of benchmark functions for bi-objective problems is expected to build the basis of the next BBOB workshop at GECCO 2016 for which a new software release is planned for January.

- Participants: Dimo Brockhoff, Arnaud Liefooghe, Thanh-Do Tran, Dejan Tušar, Tea Tušar (all Dolphin), Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara, Asma Atamna, Phillipe Sampaio, and Duc Manh Nguyen (all TAO team)
- Partners: TU Dortmund University, Germany and Czech Technical University, Czech Republic
- Contact: Dimo Brockhoff
- URL: http://coco.gforge.inria.fr/, https://github.com/numbbo/coco

6.2. MO-Mine

SCIENTIFIC DESCRIPTION

MO-Mineclust is the first package of the platform and is dedicated to clustering (unsupervised classification). Indeed, it is well-known that clustering may be seen as a bi-objective optimization problem as the goal is both to minimize distances between data belonging to a same cluster, while maximizing distances between data belonging to different clusters. Several models (objective functions used,...) and engines (optimization algorithms) have been implemented. The framework searches, for a given dataset, the best association of model/engine/parameter without specifiing the number of clusters. MO-Mineclust shows very interesting behavior and shows that the choice of the model and the engine has a great importance in the performance of the method and depends on the dataset to analyze.

FUNCTIONAL DESCRIPTION

MO-Mine is a process of tests and evaluations of multi-objective optimisation algorithms for data mining. MO-Mine platform will provide data sets (literature + synthetics benchmarks), data mining (Features selection, Clustering, Classification and Association rules) algorithms based on multi-objective metaheuristics (Evolutionary algorithm), validation methods and tools to compare algorithms. MO-Mine is based on evolutionary algorithms implemented in ParadisEO and adapted to solve problem of data mining. MO-Mine proposed to users to compare their own methods with different approaches following protocols clearly identified and shared.

- Participants: B. Fisset, L. Jourdan and C. Dhaenens
- Contact: Laetitia Jourdan
- URL: http://mo-mine.gforge.inria.fr/doku.php

6.3. ParadisEO

KEYWORD: Parallelisation
SCIENTIFIC DESCRIPTION

ParadisEO (PARallel and DIStributed Evolving Objects) is a C++ white-box object-oriented framework dedicated to the flexible design of metaheuristics. Based on EO, a template-based ANSI-C++ compliant evolutionary computation library, it is composed of four modules: * Paradiseo-EO provides tools for the development of population-based metaheuristic (Genetic algorithm, Genetic programming, Particle Swarm Optimization (PSO)...) * Paradiseo-MO provides tools for the development of single solution-based metaheuristics (Hill-Climbing, Tabu Search, Simulated annealing, Iterative Local Search (ILS), Incremental evaluation, partial neighborhood...) * Paradiseo-MOEO provides tools for the design of Multi-objective metaheuristics (MO fitness assignment shemes, MO diversity assignment shemes, Elitism, Performance metrics, Easy-to-use standard evolutionary algorithms...) * Paradiseo-PEO provides tools for the design of parallel and distributed metaheuristics (Parallel evaluation, Parallel evaluation function, Island model) Furthermore, ParadisEO also introduces tools for the design of distributed, hybrid and cooperative models: * High level hybrid metaheuristics: coevolutionary and relay model * Low level hybrid metaheuristics: coevolutionary and relay model

FUNCTIONAL DESCRIPTION

Paradiseo is a software framework for metaheuristics (optimisation algorithms aimed at solving difficult optimisation problems). It facilitates the use, development and comparison of classic, multi-objective, parallel or hybrid metaheuristics.

- Partners: CNRS - Université Lille 1
- Contact: El-Ghazali Talbi
- URL: http://paradiseo.gforge.inria.fr/

6.4. VRPsolve

KEYWORDS: C++ - Mobile Computing, Transportation - Optimization

- Participants: Clive Ferret-Canape, Arnaud Liefooghe and Sébastien Vérel
- Contact: Arnaud Liefooghe
- URL: http://gforge.inria.fr/projects/vrpsolve (limited access)

SCIENTIFIC DESCRIPTION

VRPsolve is a software for solving vehicle routing problems dealing with last-mile delivery issues that arise as we approach the final customer. When modeling and solving combinatorial optimization problems, especially problems related to the transport of goods and people, the resulting models are generally subject to a specific development in order to be validated, as industrial needs are highly dependent of the application domain. However, a set of conventional objectives and constraints, such as vehicles capacities, incompatible parcels, time windows, are now commonly encountered. In addition to being efficient and effective, VRPsolve differentiates from other tools by allowing to quickly and conveniently integrate ad-hoc constraints and objectives into a generic software. Indeed, VRPsolve effectively deal with industrial last-mile delivery vehicle routing problems and is able to cope with multiple objectives and a large number of constraints by using advanced optimization algorithms which are usually not available with existing softwares. In addition, VRPsolve allows industrial collaborations to be addressed by solving real-world problems requiring geographic information systems (GIS).

