Activity Report 2019

Section Software

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

6. New Software and Platforms

6.1. TAPASCologne

Travel and Activity PAtterns Simulation Cologne

KEYWORDS: Mobility - Traces

FUNCTIONAL DESCRIPTION: TAPASCologne is an initiative by the Institute of Transportation Systems at the German Aerospace Center (ITS-DLR), aimed at reproducing, with the highest level of realism possible, car traffic in the greater urban area of the city of Cologne, in Germany.

To that end, different state-of-art data sources and simulation tools are brought together, so to cover all of the specific aspects required for a proper characterization of vehicular traffic:

The street layout of the Cologne urban area is obtained from the OpenStreetMap (OSM) database, The microscopic mobility of vehicles is simulated with the Simulation of Urban Mobility (SUMO) software, The traffic demand information on the macroscopic traffic flows across the Cologne urban area (i.e., the O/D matrix) is derived through the Travel and Activity PAtterns Simulation (TAPAS) methodology, The traffic assignment of the vehicular flows described by the TAPASCologne O/D matrix over the road topology is performed by means of Gawron's dynamic user assignment algorithm.

- Participants: Marco Fiore and Razvan Stanica
- Contact: Marco Fiore
- URL: http://kolntrace.project.citi-lab.fr/#download

6.2. Sense in the City

KEYWORDS: Sensors - Sensors network - Wireless Sensor Networks

FUNCTIONAL DESCRIPTION: Sense in the city is a lightweight experimentation platform for wireless sensor networks in development. The main objective of this platform is to be easily transferable and deployable on the field. It allows a simplified deployment of the code running on the sensors and the collection of logs generated by the instrumentation of the code on a centralized database. In the early stage of the platform, the sensors are powered by small PCs, e.g. Raspberry Pi, but we are investigating the integration of energy harvesting capabilities such as solar panels.

- Participants: Hervé Rivano and Khaled Boussetta
- Contact: Khaled Boussetta

6.3. PrivaMovApp

KEYWORD: Crowd-sensing

FUNCTIONAL DESCRIPTION: Agora is leading the development of an Android application for user data collection purposes. The application is based on the Funf framework, and is currently available on Google Play.

- Participants: Stéphane d'Alu, Hervé Rivano, Razvan Stanica and Solohaja Rabenjamina
- Contact: Razvan Stanica

6.4. WSNet

KEYWORD: Network simulator

FUNCTIONAL DESCRIPTION: WSNet is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalabiliy, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation. We still hope to find the proper resource to make WSNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem and Fabrice Valois
- Partner: CEA-LETI
- Contact: Guillaume Chelius
- URL: https://gforge.inria.fr/projects/wsnet-3/

6.5. Platforms

6.5.1. PPAIR Plateforme LoRa - Campus Connecté

The project aims at providing a platform that offers connectivity through a long-range, low-energy network to smart objects. The platform uses LoRa technology, which offers a wide connectivity, covering the entire INSA Lyon campus and providing a data collection service to all campus users. The main purpose of the LoRa plateform is: *(i)* research (researchers can use it for studying reliability and capacity problems, privacy related challenges, etc.), and *(ii)* teaching (several courses from INSA, especially in the Telecom department can use this platform as a pedagogical tool).
Part of the software is mutualized with the University of Paris 13, where a LoRaWan testbed project is under deployment at the campus of Villetaneuse. This project, is supported by a local BQR and is lead by Khaled Boussetta. The mutualization of the software tools will allow us to conduct multi sites experiments, at Lyon and at Paris. Since 2019, this platform is used in the European Project Interreg Med ESMARTCITY and for the PHC Ulysses (joint collaboration with Nimbus Center, Ireland).

6.5.2. UrPolSens Platform

We designed from scratch an energy efficient air pollution sensor network using Atmega micro-controllers and electrochemical air pollution probes. The micro-controller is integrated into a lab-designed printed circuit which includes among others: a high precision ADC, a micro-SD card reader and a radio communication module. The designed nodes measure the nitrogen dioxide (NO2) pollutant in addition to temperature and humidity and transmit data using LoRa to a gateway, which is connected to our servers using a 4G connection. The sensors are also equipped with solar panels in order to extend their lifetime when their batteries are drained. Our platform has been operational in the downtown of the Lyon city with 12 sensor nodes deployed in the Garibaldi street from mid-July to Mid-October 2018.

