



RESEARCH CENTER  
Lille - Nord Europe

FIELD

Activity Report 2018

**Section Software**

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## GAIA Team

# 6. New Software and Platforms

## 6.1. ADHOMFI

*Adaptive Homogeneous Filtering*

KEYWORDS: Automatic differentiation - Filtering

FUNCTIONAL DESCRIPTION: allows to reconstruct a signal based on derivatives estimation and to filter high amplitude and wide frequencies spectrum perturbations.

- Contact: Denis Efimov

## 6.2. Platforms

### 6.2.1. *BLINEIDE* library

We have released the first version of the BLINEIDE library. BLINEIDE stands for Bibliothèques Lilloises dédiées à l'Intégration Numérique des Équations Intégré-Différentielles. It is an open source C library dedicated to the numerical integration of systems of integro-differential equations. for more details, see <https://pro.univ-lille.fr/francois-boulier/logiciels/blineide>.

## BONUS Team

# 6. New Software and Platforms

## 6.1. Platforms

### 6.1.1. Grid'5000 testbed: extension with GPUs at Lille

**KEYWORDS:** Experimental testbed, large-scale computing, high-performance computing, GPU computing, cloud computing, big data

**FUNCTIONAL DESCRIPTION:** Grid'5000 is a project initiated in 2003 by the French government to promote scientific research on large scale distributed systems. The project is later supported different research organizations including Inria, CNRS, the french universities, Renater which provides the wide-area network, etc. The overall objective of Grid'5000 was to build by 2007 a nation-wide experimental testbed composed of at least 5000 processing units and distributed over several sites in France. From a scientific point of view, the aim was to promote scientific research on large-scale distributed systems.

Grid'5000 was installed at the center of IT resources including supercomputing resources of Université de Lille 1 and opened to users in 2005. Since March 2017, the Grid'5000 site has moved to the premises on Inria Lille within the context of the phase 1 of the CPER data program (see Section 9.1 ) with a completely new hardware equipment. As a scientific leader of the testbed for the Lille's site, N. Melab has been strongly involved in the extension (phase 2 of CPER data) of the platform with 16 computing serveurs, 16 Nvidia GPUs (12 P100 and 4V100), 2 storage serveurs 200TB and 2 administration servers. Grid'5000 at Lille is used by more than 150 users including 100 external ones. The testbed is used for research as well as for teaching allowing a high scientific production (publications, PhD theses, etc.) and over 30 master students to get started with parallel and distributed programming.

- Participants: N. Melab, external collaborators: D. Delabroy, T. Peltier, L. Nussbaum.
- Contact: Nouredine Melab.
- URL: <https://www.grid5000.fr/mediawiki/index.php/Grid5000:Home>

## **INOCS Project-Team**

# **6. New Software and Platforms**

## **6.1. HappyChic-ApproPick**

**KEYWORDS:** Operational research - Optimization - Java

**FUNCTIONAL DESCRIPTION:** This software is a prototype developed for the bilateral contract with the company HappyChic. This software is a solver for an integrated warehouse order picking problem with manual picking operations. More precisely, the following problems are solved: (1) the assignment of references to storage positions, based on the iterative solving of minimum cost flow problems, (2) the division of clients orders into several parcels, respecting weight and size constraints, using a dynamic programming algorithm based on the split algorithm, (3) the batching of parcels into trolleys to perform picking tours, using a dynamic programming algorithm based on the split algorithm. The objective function is to minimize the total walking distance. This software is designed to deal with the large-sized industrial instances of HappyChic (considering hundreds of clients, thousands of positions and product references) in a short computation time (few minutes).

- Contact: Maxime Ogier

## **6.2. KEOLIS-MEDIATOUR**

**KEYWORDS:** Operational research - Mathematical Optimization - Staff scheduling

**FUNCTIONAL DESCRIPTION:** This software is a prototype developed under a bilateral contract with the company Keolis. This software is a solver which aims to optimize the scheduling of mediation staff. More precisely, for each member of the mediation staff working in a public transportation network, MEDIATOUR determines his/her schedule along the day, i.e. when and where he/she is present. Various operational constraints must be taken into account such as the coverage of the network. This software is designed to solve large-scale industrial instances (the subway network of Lille) in short computation times (less than 1 minute).

