informatics *mathematics*

Inria

RESEARCH CENTER
Lille - Nord Europe

FIELD

Activity Report 2016

Section Software

BONSAI Project-Team

6. New Software and Platforms

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

6.2. NORINE

Nonribosomal peptides resource
KEYWORDS: Bioinformatics - Biotechnology - Biology - Genomics - Graph algorithmics - Chemistry - Knowledge database - Drug development - 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. Norine is freely accessible from the following URL: http://bioinfo.lifl.fr/NRP.

FUNCTIONAL DESCRIPTION

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

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

6.3. Olo

KEYWORDS: Bioinformatics - Indexation - Sequence alignment - Biological sequences - Approximate string matching

SCIENTIFIC DESCRIPTION

Approximate string matching of short sequences in a text often starts by a filtering step. That step relies on seed searching, which are shorter than the pattern. Usually in those seeds the number of errors is constrained, to allow more efficient computations. We designed the 01*0 seeds which offer a good trade-off between the number of false positives and filtering time.

FUNCTIONAL DESCRIPTION

We applied the 01*0 seeds to the similarity search of miRNA targets in a reference genome (Bwolo software) and to the similarity search between a pre-miRNA and mature miRNAs (Piccolo software).

- Participants: Sébastien Bini, Mikaël Salson, Hélène Touzet and Christophe Vroland
- Partners: CNRS - Université Lille 1
- Contact: Helene Touzet
- URL: http://bioinfo.lifl.fr/olo/

6.4. Vidjil

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

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

SCIENTIFIC DESCRIPTION

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

Vidjil high-throughput algorithm extracts V(D)J junctions and gather them into clones. This analysis is based on a spaced seed heuristics and is fast and scalable, as, in the first phase, no alignment is performed with database germline sequences. Each sequence is put in a cluster depending on its V(D)J junction. Then a representative sequence of each cluster is computed in time linear in the size of the cluster. Finally, we perform a full alignment using dynamic programming of that representative sequence 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: Mathieu Giraud, Mikaël Salson, Marc Duez, Ryan Herbert, Tatiana Rocher and Florian Thonier
- Partners: CHRU Lille - CNRS - Inria - Université de Lille
- Contact: Mathieu Giraud
- URL: http://www.vidjil.org

DEFROST 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.

Since 2016, SOFA development and maintenance is now coordinated by the SOFA Consortium.

DEFROST is an active member of the consortium steering committee; beside his mission of Inria continuous integration support team coordinator, Bruno Carrez is in charge of the continuous integration setup of the SOFA consortium.

- Participants: Christian Duriez, Jeremie Dequidt, Bruno Carrez, Damien Marchal, Eulalie Coevoet, Frederick Largilliere
- Partner: Sofa consortium, projet-team Mimesis, projet-team Imagine, projet-team Asclepios, In-Simo, Anatoscope
- Contact: Hugo Talbot
- URL: http://www.sofa-framework.org

6.2. Soft-robot plugin for Sofa

Soft-robot plugin for Sofa

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

FUNCTIONAL DESCRIPTION The soft-robot plugin consists in a new framework to simulate and control soft robots. This framework is based on a mechanical modeling of the robot elements in Sofa combined with fast real-time direct/inverse FEM solvers.

The keypoint of the approach implemented is that the same modeling is used for interactive simulation of its behavior and interactive control of the fabricated robots. This plugin was developped during the ADT project SORBET that ended in 09/2016.

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

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

6. New Software and Platforms

6.1. COCO

COmparing Continuous Optimizers

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

SCIENTIFIC DESCRIPTION

COmparing Continuous Optimisers (COCO) is a tool for benchmarking algorithms for black-box optimisation. COCO facilitates systematic experimentation in the field of continuous optimization. COCO provides: (1) an experimental framework for testing the algorithms, (2) post-processing facilities for generating publication quality figures and tables, (3) LaTeX templates of articles which present the figures and tables in a single document.

The COCO software is composed of two parts: (i) an interface available in different programming languages (C/C++, Java, Matlab/Octave, R, Python) which allows to run and log experiments on multiple test functions testbeds of functions (noisy and noiseless) are provided (ii) a Python tool for generating figures and tables that can be used in the LaTeX templates.