FUNCTIONAL DESCRIPTION

The current release includes the following functional and technical specifications:

- A modular architecture which allows for an easy integration into a global information system (with respect to data standards, weak coupling with external libraries, etc),
- An independent geographic information system with graphic display,
- A resolution engine based on metaheuristics (running in a high-performance computing mode),
- The possibility of coupling with other optimization solvers and frameworks like Paradiseo (in order to enable a quick prototyping of new optimization algorithms),
- Objective- and constraint-handling that can be easily configured by the user,
- Software engineering (build system testing, continuous integration, etc).

6.5. Platforms

6.5.1. Grid'5000

The Grid'5000 experimental platform is a scientific instrument to support computer science research related to distributed systems, including parallel processing, high performance computing, cloud computing, operating systems, peer-to-peer systems and networks. It is distributed on 10 sites in France and Luxembourg, including Lyon. Grid'5000 is a unique platform as it offers to researchers many and varied hardware resources and a complete software stack to conduct complex experiments, ensure reproducibility and ease understanding of results.

- Participants: F. Desprez, F. Huet, E. Jeannot, Y. Jegou, A. Lebre, L. Lefevre, F. Loui, D. Margery, N. Melab, J-M. Menaud, P. Neyron, L. Nussbaum, C. Perez, J-M. Pierson, O. Richard., S. Varette.
- Contact: Frédéric Desprez
- URL: https://www.grid5000.fr/mediawiki/index.php/Grid5000:Home

DREAMPAL Project-Team

5. New Software and Platforms

5.1. HoMade

KEYWORDS: SoC - Multicore - Softcore
FUNCTIONAL DESCRIPTION

HoMade is a softcore processor. The current version is reflective (i.e., the program it executes is self-modifiable), and statically configurable, dynamically reconfigurable multi-processors are the next steps. Users have to add to it the functionality they need in their applications via IPs. We have also being developing a library of IPs for the most common processor functions (ALU, registers, ...). All the design is in VHDL except for some schematic specifications.

- Participant: Jean Luc Dekeyser
- Partner: LIFL
- Contact: Jean Luc Dekeyser
- URL: https://sites.google.com/site/homadeguideen/home

5.2. JHomade

FUNCTIONAL DESCRIPTION

JHomade is a software suite written in JAVA, including compilers and tools for the HoMade processor. It allows us to compile HiHope programs to Homade machine code and load the resulting binaries on FPGA boards. It was first released in 2013. The second version in 2014 includes several new features, like a C-frontend, a few optimizations (automatic inlining and more compact byte-code), a binary decoder and a code-generator for VHDL simulation. New features of the HiHope language are described in [19].

- Contact: Frédéric Guyomarch
- URL: https://gforge.inria.fr/frs/?group_id=3646

FUN Project-Team

6. New Software and Platforms

6.1. IoT-LAB robots

KEYWORDS: Internet of things - Robotics
FUNCTIONAL DESCRIPTION

IoT-LAB robots is an embedded robot controller on a Turtlebot2 providing the IoT-LAB node mobility functionality.

- Partner: Université de Strasbourg

6.2. FIT IoT-Lab

Participants: Raymond Borenstein, Nathalie Mitton [correspondant], Julien Vandaele.

FIT IoT-LAB is a very large scale open testbed that features over 2700 wireless sensor nodes and more than 200 robots spread across six different sites in France. Nodes are either fixed or mobile and can be allocated in various topologies throughout all sites. A variety of wireless sensors are available, with different processor architectures (MSP430, STM32 and Cortex-A8) and different wireless chips (802.15.4 PHY at 800 MHz or 2.4 GHz). In addition, "open nodes" can receive custom wireless sensors for inclusion in IoT-LAB testbed. This platform is completely open and can be used by any one wishing to run experiment on wireless sensors and robots.

The Lille site displays 3 subsets of the platforms:

- Euratechnologies : this site features 256 WSN430 sensor nodes operating in the 2.4GHz band. 64 nodes are mobile, embedded on mobile trains.

- Haute Borne : this site features 256 M3 sensor nodes operating in the 2.4GHz band and 64 mobile robots (32 turtlebots and 32 wifibots) completely remotely programmable.

- Opennodes : this site will feature (opening beginning 2015) 64 hardware open slots to allow any one to plug his own hardware and benefits from the platform debugging and monitoring tools.