- Contact: Frédéric Semet

## **6.3. PARROT**

*Planning Adapter Performing ReRouting and Optimization of Timing*

**KEYWORDS:** Decision aid - Railway - Scheduling

**FUNCTIONAL DESCRIPTION:** This is a decision support system addressing the problem of the rescheduling railway schedules on the Belgian network when maintenance operations are planned in the short term (2-3 weeks in advance). The deliverable is a software tool that will take as input: (1) the schedules initially planned for the different trains, (2) the initial routes of the trains, (3) maintenance operations / changes of elements in the form of constraints (unavailable routes etc.). It then provides in output: (1) the new train schedule, (2) the new routing of the fleet. The modifications must respect the constraints corresponding to the operations of maintenance. For example, in some cases it is common to leave at least a few minutes interval between two trains using the same track in the station. This constraint must then be propagated if a maintenance operation delays the arrival of a train. New schedules and routings have to be created following a specific goal. Changes made to schedules and routings must minimize: (1) variations on the time spent at the station, (2) the number of partially canceled trains (additional correspondence (s) or stations that are no longer served), (2) the number of fully canceled trains (no stations served).

- Contact: Martine Labbe

**MEPHYSTO-POST Team (section vide)**

## MODAL Project-Team

# 6. New Software and Platforms

## 6.1. MixtComp

### *Mixture Computation*

KEYWORDS: Clustering - Statistics - Missing data

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: Christophe Biernacki, Étienne Goffinet, Matthieu Marbac-Lourdelle, Quentin Grimonprez, Serge Iovleff and Vincent Kubicki
- Contact: Christophe Biernacki
- URL: <https://modal-research.lille.inria.fr/BigStat>

## 6.2. BlockCluster

### *Block Clustering*

KEYWORDS: Statistic analysis - Clustering package

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

## 6.3. CloHe

### *Clustering of Mixed data*

KEYWORDS: Classification - Clustering - Missing data



FUNCTIONAL DESCRIPTION: Software of classification for mixed data with missing values with application to multispectral satellite image time-series

- Partners: CNRS - INRA
- Contact: Serge Iovleff
- URL: <https://modal.lille.inria.fr/CloHe/>

## 6.4. PACBayesianNMF

KEYWORDS: Statistics - Machine learning

FUNCTIONAL DESCRIPTION: Implementing NMF with a PAC-Bayesian approach relying upon block gradient descent

- Participants: Benjamin Guedj and Astha Gupta
- Contact: Benjamin Guedj
- URL: <https://github.com/astha736/PACbayesianNMF>

## 6.5. pycobra

KEYWORDS: Statistics - Data visualization - Machine learning

SCIENTIFIC DESCRIPTION: pycobra is a python library for ensemble learning, which serves as a toolkit for regression, classification, and visualisation. It is scikit-learn compatible and fits into the existing scikit-learn ecosystem.

pycobra offers a python implementation of the COBRA algorithm introduced by Biau et al. (2016) for regression.

Another algorithm implemented is the EWA (Exponentially Weighted Aggregate) aggregation technique (among several other references, you can check the paper by Dalalyan and Tsybakov (2007).

Apart from these two regression aggregation algorithms, pycobra implements a version of COBRA for classification. This procedure has been introduced by Mojirsheibani (1999).

pycobra also offers various visualisation and diagnostic methods built on top of matplotlib which lets the user analyse and compare different regression machines with COBRA. The Visualisation class also lets you use some of the tools (such as Voronoi Tesselations) on other visualisation problems, such as clustering.

- Participants: Bhargav Srinivasa Desikan and Benjamin Guedj
- Contact: Benjamin Guedj
- Publication: [Pycobra: A Python Toolbox for Ensemble Learning and Visualisation](#)
- URL: <https://github.com/bhargavvader/pycobra>

## 6.6. STK++

*Statistical ToolKit*

KEYWORDS: Statistics - Linear algebra - Framework - Learning - Statistical learning

FUNCTIONAL DESCRIPTION: STK++ (Statistical ToolKit in C++) 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>

## 6.7. rtkore

*STK++ core library integration to R using Rcpp*

KEYWORDS: C++ - Data mining - Clustering - Statistics - Regression

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 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>

## 6.8. MixAll

*Clustering using Mixture Models*

KEYWORDS: Clustering - Clustering package - Generative Models

FUNCTIONAL DESCRIPTION: MixAll 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](http://www.stkpp.org)) for faster computation.

- Participant: Serge Iovleff
- Partner: Université Lille 1
- Contact: Serge Iovleff
- URL: <https://cran.r-project.org/web/packages/MixAll/>

## 6.9. simerge

*Statistical Inference for the Management of Extrem Risks, Genetics and Global epidemiology*

KEYWORD: Biclustering

FUNCTIONAL DESCRIPTION: Allows to perform Co-Clustering on binary (Bernoulli) and counting variables (Poisson) using co-variables.