6.5.3. 3M'air sensor platform

We developed the 3M'Air sensor platform to be used in participatory sensing of temperature and air quality. We have built our own nodes equipped with multiple sensors measuring Nitrogen-Dioxide (NO2), Particulate Matter (PM1, PM2.5, PM10), temperature and humidity. They are battery-powered and equipped with a GPS module to have the position of the measurements. Data are stored on a micro SD card and at the same time sent over LoRa to a server we have developed that is responsible to store these data for future analyses. A web platform has also been developed to display the collected concentration measurements in real time. This developed solution is used in several participatory planned measurement campaigns in Lyon city.

AIRSEA Project-Team

5. New Software and Platforms

5.1. AGRIF

Adaptive Grid Refinement In Fortran

KEYWORD: Mesh refinement

SCIENTIFIC DESCRIPTION: AGRIF is a Fortran 90 package for the integration of full adaptive mesh refinement (AMR) features within a multidimensional finite difference model written in Fortran. Its main objective is to simplify the integration of AMR potentialities within an existing model with minimal changes. Capabilities of this package include the management of an arbitrary number of grids, horizontal and/or vertical refinements, dynamic regridding, parallelization of the grids interactions on distributed memory computers. AGRIF requires the model to be discretized on a structured grid, like it is typically done in ocean or atmosphere modelling.

NEWS OF THE YEAR: In 2019, a new contract has been signed with CMEMS (Copernicus Marine Environment Moniroting Service) in order to extent the multiresolution capabilities of the AGRIF and its integration into the NEMO ocean system.

- Participants: Roland Patoum and Laurent Debreu
- Contact: Laurent Debreu
- Publications: Numerical and experimental approach for a better physical description of submesoscale processes : A north-western Mediterranean Sea case - AGRIF: Adaptive Grid Refinement in Fortran
- URL: http://www-ljk.imag.fr/MOISE/AGRIF

5.2. BALAISE

Bilbliothèque d'Assimilation Lagrangienne Adaptée aux Images Séquencées en Environnement

KEYWORDS: Multi-scale analysis - Data assimilation - Optimal control

FUNCTIONAL DESCRIPTION: BALAISE (Bilbliothèque d'Assimilation Lagrangienne Adaptée aux Images Séquencées en Environnement) is a test bed for image data assimilation. It includes a shallow water model, a multi-scale decomposition library and an assimilation suite.

- Contact: Arthur Vidard

5.3. NEMOVAR

Variational data assimilation for NEMO

KEYWORDS: Oceanography - Data assimilation - Adjoint method - Optimal control

FUNCTIONAL DESCRIPTION: NEMOVAR is a state-of-the-art multi-incremental variational data assimilation system with both 3D and 4D var capabilities, and which is designed to work with NEMO on the native ORCA grids. The background error covariance matrix is modelled using balance operators for the multivariate component and a diffusion operator for the univariate component. It can also be formulated as a linear combination of covariance models to take into account multiple correlation length scales associated with ocean variability on different scales. NEMOVAR has recently been enhanced with the addition of ensemble data assimilation and multi-grid assimilation capabilities. It is used operationnaly in both ECMWF and the Met Office (UK)

- Partners: CERFACS - ECMWF - Met Office
- Contact: Arthur Vidard

5.4. Sensitivity

FUNCTIONAL DESCRIPTION: This package is useful for conducting sensitivity analysis of complex computer codes.

- Contact: Laurent Gilquin
- URL: https://cran.r-project.org/web/packages/sensitivity/index.html

ARIC Project-Team

6. New Software and Platforms

6.1. FPLLL

KEYWORDS: Euclidean Lattices - Computer algebra system (CAS) - Cryptography

SCIENTIFIC DESCRIPTION: The fplll library is used or has been adapted to be integrated within several mathematical computation systems such as Magma, Sage, and PariGP. It is also used for cryptanalytic purposes, to test the resistance of cryptographic primitives.

FUNCTIONAL DESCRIPTION: fplll contains implementations of several lattice algorithms. The implementation relies on floating-point orthogonalization, and LLL is central to the code, hence the name.

