



RESEARCH CENTER
Lille - Nord Europe

FIELD

Activity Report 2013

Section Software

Edition: 2014-03-19

1. ADAM Project-Team	4
2. ATEAMS Project-Team	6
3. BONSAI Project-Team	10
4. DOLPHIN Project-Team	14
5. DREAMPAL Team	16
6. FUN Project-Team	17
7. LINKS Team	18
8. MAGNET Team	19
9. MINT Project-Team	20
10. MODAL Project-Team	22
11. NON-A Project-Team	25
12. RMOD Project-Team	26
13. SequeL Project-Team	30
14. SHACRA Project-Team	31
15. SIMPAF Project-Team	32

ADAM Project-Team

5. Software and Platforms

5.1. APISENSE

Participants: María Gómez Lacruz, Nicolas Haderer, Christophe Ribeiro, Romain Rouvoy [correspondant].

APISENSE[®] is a distributed platform dedicated to crowdsensing activities [30], [31], [24], [77], [67], [66]. Crowdsensing 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, epidemic predictions, emergency crisis support, open maps initiatives, wild applications debugging. APISENSE[®] is composed of a HIVE and an HONEYCOMB delivered as a *Platform-as-a-Service* (PaaS) to the stakeholders who can pilot and customize their own crowdsensing environment [77], and *Bee.mob* supporting participants with a mobile application to control the sensors to be shared with the rest of the world [30], [31]. The platform is used by the **Metroscope** project, an Internet scientific observatory initiative supported by Inria.

Web site: <http://www.apisense.fr>. Registered with the APP (*Agence pour la Protection des Programmes*) under reference IDDN.FR.001.080006.000.S.P.2013.000.10000 is pending. License: Proprietary.

5.2. FraSCaTi

Participants: Gwenaël Cattez, Philippe Merle [correspondant], Fawaz Paraíso, Romain Rouvoy, Lionel Seinturier.

FraSCaTi is a service-oriented component-based middleware platform implementing OASIS *Service Component Architecture* (SCA) specifications. The main originality of OW2 FraSCaTi is to bring FRACTAL-based reflectivity to SCA, *i.e.*, any FraSCaTi software component is equipped with both the SOA capabilities brought by SCA and the reflective capabilities (*i.e.*, introspection and reconfiguration) brought by FRACTAL. Various micro-benchmarks have shown that FraSCaTi reflectivity is achieved without hindering its performance relative to the de facto reference SCA implementation, *i.e.*, Apache Tuscany. Non-functional concerns (logging, transaction, security, etc.), so called intents in SCA terms, are also programmed as FraSCaTi components and are (un)woven on business components dynamically at runtime, this is based on aspect-oriented concepts defined in FAC [78]. OW2 FraSCaTi supports various implementation technologies (SCA Composite, Java, WS-BPEL, Spring Framework, OSGi, Fractal ADL, native C library, Apache Velocity templates, and seven scripting languages as BeanShell, FScript, Groovy, JavaScript, JRuby, Jython, XQuery) for programming services or integrating legacy code, various binding protocols (SOAP, REST, JSON-RPC, UPnP, HTTP servlets, Java RMI, JMS, JGroups) and interface definition languages (WSDL, Java, WADL) for inter-operating with existing services. OW2 FraSCaTi provides management tools like standalone, Web-based, and JMX-based graphical consoles and a dedicated scripting language for reconfiguring SCA applications. The whole OW2 FraSCaTi platform is itself built as a set of reflective SCA components.

Inria Evaluation Committee Criteria for Software Self-Assessment: A-4-up, SO-4, SM-4-up, EM-3-up, SDL-4-up, DA-4, CD-4, MS-4, TPM-4. FraSCaTi is a project of the OW2 consortium for open-source middleware. Web site: <http://frascati.ow2.org>. 292 Kloc (mainly Java). Registered with the APP (*Agence pour la Protection des Programmes*) under reference FR.001.050017.000.S.P.2010.000.10000. License: LGPL. Embedded into several industrial software systems: EasySOA, Petals Link EasyViper, EasyBPEL, EasyESB, OW2 PETALS, OW2 Scarbo. Various demonstrators built during funded projects: ANR SCORWare, FP7 SOA4All, ANR ITeMIS, ANR SALTY, ANR SocEDA, FUI Macchiato, FUI EasySOA, ADT Galaxy and ADT Adapt. Main publications: [82], [81], [70], [71], [62], [61].

5.3. PowerAPI

Participants: Aurélien Bourdon, Maxime Colmant, Loïc Huertas, Adel Noureddine, Romain Rouvoy [correspondant].

PowerAPI is a Scala-based library for monitoring energy at the process-level. 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 [74], [50], [49], [23], energy hotspots and bugs detection [75], [76] and real-time distributed system monitoring.

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.

ATEAMS Project-Team

4. Software and Platforms

4.1. MicroMachinations

Participant: Riemer Van Rozen [correspondent].

Characterization: A-2-up3, SO-4, SM-2-up3, EM-3, SDL-3-up4, OC-DA-3-CD-3-MS-3-TPM-3.

WWW:

Objective: To create an integrated, live environment for modeling and evolving game economies. This will allow game designers to experiment with different strategies to realize 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.

Users: Game designers

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 behaviors.

Competition: None.

Engineering: The front-end of MicroMachinations is built using the Rascal language workbench, including visualization, model checking, debugging and standard IDE features. The runtime library is implemented in C++ and will be evaluated in the context of industrial game design.

Publications: [28]

4.1.1. Novelties

- Development on MMLib was started which allows the execution of game economies directly within games.

4.2. Derric

Participants: Tijds Van Der Storm, Jeroen Van Den Bos [correspondent].

Characterization: A-2-up3, SO-4, SM-2-up3, EM-3, SDL-3-up4, OC-DA-3-CD-3-MS-3-TPM-3.

WWW: <http://www.derric-lang.org>

Objective: Encapsulate all the variability in the construction of so-called “carving” algorithms, then generate the fastest and most accurate implementations. Carving algorithms recover information that has been deleted or otherwise scrambled on digital media such as hard-disks, usb sticks and mobile phones.

Users: Digital forensic investigation specialists

Impact: Derric has the potential of revolutionizing the carving area. It does in 1500 lines of code what other systems need tens of thousands of lines for with the same accuracy. Derric will be an enabler for faster, more specialized and more successful location of important evidence material.

Competition: Derric competes in a small market of specialized open-source and commercial carving tools.

Engineering: Derric is a Rascal program of 1.5 kloc designed by two persons.

Publications: [35], [34][14], [16], [15]

4.2.1. Novelties

- Construction of a 1TB benchmark based on Wikipedia images.
- The Derric DSL for digital forensics now features Trinity, a runtime IDE to debug file format descriptions [35].

4.3. Rascal

Participants: Paul Klint, Jurgen Vinju [correspondent], Tijs Van Der Storm, Jeroen Van Den Bos, Mark Hills, Bert Lissner, Atze Van Der Ploeg, Vadim Zaytsev, Anastasia Izmaylova, Michael Steindorfer, Ali Afroozeh, Ashim Shahi.

Characterization: A5, SO-4, SM-4, EM-4, SDL-4-up5, OC-DA-3-CD-3-MS-3-TPM-3.

WWW: <http://www.rascal-mpl.org>

Objective: Provide a completely integrated programming language parametric meta programming language for the construction of any kind of meta program for any kind of programming language: analysis, transformation, generation, visualization.