- Partner: Inria
- Contact: Serge Iovleff

## 6.10. Platforms

### 6.10.1. MASSICCC Platform

MASSICCC is a demonstration platform giving access through a SaaS (service as a software) concept to data analysis libraries developed at Inria. It allows to obtain results either directly through a website specific display (specific and interactive visual outputs) or through an R data object download. It started in October 2015 for two years and is common to the Modal team (Inria Lille) and the Select team (Inria Saclay). In 2016, two packages have been integrated: Mixmod and MixtComp (see the specific section about MixtComp). In 2017, the BlockCluster package has been integrated and also a particular attention to provide meaningful graphical outputs (for Mixmod, MixtComp and BlockCluster) directly in the web platform itself has led to some specific developments.

## **NON-A POST Team**

# **5. New Software and Platforms**

## **5.1. ADHOMFI**

*Adaptive Homogeneous Filtering*

KEYWORDS: Automatic differentiation - Filtering

FUNCTIONAL DESCRIPTION: allows to reconstruct a signal based on derivatives estimation and to filter high amplitude and wide frequencies spectrum perturbations.

- Contact: Denis Efimov

## RAPSODI Project-Team

# 6. New Software and Platforms

## 6.1. Platform NS2DDV-M

**NS2DDV-M** is a Matlab code, developed by C. Calgaro Zotto, E. Creusé, and A. Mouton (CNRS research engineer at Université de Lille), for the simulation of homogeneous and inhomogeneous fluid flows by a combined Finite Volume-Finite Element method. The code is freely distributed, to allow for easy comparisons with concurrent codes on benchmark test-cases, and to promote new collaborations in the domain.

In 2018, a new version (v. 2.0) has been released, which contains a detailed documentation as well as some new functionalities, such as some post-processing tools and parallel computation capabilities.

## SEQUEL Project-Team

### 6. New Software and Platforms

#### 6.1. BAC

*Bayesian Policy Gradient and Actor-Critic Algorithms*

KEYWORDS: Machine learning - Incremental learning - Policy Learning

FUNCTIONAL DESCRIPTION: To address this issue, we proceed to supplement our Bayesian policy gradient framework with a new actor-critic learning model in which a Bayesian class of non-parametric critics, based on Gaussian process temporal difference learning, is used. Such critics model the action-value function as a Gaussian process, allowing Bayes' rule to be used in computing the posterior distribution over action-value functions, conditioned on the observed data. Appropriate choices of the policy parameterization and of the prior covariance (kernel) between action-values allow us to obtain closed-form expressions for the posterior distribution of the gradient of the expected return with respect to the policy parameters. We perform detailed experimental comparisons of the proposed Bayesian policy gradient and actor-critic algorithms with classic Monte-Carlo based policy gradient methods, as well as with each other, on a number of reinforcement learning problems.

- Contact: Michal Valko
- URL: <https://team.inria.fr/sequel/Software/BAC/>

#### 6.2. GuessWhat?!

*GuessWhat?! Visual object discovery through multi-modal dialogue*

KEYWORDS: Deep learning - Dialogue System

FUNCTIONAL DESCRIPTION: This project train a AI to play the GuessWhat?! game. Thus, you can train an AI to ask questions, to answer questions about images. You can also perform basic visual reasoning. This project is a testbed for future interactive dialogue system.

- Partner: Universite de Montreal
- Contact: Florian Strub
- Publications: [GuessWhat?! Visual object discovery through multi-modal dialogue - End-to-end optimization of goal-driven and visually grounded dialogue systems Harm de Vries](#)

#### 6.3. Squeak

*Sequential sampling for kernel matrix approximation*

KEYWORD: Machine learning

- Contact: Daniele Calandriello
- URL: <http://researchers.lille.inria.fr/~valko/hp/serve.php?what=publications/squeak.py>

#### 6.4. OOR

*Optimistic Optimization in R*

KEYWORDS: Black-box optimization - Machine learning

- Contact: Mickael Binois
- URL: <https://cran.r-project.org/web/packages/OOR/index.html>

## 6.5. DPPy

*Sampling Determinantal Point Processes with Python*

KEYWORD: Determinantal point processes

FUNCTIONAL DESCRIPTION: Determinantal point processes (DPPs) are specific probability distributions over clouds of points that are used as models and computational tools across physics, probability, statistics, and more recently machine learning. Sampling from DPPs is nontrivial and therefore we present DPPy, a Python toolbox that gathers known exact and approximate sampling algorithms. The project is hosted on GitHub and equipped with an extensive documentation.

- Contact: Guillaume Gautier
- URL: <https://github.com/guilgautier/DPPy/>

## 6.6. SMPyBandits

*Open-Source Python package for Single- and Multi-Players multi-armed Bandits algorithms.*

KEYWORD: Machine learning

FUNCTIONAL DESCRIPTION: The library contains the implementation of many single-player multi-armed bandit algorithms as well as the implementation of all the state-of-the-art multi-player algorithms.