FUNCTIONAL DESCRIPTION

The Coco Platform provides the functionality to automatically benchmark optimization algorithms for unbounded, unconstrained optimization problems in continuous domains. Benchmarking is a vital part of algorithm engineering and a necessary path to recommend algorithms for practical applications. The Coco platform releases algorithm developers and practitioners alike from (re-)writing test functions, logging, and plotting facilities by providing an easy-to-handle interface in several programming languages. The Coco platform has been developed since 2007 and has been used extensively within the "Blackbox Optimization Benchmarking (BBOB)" workshop series since 2009. Overall, 140+ algorithms and algorithm variants by contributors from all over the world have been benchmarked with the platform so far and all data is publicly available for the research community). A new extension towards bi-objective problems will be used for the BBOB-2016 workshop at GECCO.

- Participants: Dimo Brockhoff, Arnaud Liefooghe, Thanh-Do Tran, Nikolaus Hansen, Anne Auger, Marc Schoenauer, Ouassim Ait Elhara, Asma Atamna, Tea Tusar and Dejan Tusar
- Partners: Université technique de Dortmund - Université technique de Prague
- Contact: Dimo Brockhoff
- URL: https://github.com/numbbo/coco

6.2. ParadisEO

KEYWORD: Metaheuristics, multi-objective optimization, Parallel metaheuristics

SCIENTIFIC DESCRIPTION

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

FUNCTIONAL DESCRIPTION

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

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

6.3. VRPsolve

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

- Participants: Clive Ferret-Canape, Arnaud Liefooghe and Sebastien Verel
- URL: http://gforge.inria.fr/projects/vrpsolve

6.4. Platform Grid'5000

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

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

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

5. New Software and Platforms

5.1. HoMade

KEYWORDS: SoC - Multicore - Softcore

FUNCTIONAL DESCRIPTION

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

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

5.2. JHomade

FUNCTIONAL DESCRIPTION

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

- Contact: Vlad Rusu
- URL: https://gforge.inria.fr/frs/?group_id=3646

FUN Project-Team

6. New Software and Platforms

6.1. FIT IoT-Lab

Participants: Nathalie Mitton [correspondant], Julien Vandaele.

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

The Lille site displays 3 subsets of the platforms:

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

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

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

INOCS Team (section vide)

<div align="center">

LINKS Project-Team

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6. New Software and Platforms

6.1. ShEx Validator

KEYWORDS: RDF Data management - RDF - Shape Expression
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.

- Participants: Iovka Boneva
- Contact: Iovka Boneva
- URL: https://gforge.inria.fr/projects/shex-impl

6.2. gMark

KEYWORDS: graph benchmark - Graph Database - Graph Query
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 and queries with a desired selectivity .

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

6.3. QuiXPath

KEYWORDS: XML Streams - XPath 3.0 Queries - Aggregation - Data Joins
FUNCTIONAL DESCRIPTION

QuiXPath is a streaming implementation that covers most of XPath 3.0. It was developed during the PhD thesis of T. Sebastian funded by our industrial transfer partner Innovimax.

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

6.4. X-FUN

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

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

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

MAGNET Project-Team

6. New Software and Platforms

6.1. CoRTex

Python library for noun phrase COreference Resolution in natural language TEXts
FUNCTIONAL DESCRIPTION

CoRTex is a LGPL-licensed Python library for Noun Phrase coreference resolution in natural language texts. This library contains implementations of various state-of-the-art coreference resolution algorithms, including those developed in our research. In addition, it provides a set of APIs and utilities for text 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.

- Participants: Pascal Denis and David Chatel
- Contact: Pascal Denis
- URL: https://team.inria.fr/magnet/software/

6.2. Magneto

Python toolbox for generating and evaluating vector space representations for Natural Language Processing
FUNCTIONAL DESCRIPTION

Version 1.0 of Magneto contains preprocessing methods for texts in french and english. It includes classical methods for generating vector space representations: count based models, dimensionality reduction based methods and predictive methods (word2vec and Glove). For version 1.0, vector space representations can be evaluated on dedicated evaluation tasks such as similarity and analogy.

- Participants: Pascal Denis, Rémi Gilleron, Mikaela Keller, François Noyer and Nathalie Vauquier
- Contact: Pascal Denis
- URL: https://team.inria.fr/magnet/software/

MEPHYSTO Project-Team

6. New Software and Platforms

6.1. MODULEF

FUNCTIONAL DESCRIPTION

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

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

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

MINT Project-Team

5. New Software and Platforms

5.1. ControllAR

FUNCTIONAL DESCRIPTION

ControllAR is a novel system that facilitates the appropriation of rich visual feedback on control surfaces through remixing of graphical user interfaces and augmented reality display.

- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/ControllAR

5.2. GINA

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

5.3. Revil

FUNCTIONAL DESCRIPTION

Revil is an application for building and manipulating 3D SceneGraphs for Mixed-Reality Artistic Performances. It is based on OpenGL/GLSL(glfw, glm), OpenNI2, FLTK and is entirely controllable via Open-SoundControl messages. It relies on the approach of revealing virtual content in the physical space by intersecting it with performers and spectator's bodies and props.

- Contact: Florent Berthaut
- URL: http://forge.lifl.fr/Revil

5.4. TaxtelOSC

FUNCTIONAL DESCRIPTION

TaxtelOSC is a software wich uses the concept of taxtel to reproduce rich and dense tactile feedback on

- Contact: Laurent Grisoni
- URL: http://forge.lifl.fr/ControllAR

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

6. New Software and Platforms

6.1. Introduction

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

6.2. Libpointing

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

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

The library has been thoroughly improved in 2016. Notable changes concern the migration of code on GitHub, the set up of continuous integration and the automated release of buildings for Windows, Linux and MacOS. libpointing can be easily installed using apt-get command on Linux and and Homebrew and Macport package installers on MacOS. New features like the estimation of the input frequency have been added and different demos have been developed. Code has been re-factored and various bugs fixed.

Web site: http://libpointing.org/

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

6.3. Liblag

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

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

Sébastien Poulmane was recruited in May as an engineer on the TurboTouch project. He has been contributing to refactor the code, integrate new input devices and new prediction techniques and also develop associated demos and experiments.

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

6.4. Mouse-based lagmeter

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

As part of the work reported in [46], we implemented our mouse-based method for measuring end-to-end latency using Java/Swing, C++/GLUT, C++/Qt and JavaScript/HTML5. We also wrote Python scripts to parse the logs generated by these implementations in order to compare them. This software (about 2,500 lines of code) was made available in 2016 on a public git repository. The online interactive demo has been improved to collect anonymous latency measurement data from users and integrate libpointing in order to get information about the input and output devices connected. A native Android version has also been developed.

Web site: http://mjolnir.lille.inria.fr/turbotouch/lagmeter/

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

6.5. TAN

Participants: Fanny Chevalier [correspondent], Nicolas Roussel, Stéphane Huot.

TAN stands for *Transitions animées*, i.e. *Animated transitions*. This web site illustrates some of our past research on this topic. It combines videos and live demonstrations of Histomages, an image editing tool that associates pixel and color space; Diffamation, an animation tool to follow and understand the modifications made to a document over time; and Gliimpse, a markup language editor (e.g. HTML, LaTeX, Wiki) to instantly switch from source code to the document it produces and vice versa. The source code for the three demonstrators (about 87,000 lines of Java and JavaScript) is not distributed for the moment.

Web site: http://tan.lille.inria.fr/

Software characterization: [A-4] [SO-2] [SM-3] [EM-2] [SDL-4]

6.6. InspectorWidget

Participants: Christian Frisson [correspondent], Sylvain Malacria.

InspectorWidget [26] is an HTML5/nodejs/C++ software suite that can be used by an experimenter to track and analyze users' behaviors in closed interactive software. The suite has a *recording* module that records users' display and captures low-level events while she carries her task, and an *annotation* module that combines OCR and low-level inputs analysis so the experimenter post-annotate users' activity afterwards. InspectorWidget is cross-platform, open-source and publicly available under the GPLv3 license. New features, notably recording and exploiting accessibility API, are currently under development in order to be tested and added to the software suite.

Web site: https://github.com/InspectorWidget/InspectorWidget/

Software characterization: [A-2↑] [SO-3] [SM-3↑] [EM-3] [SDL-4]

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

6. New Software and Platforms

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

6.2. Clustericat

FUNCTIONAL DESCRIPTION

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

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

6.3. CoModes

FUNCTIONAL DESCRIPTION

CoModes is another R package for model-based clustering of categorical data. In this package, the Conditional Modes Model (CMM) (published in 2016) takes into account the main conditional dependencies between variables through particular modality crossings (so-called modes). CoModes performs the model selection and provides the best model according to the exact integrated likelihood criterion and the maximum likelihood estimates.

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

6.4. CorReg

FUNCTIONAL DESCRIPTION

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

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

6.5. FunFEM

FUNCTIONAL DESCRIPTION

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

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

6.6. FunHDDC

FUNCTIONAL DESCRIPTION

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

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

6.7. Galaxy - MPAgenomics

KEYWORDS: Bioinformatics - Data mining - Statistics - Genomics
FUNCTIONAL DESCRIPTION

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

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

6.8. HDPenReg

High-Dimensional Penalized Regression
FUNCTIONAL DESCRIPTION

HDPenReg is an R-package based on a C++ code dedicated to the estimation of regression model with l1-penalization.