Users: Researchers in model driven engineering, programming languages, software engineering, software analysis, as well as practitioners that need specialized tools.

Impact: Rascal is making the mechanics of meta programming into a non-issue. We can now focus on the interesting details of the particular fact extraction, model, source analysis, domain analysis as opposed to being distracted by the engineering details. Simple things are easy in Rascal and complex things are manageable, due to the integration, the general type system and high-level programming features.

Competition: There is a plethora of meta programming toolboxes and frameworks available, ranging from plain parser generators to fully integrated environments. Rascal is distinguished because it is a programming language rather than a specification formalism and because it completely integrates different technical domains (syntax definition, term rewriting, relational calculus). For simple tools, Rascal competes with scripting languages and for complex tools it competes context-free general parser generators, with query engines based on relational calculus and with term rewriting and strategic programming languages.

Engineering: Rascal is about 100 kLOC of Java code, designed by a core team of three and with a team of around 8 phd students and post-docs contributing to its design, implementation and maintenance. The goal is to work towards more bootstrapping and less Java code as the project continues.

Publications: [7], [6], [8], [5], [6]

4.3.1. Novelties

- A new language-parametric model to represent software projects, called M3 [38].
- Performance improvements of the Rascal interpreter throughout.
- Initial version of a compiler for Rascal, based on new language construct guarded coroutines.
- Origin tracking for values and expressions of type string.
- A library for accessing and analyzing Excel and Word documents.
- Improvements to the Rascal IDE: better output handling, hyper linked source code locations in the console, dedicated project explorer view.
- Content completion for DSLs implemented in Rascal.
- Significant improvements to the Rascal static type checker.
- Experiments with improved GLL parsing (Iguana).
- Several new example DSL implementations to illustrate Rascal as a language workbench: Marvol, a DSL for controlling NAO robots, and two implementations of a DSL for questionnaires (DemoQLes and QL-R-Kemi).

4.4. IDE Meta-tooling Platform

Participants: Jurgen Vinju [correspondent], Michael Steindorfer.

IMP, the IDE meta tooling platform is an Eclipse plugin developed mainly by the team of Robert M. Fuhrer at IBM TJ Watson Research institute. It is both an abstract layer for Eclipse, allowing rapid development of Eclipse based IDEs for programming languages, and a collection of meta programming tools for generating source code analysis and transformation tools.

Characterization: A5, SO-3, SM4-up5, EM-4, SDL-5, DA-2-CD-2-MS-2-TPM-2

WWW: <https://github.com/impulse-org/>

Objective: The IDE Meta Tooling Platform (IMP) provides a high-level abstraction over the Eclipse API such that programmers can extend Eclipse with new programming languages or domain specific languages in a few simple steps. IMP also provides a number of standard meta tools such as a parser generator and a domain specific language for formal specifications of configuration parameters.

Users: Designers and implementers of IDEs for programming languages and domain specific languages. Also, designers and implementers of meta programming tools.

Impact: IMP is popular among meta programmers especially for it provides the right level of abstraction.

Competition: IMP competes with other Eclipse plugins for meta programming (such as Model Driven Engineering tools), but its API is more general and more flexible. IMP is a programmers framework rather than a set of generators.

Engineering: IMP is a long-lived project of many contributors, which is managed as an Eclipse incubation project at eclipse.org. Currently we are moving the project to Github to explore more different ways of collaboration.

Publications: [2]

4.4.1. Novelties

- The IMP program database (PDB) was completely redesigned.

4.5. Ensō

Participant: Tijds Van Der Storm [correspondent].

Characterization: A5, SO-4, SM-3-up-4, EM-2-up-4, SDL-4, OC-DA-4-CD-4-MS-4-TPM-4

WWW: <http://www.enso-lang.org>

Objective: Together with Prof. Dr. William R. Cook of the University of Texas at Austin, and Alex Loh, Tijds van der Storm has been designing and implementing a new programming system, called Ensō. Ensō is theoretically sound and practical reformulation of model-based development. It is based on model-interpretation as opposed to model transformation and code generation. Currently, the system already supports models for schemas (data models), web applications, context-free grammars, diagram editors and security.

Users: All programmers.

Impact: Ensō has the potential to revolutionize the activity of programming. By looking at model driven engineering from a completely fresh perspective, with as key ingredients interpreters and partial evaluation, it may make higher level (domain level) program construction and maintenance as effective as normal programming.

Competition: Ensō competes as a programming paradigm with model driven engineering tools and generic programming and languages that provide syntax macros and language extensions.

Engineering: Ensō is a completely self-hosted system in 7000 lines of code.

Publications: [12], [17], [11]

4.5.1. Novelties

- A compiler for a dedicated Ensō language, which targets JavaScript.
- Added a demo based on the LWC'13 questionnaire language assignment.

4.6. LiveQL

Participant: Tijds Van Der Storm [correspondent].

Characterization: A1, SO-3, SM-1, EM-2, SDL-4, OC-DA-4-CD-4-MS-4-TPM-4

WWW: <https://github.com/cwi-swat/liveql>

Objective: Experimenting with live programming concepts and techniques in the context of domain specific languages (DSLs).

Users: End-user programmers.

Impact: LiveQL is an experiment in making a DSL “live”, i.e. any change to the DSL program is immediately reflected in the running program. This has the potential to widen the audience of DSL users to include end-user programmers.

Competition: The end-goal is to provide live end-user programming environments with domain-specific checking and optimization. The most similar tools are spreadsheet applications. However, these are still quite general.

Engineering: LiveQL is built in Java, using the ANTLR parser generator.

Publications: [36]

4.7. QL-R-Kemi

Participant: Tijds Van Der Storm [correspondent].

Characterization: A1, SO-3, SM-1, EM-2, SDL-4, OC-DA-4-CD-4-MS-4-TPM-4

WWW: <https://github.com/cwi-swat/QL-R-Kemi>

Objective: Demonstrate the language workbench features of the Rascal meta programming language and environment. Investigate domain specific language application in the domain of questionnaires and surveys.

Users: Students, scientists.

Impact: Questionnaires are common in social science, tax administration and statistics. Discovering the right abstractions for describing questionnaires has the potential to significantly improve the practice of constructing questionnaire software.

Competition: Traditional survey tools are often wizard-based, lack computational capabilities and lack a formal foundation. The same language is built in a number of different language workbenches which served as a benchmark to compare such tools [24].

Engineering: Uses all features of the Rascal language workbench.

Publications: [24]

BONSAI Project-Team

5. Software and Platforms

5.1. YASS – Local homology search

Actively maintained.

Software self-assessment following the mechanisms provided by Inria Evaluation Committee for software evaluation: **A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://bioinfo.lifl.fr/yass/>

Licence: GPL

YASS is a software devoted to the classical problem of genomic pairwise alignment, and use most of our knowledge to design and implement efficient seeding techniques these last years. It is frequently used, it always receives more than 300 web queries per month (excluding local queries), and is also frequently downloaded and cited.