- Contact: Lilian Besson

## BONSAI Project-Team

# 5. New Software and Platforms

## 5.1. BCALM 2

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

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

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

- Participants: Antoine Limasset, Paul Medvedev and Rayan Chikhi
- Contact: Rayan Chikhi
- Publication: [Compacting de Bruijn graphs from sequencing data quickly and in low memory](#)
- URL: <https://github.com/GATB/bcalm>

## 5.2. NORINE

*Nonribosomal peptides resource*

KEYWORDS: Drug development - Knowledge database - Chemistry - Graph algorithmics - Genomics - Biology - Biotechnology - Bioinformatics - Computational biology

SCIENTIFIC DESCRIPTION: Since its creation in 2006, Norine remains the unique knowledgebase dedicated to non-ribosomal peptides (NRPs). These secondary metabolites, produced by bacteria and fungi, harbor diverse interesting biological activities (such as antibiotic, antitumor, siderophore or surfactant) directly related to the diversity of their structures. The Norine team goal is to collect the NRPs and provide tools to analyze them efficiently. We have developed a user-friendly interface and dedicated tools to provide a complete bioinformatics platform. The knowledgebase gathers abundant and valuable annotations on more than 1100 NRPs. To increase the quantity of described NRPs and improve the quality of associated annotations, we are now opening Norine to crowdsourcing. We believe that contributors from the scientific community are the best experts to annotate the NRPs they work on. We have developed MyNorine to facilitate the submission of new NRPs or modifications of stored ones.

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: Areski Flissi, Juraj Michalik, Laurent Noé, Maude Pupin, Stéphane Janot, Valerie Leclère and Yoann Dufresne
- Partners: CNRS - Université Lille 1 - Institut Charles Viollette
- Contact: Maude Pupin
- Publications: [Norine, the knowledgebase dedicated to non-ribosomal peptides, is now open to crowdsourcing](#) - [Smiles2Monomers: a link between chemical and biological structures for polymers](#) - [Norine: a powerful resource for novel nonribosomal peptide discovery](#) - [NORINE: a database of nonribosomal peptides](#). - [Bioinformatics Tools for the Discovery of New Nonribosomal Peptides](#)
- URL: <http://bioinfo.lille.inria.fr/NRP>

### 5.3. Vidjil

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

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

SCIENTIFIC DESCRIPTION: Vidjil is made of three components: an algorithm, a visualization 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 gathers 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 against 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 an 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: Florian Thonier, Marc Duez, Mathieu Giraud, Mikaël Salson, Ryan Herbert and Tatiana Rocher
- Partners: CNRS - Inria - Université de Lille - CHRU Lille
- Contact: Mathieu Giraud
- Publications: [High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges.](#) - [High-throughput sequencing in acute lymphoblastic leukemia: Follow-up of minimal residual disease and emergence of new clones](#) - [Diagnostic et suivi des leucémies aiguës lymphoblastiques \(LAL\) par séquençage haut-débit \(HTS\)](#) - [Multiclonal Diagnosis and MRD Follow-up in ALL with HTS Coupled with a Bioinformatic Analysis](#) - [A dataset of sequences with manually curated V\(D\)J designations](#) - [Vidjil: A Web Platform for Analysis of High-Throughput Repertoire Sequencing](#) - [Multi-loci diagnosis of acute lymphoblastic leukaemia with high-throughput sequencing and bioinformatics analysis](#) - [Fast multiclonal clusterization of V\(D\)J recombinations from high-throughput sequencing](#) - [The predictive strength of next-generation sequencing MRD detection for relapse compared with current methods in childhood ALL.](#)
- URL: <http://www.vidjil.org>

### 5.4. MATAM

#### *Mapping-Assisted Targeted-Assembly for Metagenomics*

KEYWORDS: Metagenomics - Genome assembling - Graph algorithmics

SCIENTIFIC DESCRIPTION: MATAM relies on the construction of a read overlap graph. Overlaps are computed using SortMeRNA. The overlap graph is simplified into relevant components related to specific and conserved regions. Components are assembled into contigs using SGA and contigs are finally assembled into scaffolds. The process yields nearly full length marker sequences with a very low error rate compared to the state of the art approaches. Taxonomic assignation of the obtained scaffolds is performed using the RDP classifier and is represented using Krona.



FUNCTIONAL DESCRIPTION: MATAM provides targeted genes assembly from the short metagenomic reads issued from environmental samples sequencing. Its default application focuses on the gold standard for species identification, 16S / 18S ribosomal RNA SSU genes. The produced gene scaffolds are highly accurate and suitable for precise taxonomic assignation. The software also provides a RDP classification for the reconstructed scaffolds as well as an estimation of the relative population sizes.