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

6.9. MPAGenomics

Multi-Patient Analysis of Genomic markers
KEYWORDS: Segmentation - Genomics - Marker selection - Biostatistics
SCIENTIFIC DESCRIPTION

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

FUNCTIONAL DESCRIPTION

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

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

6.10. MetaMA

Meta-analysis for MicroArrays
KEYWORDS: Transcriptomics - Meta-analysis - Differential analysis - Microarrays - Biostatistics
FUNCTIONAL DESCRIPTION

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

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

6.11. MetaRNASeq

KEYWORDS: Transcriptomics - Meta-analysis - Differential analysis - High throughput sequencing - Biostatistics
FUNCTIONAL DESCRIPTION

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

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

6.12. MixAll

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 (http://www.stkpp.org) for faster computation.

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

6.13. MixCluster

FUNCTIONAL DESCRIPTION

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

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

6.14. Mixmod

Many-purpose software for data mining and statistical learning
KEYWORDS: Data mining - Classification - Mixed data - Data modeling - Big data
FUNCTIONAL DESCRIPTION

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

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

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

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

6.15. 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). A new advanced model concerning functional data is also available in 2016. MixtComp has the ability to natively manage missing data (completely or by interval). MixtComp is used as an R package, but its internals are coded in C++ using state of the art libraries for faster computation.

- Participants: Vincent Kubicki, Christophe Biernacki and Serge Iovleff
- Contact: Christophe Biernacki
- URL: https://massiccc.lille.inria.fr/#/

6.16. RankCluster

FUNCTIONAL DESCRIPTION

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

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

6.17. STK++

Statistical ToolKit
KEYWORDS: Statistics - Linear algebra - Framework
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

6.18. clere

FUNCTIONAL DESCRIPTION

The clere package for R proposes variable clustering in high dimensional linear regression. Available on CRAN and now published to an international journal dedicated to software: [24].

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

6.19. rtkore

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

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

6. New Software and Platforms

6.1. Blimp

FUNCTIONAL DESCRIPTION

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

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

- Contact: Jean-Pierre Richard
- URL: https://bil.inria.fr/fr/software/view/2279/tab

6.2. ControlHub

The driving idea is to interconnect a group of actors (researchers, engineers, etc.) around a control problem and grant them remote access to existing experimental facilities, thus allowing them to verify their theoretical results online, and finally share them with the project members.

The platform architecture relies on three key principles:

- Problem centric: The control problem to be solved is the core project, whereas the software resources, tools and online experiments are web services available to support experimental verification of the solutions.
- Separation of concerns: setup and maintenance of experiment facilities, installation of software tools, problem formulation and theoretical analysis, etc.
- Resource sharing: software packages, experimental facilities, open problems.
- Contact: R. Dagher, A. Polyakov, J.-P. Richard
- URL: https://bil.inria.fr/fr/software/view/2830/tab

6.3. SLIM

FUNCTIONAL DESCRIPTION

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

- Contact: G. Zheng
- URL: https://bil.inria.fr/fr/software/view/2278/tab

RAPSODI Team

6. New Software and Platforms

6.1. New Software

6.1.1. NS2DDV-M: a code for the simulation of inhomogeneous fluid flow

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

6.1.2. A scientific computing software for fast simulation of large systems of interacting particles

Benoît Merlet and Thomas Rey have developed a set of numerical codes for the numerical simulation of large systems of interacting particles. For a system of N particles, the number of interactions is a quadratic functions of N, leading to a quadratic cost of a brut force implementation. This fact limits simulations by "naïve" methods to systems with "only" tenth of thousands of particles. In order to treat larger systems (involving millions of particles), the team has implemented a method based on the Non Uniform Fast Fourier Transform which reduces the computation cost of the interactions to $O(N \log N)$. The NUFFT is used to handle the long range smooth interactions. To treat the possibly singular short range interactions (involving only neighboring particles) a quadtree-like method is used. The method is applied to two kind of problems : computations of the dynamics of interacting particles where a standard ordinary differential equation is used; numerical optimization of the energy of a system of interacting particles thanks to a Nonlinear Conjugate Gradient method.

As an illustration of the efficiency of the code, the team has performed numerical experiments which support the following crystallization conjecture : in 2D, a large number of identical charged particles tend to arrange themselves into a regular triangular lattice.

A user friendly version will be released to the public in 2017.