5.2. RNA tools – RNA structure prediction and comparison

<http://bioinfo.lifl.fr/rna/>

Actively maintained/Actively developed

Inria Evaluation Committee Criteria for Software Self-Assessment: **A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

The RNA tools provide a suite of programs to help analysing RNA secondary structures, together with visualisation tools for RNA 2D structures and RNA multiple alignments. Our first tool was *carnac* for RNA structure prediction by comparative analysis. *carnac* was issued in 2004 ¹, independently benchmarked ², and re-designed in 2009. It is still cited and used. Over the years, we have add new programs: *regliss* for locally optimal secondary structures, *gardenia* for structure comparison, *CG-seq* for gene prediction by comparative analysis, ...

5.3. TFM-Explorer – Identification and analysis of transcription factor binding sites

Actively maintained.

Software self-assessment: **A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://bioinfo.lifl.fr/TFM/>

Licence: GPL

The TFM suite is a set of tools for analysis of transcription factor binding sites modeled by Position Weight Matrices. In this suite, the TFM-EXPLORER tool is designed to analyze regulatory regions of eukaryotic genomes using comparative genomics and local over-representation.

5.4. RNAspace – A platform for noncoding RNA annotation

Actively developed.

Software self-assessment: **A-5, SO-3, SM-3-up4, EM-2-up3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://www.rnaspaces.org/>

¹CARNAC: folding families of related RNAs. H. Touzet *et al.*, Nucleic Acids Research, 2004

²A comprehensive comparison of comparative RNA structure prediction approaches. P. Gardner *et al.*, BMC Bioinformatics, 2004

Licence: GPL

RNAspace is a national collaborative initiative conducted with Genopole Midi-Pyrénées and originally supported by IBISA³. The goal is to develop an open source platform for structural and functional noncoding RNA annotation in genomes (see Section 6.2): <http://www.rnaspaces.org>. The project will be pursued within France Génomique (see Section 7.2.1).

5.5. CGseq – A toolbox for comparative analysis

Actively maintained.

Software self-assessment: **A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://bioinfo.lifl.fr/CGseq/>

Licence: GPL

CG-seq is a toolbox for identifying functional regions in a genomic sequence by comparative analysis using multispecies comparison.

5.6. SortMeRNA – Metatranscriptome classification

Actively developed.

Software self-assessment: **A-4, SO-3, SM-2, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site: <http://bioinfo.lifl.fr/RNA/sortmerna>

Licence: GPL

+ *SortMeRNA*: Metatranscriptome classification

<http://bioinfo.lifl.fr/RNA/sortmerna/>

Actively developed

Inria Evaluation Committee Criteria for Software Self-Assessment: **A-4, SO-3, SM-3, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

SortMeRNA is a tool designed to rapidly filter ribosomal RNA fragments from metatranscriptomic data produced by next-generation sequencers. The distribution includes curated ribosomal RNA databases. It is available for download from our website, or through the open web-based platform Galaxy. *SortMeRNA* was released in October 2012, and is used in production by Genoscope (French National Center for Sequencing) to process metatranscriptomic data. Moreover, it has already been integrated in two published computational pipelines^{4,5} and have identified users in multiple research laboratories worldwide⁶.

5.7. Vidjil – Quantifying lymphocytes rearrangements in high-throughput sequencing data

Actively developed

Software self-assessment: **A-3-up4, SO-3, SM-2-up3, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://bioinfo.lifl.fr/vidjil>

³IBISA is a French consortium for evaluating and funding national technological platforms in life sciences.

⁴A comprehensive metatranscriptome analysis pipeline and its validation using human small intestine microbiota datasets. M. Leimena et al., *BMC genomics*, 2013

⁵Metagenome survey of a multispecies and algae-associated biofilm reveals key elements of bacterial-algae interactions in photobioreactors. I. Krohn-Molt et al. *Applied and environmental microbiology*, 2013

⁶Umeå University (Sweden), Leibniz Institute DSMZ (Germany), NGS department of Campus Science Support Facilities GmbH (Austria), Oxford Centre for Integrative Systems Biology (Great Britain), Laboratoire d'Ecologie Alpine (Grenoble), PRABI (Lyon), Wageningen University (Netherlands), ...

Vidjil implements a two-stage strategy for fast clustering and quantification of clones coming from immunological rearrangements in genomic sequences. It is currently used in “minimal residual disease” following, but could have other uses in immunology research. *Vidjil* is currently under test at the Lille hospital, and is planned to be tested in another hematological lab. In 2013, the development of *Vidjil* was supported by the regional project ABILES: an engineer (Marc Duez) developed for 5 months a graphical interface for using *Vidjil*. We plan to release a first production version to the hospital during 2014.

5.8. Biomanycores.org – A community for bioinformatics on manycore processors

Actively developed.

Software self-assessment: **A-3, SO-2, SM-3, EM-3down2, SDL-4up5, OC-4** (DA-4, CD-4, MS-4, TPM-4)

Software web site : <http://biomanycores.org/>

Manycore architectures are an emerging field of research full of promises for parallel bioinformatics. However the usage of GPUs is not so widespread in the end-user bioinformatics community. The goal of the biomanycores.org project is to gather open-source CUDA and OpenCL parallel codes and to provide easy installation, benchmarking, and interoperability. The last point includes interfaces to popular frameworks such as Biopython, BioPerl and BioJava.

The development of Biomanycores was supported by a national ADT ⁷ from October 2010 to October 2012.

5.9. Norine – A resource for nonribosomal peptides

Actively maintained.

Software self-assessment: **A-5, SO-3, SM-3-up4, EM-2-up3, SDL-4, DA-4, CD-4, MS-4, TPM-4**

Software web site : <http://bioinfo.lifl.fr/norine/> Norine is a public computational resource that contains a database of NRPs with a web interface and dedicated tools, such as a 2D graph viewer and editor for peptides or comparison of NRPs. Norine was created and is maintained by members of BONSAI team, in tight collaboration with members of the ProBioGEM lab, a microbial laboratory of Lille1 University. Since its creation in 2006, Norine has gained an international recognition as the unique database dedicated to non-ribosomal peptides because of its high quality and manually curated annotations, and has been selected by wwPDB as a reference database. It is queried from all around the world by biologists or biochemists. It receives more than 3000 queries per month. Norine main users come for 13% from the United States of America, for 12% from the United Kingdom, for 5% from China or for 4% from Germany where renowned biology laboratories work on nonribosomal peptides (NRPs) or on their synthetases.

5.10. Crac – RNA-seq read analysis

Actively maintained.

Software self-assessment: **A-4, SO-3, SM-3, EM-3, SDL-4, DA-4, CD-4, MS-4, TPM-3**

Software web site: <http://crac.gforge.inria.fr/>

Objective: CRAC aims at identifying biological variations in RNAs by comparing short reads to a reference genome. It detects point mutations, short indels, splice events, and fusion genes or transcripts.

This library is the result of a collaboration with N. Philippe and T. Commes (IGH laboratory, Montpellier) and É. Rivals (LIRMM laboratory, Montpellier).

5.11. GkArrays – Indexing high throughput sequencer reads

Actively maintained.

Software self-assessment: **A-3, SO-3, SM-3, EM-2, SDL-4, DA-4, CD-4, MS-4, TPM-3**

⁷ADT (Action for Technological Development) is an Inria internal call

Software web site : <http://crac.gforge.inria.fr/gkarrays/>

Objective : Gk-Arrays is a C++ library specifically dedicated to indexing reads produced by high-throughput sequencers. This index allows to answer queries centred on reads. It also takes benefits from the input specificity to lower space consumption.