- Participants: H  l  ne Touzet, Pierre Pericard, Yoann Dufresne, Samuel Blanquart and Lo  c Couderc
- Contact: H  l  ne Touzet
- Publication: **MATAM: reconstruction of phylogenetic marker genes from short sequencing reads in metagenomes**
- URL: <https://github.com/bonsai-team/matam>

## **FUN Project-Team**

# **6. New Software and Platforms**

## **6.1. AspireRFID ALE**

**FUNCTIONAL DESCRIPTION:** 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. This module has been implemented in the framework of the MIAOU project.

- Participants: Ibrahim Amadou, Julien Vandaële, Nathalie Mitton and Rim Driss
- Contact: Nathalie Mitton

## **6.2. ETINODE-CONTIKI-PORT**

**FUNCTIONAL DESCRIPTION:** Contiki is an open source embedded OS for Internet of Things (IoT). It is light and portable to different hardware architectures. It embeds communication stacks for IoT Il embarque aussi des piles de communication pour l'internet des objets. This driver allows the running of Contiki OS over Etinode-MSP430. The code also allows the use of radio chip and embedded sensors. This module has been implemented in the framework of the ETIPOPS project.

- Participants: Nathalie Mitton, Roudy Dagher and Salvatore Guzzo Bonifacio
- Contact: Salvatore Guzzo Bonifacio

## **6.3. ETINODE-DRIVERS**

**FUNCTIONAL DESCRIPTION:** These drivers for Etinode-MSP430 control the different embedded sensors and hardware components available on an Etinode-MSP430 node such as gyroscope, accelerometer and barometric sensor. This module has been implemented in the framework of the ETIPOPS project.

- Participants: Nathalie Mitton, Roudy Dagher and Salvatore Guzzo Bonifacio
- Contact: Salvatore Guzzo Bonifacio

## **6.4. EVe-TCF**

*Embedded Verifier for Transitive Control Flow*

**KEYWORDS:** Control Flow - JavaCard - Embedded systems - Embedded - Security - Code analysis

**FUNCTIONAL DESCRIPTION:** Verification of transitive control flow policies on JavaCard 2.x bytecode. Control flow policies expressed using a DSL language are embedded in JavaCard packages (CAP files) using EVe-TCF convert tool. Control flow policies are then statically verified on-device at loading-time thanks to an embedded verifier (designed for smart cards in EVe-TCF). EVe-TCF (Embedded Verifier for Transitive Control Flow ) also contains an off-device (i.e. PC tool) to simulate on-device loading process of JavaCard 2.x platforms with GlobalPlatform 2.x installed.

- Participants: Arnaud Fontaine and Isabelle Simplot Ryl
- Contact: Nathalie Mitton

## **6.5. GOLIATH**

*Generic Optimized Lightweight communication stack for Ambient Technologies*

**KEYWORDS:** WSN - WSN430

**FUNCTIONAL DESCRIPTION:** GOLIATH (Generic Optimized LIghtweight communication stack for Ambient TecHnologies) is a full protocol stack for wireless sensor networks. This module has been implemented in the framework of the ETIPOPS project.

- Participants: David Simplot Ryl, Fadila Khadar, Nathalie Mitton and Salvatore Guzzo Bonifacio
- Contact: Nathalie Mitton
- URL: <https://gforge.inria.fr/projects/goliath/>

## 6.6. 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
- Contact: Julien Vandaële
- URL: <https://github.com/iot-lab/>

## 6.7. T-SCAN

**KEYWORDS:** Rfid - RFID Middleware

**FUNCTIONAL DESCRIPTION:** T-Scan is an interface ensuring the translation from a SGTIN tag format to an ONS hostname format according to the EPCGlobal standards. It allows the sending of a DNS request to look up the EPC-IS aides to which the product belongs in order to access the data relative to that product. This module has been implemented in the framework of the TRACAVERRERRE project.

- Participants: Gabriele Sabatino and Nathalie Mitton
- Contact: Gabriele Sabatino

## 6.8. FIT IoT-Lab

**Participants:** Nathalie Mitton [correspondant], Julien Vandaele, Matthieu Berthome.

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.

## RMOD Project-Team

# 6. New Software and Platforms

## 6.1. Moose

*Moose: Software and Data Analysis Platform*

KEYWORDS: Software engineering - Meta model - Software visualisation

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. The development of Moose has been evaluated to 200 man/year.

Mots-cles : MetaModeling, Program Visualization, Software metrics, Code Duplication, Software analyses, Parsers

- Participants: Anne Etien, Nicolas Anquetil, Olivier Auverlot, Stéphane Ducasse, Julien Delplanque, Guillaume Larcheveque, Cyril Ferlicot-Delbecque and Pavel Krivanek
- 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 - Web Application

FUNCTIONAL DESCRIPTION: Pharo is a pure object reflective and dynamic language inspired by Smalltalk. In addition, Pharo comes with a full advanced programming environment developed under the MIT License. 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. Pharo 60 got 100 contributors world-wide. It is used by around 30 universities, 15 research groups and around 40 companies.