INOCS Team (section vide)

LINKS Team

6. New Software and Platforms

6.1. QuiX Tool suite

KEYWORDS: XML - JSon - Xproc - XSLT - Schematron - Xquery - NoSQL
SCIENTIFIC DESCRIPTION

The QuiX-Tool Suite provides tools to process XML streams and documents. The QuiX-Tool Suite is based on early algorithms: query answers are delivered as soon as possible and in all practical cases at the earliest time point. The QuiX-Tool Suite provides an implementation of the main XML standart over streams. XPath, XSLT, XQuery and XProc are W3C standarts while Schematron is an ISO one. The QuiX-Tool suite is developed in the Inria transfer project QuiXProc in cooperation with Innovimax. It includes among the others existing tools such as FXP and QuixPath, along with new tools, namely X-Fun. Both, a free and a professional version are available. The ownership of QuiX-Tool Suite is shared between Inria and Innovimax. The main application of QuiX-Tool Suite is its usage in QuiXProc, an professional implementation of the W3C pipeline language XProc owned by Innovimax.

The QuiXPath language is a large fragment of XPath with full support for the XML data model. The QuiXPath library provides a compiler from QuiXPath to FXP, which is a library for querying XML streams with a fragment of temporal logic.

The X-Fun language is a functional language for defining transformations between XML data trees, while providing shredding instructions. X-Fun can be understood as an extension of Frisch's XStream language with output shredding, while pattern matching is replaced by tree navigation with XPath expressions. The QuiX-Tool suite includes QuiXSLT, which is a compiler from XSLT into a fragment of X-Fun, which can be considered as the core of XSLT. It also provides QuiXSchematron, which is a compiler from Schematron to X-Fun, and QuiXQuery, which is a compiler from XQuery to X-Fun.
FUNCTIONAL DESCRIPTION

QuiX Tool suite reads and processes large XML files without loading the entire file in main memory. Instead of building a tree representation of the XML document, QuiXProc manages data as streams (sequence of opening and closing tags).

- Participants: Joachim Niehren and Tom Sebastian
- Partner: Innovimax
- Contact: Joachim Niehren
- URL: https://project.inria.fr/quix-tool-suite/

6.2. SmartHal

FUNCTIONAL DESCRIPTION

SmartHal is a better tool for querying the HAL bibliography database, while is based on Haltool queries. The idea is that a Haltool query returns an XML document that can be queried further. In order to do so, SmartHal provides a new query language. Its queries are conjunctions of Haltool queries (for a list of laboratories or authors) with expressive Boolean queries by which answers of Haltool queries can be refined. These Boolean refinement queries are automatically translated to XQuery and executed by Saxon. A java application for extraction from the command line is available.

- Participants: Guillaume Bagan and Joachim Nierhen
- Contact: Joachim Niehren
- URL: http://smarthal.lille.inria.fr/

6.3. X-FUN

KEYWORDS: XML - Transformation - Functional programming - Compilers - Programming language
FUNCTIONAL DESCRIPTION

X-FUN is a core language for implementing various XML, standards in a uniform manner. X-Fun is a higher-order functional programming language for transforming data trees based on node selection queries.

- Participants: Pavel Labath and Joachim Niehren
- Contact: Joachim Niehren

MAGNET Team

6. New Software and Platforms

6.1. CoRTex

Python library for noun phrase COreference Resolution in natural language TEXts

FUNCTIONAL DESCRIPTION

CoRTex is a LGPL-licensed Python library for Noun Phrase coreference resolution in natural language texts. This library contains implementations of various state-of-the-art coreference resolution algorithms, including those developed in our research. In addition, it provides a set of APIs and utilities for text preprocessing, reading the main annotation formats (ACE, CoNLL and MUC), and performing evaluation based on the main evaluation metrics (MUC, B-CUBED, and CEAF). As such, CoRTex provides benchmarks for researchers working on coreference resolution, but it is also of interest for developers who want to integrate a coreference resolution within a larger platform.

- Participants: Pascal Denis and David Chatel
- Contact: Pascal Denis
- URL: https://gforge.inria.fr/projects/cortex/

MEPHYSTO Team

6. New Software and Platforms

6.1. MODULEF

FUNCTIONAL DESCRIPTION

The numerical method to approximate the constitutive laws for rubber elasticity derived from polymer physics are implemented in the Inria software Modulef.

It is based on : - algorithms from stochastic geometry to generate suitable polymer networks, - Delaunay tessellation algorithms to deal with steric effects (courtesy of the Inria project-team GAMMA2), - the introduction of 1-dimensional finite elements for the polymer-chains in Modulef.

- Participants: Marina Vidrascu and Antoine Gloria
- Contact: Marina Vidrascu
- URL: https://www.rocq.inria.fr/modulef/

MINT Project-Team

5. New Software and Platforms

5.1. Revil

SCIENTIFIC DESCRIPTION

Revil is an application for building and manipulating 3D SceneGraphs for Mixed-Reality Artistic Performances.It relies on the approach of revealing virtual content in the physical space by intersecting it with performers and spectator's bodies and props.