This library is the result of a collaboration with N. Philippe and T. Combes (IGH laboratory, Montpellier), M. Léonard and T. Lecroq (LITIS laboratory, Rouen) and É. Rivals (LIRMM laboratory, Montpellier).

DOLPHIN Project-Team

5. Software and Platforms

5.1. ParadisEO

Participants: Clive Canape, Laetitia Jourdan, Arnaud Liefvooghe, Nouredine Melab, Alexandre Quemy, El-Ghazali Talbi [correspondent], Sébastien Verel.

ParadisEO (PARallel and DIStributed Evolving Objects) is a C++ white-box object-oriented framework dedicated to the flexible design of metaheuristics. See web site <http://paradisEO.gforge.inria.fr>. Based on EO, a template-based ANSI-C++ compliant evolutionary computation library, it is composed of five modules:

- ParadisEO-EO provides tools for the development of population-based metaheuristic (evolutionary and genetic algorithm, genetic programming, particle swarm optimization, etc.)
- ParadisEO-MO provides tools for the development of single solution-based metaheuristics (hill-climbing, tabu search, simulated annealing, iterative local search, variable neighborhood search, incremental evaluation, partial neighborhood, etc.)
- ParadisEO-MOEO provides tools for the design of multi-objective metaheuristics (MO fitness assignment, MO diversity preservation, elitism, performance indicators, easy-to-use state-of-the-art algorithms, etc)
- ParadisEO-PEO provides tools for the design of parallel and distributed metaheuristics (parallel evaluation, parallel evaluation function, island model)
- ParadisEO-SMP provides tools for the design of shared memory parallel metaheuristics (parallel evaluation, island model)

Furthermore, ParadisEO also introduces tools for the design of distributed, hybrid and cooperative models:

- High level hybrid metaheuristics: coevolutionary and relay models.
- Low level hybrid metaheuristics: coevolutionary and relay models.

The ParadisEO framework has been especially designed to best suit to the following objectives:

- Maximum design and code reuse: ParadisEO is based on a clear conceptual separation of the solution methods from the problems they are intended to solve. This separation confers to the user a maximum code and design reuse.
- Flexibility and adaptability: The fine-grained nature of the classes provided by the framework allows a higher flexibility compared to other frameworks.
- Utility: ParadisEO allows the user to cover a broad range of metaheuristics, problems, parallel distributed models, hybridization mechanisms, etc.
- Transparent and easy access to performance and robustness: As the optimization applications are often time-consuming the performance issue is crucial. Parallelism and distribution are two important ways to achieve high performance execution. ParadisEO is one of the rare frameworks that provide the most common parallel and distributed models. These models can be exploited in a transparent way, one has just to instantiate their associated provided classes.
- Portability: The implemented models are portable on distributed-memory machines as well as on shared-memory multiprocessors, as they use standard libraries such as MPI and `std::threads`. ParadisEO supports the most recent version of standard of the C++ programming, `c++11`.

This year a new module, ParadisEO-SMP, has been released. All the new features is managed via the Inria Gforge project <http://paradisEO.gforge.inria.fr>. The version 2.0 has been released in Septembre 2012.

5.1.1. *Paradiseo-SMP: a new module for shared memory parallel*

This year, we released a new module dedicated to shared memory parallel. This module improves the technical mechanisms of Paradiseo-PEO thanks a new software architecture and the new c++11 features.

Paradiseo-SMP implements parallel evaluation, dynamic heterogeneous island model, and their hybridization. The main features are:

- Dynamic Island Model: topology can be changed during the execution.
- Heterogeneous Islands: different kinds of population-based metaheuristics can communicate (evolutionary and genetic algorithm, particle swarm optimization, etc.).
- Island Model and master/slave model can be hybridized.

All these new features are developed in c++11.

5.1.2. *New technical features*

Regarding the technical aspects, the compatibility with dependencies taken into account is:

- c++11 features supporting.
- Checked compatibility with different operating systems.
- Reviewed and checked compatibility with new versions of the tools used (CMake, g++, clang, MinGW...).
- Unit and integration test of all additional components, and experiments on classical applications.

5.1.3. *Contributions and documentations*

Many investigations were made in this context in order to help users to manipulate the framework.

- New quick start guide is available.
- New tutorials:
 - Tutorials SMP.
 - Tutorials GPU.
- Updated implementation for classical problems.

Self-assessment of the team effort (software criteria: <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>)

(A-4-up5) Audience: 4 - Used in many universities for teaching and several companies.

(SO-4) Software Originality: 4 - ParadisEO aggregates the last results of the Dolphin team.

(SM-4) Software Maturity: 4 - Extensive documentation, strong software engineering and testing, regression testing, user feedback ...

(EM-2-up3) Evolution and Maintenance: 2 - Basic maintenance with persistent attention to users.

(SDL-4) Software Distribution and Licensing: 4 - CeCILL license, public source, Windows and Mac installer, Linux packages.

(OC) Own Contribution: (Design/Architecture) DA-4, (Coding/Debugging) CD-4, (Maintenance/Support)

MS-4, (Team/Project Management) TPM-4

DREAMPAL Team

5. Software and Platforms

5.1. Software and Platforms

Download page : https://gforge.inria.fr/frs/?group_id=3646

5.1.1. HoMade

HoMade V4 is available and was used by 140 students this year on a Xilinx Nexys3 board. The Xilinx Virtex6 and Virtex7 are also supporting this new release. All the design is in VHDL except some ISE schematic specifications.

The main novelty of this release concerns :

- three stage pipe-lining of the HoMade core,
- new execution stack to improve frequency,
- instruction memory loading via UART port,
- MSPMD support
- reflexive features: Write-In-Program-Memory (WIM) instruction
- development of new IPs.

A test with 56 HoMade Slaves on a ring topology was running on a Virtex6 on a parallel matrix-vector multiplication example.

A low-level stack-based assembler supports binary generation from a Forth-like post-fixed syntax. It is written in Forth and can automatically generate binary code for the UART Port loading. This assembler will be merged with the JHomade software.

5.1.2. JHomade

JHomade is a software suite including a compiler for the HoMade processor. It allows us to compile HiHope programs (or HoMade assembly) and load the binary on the FPGA board. Its first release was in december 2013.

5.1.3. \mathbb{K} -based language-independent symbolic execution and verification tool

The results in [9], [14] were implemented in the \mathbb{K} framework and are distributed with it. The implementation allows users to symbolically execute programs in arbitrary languages defined in \mathbb{K} , with the only restriction that data cannot become code (and reciprocally). It also allows users to formally verify programs against specifications written in Reachability Logic, a specification formalism that can be seen as a language-independent Hoare logic. These language-independent tools will be specialized to the languages of interest in the project (HiHope, HoMade assembly and machine code).

FUN Project-Team

4. Software and Platforms

4.1. Distributed ONS

Participants: Nathalie Mitton, Roberto Quilez [correspondant].

This module implements a DHT-based Distributed EPC Global ONS issued from the ANR WINGS project and published in [61]. APP number: IDDN.FR.001.180033.000.S.P.2012.000.10000.

- Version: version 1

4.2. GOLIATH 1.0

Participants: Fadila Khadar [correspondant], Nathalie Mitton.

GOLIATH (Generic Optimized LIghtweight communication stack for Ambient TecHnologies) is a full protocol stack for wireless sensor networks.

See also the web page <https://gforge.inria.fr/projects/goliath/>.