It includes implementations of floating-point LLL reduction algorithms, offering different speed/guarantees ratios. It contains a 'wrapper' choosing the estimated best sequence of variants in order to provide a guaranteed output as fast as possible. In the case of the wrapper, the succession of variants is oblivious to the user.

It includes an implementation of the BKZ reduction algorithm, including the BKZ-2.0 improvements (extreme enumeration pruning, pre-processing of blocks, early termination). Additionally, Slide reduction and self dual BKZ are supported.

It also includes a floating-point implementation of the Kannan-Fincke-Pohst algorithm that finds a shortest non-zero lattice vector. For the same task, the GaussSieve algorithm is also available in fplll. Finally, it contains a variant of the enumeration algorithm that computes a lattice vector closest to a given vector belonging to the real span of the lattice.

- Author: Damien Stehlé
- Contact: Damien Stehlé
- URL: https://github.com/fplll/fplll

6.2. Gfun

generating functions package

KEYWORD: Symbolic computation

FUNCTIONAL DESCRIPTION: Gfun is a Maple package for the manipulation of linear recurrence or differential equations. It provides tools for guessing a sequence or a series from its first terms, for manipulating rigorously solutions of linear differential or recurrence equations, using the equation as a data-structure.

- Contact: Bruno Salvy
- URL: http://perso.ens-lyon.fr/bruno.salvy/software/the-gfun-package/

6.3. GNU-MPFR

KEYWORDS: Multiple-Precision - Floating-point - Correct Rounding

FUNCTIONAL DESCRIPTION: GNU MPFR is an efficient arbitrary-precision floating-point library with well-defined semantics (copying the good ideas from the IEEE 754 standard), in particular correct rounding in 5 rounding modes. It provides about 80 mathematical functions, in addition to utility functions (assignments, conversions...). Special data (Not a Number, infinities, signed zeros) are handled like in the IEEE 754 standard. GNU MPFR is based on the mpn and mpz layers of the GMP library.

- Participants: Guillaume Hanrot, Paul Zimmermann, Philippe Théveny and Vincent Lefèvre
- Contact: Vincent Lefèvre
- Publications: Correctly Rounded Arbitrary-Precision Floating-Point Summation - Optimized Binary64 and Binary128 Arithmetic with GNU MPFR - Évaluation rapide de fonctions hypergéométriques - Arbitrary Precision Error Analysis for computing $\zeta(s)$ with the Cohen-Olivier algorithm: Complete description of the real case and preliminary report on the general case - MPFR: A Multiple-Precision Binary Floating-Point Library with Correct Rounding. - The Generic Multiple-Precision Floating-Point Addition With Exact Rounding (as in the MPFR Library)
- URL: https://www.mpfr.org/

6.4. Sipe

KEYWORDS: Floating-point - Correct Rounding

FUNCTIONAL DESCRIPTION: Sipe is a mini-library in the form of a C header file, to perform radix-2 floating-point computations in very low precisions with correct rounding, either to nearest or toward zero. The goal of such a tool is to do proofs of algorithms/properties or computations of tight error bounds in these precisions by exhaustive tests, in order to try to generalize them to higher precisions. The currently supported operations are addition, subtraction, multiplication (possibly with the error term), fused multiply-add/subtract (FMA/FMS), and miscellaneous comparisons and conversions. Sipe provides two implementations of these operations, with the same API and the same behavior: one based on integer arithmetic, and a new one based on floating-point arithmetic.

- Participant: Vincent Lefèvre
- Contact: Vincent Lefèvre
- Publications: SIPE: Small Integer Plus Exponent - Sipe: a Mini-Library for Very Low Precision Computations with Correct Rounding
- URL: https://www.vinc17.net/research/sipe/

6.5. LinBox

KEYWORD: Exact linear algebra

FUNCTIONAL DESCRIPTION: LinBox is an open-source C++ template library for exact, high-performance linear algebra computations. It is considered as the reference library for numerous computations (such as linear system solving, rank, characteristic polynomial, Smith normal forms,...) over finite fields and integers with dense, sparse, and structured matrices.