- Participants: Christophe Demarey, Clement Bera, Damien Pollet, Esteban Lorenzano, Marcus Denker, Stéphane Ducasse and Guillermo Polito
- Partners: BetaNine - Reveal - Inceptive - Netstyle - Feenk - ObjectProfile - GemTalk Systems - Greyc Université de Caen - Basse-Normandie - Université de Berne - Yesplan - RMod - Pleiad - Sensus - Université de Bretagne Occidentale - École des Mines de Douai - ENSTA - Uqbar foundation Argentina - LAM Research - ZWEIDENKER - LifeWare - JPMorgan Chase - KnowRoaming - ENIT - Spesenfuchs - FINWorks - Esug - FAST - Ingenieubüro Schmidt - Projector Software - HRWorks - Inspired.org - Palantir Solutions - High Octane - Soops - Osoco - Ta Mère SCRL - University of Yaounde 1 - Software Quality Laboratory, University of Novi Sad - Software Institute Università della Svizzera italiana - Universidad Nacional de Quilmes - UMMISCO IRD - Université technique de Prague
- 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. It is used in the tools developed by Feenk.com.

- Partner: Feenk
- Contact: Stéphane Ducasse
- URL: <https://github.com/Pillar-markup/pillar>

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## SPIRALS Project-Team

## 6. New Software and Platforms

### 6.1. APISENSE

KEYWORDS: Mobile sensing - Crowd-sensing - Mobile application - Crowd-sourcing - Android

FUNCTIONAL DESCRIPTION: APISENSE platform is a software solution to collect various contextual information from Android devices (client application) and automatically upload collected data to a server (deployed as a SaaS). APISENSE is based on a Cloud computing infrastructure to facilitate datasets collection from significant populations of mobile users for research purposes.

- Participants: Antoine Veullier, Christophe Ribeiro, Julien Duribreux, Nicolas Haderer, Romain Rouvoy, Romain Sommerard and Lakhdar Meftah
- Partner: Université de Lille
- Contact: Romain Rouvoy
- URL: <https://apisense.io>

### 6.2. PowerAPI

KEYWORDS: Energy efficiency - Energy management

FUNCTIONAL DESCRIPTION: PowerAPI is a library for monitoring the energy consumption of software systems.

PowerAPI differs from existing energy process-level monitoring tool in its software orientation, with a fully customizable and modular solution that let the user to precisely define what he/she wants to monitor. PowerAPI is based on a modular and asynchronous event-driven architecture using the Akka library. PowerAPI offers an API which can be used to define requests about energy spent by a process, following its hardware resource utilization (in term of CPU, memory, disk, network, etc.).

- Participants: Adel Noureddine, Loïc Huertas, Maxime Colmant and Romain Rouvoy
- Contact: Romain Rouvoy
- URL: <http://powerapi.org>

### 6.3. Saloon

KEYWORDS: Feature Model - Software Product Line - Cloud computing - Model-driven engineering - Ontologies

FUNCTIONAL DESCRIPTION: 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.

- Participants: Clément Quinton, Daniel Romero Acero, Laurence Duchien, Lionel Seinturier and Romain Rouvoy
- Partner: Université Lille 1
- Contact: Lionel Seinturier
- URL: <https://gitlab.irisa.fr/drome00A/saloon>

## 6.4. SPOON

KEYWORDS: Java - Code analysis

FUNCTIONAL DESCRIPTION: Spoon is an open-source library that enables you to transform (see below) and analyze Java source code (see example) . Spoon provides a complete and fine-grained Java metamodel where any program element (classes, methods, fields, statements, expressions...) can be accessed both for reading and modification. Spoon takes as input source code and produces transformed source code ready to be compiled.

- Participants: Gérard Paligot, Lionel Seinturier, Martin Monperrus and Nicolas Petitprez
- Contact: Martin Monperrus
- URL: <http://spoon.gforge.inria.fr>

## DEFROST Project-Team

# 6. New Software and Platforms

## 6.1. SOFA

*Simulation Open Framework Architecture*

KEYWORDS: Real time - Multi-physics simulation - Medical applications

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: Christian Duriez, François Faure, Hervé Delingette and Stéphane Cotin
- Partner: IGG
- Contact: Stéphane Cotin
- URL: <http://www.sofa-framework.org>

## 6.2. SoftRobots

*SoftRobots plugin for Sofa*

KEYWORDS: Numerical simulations - Problem inverse - Soft robotics

FUNCTIONAL DESCRIPTION: This plugin allows the modeling of deformable robots in the Sofa platform. It allows the modeling of different actuators, such as cable, pneumatic pressure, hydraulics and other simpler types of actuation. It also contains useful tools for animation design or communication with the robot. Coupled with the SoftRobots.Inverse plugin, it also allows the control of these robots. More information can be found on the dedicated website <https://project.inria.fr/softrobot/>.