4.3. Linear variable energy module for WSNET.

Participants: Tony Ducrocq [correspondant], Nathalie Mitton.

This module is to be integrated in the WSNET event-based simulator for wireless networks. It implements a Linear transmission variable energy module for WSNET.

- Version: 1.0

4.4. New ALE module for ASPIRERFID middleware.

Participants: Rim Driss [correspondant], Nathalie Mitton, Ibrahim Amadou, Julien Vandaele.

AspireRFID middleware is a modular OW2 open source RFID middleware. It is compliant with EPC Global standards. This new module integrates the modifications of the new standard release, including new RP and LLRP definitions and fixing bugs.

- Version: 1.0

LINKS Team

4. Software and Platforms

4.1. QuiX-Tool Suite

Participants: Joachim Niehren [correspondant], Denis Debarbieux, Tom Sebastian.

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.

See also the web page <https://project.inria.fr/quix-tool-suite/>.

- Version: QuixPath v2.0.0
- Version: X-Fun v0.5.0
- Version: QuiXSLT v0.5.0
- Version: QuiXSchematron v1.0.0

4.2. SmartHal

Participants: Joachim Niehren [correspondant], Antoine Ndione.

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. On top of this, we have build a tool for producing the citation lists for the evaluation report of the LIFL, which can be easily adapter to other Labs.

See also the web page <http://smarthal.lille.inria.fr/>.

- Version: SmartHal v1.0.0

MAGNET Team

5. Software and Platforms

5.1. CoRTex

Participants: Pascal Denis [correspondent], David Chatel.

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 my own research, such as [3]. In addition, it provides a set of APIs and utilities for text pre-processing, 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. This project is hosted on Inria gforge: <https://gforge.inria.fr/projects/cortex/>.

5.2. JProGraM

Participant: Antonino Freno [correspondent].

JProGraM is a GPL-licensed Java library for machine learning and statistical analysis over graphs and through graphs. Supported models for vectorial data include e.g. Bayesian networks, Markov random fields, Gaussian mixtures, kernel density estimators, and neural networks, whereas random graph tools include small-world networks, preferential-attachment, exponential random graphs, and spectral models (as well as subgraph sampling algorithms). One strong point of the library is the extensive support for continuous random variables. JProGraM integrates implementations for the recent results in [20] and [21]. For more information, see the associated webpage at <http://researchers.lille.inria.fr/~freno/JProGraM.html>.

MINT Project-Team

5. Software and Platforms

5.1. LibGINA

Participant: Laurent Grisoni [correspondant].

This library has been developed within the context of the ADT GINA, for one of the installation that have been made in collaboration with Le Fresnoy national studio (Damassama, Léonore Mercier). This library is currently being posted as APP, and has been used by Idées-3com small company, in the context of our join I-lab program. This library allows for use of gesture for command, and is able to handle strong variability into recognized patterns.

Current version: version 1.0

Software characterization: A-2 SO-3 SM-2-up EM-3 SDL-3 OC-DA4-CD4-MS2-TPM4

5.2. 3D interaction using mobile phone

Participants: Samuel Degrande [correspondant], Laurent Grisoni.

This work has been achieved in the context of the Idées-3com I-lab. In this context a module, that allows to use any android based smartphone to control an Explorer module for navigation and interaction with VRML-based content. This module was used as a basis by Idées-3com in their commercial product this year.

Current version: version 1.0

Software characterization: A-2 SO-3 SM-2-up EM-2-up SDL-3 OC-DA4-CD4-MS2-TPM4

5.3. tIO (tactile input & output)

Participants: Marc-Antoine Dupré, Nicolas Roussel [correspondant], Takashi Miyaki.

tIO is a library designed to facilitate the implementation of doubly tactile interaction techniques (tactile input coupled with tactile feedback) based on the STIMTAC technology. Supporting all current STIMTAC prototypes, it makes it easy to move the system pointer of the host computer according to motions detected on them and adapt their vibration amplitude based on the color of the pointed pixel or the nature of the pointed object. The library includes a set of Qt demo applications that illustrate these two different approaches and makes it easy to “augment” existing Qt applications with tactile feedback. It also makes it possible to supplement or substitute tactile feedback with basic auditory feedback synthesized using `portaudio` (friction level is linearly mapped to the frequency of a sine wave). This not only facilitates the development and documentation of tactile-enhanced applications but also makes it easier to demonstrate them to a large audience.

Software characterization: A2, SO3-up, SM-2, EM2, SDL1.

5.4. libpointing

Participants: Géry Casiez [correspondant], Damien Marchal, Nicolas Roussel.

Libpointing is a software toolkit that provides direct access to HID pointing devices and supports the design and evaluation of pointing transfer functions [2]. 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 and Java bindings available. It is publicly available under the GPLv2 license.

Web site: <http://libpointing.org/>

Software characterization: A3, SO3, SM-2, EM2, SDL4

5.5. Platform PIRVI

MINT is associated to the CPER-CIA (2007-2013), and participates to the PIRVI platform (Framework for Computer Human Animation, Virtual Reality and Images, handled by F. Aubert, co-animated by F. Aubert and D. Marchal), which aims at promoting research achieved by participant research teams (6 research teams, among which MINT), as well as encouraging collaborations with regional economical tissue on the knowledge fields covered within the associated research teams. The PIRVI allows these research teams to share a Virtual-Reality Room and various mid-size research equipments : multitouch tables, cameras (depth, infrared, ...), interactive devices (force-feedback, multitouch, smartphones...), a configurable multitouch wall. This dissemination activity has been supported with a regional contract 500 Keuros.

MODAL Project-Team

5. Software and Platforms

5.1. Rmixmod package for mixed data

Participants: Christophe Biernacki, Serge Iovleff, Parmeet Bhatia.

MIXMOD (MIXture MODelling) is an important software for the mØdal team since it concerns its main topics: model-based supervised, unsupervised and semi-supervised classification for various data situations. MIXMOD is now a well-distributed software with over 250 downloads/month are recorded for several years. MIXMOD is written in C++ (more than 10 000 lines) and distributed under GNU General Public License. Several other institutions participate in the MIXMOD development since several years: CNRS, Inria Saclay-Île de France, Université de Franche-Comté, Université Lille 1. The software already benefits from several APP depositions and an R package (Rmixmod) has been associated to MIXMOD in 2012.

In 2013, Parmeet Bhatia, under scientific supervision of Christophe Biernacki and Serge Iovleff, has developed possibility in Rmixmod to cluster simultaneously continuous and categorical data with the restrictive conditional independence assumption. It is an important first step towards the long term purpose of mØdal to cluster heterogeneous (or mixed) data sets. It is a joint work with Florent Langrognet, Rémi Lebre, Gilles Celeux and Gérard Govaert.

5.2. RankClust package for rank data

Participants: Christophe Biernacki, Quentin Grimonprez, Julien Jacques.

Rankcluster package for R proposes a clustering tool for ranking data. Multivariate and partial rankings can be also taken into account. Available on CRAN.

5.3. Clere package for high dimensional regression

Participants: Christophe Biernacki, Loïc Yengo, Julien Jacques.

The Clere package for R proposes variable clustering in high dimensional linear regression. Available on CRAN.

5.4. Clustericat package for correlated categorical variable

Participants: Christophe Biernacki, Matthieu Marbac-Lourdelle, Vincent Vandewalle.