FUNCTIONAL DESCRIPTION

It provides a GUI for setting up the projectors, depth cameras and scene objects. It is based on OpenScene-Graph, OpenNI2 and is entirely controllable via OpenSoundControl messages so that it can be connected to Digital Musical Instruments and other interactive systems.

- Participants: Florent Berthaut, Cagan Arslan
- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/Revil

5.2. libgina

FUNCTIONAL DESCRIPTION

LibGINA is a library for fast prototyping of gestural interaction.
In 2015, new features were added in the context of Nicolas Bremard's thesis. The software was used in various projects.

- Participants: Nicolas Bremard and Laurent Grisoni
- Contact: Laurent Grisoni

5.3. SmartInteraction

FUNCTIONAL DESCRIPTION

SmartInteraction is a library, result from the FUI SmartStore project. It allows mobile services to be activated easily through automatic connection to interaction public spots, without specific user action.

- Participants: Samuel Degrande, Laurent Grisoni
- Contact: Samuel Degrande

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

6. New Software and Platforms

6.1. Introduction

Each software listed below is characterized according to the *criteria for software self-assessment* proposed by Inria's Evaluation Committee. Note that the only software mentioned here are those that were created or significantly modified during the year.

6.2. Libpointing

Participants: Géry Casiez [correspondent], Nicolas Roussel, Izzatbek Mukhanov, Sébastien Poulmane.

Libpointing is a software toolkit that provides direct access to HID pointing devices and supports the design and evaluation of pointing transfer functions [3]. The toolkit provides resolution and frequency information for the available pointing and display devices and makes it easy to choose between them at run-time through the use of URIs. It allows to bypass the system's transfer functions to receive raw asynchronous events from one or more pointing devices. It replicates as faithfully as possible the transfer functions used by Microsoft Windows, Apple OS X and Xorg (the X.Org Foundation server). Running on these three platforms, it makes it possible to compare the replicated functions to the genuine ones as well as custom ones. The toolkit is written in C++ with Python, Java and Node.js bindings available (about 49,000 lines of code in total). It is publicly available under the GPLv2 license.

The library has been thoroughly improved in 2015. Notable changes concern the management of pointing devices and displays, the standardization of URIs on all platforms, HID reports parsing on Linux and OS X, the integration of floating pixel coordinates and subpixel interaction [34], the improvement of existing bindings and the addition of Node.js ones, and support for Web browser integration.

Web site: http://libpointing.org/

Software characterization: [A-3] [SO-3] [SM-2] [EM-2↑] [SDL-5]

6.3. Liblag

Participants: Géry Casiez [correspondent], Matthieu Falce, Nicolas Roussel.

Liblag is a software toolkit designed to support the comparison of latency compensation techniques. The toolkit notably includes a playground application that allows to compare different trajectory prediction algorithms on desktop (OS X and Ubuntu) and mobile (iOS and Android) systems. The source code for this toolkit (about 8,500 lines of code) is only available to Turbotouch partners for now.

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

6.4. Mouse-based lagmeter

Participants: Géry Casiez [correspondent], Stéphane Huot, Matthieu Falce, Nicolas Roussel.

As part of the work reported in [18], we implemented our mouse-based method for measuring end-to-end latency using Java/Swing, C++/GLUT, C++/Qt and JavaScript/HTML5. We also wrote Python scripts to parse the logs generated by these implementations in order to compare them. This software (about 2,500 lines of code) should be made available in 2016.

Software characterization: [A-1] [SO-4] [SM-1] [EM-2] [SDL-1]

MODAL Project-Team

6. New Software and Platforms

6.1. BlockCluster

SCIENTIFIC DESCRIPTION

Simultaneous clustering of rows and columns, usually designated by biclustering, co-clustering or block clustering, is an important technique in two way data analysis. It consists of estimating a mixture model which takes into account the block clustering problem on both the individual and variables sets. The blockcluster package provides a bridge between the C++ core library and the R statistical computing environment. This package allows to co-cluster binary, contingency, continuous and categorical data-sets. It also provides utility functions to visualize the results. This package may be useful for various applications in fields of Data mining, Information retrieval, Biology, computer vision and many more.

FUNCTIONAL DESCRIPTION

BlockCluster is an R package for co-clustering of binary, contingency and continuous data based on mixture models.

- Participants: Parmeet Bhatia, Serge Iovleff, Vincent Brault, Christophe Biernacki, Gilles Celeux and Vincent Kubicki
- Partner: Université de Technologie de Compiègne
- Contact: Serge Iovleff
- URL: http://cran.r-project.org/web/packages/blockcluster/index.html

6.2. Clustericat

FUNCTIONAL DESCRIPTION

Clustericat is an R package for model-based clustering of categorical data. In this package, the Conditional Correlated Model (CCM), published in 2014, takes into account the main conditional dependencies between variables through extreme dependence situations (independence and deterministic dependence). Clustericat performs the model selection and provides the best model according to the BIC criterion and the maximum likelihood estimates.