- Participants: Clément Pernet and Thierry Gautier
- Contact: Clément Pernet
- URL: http://linalg.org/

6.6. HPLLL

KEYWORDS: Euclidean Lattices - Computer algebra system (CAS)

FUNCTIONAL DESCRIPTION: Software library for linear algebra and Euclidean lattice problems

- Contact: Gilles Villard
- URL: http://perso.ens-lyon.fr/gilles.villard/hplll/

AVALON Project-Team

5. New Software and Platforms

5.1. DIET

Distributed Interactive Engineering Toolbox

KEYWORDS: Scheduling - Clusters - Grid - Cloud - HPC - Middleware - Data management.

FUNCTIONAL DESCRIPTION: Middleware for grids and clouds. Toolbox for the use and porting of intensive computing applications on heterogeneous architectures.

RELEASE FUNCTIONAL DESCRIPTION: - Native Google Drive Support for the data manager - Standardization of internal integer types. - New types (see Changelog for more information)

NEWS OF THE YEAR: New DIET release (DIET 2.11) is avaible since may 2019 Batch's GENCI support to use the GENCI resources

- Participants: Joel Faubert, Hadrien Croubois, Abdelkader Amar, Arnaud Lefray, Aurélien Bouteiller, Benjamin Isnard, Daniel Balouek, Eddy Caron, Eric Bois, Frédéric Desprez, Frédéric Lombart, Gaël Le Mahec, Guillaume Verger, Huaxi Zhang, Jean-Marc Nicod, Jonathan Rouzaud-Cornabas, Lamiel Toch, Maurice Faye, Peter Frauenkron, Philippe Combes, Philippe Laurent, Raphaël Bolze, Yves Caniou and Cyril Seguin
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - Sysfera
- Contact: Eddy Caron
- URL: http://graal.ens-lyon.fr/diet/

5.2. SimGrid

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

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

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

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

NEWS OF THE YEAR: There were 3 major releases in 2019: Python bindings were introduced, SMPI now partially supports some of the MPI/IO functions, a new model for Wifi networks was proposed, and the API for the simulation of storage resources was completely revisited. We also pursued our efforts to improve the documentation of the software, simplified the web site, and made a lot of bug fixing and code refactoring.

- Participants: Adrien Lèbre, Arnaud Legrand, Augustin Degomme, Florence Perronnin, Frédéric Suter, Jean-Marc Vincent, Jonathan Pastor, Luka Stanisic and Martin Quinson
- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson
- URL: https://simgrid.org/

5.3. SeeDep

Seed based Deployment

KEYWORDS: Reproducibility - Deployment - Cloud

SCIENTIFIC DESCRIPTION: SeeDep aims at devising a new way where researchers can communicate in a comprehensive and accurate way the experimentation set-up used in their work. It lies on two components: (i) a public algorithm that generates experimentation networks, and (ii) a generation key (i.e. a seed) that can be shared which specifies the said network. Therefore, researchers only need to share (in their paper for instance) the "generation key" that corresponds to their experimentation network. With such key, any other researcher/professional will be able to re-generate a comprehensive and accurate model of the same network.

FUNCTIONAL DESCRIPTION: SeeDep is a framework aiming at generating, reproducing and deploying experiments set-up on different Cloud platforms.

- Participants: Cyril Seguin and Eddy Caron
- Partner: Nokia Bell Labs
- Contact: Eddy Caron

5.4. libkomp

Runtime system libkomp

KEYWORDS: HPC - Multicore - OpenMP

FUNCTIONAL DESCRIPTION: libKOMP is a runtime support for OpenMP compatible with différent compiler: GNU gcc/gfortran, Intel icc/ifort or clang/llvm. It is based on source code initially developed by Intel for its own OpenMP runtime, with extensions from Kaapi software (task representation, task scheduling). Moreover it contains an OMPT module for recording trace of execution.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Contact: Thierry Gautier
- URL: http://gitlab.inria.fr/openmp/libkomp

5.5. XKBLAS

KEYWORDS: BLAS - Dense linear algebra - GPU

FUNCTIONAL DESCRIPTION: XKBLAS is yet an other BLAS library (Basic Linear Algebra Subroutines) that targets multi-GPUs architecture thanks to the XKaapi runtime and with block algorithms from PLASMA library. The library offers a wrapper library able to capture calls to BLAS (C or Fortran). The internal API is based on asynchronous invocations in order to enable overlapping between communication by computation and also to better composed sequences of calls to BLAS.