Clustericat is a R package for model-based clustering of categorical data. In this package, the model CCM [41] where the main conditional dependencies between variables are taken into account is implemented. Clustericat performs the model selection and provides the best model according to the BIC criterion and the maximum likelihood estimates. It is available online on Rforge (https://r-forge.r-project.org/R/?group_id=1803).

5.5. CorReg package for correlated variables in regression

Participants: Christophe Biernacki, Clément Théry.

Databases from the steel industry are often large (very long process with many parameters) and have strong correlations between variables. Some variables may be written directly in terms of other via physical models or related by definition. Moreover the process, which is specific to the type of finished product, conditions most of the process parameters and therefore induces strong correlations between variables. The main idea 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. This research is placed in a steel industry context (Arcelor-Mittal Dunkerque).

The associated CorReg package is now available on Rforge. It is a joint work with Gaétan Loridant.

5.6. AAM

Participant: Serge Iovleff.

A console based program written in C++ and dedicated to the estimation of the Auto-Associative Models.

5.7. BlockCluster

Participants: Serge Iovleff, Parmeet Bathia.

Serge Iovleff, Parmeet Bathia

BlockCluster: An R package on top of the coclust C++ library.

5.8. HDPenReg

Participants: Quentin Grimonprez, Serge Iovleff.

R-package written in collaboration based on a C++ code dedicated to the estimation of regression model with l1-penalization.

5.9. STK++ release 0.5

Participant: Serge Iovleff.

New release including new functionalities for templated expression evaluation (similar to the Eigen library offer) and a new subproject offering tools for Clustering.

5.10. Funclustering package for R

Participants: Cristian Preda, Julien Jacques.

Funclustering package for R proposes a clustering tool for functional data. Multivariate curves can be also taken into account. Available on CRAN.

5.11. metaMA

metaMA is a specialised software for microarrays. It is a 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.

Guillemette Marot is the main contributor and the maintainer of this package.

This software is routinely used by biologists from INRA, Jouy en Josas (it has been included in a local analysis pipeline) but its diffusion on the CRAN makes it available to a wider community, as attested by the citations of publications related to the methods implemented in the software.

More information is available on the website <http://cran.r-project.org/web/packages/metaMA/>

5.12. metaRNASeq

Participant: Guillemette Marot.

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. Guillemette Marot and Andrea Rau are the main contributors of this package and Guillemette Marot is the maintainer of this package.

5.13. MPAGenomics

Participants: Quentin Grimonprez, Guillemette Marot, Alain Celisse.

MPAGenomics is a R package for multi-patients analysis of genomics markers. Its main contributor is Quentin Grimonprez. 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. It is available on the Inria forge and should be released on the R-forge in January.

5.14. SMVar

Participant: Guillemette Marot.

SMVar is a specialised software for microarrays. This R package implements the structural model for variances in order to detect differentially expressed genes from gene expression data. It performs gene expression differential analysis, based on a particular variance modelling. Its main competitor is the Bioconductor R package limma but limma assumes a common variance between the two groups to be compared while SMVar relaxes this assumption.

Guillemette Marot is the main contributor and the maintainer of this package.

More information is available on the website <http://cran.r-project.org/web/packages/SMVar/index.html>

NON-A Project-Team

5. Software and Platforms

5.1. SLIM

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.

RMOD Project-Team

5. Software and Platforms

5.1. Moose

Participants: Stéphane Ducasse [correspondant], Muhammad Bhatti, Andre Calvante Hora, Nicolas Anquetil, Anne Etien, Guillaume Larcheveque, Tudor Gîrba [University of Bern].

Web: <http://www.moosetechnology.org/>

The platform. Moose is a language-independent environment for reverse- and re-engineering complex software systems. Moose provides a set of services including a common meta-model, metrics evaluation and visualization, a model repository, and generic GUI support for querying, browsing and grouping. The development of Moose began at the Software Composition Group in 1997, and is currently contributed to and used by researchers in at least seven European universities. Moose offers an extensible meta-described metamodel, a query engine, a metric engine and several visualizations. Moose is currently in its fourth major release and comprises 55,000 lines of code in 700 classes.

The RMoD team is currently the main maintainer of the Moose platform. There are 200 publications (journal, international conferences, PhD theses) based on execution or use of the Moose environment.

The first version running on top of Pharo (Moose 4.0) was released in June 2010. In 2013, three releases of Moose were done: 4.7 to 4.9. The current focus is Moose 5.0, which is running on Pharo3 and will be released together with Pharo3 in spring 2014.

Here is the self-assessment of the team effort following the grid given at <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>.

- **(A5)** Audience : 5 – Moose is used by several research groups, a consulting company, and some companies using it in ad-hoc ways.
- **(SO4)** Software originality : 4 – Moose aggregates the last results of several research groups.
- **(SM4)** Software Maturity : 4 – Moose is developed since 1996 and got two main redesign phases.
- **(EM4)** Evolution and Maintenance : 4 – Moose will be used as a foundation of our Synectique start up so its maintenance is planned.
- **(SDL4)** Software Distribution and Licensing : 4 – Moose is licensed under BSD
- **(OC)** Own Contribution : (Design/Architecture)DA-4, (Coding/Debugging)-4, (Maintenance/Support)-4, (Team/Project Management)-4

5.2. Pharo

Participants: Marcus Denker [correspondant], Damien Cassou, Stéphane Ducasse, Esteban Lorenzano, Damien Pollet, Igor Stasenko, Camillo Bruni, Camille Teruel, Clément Bera.

Web: <http://www.pharo.org/>

The platform. Pharo is a new 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.

The first stable version, Pharo 1.0, was released in 2010. The development of Pharo accelerated in 2011 and 2012: Versions 1.2 to 1.4 have been released (with more than 2400 closed issues). In 2013, Pharo 2.0 was released. The development cycle will now be one major release per year, with Pharo3 to be released in March 2014.

In 2012, RMoD organized the first *Pharo Conference* during two days in May with 60 participants, the second Pharo conference was held in Bern, Switzerland in 2013.

Additionally, in November 2012 RMoD launched the Pharo Consortium (<http://consortium.pharo.org/>) and the Pharo Association (<http://association.pharo.org/>). Over 10 companies are now paying members of the Consortium.

RMoD is the main maintainer and coordinator of Pharo.

Here is the self-assessment of the team effort following the grid given at <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>.

- **(A5)** Audience: 5 – Used in many universities for teaching, more than 25 companies.
- **(SO3)** Software originality : 3 – Pharo offers a classical basis for some aspects (UI). It includes new frameworks and concepts compared to other Smalltalk implementations.
- **(SM4)** Software Maturity: 4 – Bug tracker, continuous integration, large test suites are on place.
- **(EM4)** Evolution and Maintenance: 4 – Active user group, consortium and association had just been set up.
- **(SDL4)** Software Distribution and Licensing: 4 – Pharo is licensed under MIT.
- **(OC5)** Own Contribution: (Design/Architecture) DA-5, (Coding/Debugging) CD-5, (Maintenance/Support) MS-5, (Team/Project Management) TPM-5

5.3. Fuel

Participants: Martin Dias [Correspondant], Mariano Martinez-Peck.