- Participants: Matthieu Marbac-Lourdelle, Vincent Vandewalle and Christophe Biernacki
- Contact: Matthieu Marbac-Lourdelle
- URL: https://r-forge.r-project.org/R/?group_id=1803

6.3. CoModes

FUNCTIONAL DESCRIPTION

CoModes is another R package for model-based clustering of categorical data. In this package, the Conditional Modes Model (CMM), submitted for publication in 2014, takes into account the main conditional dependencies between variables through particular modality crossings (so-called modes). CoModes performs the model selection and provides the best model according to the exact integrated likelihood criterion and the maximum likelihood estimates.

- Participants: Matthieu Marbac-Lourdelle, Vincent Vandewalle and Christophe Biernacki
- Contact: Christophe Biernacki
- URL: https://r-forge.r-project.org/R/?group_id=1809

6.4. CorReg

FUNCTIONAL DESCRIPTION

The main idea of the CorReg package is to consider some form of sub-regression models, some variables defining others. We can then remove temporarily some of the variables to overcome ill-conditioned matrices inherent in linear regression and then reinject the deleted information, based on the structure that links the variables. The final model therefore takes into account all the variables but without suffering from the consequences of correlations between variables or high dimension.

- Participants: Clément Thery and Christophe Biernacki
- Contact: Clément Thery
- URL: https://cran.r-project.org/web/packages/CorReg/index.html

6.5. FunFEM

FUNCTIONAL DESCRIPTION

FunFEM package for R proposes a clustering tool for functional data. The model-based algorithm clusters the functional data into discriminative subspaces.

- Participants: Charles Bouveyron and Julien Jacques
- Contact: Charles Bouveyron
- URL: https://cran.r-project.org/web/packages/funFEM/index.html

6.6. FunHDDC

FUNCTIONAL DESCRIPTION

FunHDDC package for R proposes a clustering tool for functional data. The model-based clustering algorithm considers that functional data live in cluster-specific subspaces.

- Participants: Charles Bouveyron and Julien Jacques
- Contact: Charles Bouveyron
- URL: https://cran.r-project.org/web/packages/funHDDC/index.html

6.7. Galaxy - MPAgenomics

FUNCTIONAL DESCRIPTION

Galaxy is an open, web-based platform for data intensive biomedical research. Galaxy features user friendly interface, workflow management, sharing functionalities and is widely used in the biologist community. The MPAgenomics R package developped by Modal has been integrated into Galaxy, and the Galaxy-Modal instance has been publicly deployed thanks to the IFB-cloud infrastructure.

- Participants: Guillemette Marot and Samuel Blanck
- Contact: Guillemette Marot
- URL: https://cloud.france-bioinformatique.fr/accounts/login/

6.8. HDPenReg

FUNCTIONAL DESCRIPTION

HDPenReg (High-Dimensional Penalized Regression) is an R-package based on a C++ code dedicated to the estimation of regression model with l1-penalization.

- Participants: Quentin Grimonprez and Serge Iovleff
- Contact: Quentin Grimonprez
- URL: https://cran.r-project.org/web/packages/HDPenReg/index.html

6.9. MPAGenomics

KEYWORDS: Segmentation - Genomics - Marker selection - Biostatistics
SCIENTIFIC DESCRIPTION

MPAgenomics (Multi-Patient Analysis of Genomic markers) is an R package for multi-patients analysis of genomics markers. It enables to study several copy number and SNP data profiles at the same time. It offers wrappers from commonly used packages to offer a pipeline for beginners in R. It also proposes a special way of choosing some crucial parameters to change some default values which were not adapted in the original packages. For multi-patients analysis, it wraps some penalized regression methods implemented in HDPenReg.

FUNCTIONAL DESCRIPTION

MPAgenomics provides functions to preprocess and analyze genomic data. It is devoted to: (i) efficient segmentation and (ii) genomic marker selection from multi-patient copy number and SNP data profiles.

- Participants: Quentin Grimonprez, Guillemette Marot and Samuel Blanck
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/MPAgenomics/index.html

6.10. MetaMA

FUNCTIONAL DESCRIPTION

MetaMA (Meta-analysis for MicroArrays) is a specialised software for microarrays. It is an R package which combines either p-values or modified effect sizes from different studies to find differentially expressed genes. The main competitor of metaMA is geneMeta. Compared to geneMeta, metaMA offers an improvement for small sample size datasets since the corresponding modelling is based on shrinkage approaches.

- Participant: Guillemette Marot
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/metaMA/index.html

6.11. MetaRNASeq

FUNCTIONAL DESCRIPTION

This is joint work with Andrea Rau (INRA, Jouy-en-Josas). MetaRNASeq is a specialised software for RNA-seq experiments. It is an R package which is an adaptation of the MetaMA package presented previously. Both implement the same kind of methods but specificities of the two types of technologies require some adaptations to each one.