- Participants: Christian Duriez, Olivier Goury, Jérémie Dequidt, Damien Marchal, Eulalie Coevoet, Erwan Douaille and Félix Vanneste
- Contact: Christian Duriez
- URL: <https://project.inria.fr/softrobot/>

## 6.3. Model Order Reduction Plugin for SOFA

KEYWORDS: Model Order Reduction - Sofa - Finite element modelling

SCIENTIFIC DESCRIPTION: This plugin allows speed-up of SOFA simulations by providing tools to create a reduced version of the SOFA simulation that runs at much higher rates but remains accurate. Starting with a snapshot of the object deformations on a high-dimensional Finite Element mesh, Proper Orthogonal Decomposition (POD) is used to compute a reduced basis of small dimension representing correctly all the possible deformations of the object. The original system describing the object motion is then greatly reduced. To keep numerical efficiency, a hyper-reduction method is used to speed-up the construction of the reduced system.

**FUNCTIONAL DESCRIPTION:** This plugin allows to dramatically reduce computational time in mechanical simulation in the SOFA framework. A reduced simulation, of much smaller dimension but still accurate is created in an automatic way by the plugin. Building the reduced model may take time, but this operation is made once only. The user can then benefit from a reduced and interactive version of his/her simulation without significant loss of accuracy.

**RELEASE FUNCTIONAL DESCRIPTION:** This is the first version of the plugin.

**NEWS OF THE YEAR:** Publication using this plugin accepted dans IEEE Transactions on Robotics

- Participants: Olivier Goury, Félix Vanneste, Christian Duriez and Eulalie Coevoet
- Contact: Olivier Goury
- Publication: **Fast, generic and reliable control and simulation of soft robots using model order reduction**
- URL: <https://project.inria.fr/modelorderreduction/>

## 6.4. SoftRobots.Inverse

**KEYWORDS:** Sofa - SoftRobots

**FUNCTIONAL DESCRIPTION:** This plugin builds on the plugin SoftRobots ( <https://project.inria.fr/softrobot/> ). Inside the plugin, there is some constraint components that are used to describe the robot (effectors, actuators, sensors). An optimisation algorithm is provided to find the efforts to put on actuators in order to place the robot in a the closest possible configuration than the one described by "effectors", or to a state described by "sensors". This method used to control the soft-robots in the task space is patented.

- Partners: CNRS - Université de Lille - Ecole Centrale de Lille
- Contact: Christian Duriez
- URL: <https://project.inria.fr/softrobot.inverse>



## LINKS Project-Team

# 6. New Software and Platforms

## 6.1. ShEx validator

*Validation of Shape Expression schemas*

KEYWORDS: Data management - RDF

FUNCTIONAL DESCRIPTION: Shape Expression schemas is a formalism for defining constraints on RDF graphs. This software allows to check whether a graph satisfies a Shape Expressions schema.

RELEASE FUNCTIONAL DESCRIPTION: ShExJava now uses the Commons RDF API and so support RDF4J, Jena, JSON-LD-Java, OWL API and Apache Clerezza. It can parse ShEx schema in the ShEcC, ShEJ, ShExR formats and can serialize a schema in ShExJ.

To validate data against a ShExSchema using ShExJava, you have two different algorithms: - the refine algorithm: compute once and for all the typing for the whole graph - the recursive algorithm: compute only the typing required to answer a validate(node,ShapeLabel) call and forget the results.

- Contact: Iovka Boneva
- URL: <http://shexjava.lille.inria.fr/>

## 6.2. gMark

*gMark: schema-driven graph and query generation*

KEYWORDS: Semantic Web - Data base

FUNCTIONAL DESCRIPTION: gMark allow the generation of graph databases and an associated set of query from a schema of the graph.gMark is based on the following principles: - great flexibility in the schema definition - ability to generate big size graphs - ability to generate recursive queries - ability to generate queries with a desired selectivity

- Contact: Aurélien Lemay
- URL: <https://github.com/graphMark/gmark>

## 6.3. SmartHal

KEYWORD: Bibliography

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. 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.

- Contact: Joachim Niehren
- URL: <http://smarthal.lille.inria.fr/>

## 6.4. QuiXPath

KEYWORDS: XML - NoSQL - Data stream

SCIENTIFIC DESCRIPTION: The QuiXPath tools supports a very large fragment of XPath 3.0. The QuiXPath library provides a compiler from QuiXPath to FXP, which is a library for querying XML streams with a fragment of temporal logic.