Web: <http://rmod.lille.inria.fr/web/pier/software/fuel>

Objects in a running environment are constantly being born, mutating their status and dying in the volatile memory of the system. The goal of serializers is to store and load objects either in the original environment or in another one. Fuel is a general-purpose serializer based on four principles: (1) speed, through a compact binary format and a pickling algorithm which obtains the best performance on materialization; (2) good object-oriented design, without any special help from the virtual machine; (3) specialized for Pharo, so that core objects (such as contexts, block closures and classes) can be serialized too; (4) flexible about how to serialize each object, so that objects are serialized differently depending on the context.

Since Pharo 2.0, Fuel is part of the standard distribution.

Here is the self-assessment of the team effort following the grid given at <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>.

- **(A4)** Audience: 4 – Large audience software, usable by people inside and outside the field with a clear and strong dissemination, validation, and support action plan.
- **(SO3)** Software originality : 3.
- **(SM4)** Software Maturity: 4 – Bug tracker, continuous integration, large test suites are on place.
- **(EM4)** Evolution and Maintenance: 4.
- **(SDL4)** Software Distribution and Licensing: 4 – Fuel is licensed under MIT.
- **(OC5)** Own Contribution: (Design/Architecture) DA-5, (Coding/Debugging) CD-5, (Maintenance/Support) MS-5, (Team/Project Management) TPM-5

5.4. Athens

Participant: Igor Stasenko [Correspondant].

Athens is a vector graphics framework for Pharo. Athens is now part of Pharo since version 3 as a technology Preview. We plan to make Athens the default graphics framework with Pharo4 in 2015.

5.5. Citezen

Participants: Damien Pollet [Correspondant], Stéphane Ducasse.

Web: <http://people.untyped.org/damien.pollet/software/citezen/>

Citezen is a suite of tools for parsing, validating, sorting and displaying BibTeX databases. This tool suite is integrated within the Pier Content Management System (CMS) and both are implemented on top of Pharo. Citezen aims at replacing and extending BibTeX, in Smalltalk; ideally, features would be similar to BibTeX, CrossTeX, and CSL.

5.6. Handles

Participant: Jean-Baptiste Arnaud [Correspondant].

Web: <http://jeanbaptiste-arnaud.eu/handles/>

An Handle is a first-class reference to a target object. Handles can alter the behavior and isolate the state of the target object. Handles provide infrastructure to automatically create and wrap new handles when required. A real-time control of handles is possible using a special object called metaHandle.

5.7. Hazelnut

Participants: Guillermo Polito [Correspondant], Benjamin Van Ryseghem, Nicolas Paez, Igor Stasenko.

Web: <http://rmod.lille.inria.fr/web/pier/software/Seed>

Traditionally, Smalltalk-based systems are not bootstrapped because of their ability to evolve by self-modification. Nevertheless, the absence of a bootstrap process exposes many problems in these systems, such as the lack of reproducibility and the impossibility to reach certain evolution paths. Hazelnut is a tool that aims to introduce a bootstrap process into these systems, in particular Pharo.

5.8. LegacyParsers

Participants: Muhammad Bhatti [Correspondant], Nicolas Anquetil, Guillaume Larcheveque, Esteban Lorenzano, Gogui Ndong.

As part of our research on legacy software and also for the Synectique company), we started to define several parsers for old languages like Cobol for example. This work is important to help us validate our meta-model and tools against a larger range of existing technologies and to discover the limits of our approach. From our initial results, and the in-depth understanding that it gave us, we are formulating new research objectives in meta-model driven reverse engineering. This work is also important for the spin-off company, as being able to work with such technologies is fundamental.

5.9. Mate

Participants: Marcus Denker [Correspondant], Clement Bera, Camillo Bruni.

Mate is the future research-oriented virtual machine for Pharo. Its goal is to serve as a prototype for researchers to experiment with. As a result, the design of Mate is very simple to understand. As of today, Mate consists of an AST interpreter, a new object memory layout, and a simple garbage collector.

5.10. NativeBoost

Participant: Igor Stasenko [Correspondant].

Web: <http://code.google.com/p/nativeboost/>

NativeBoost is a Smalltalk framework for generating and running machine code from the language side of Pharo. As part of it comes a foreign function interface that enables calling external C functions from Smalltalk code with minimal effort.

5.11. Nabujito

Participants: Camillo Bruni [Correspondant], Marcus Denker.

Nabujito is an experimental Just In Time compiler implemented as a Smalltalk application, based on Native-Boost, that does not require changes in the virtual machine.

5.12. Nautilus

Participants: Benjamin Van Ryseghem [Correspondant], Stéphane Ducasse, Igor Stasenko, Camillo Bruni, Esteban Lorenzano.

Nautilus is a new source code browser based on the latest infrastructure representations. Its goal is mainly to replace the current system browser that was implemented in the 80s and that doesn't provide optimal tools for the system as it has evolved.

5.13. Spec

Participants: Benjamin Van Ryseghem [Correspondant], Stéphane Ducasse, Johan Fabry.

Spec is a programming framework for generating graphical user interfaces inspired by VisualWorks' Subcanvas. The goal of Spec is to tackle the lack of reuse experienced in existing tools. Spec serves as a pluggable layer on top of multiple lower-level graphical frameworks. Many improvements have been noticed in Pharo after the introduction of Spec in terms of speed or number of lines of code while we re-implemented existing tools using Spec.

SequeL Project-Team

5. Software and Platforms

5.1. Computer Games

Participant: Rémi Coulom.

- *Crazy Stone* is a top-level Go-playing program that has been developed by Rémi Coulom since 2005. Crazy Stone won several major international Go tournaments in the past. In 2013, a new version was released in Japan. This new version won the 6th edition of the UEC Cup (the most important international computer-Go tournament). It also won the first edition of the Densen, by winning a 4-stone handicap game against 9-dan professional player Yoshio Ishida. It is distributed as a commercial product by *Unbalance Corporation* (Japan). 6-month work in 2013. URL: <http://remi.coulom.free.fr/CrazyStone/>
- *Kifu Snap* is an Android image-recognition app. It can automatically recognize a Go board from a picture, and analyze it with Crazy Stone. It was released on Google Play in November, 2013. 6-month work in 2013. URL: <http://remi.coulom.free.fr/kifu-snap/>

SHACRA Project-Team

5. Software and Platforms

5.1. SOFA

SOFA <http://www.sofa-framework.org> is an open-source software framework targeted at interactive computational (medical) simulation. The idea of SOFA was initiated by members of the SHACRA team, and strongly supported by Inria through a development program that we lead. SOFA facilitates collaborations between specialists from various domains, by decomposing complex simulators into components designed independently. Each component encapsulates one of the key aspects of a simulation, such as the degrees of freedom, the forces and constraints, the differential equations, the linear solvers, the collision detection algorithms or the interaction devices. The simulated objects can be represented using several models, each of them optimized for a different task such as the computation of internal forces, collision detection, haptics or visual display. These models are synchronized during the simulation using a mapping mechanism. CPU and GPU implementations can be transparently combined to exploit the computational power of modern hardware architectures. Thanks to this flexible yet efficient architecture, SOFA can be used as a test-bed to compare models and algorithms, or as a basis for the development of complex, high-performance simulators. As proof of its success, SOFA has been downloaded nearly 150,000 times, and is used today by many research groups around the world, as well as a number of companies. The mailing list used to exchange with the community includes several hundreds of researchers, from about 50 different institutions. SOFA is at the heart of a number of research projects, including cardiac electro-physiology modeling, interventional radiology planning and guidance, planning for cryosurgery and deep brain stimulation, robotics, percutaneous procedures, laparoscopic surgery, non-rigid registration, etc. SOFA is the only software developed by our team, but practically speaking it is a collection of plugins (each one aimed at a specific application) organized around a common core that provides a large number of functionalities. As mentioned previously, SOFA is currently used by a number of companies (Siemens Corporate Research, Digital Trainers, Epona Medical, Moog, SenseGraphics, etc.) and also provides the key technology on which our newly created start-up (InSimo) is relying. We strongly believe that today SOFA has become a reference for academic research, and is increasingly gaining recognition for product prototyping and development. The best illustration of this worldwide positioning is the role of SOFA in the challenge set by the HelpMeSee foundation to win the contract for the development of a very ambitious and high-risk project on cataract surgery simulation.