6.1.3. The Fast Spectral Kinetic Scheme

The Fast Spectral Kinetic Scheme (FSKS), has been jointly developed by researchers from the universities of Ferrara, Toulouse, and Lille, and is the first high-order 7-dimensional deterministic numerical method capable of dealing with the complete physics of rarefied gas dynamics. The FSKM indeed solves the Boltzmann equation in 1 dimension of time, 3 of physical space and 3 of velocity space, and has been used to model accurately aerospace engineering problems such as space shuttle re-entry in the atmosphere or very rarefied gas flow in microscopic devices (Knudsen pump).

<div align="center">

RMOD Project-Team

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6. New Software and Platforms

6.1. Pharo

KEYWORDS: Live programming objet - Reflective system
FUNCTIONAL DESCRIPTION

The platform Pharo is an open-source Smalltalk-inspired language and environment. It provides a platform for innovative development both in industry and research. By providing a stable and small core system, excellent developer tools, and maintained releases, Pharo's goal is to be a platform to build and deploy mission critical applications, while at the same time continue to evolve. In 2016, we released a new version Pharo (Pharo 5.0) completely revisited with fundamental changes in the VM (object representation, compiler, ...)

- Participants: Marcus Denker, Damien Cassou, Stephane Ducasse, Esteban Lorenzano, Damien Pollet, Igor Stasenko, Camillo Bruni, Camille Teruel and Clement Bera
- Partners: BetaNine - Debris publishing - École des Mines de Douai - HR Works - MAD - Pleiad - Sensus - Synectique - Université de Berne - Uqbar foundation Argentina - Vmware - Yesplan
- Contact: Marcus Denker
- URL: http://www.pharo.org

6.2. Moose

FUNCTIONAL DESCRIPTION

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

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

6.3. Pillar

KEYWORDS: HTML - LaTeX - HTML5
FUNCTIONAL DESCRIPTION

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

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

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

6. New Software and Platforms

6.1. 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. Collaborative Filtering Network

KEYWORDS: Recommender system - Neural networks - Deep learning
FUNCTIONAL DESCRIPTION

Recommendation systems advise users on which items (movies, musics, books etc.) they are more likely to be interested in. A good recommendation system may dramatically increase the amount of sales of a firm or retain customers. For instance, 80% of movies watched on Netflix come from the recommender system of the company. Colaborative Filtering (CF) aims at recommending an item to a user by predicting how a user would rate this item. To do so, the feedback of one user on some items is combined with the feedback of all other users on all items to predict a new rating. For instance, if someone rated a few books, CF objective is to estimate the ratings he would have given to thousands of other books by using the ratings of all the other readers.

The following module tackles Collaborative Filtering tasks by using a novel approach based on neural networks (sparse denoising autoencoders). In a few words, the module lets the user train neural networks to predict unknown entries in a history files.

The input files are classic csv files. The output files can either be the full matrix of ratings and/or the network weights. The root mean square error is computed to assess the quality of the training.

This module is based on Lua/Torch Framework. It works on both CPU/GPU and it is multithreaded.

- Contact: Florian Strub
- URL: https://github.com/fstrub95/Autoencoders_cf

SPIRALS Project-Team

6. New Software and Platforms

6.1. APISENSE

KEYWORDS: Mobile sensing - Crowd-sensing - 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: Nicolas Haderer, Romain Rouvoy, Christophe Ribeiro, Julien Duribreux and Antoine Veuiller
- Partner: Université Lille 1
- Contact: Romain Rouvoy
- URL: http://www.apisense.io

6.2. Nopol

KEYWORD: Automatic software repair
FUNCTIONAL DESCRIPTION

Nopol is an automatic software repair tool for buggy conditional statements (i.e., if-then-else statements) in Java programs. Nopol takes a buggy program as well as a test suite as input and generates a patch with a conditional expression as output. The test suite is required to contain passing test cases to model the expected behavior of the program and at least one failing test case that reveals the bug to be repaired. The process of Nopol consists of three major phases. First, Nopol employs angelic fix localization to identify expected values of a condition during the test execution. Second, runtime trace collection is used to collect variables and their actual values, including primitive data types and objected-oriented features (e.g., nullness checks), to serve as building blocks for patch generation. Third, Nopol encodes these collected data into an instance of a Satisfiability Modulo Theory (SMT) problem, then a feasible solution to the SMT instance is translated back into a code patch.

- Contact: Martin Monperrus
- URL: https://github.com/SpoonLabs/nopol/

6.3. PowerAPI

KEYWORD: 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: Romain Rouvoy, Adel Noureddine, Loic Huertas and Maxime Colmant
- Contact: Romain Rouvoy
- URL: http://www.powerapi.org

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

6.5. 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: Clement 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