- Participants: Guillemette Marot and Andrea Rau
- Contact: Guillemette Marot
- URL: https://cran.r-project.org/web/packages/metaRNASeq/index.html

6.12. MixAll

FUNCTIONAL DESCRIPTION

MixAll (Clustering using Mixture Models) is a model-based clustering package for modelling mixed data sets. It has been engineered around the idea of easy and quick integration of any kind of mixture models for any kind of data, under the conditional independence assumption. Currently five models (Gaussian mixtures, categorical mixtures, Poisson mixtures, Gamma mixtures and kernel mixtures) are implemented. MixAll has the ability to natively manage completely missing values when assumed as random. MixAll is used as an R package, but its internals are coded in C++ as part of the STK++ library (www.stkpp.org) for faster computation.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/MixAll/

6.13. MixCluster

FUNCTIONAL DESCRIPTION

MixCluster is an R package for model-based clustering of mixed data (continuous, binary, integer). In this package, the model, submitted for publication in 2014, takes into account the main conditional dependencies between variables through Gaussian copula. Mixcluster performs the model selection and provides the best model according to Bayesian approaches.

- Participants: Matthieu Marbac-Lourdelle, Christophe Biernacki and Vincent Vandewalle
- Contact: Christophe Biernacki
- URL: https://r-forge.r-project.org/R/?group_id=1939

6.14. Mixmod

FUNCTIONAL DESCRIPTION

Mixmod is a free toolbox for data mining and statistical learning designed for large and highdimensional data sets. Mixmod provides reliable estimation algorithms and relevant model selection criteria.

It has been successfully applied to marketing, credit scoring, epidemiology, genomics and reliability among other domains. Its particularity is to propose a model-based approach leading to a lot of methods for classification and clustering.

Mixmod allows to assess the stability of the results with simple and thorough scores. It provides an easy-to-use graphical user interface (mixmodGUI) and functions for the R (Rmixmod) and Matlab (mixmodForMatlab) environments.

- Participants: Christophe Biernacki, Gilles Celeux, Gérard Govaert, Florent Langrognet, Serge Iovleff, Remi Lebret and Benjamin Auder
- Partners: CNRS - Université Lille 1 - LIFL - Laboratoire Paul Painlevé - HEUDIASYC - LMB
- Contact: Christophe Biernacki
- URL: http://www.mixmod.org

6.15. MixtComp

FUNCTIONAL DESCRIPTION

MixtComp (Mixture Computation) is a model-based clustering package for mixed data originating from the Modal team (Inria Lille). It has been engineered around the idea of easy and quick integration of all new univariate models, under the conditional independence assumption. New models will eventually be available from researches, carried out by the Modal team or by other teams. Currently, central architecture of MixtComp is built and functionality has been field-tested through industry partnerships. Three basic models (Gaussian, multinomial, Poisson) are implemented, as well as two advanced models (Ordinal and Rank). MixtComp has the ability to natively manage missing data (completely or by interval). MixtComp is used as an R package, but its internals are coded in C++ using state of the art libraries for faster computation.

- Participants: Vincent Kubicki, Christophe Biernacki and Serge Iovleff
- Contact: Christophe Biernacki
- URL: https://modal-research.lille.inria.fr/BigStat

6.16. RankCluster

FUNCTIONAL DESCRIPTION

Rankcluster package for R proposes a clustering tool for ranking data. Multivariate and partial rankings can be also taken into account. Rankcluster now supports tied ranking data.

- Participants: Christophe Biernacki, Julien Jacques and Quentin Grimonprez
- Contact: Quentin Grimonprez
- URL: https://cran.r-project.org/web/packages/Rankcluster/index.html

6.17. STK++

FUNCTIONAL DESCRIPTION

STK++ (C++ Statistical ToolKit) is a versatile, fast, reliable and elegant collection of C++ classes for statistics, clustering, linear algebra, arrays (with an API Eigen-like), regression, dimension reduction, etc. The library is interfaced with lapack for many linear algebra usual methods. Some functionalities provided by the library are available in the R environment using rtkpp and rtkore.

STK++ is suitable for projects ranging from small one-off projects to complete data mining application suites.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: http://www.stkpp.org

6.18. clere

FUNCTIONAL DESCRIPTION

The clere package for R proposes variable clustering in high dimensional linear regression. Available on CRAN and now submitted to an international journal dedicated to software.