This current version of XKBlas is the first public version and contains only BLAS level 3 algorithms, including XGEMMT:

XGEMM XGEMMT: see MKL GEMMT interface XTRSM XTRMM XSYMM XSYRK XSYR2K XHEMM XHERK XHER2K

For classical precision Z, C, D, S.

RELEASE FUNCTIONAL DESCRIPTION: XKBlas has following limitations:

0.1 versions: calls to BLAS kernels must be initiate by the same thread that initializes the XKBlas library.

- Participants: Thierry Gautier and João Vicente Ferreira Lima
- Contact: Thierry Gautier
- URL: https://gitlab.inria.fr/xkblas/versions

5.6. Concerto

KEYWORDS: Reconfiguration - Distributed Software - Component models - Dynamic software architecture

FUNCTIONAL DESCRIPTION: Concerto is an implementation of the formal model Concerto written in Python. Concerto aloows to : 1. describe the life-cycle and the dependencies of software components, 2. describe a components assembly that forms the overall life-cycle of a distributed software, 3. automatically reconfigure a Concerto assembly of components by using a set of reconfiguration instructions as well as a formal operational semantics.

- Partners: IMT Atlantique - LS2N - LIP
- Contact: Maverick Chardet
- URL: https://gitlab.inria.fr/VeRDi-project/concerto

5.7. Kwapi

KiloWatt API

KEYWORD: Power monitoring

FUNCTIONAL DESCRIPTION: Kwapi is a software framework dealing with energy monitoring of large scale infrastructures through heterogeneous energy sensors. Kwapi has been designed inside the FSN XLCloud project for Openstack infrastructures. Through the support of Hemera Inria project, kwapi has been extended and deployed in production mode to support easy and large scale energy profiling of the Grid5000 resources. Kwapi now supports high frequency powermeters of the Grid5000 Lyon platform.

RELEASE FUNCTIONAL DESCRIPTION: - many bugfixes - multiprocessing instead of multithreading - many optimizations

- Participants: François Rossigneux, Jean-Patrick Gelas, Laurent Lefèvre, Laurent Pouilloux, Simon Delamare and Matthieu Imbert
- Contact: Laurent Lefèvre
- URL: https://launchpad.net/kwapi

5.8. execo

KEYWORDS: Toolbox - Deployment - Orchestration - Python

FUNCTIONAL DESCRIPTION: Execo offers a Python API for asynchronous control of local or remote, standalone or parallel, unix processes. It is especially well suited for quickly and easily scripting workflows of parallel/distributed operations on local or remote hosts: automate a scientific workflow, conduct computer science experiments, perform automated tests, etc. The core python package is execo. The execo_g5k package provides a set of tools and extensions for the Grid5000 testbed. The execo_engine package provides tools to ease the development of computer sciences experiments.

RELEASE FUNCTIONAL DESCRIPTION: - misc python3 support fixes - basic documentation for wheezy compatible package build - remove some debug outputs - fix crash in processes conductor in some situations - improve/fix process stdout/stderr handlers - fix get_cluster_network_equipments - add a FAQ

- Participants: Florent Chuffart, Laurent Pouilloux and Matthieu Imbert
- Contact: Matthieu Imbert
- URL: http://execo.gforge.inria.fr

5.9. Platforms

5.9.1. Platform: Grid'5000

Participants: Laurent Lefèvre, Simon Delamare, David Loup, Christian Perez.

FUNCTIONAL DESCRIPTION

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. In 2018, a new generation of high speed wattmeters has been deployed on the Lyon site. They allow energy monitoring with up to 50 measurements per second. In parallel, a new version of kwapi (software stack for energy monitoring) has been proposed and redesigned.

- Contact: Laurent Lefèvre
- URL: https://www.grid5000.fr/

5.9.2. Platform: Leco

Participants: Thierry Gautier, Laurent Lefèvre, Christian Perez.