FUNCTIONAL DESCRIPTION: QuiXPath is a streaming implementation of XPath 3.0. It can query large XML files without loading the entire file in main memory, while selecting nodes as early as possible.

- Contact: Joachim Niehren
- URL: <https://project.inria.fr/quix-tool-suite/>

## **6.5. X-FUN**

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

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: Joachim Niehren and Pavel Labath
- Contact: Joachim Niehren

## LOKI Team

# 6. New Software and Platforms

## 6.1. ParkEvolution

*Longitudinal analysis of fine motor movement in an ecological context for patients with Parkinson disease*

KEYWORD: Parkinson disease

FUNCTIONAL DESCRIPTION: The originality of this application relies on the acquisition of data in an ecological context. Thanks to this application that patients download on their personal computer, the data corresponding to cursor displacement on screen and raw input from pointing devices are collected, encrypted and sent to a server. The analysis of this data allows to compute a motor score according to the parameters of movement, in order to identify alterations in fine motor control. We ensure a realistic score based on the important quantity of data collected. This software is written in C++ and runs on Windows. It uses the libpointing library to access raw data from pointing devices.

RELEASE FUNCTIONAL DESCRIPTION: Fixed bugs and developed new features.

NEWS OF THE YEAR: Release of the 1.3.0 version fixing a number of bugs and introducing a number of new small features. An APP request is close of getting approved.

- Participants: Géry Casiez and Laure Fernandez
- Partners: Aix-Marseille Université - CNRS Laboratoire de Psychologie Cognitive - UMR 7290 - Team 'Perception and attention' - Institut de Neurosciences de la Timone
- Contact: Géry Casiez
- URL: <http://parkevolution.org/>

## 6.2. liblag

*Library implementing latency compensation techniques for interactive systems*

KEYWORDS: Interaction - Latency

FUNCTIONAL DESCRIPTION: The library comprises the management of a set of multitouch input devices, the implementation of latency compensation techniques from the state-of-the-art and new latency compensation techniques developed in the project, and a system to handle artificial latency.

The library is developed in C++ using the Qt framework to allow compiling the same code on a wide range of devices and platforms.

NEWS OF THE YEAR: Finished the work on the latency compensation algorithm "TurboTouch predictor" and development of the demonstrator presented at Euratechnologies. Development of an on-line interactive demo available at <http://ns.inria.fr/loki/TTp/>

- Contact: Géry Casiez
- Publications: [Dispositif à affichage prédictif - Next-Point Prediction for Direct Touch Using Finite-Time Derivative Estimation](#)
- URL: <http://mjolnir.lille.inria.fr/turbotouch/>

## MAGNET Project-Team

# 6. New Software and Platforms

## 6.1. CoRTeX

*Python library for noun phrase COreference Resolution in natural language TEXTs*

KEYWORD: Natural language processing

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 pre-processing, reading the CONLL2012 and CONLLU annotation formats, and performing evaluation, notably 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. It currently supports use of the English or French language.

- Participant: Pascal Denis
- Partner: Orange Labs
- Contact: Pascal Denis
- URL: <https://gitlab.inria.fr/magnet/CoRTeX>

## 6.2. Mangoes

*MAgnet liNGuistic wOrd vEctorS*

KEYWORDS: Word embeddings - NLP

FUNCTIONAL DESCRIPTION: Process textual data and compute vocabularies and co-occurrence matrices. Input data should be raw text or annotated text. Compute word embeddings with different state-of-the-art unsupervised methods. Propose statistical and intrinsic evaluation methods, as well as some visualization tools.

- Contact: Nathalie Vauquier
- URL: <https://gitlab.inria.fr/magnet/mangoes>

## 6.3. metric-learn

KEYWORDS: Machine learning - Python - Metric learning

FUNCTIONAL DESCRIPTION: Distance metrics are widely used in the machine learning literature. Traditionally, practitioners would choose a standard distance metric (Euclidean, City-Block, Cosine, etc.) using a priori knowledge of the domain. Distance metric learning (or simply, metric learning) is the sub-field of machine learning dedicated to automatically constructing optimal distance metrics.

This package contains efficient Python implementations of several popular metric learning algorithms.

- Partner: Parietal
- Contact: William De Vazelhes
- URL: <https://github.com/metric-learn/metric-learn>

## 6.4. MyLocalInfo

KEYWORDS: Privacy - Machine learning - Statistics

FUNCTIONAL DESCRIPTION: Decentralized algorithms for machine learning and inference tasks which (1) perform as much computation as possible locally and (2) ensure privacy and security by avoiding personal data leaves devices.

- Contact: Nathalie Vauquier
- URL: <https://gitlab.inria.fr/magnet/mylocalinfo>