- Participants: Loïc Yengo, Christophe Biernacki and Julien Jacques
- Contact: Loïc Yengo
- URL: https://cran.r-project.org/web/packages/clere/index.html

6.19. rtkore

FUNCTIONAL DESCRIPTION

STK++ (http://www.stkpp.org) is a collection of C++ classes for statistics, clustering, linear algebra, arrays (with an Eigen-like API), regression, dimension reduction, etc. The integration of the library to R is using Rcpp. The rtkore (STK++ core library integration to R using Rcpp) package includes the header files from the STK++ core library. All files contain only templated classes or inlined functions. STK++ is licensed under the GNU LGPL version 2 or later. rtkore (the stkpp integration into R) is licensed under the GNU GPL version 2 or later. See file LICENSE.note for details.

- Participant: Serge Iovleff
- Contact: Serge Iovleff
- URL: https://cran.r-project.org/web/packages/rtkore/index.html

NON-A Project-Team

5. New Software and Platforms

5.1. Blimp

FUNCTIONAL DESCRIPTION

Scientific research and development on the control of autonomous airships have shown a significant growth in recent years. New applications appear in the areas such as freight carrier, advertising, monitoring, surveillance, transportation, military and scientific research. The control of autonomous airships is a very important problem for the aerial robots research.

The development of Blimp by Non-A is used for experimentation and demonstration of controlling algorithms. The blimp is required to provide some environment information and status of itself, such as surveillance video of surrounding environment, gesture of blimp, altitude of blimp. With these basic information, one could localize blimp with certain algorithm (visual SLAM for example) or implement one controller in order to improve the stability and maneuverability of blimp.

- Contact: Jean-Pierre Richard

5.2. SLIM

FUNCTIONAL DESCRIPTION

Multi-robots cooperation can be found as an application in many domains of science and technology: manufacturing, medical robotics, personal assistance, military/security and spatial robots. The market of robots is quickly developing and its capacity is continuously growing. Concerning cooperation of mobile multi-robots, 3 key issues have to be studied: Localization, path planning and robust control, for which Non-A team has worked and proposed new algorithms. Due to the ADT SLIM, we implement our algorithms (localization, path planning and robust control) and integrate them into ROS (Robotic Operating System) as a package, named SLIM.

- Contact: Jean-Pierre Richard

RAPSODI Team

6. New Software and Platforms

6.1. New Software and Platforms

We develop and freely distribute a new version of the matlab code NS2DDV-M (equipped with a graphic interface and an accurate documentation) to promote new collaborations in the domain, allow some easy comparisons with concurrent codes on the same benchmark cases, and compare alternative numerical solution methods. Contacts: Caterina Calgaro & Emmanuel Creusé.

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

6. New Software and Platforms

6.1. Moose

FUNCTIONAL DESCRIPTION

Moose is an extensive platform for software and data analysis. It offers multiple services ranging from importing and parsing data, to modeling, to measuring, querying, mining, and to building interactive and visual analysis tools.

- Participants: Stéphane Ducasse, Muhammad Bhatti, Andre Cavalcante Hora, Nicolas Anquetil, Anne Etien, Guillaume Larcheveque and Alexandre Bergel
- Partners: Université de Berne - Sensus - Synectique - Pleiad - USI - Vrije Universiteit Brussel
- Contact: Stéphane Ducasse
- URL: http://www.moosetechnology.org

6.2. Pharo

KEYWORDS: Live programmation objet - Reflective system
FUNCTIONAL DESCRIPTION

The platform Pharo is an open-source Smalltalk-inspired language and environment. It provides a platform for innovative development both in industry and research. By providing a stable and small core system, excellent developer tools, and maintained releases, Pharo's goal is to be a platform to build and deploy mission critical applications, while at the same time continue to evolve.

- Participants: Marcus Denker, Damien Cassou, Christophe Demarey, Stéphane Ducasse, Esteban Lorenzano, Damien Pollet, Camille Teruel and Clément Béra
- Partners: Université de Berne - École des Mines de Douai - Uqbar foundation Argentina - Sensus - Synectique - Pleiad - Debris publishing - Yesplan - HR Works - MAD - BetaNine - Vmware
- Contact: Marcus Denker
- URL: http://www.pharo.org

6.3. Pillar

KEYWORDS: HTML - LaTeX - HTML5
FUNCTIONAL DESCRIPTION

Pillar is a markup syntax and associated tools to write and generate documentation and books. Pillar is currently used to write several books and other documentation. Two platforms have already been created on top of Pillar: PillarHub and Marina.

- Contact: Damien Cassou
- URL: http://www.smalltalkhub.com/#!/~Pier/Pillar

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

6. New Software and Platforms

6.1. Function optimization

Participants: Jean-Bastien Grill, Michal Valko, Rémi Munos.

6.1.1. POO

This is a black-box function optimization toolkit that finds the global optimum of a function given a finite budget of noisy evaluations. The algorithm does not require the knowledge of the function's smoothness. It works for a larger class of functions than what was previously considered, especially for functions that are difficult to optimize, in a precise sense.