We also gave a 4 hours workshop on SOFA at MMVR/NextMed conference in february 2013 in San Diego. This workshop was done in collaboration with the swedish company SenseGraphics. The topic was to demonstrate the setup of a dental surgery simulation in Sofa, and use SenseGraphics visual tools for the rendering. The attendees feedback was beyond our expectations, with an unexpected interest in new SOFA features like the SofaPython plugin. Still about SOFA, like last year we gave in october a 3 days training session in Montpellier for about twenty SOFA beginners (mostly engineers). These are new engineers of the three teams involved in SOFA development, and employees of companies using SOFA in their business. Last, a "SOFA Day" in november in prelude of the Vriphys conference gave us a unique opportunity to meet SOFA users from various research institutes or companies, and exchange about the future improvements and development of the engine. We use these occasions to share and discuss with SOFA users, to refine the roadmap and stay tuned with our audience.

SIMPAF Project-Team

5. Software and Platforms

5.1. ns2ddv-M

Participants: Caterina Calgaro [correspondant (Univ. Lille 1)], Emmanuel Creusé [correspondant (Univ. Lille 1)].

Incompressible Navier-Stokes, Variable Density, Rayleigh-Taylor Instability The NS2DDV-M code is based on a hybrid method coupling FV and FE approaches for solving the variable density Navier-Stokes equation in dimension 2. This original approach for variable density flows is described in [41].

Here is the self-assessment of the team effort following the grid provided by Inria (see : <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>): A3, SO3-up4, SM2-up3, EM3, SDL4, DA1, CD4, MS4, TPM4.

Software web site : <http://math.univ-lille1.fr/~simpaf/SITE-NS2DDV/home.html>

5.2. ns2ddv-C++

Participants: Caterina Calgaro [correspondant (Univ. Lille 1)], Emmanuel Creusé [correspondant (Univ. Lille 1)], Thierry Goudon.

Incompressible Navier-Stokes, Variable Density, Kazhikhov-Smagulov model, Rayleigh-Taylor Instability, avalanches phenomena The NS2DVD-C++ code is based on a hybrid method coupling FV and FE approaches for solving the variable density Navier-Stokes equation in dimension 2. The code is developed around the GetFem++ and the Bamg softwares. It allows in particular mesh refinement strategies so that very relevant simulations can be reached (as the falling droplet with very high density ratios, see for example [38]). The current version of the code consider the additional terms in the Kazhikhov-Smagulov model.

Webpage : <http://math.univ-lille1.fr/~simpaf/SITE-NS2DDV>

Here is the self-assessment of the team effort following the grid provided by Inria (see : <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>): A1, SO3-up4, SM1, EM2, SDL1, DA1, CD4, MS4, TPM1.

5.3. RTcodes

Participants: Pauline Lafitte [correspondant (ECP)], Jean-François Coulombel [(CNRS & Univ. Nantes)], Christophe Besse [(Univ. Lille 1)], Thierry Goudon [(Inria)], Giovanni Samaey [(KU Leuven)].

Radiative Transfer, Radiative shocks, AP schemes

We have developed a set of numerical codes, written in Scilab, to compute the solutions of the system coupling the Euler equations to the radiation through energy exchanges, in the non equilibrium regime. This covers several situations in the hierarchy of asymptotic problems. The code treats the one-dimensional framework. In particular the code can be used to investigate radiative shocks profiles. The main advantage of our numerical codes is that they do not require any refinement near the singularities. The numerical tests show a very good agreement with the theoretical predictions. See reference [48].

Here is the self-assessment of the team effort following the grid provided by Inria (see : <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>): A2, SO3, SM2, EM1, SDL1.

5.4. FPcodes

Participants: Pauline Lafitte [correspondant (ECP)], Thierry Goudon [(Inria)], Benjamin Boutin [(Univ. Rennes)].

Fluid-Particles flows, Gravity driven flows, AP schemes

We have developed a numerical code, written in Scilab, to compute the solutions of the two-phase flows equations describing particles interacting with a fluid through friction forces. The code treats one-dimensional situation and is well adapted to describe gravity driven flows in either bubbling or flowing regimes. In particular, it can be used to describe the evolution of pollutants in the atmosphere. The numerical strategy, based on an asymptotic-based scheme, is described in details in [43].

Here is the self-assessment of the team effort following the grid provided by Inria (see : <http://www.inria.fr/institut/organisation/instances/commission-d-evaluation>): A2, SO3, SM2, EM1, SDL1.

5.5. CLAToolBox

Participants: Christophe Besse [correspondant (Univ. Lille 1)], Pauline Klein [Univ. Besançon].

Absorbant boundary conditions, Schrödinger equation

As a byproduct of the review paper [30], a user-friendly interface is offered ¹ to trial and compare various numerical methods to solve the 1D Schrödinger equation with absorbant boundary conditions. We also mention [34] for a numerical investigation of blow-up phenomena in the nonlinear Schrödinger equation.

5.6. SPARCS

Participants: Christophe Besse [Univ. Lille 1], Thierry Goudon [correspondant (Inria)], Ingrid Lacroix-Violet [Univ. Lille 1].

Vlasov-Poisson system, Euler-Poisson system. Back-Trajectory method

SPARCS is the code developed by Thales Alenia Space for the simulation of the charge phenomena the spacecrafts are subject to. The current version of the code, according to the PhD thesis of O. Chanrion and M. Chaneyook performed in collaboration with the team Caiman at Sophia Antipolis, is specialized to geostationary atmospheres. The model consists in the stationary Vlasov-Poisson system, but where instationary effects are taken into account with the boundary condition for the electric field. We participate, in particular through the post doc of N. Vauchelet, to the elaboration of an improved version of the code which includes parallization optimized procedures, the modelling of the natural difference of potential between different dielectric surfaces of the spacecraft, as well as the possible presence of devices emitting charged particles.

5.7. Code-Carmel3D

Participant: Emmanuel Creusé [correspondant (Univ. Lille 1)].

This numerical code, developed in collaboration between EDF R&D and Lille 1 University, is devoted to the electromagnetic fields computation by the use of finite element methods. This code allows in particular to perform nondestructive control by the use of Foucault currents in steam generator pipes, and should be soon coupled with the thermal simulation of Code-Aster. Code-Carmel3D uses the Salomé platform (mesh-generator and post-processing) and Open Turns (uncertainties computation). It will consequently allow to solve multi-physics problems, both for the temporal and harmonic formulations.

¹<http://math.univ-lille1.fr/~besse/site/recherche/logiciels/index.html>