SPIRALS Project-Team

6. New Software and Platforms

6.1. APISENSE®

Participants: Clive Ferret-Canape, Julien Duribreux, Maria Gomez Lacruz, Christophe Ribeiro, Romain Rouvoy, Antoine Veuiller.

- Contact: Romain Rouvoy
- URL: https://bil.inria.fr/fr/software/view/614/tab

In 2015, APISENSE® has been extended to include the support for iOS smartphones and tablets. The infrastructure, hosted by the LHS (*Laboratoire Haute Sécurité*), is now fully secured to protect the privacy of contributors.

APISENSE® is a distributed platform dedicated to crowd-sensing activities. Crowd-sensing intends to leverage mobile devices to seamlessly collect valuable dataset for different categories of stakeholders. APISENSE® intends to be used in a wide variety of scientific and industrial domains, including network quality monitoring, social behavior analysis, epidemy predictions, emergency crisis support, open maps initiatives, debugging of applications in the wide. APISENSE® is composed of HIVE delivered as a *Platform-as-a-Service* (PaaS) to the stakeholders who can pilot and customize their own crowd-sensing environment [79], and *Bee* supporting participants with a mobile application to control the sensors to be shared with the rest of the world [68], [69]. The platform is used by the Metroscope consortium, an Internet scientific observatory initiative supported by Inria. APISENSE® originates as the output of Nicolas Haderer PhD thesis [67].

APISENSE® is at the core of the Inria ADT Focus CrowdLab project (see Section 9.2) and of an industrial transfer action that aims at creating the Crowdify spin-off company.

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6.2. PowerAPI

Participants: Maxime Colmant, Loïc Huertas, Romain Rouvoy.

- Contact: Romain Rouvoy
- URL: https://bil.inria.fr/fr/software/view/1642/tab

In 2015, POWERAPI has been further extended to support the monitoring of *Software-as-a-Service* (SaaS) [23] by including a support for hypervision technologies like KVM (*Kernel-based Virtual Machine*), and Docker.

POWERAPI is a Scala-based library for monitoring energy in software systems. It is based on a modular and asynchronous event-driven architecture using the Akka library. POWERAPI differs from existing energy process-level monitoring tool in its pure software, fully customizable and modular aspect which let users precisely define what they want to monitor, without plugging any external device. POWERAPI offers an API which can be used to express requests about energy spent by a process, following its hardware resource utilization (in terms of CPU, memory, disk, network, etc.). Its applications cover energy-driven benchmarking [75], [62], [60], [61], energy hotspots and bugs detection [76], [77], and real-time distributed system monitoring. POWERAPI originates as the output of Adel Noureddine PhD thesis [78].

POWERAPI is at the core of the Inria ADT eSurgeon project (see Section 9.2).

Web site: http://www.powerapi.org. Registered with the APP (Agence pour la Protection des Programmes) under reference IDDN.FR.001.400015.000.S.P.2012.000.10000. License: AGPL.

6.3. Saloon

Participants: Laurence Duchien, Daniel Romero Acero, Lionel Seinturier [correspondant].

- Contact: Lionel Seinturier
- URL: https://bil.inria.fr/fr/software/view/1492/tab

In 2015, SALOON was extended to fit with the requirements of the FP7 PaaSage project (see Section 9.3). New mechanisms were added to deal with ontologies for describing cloud computing commercial offers.

SALOON is a framework for the selection and configuration of Cloud providers according to application requirements. The framework enables the specification of such requirements by defining ontologies. Each ontology provides a unified vision of provider offers in terms of frameworks, databases, languages, application servers and computational resources (i.e., memory, storage and CPU frequency). Furthermore, each provider is related to a Feature Model (FM) with attributes and cardinalities, which captures its capabilities. By combining the ontology and FMs, the framework is able to match application requirements with provider capabilities and select a suitable one. Specific scripts to the selected provider are generated in order to enable its configuration. SALOON originates as the output of Clément Quinton PhD thesis [82].

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6.4. Spoon

Participants: Thomas Durieux, Matias Martinez, Martin Monperrus, Gérard Paligot, Nicolas Petitprez.

- Contact: Martin Monperrus
- URL: https://bil.inria.fr/fr/software/view/251/tab

SPOON is a library for analyzing and transforming Java source code [18] [80]. In 2015, there was one engineer (Géradar Paligot) working full-time on Spoon. This has incredibly boosted the project. In particular, the new features of SPOON are: a) the complete support for Java 8 (incl. lambda expressions) b) the support for Maven and Gradle build systems. Also, a major testing effort has been done and consequently, the code quality now meets the highest standards, using a comprehensive test suite as well three continuous integration servers (incl. the Inria one). Spoon has an an international community of users and contributors, which is very active on the Github project.

SPOON is at the core of the Inria ADT Spoon3R project (see Section 9.1) SPOON is the foundation behind an industrial transfer action that aims at creating the Spoonware spin-off company on automatic hot patching.

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