FUNCTIONAL DESCRIPTION

The LECO experimental platform is a new medium size scientific instrument funded by DRRT to investigate research related to BigData and HPC. It is located in Grenoble as part of the the HPCDA computer managed by UMS GRICAD. The platform has been deployed in 2018 and was available for experiment since the summer. All the nodes of the platform are instrumented to capture the energy consumption and data are available through the Kwapi software.

- Contact: Thierry Gautier

5.9.3. Platform: SILECS

Participants: Laurent Lefèvre, Simon Delamare, Christian Perez.

FUNCTIONAL DESCRIPTION

The SILECS infrastructure (IR ministère) aims at providing an experimental platform for experimental computer Science (Internet of things, clouds, HPC, big data, *etc.*). This new infrastructure is based on two existing infrastructures, Grid'5000 and FIT.

- Contact: Christian Perez
- URL: https://www.silecs.net/

BEAGLE Project-Team

6. New Software and Platforms

6.1. aevol

Artificial Evolution

KEYWORDS: Bioinformatics - Genomics - Evolution

FUNCTIONAL DESCRIPTION: Aevol is a digital genetics model: populations of digital organisms are subjected to a process of selection and variation, which creates a Darwinian dynamics. By modifying the characteristics of selection (e.g. population size, type of environment, environmental variations) or variation (e.g. mutation rates, chromosomal rearrangement rates, types of rearrangements, horizontal transfer), one can study experimentally the impact of these parameters on the structure of the evolved organisms. In particular, since Aevol integrates a precise and realistic model of the genome, it allows for the study of structural variations of the genome (e.g. number of genes, synteny, proportion of coding sequences).

The simulation platform comes along with a set of tools for analysing phylogenies and measuring many characteristics of the organisms and populations along evolution.

An extension of the model (R-Aevol), integrates an explicit model of the regulation of gene expression, thus allowing for the study of the evolution of gene regulation networks.

RELEASE FUNCTIONAL DESCRIPTION: Fix compilation error on Mac (tr1 included in std). The new mac compiler includes the tr1 directly in std which caused a compilation error. This issue was specific to aevol-4.4.1

- Participants: Antoine Frénoy, Bérénice Batut, Carole Knibbe, David P. Parsons, Dusan Misevic, Guillaume Beslon, Jonathan Rouzaud-Cornabas and Vincent Liard
- Partners: UCBL Lyon 1 - INSERM - Université Paris-Descartes - Insa de Lyon
- Contact: Guillaume Beslon
- URL: http://www.aevol.fr/

6.2. Treerecs

KEYWORDS: Bioinformatics - Biology - Computational biology

SCIENTIFIC DESCRIPTION: The reconciliation between gene trees and species trees is a modern method of molecular phylogeny, which does not yet have its standard software, as for example phylogeny from DNA or amino acid sequences. Treerecs has this ambition, incorporating the classic functionalities of reconciliation: annotating the vertices of a gene tree with the tops of a species tree, rooting and correcting the gene tree. Rooting and correction are calculated to minimize the number of duplications and losses in reconciliation. Medium-sized solutions are randomly sampled according to a uniform law. A likelihood can then be calculated using probabilistic methods. In addition, Treerecs is integrated into a standard software ecosystem of phylogeny, bio ++, ALE, Seaview, and has a graphical interface. Some original features are implemented, such as the possibility of combining two types of likelihoods, the one calculated from the sequences and the one calculated from the reconciliations, the possibility of estimating the costs of the evolutionary events, the possibility of exploring the space of trees according to a joined likelihood.

FUNCTIONAL DESCRIPTION: Treerecs takes as minimum input a gene tree and a species tree. It "reconciles" them, that is, it annotates gene tree nodes with events and assign them to species tree nodes. Biologically, it is a reconstruction of the gene history, given the species history, in terms of duplications, speciations, losses.

With the appropriate options Treerecs can root and correct the gene tree.

NEWS OF THE YEAR: Release of a 0.1 stable version

- Participants: Nicolas Comte, David P. Parsons, Eric Tannier and Benoît Morel
- Partner: Laboratoire de Biométrie et Biologie Evolutive (LBBE) - UMR CNRS 5558
- Contact: Eric Tannier

CASH Project-Team

5. New Software and Platforms

5.1. DCC

DPN C Compiler

KEYWORDS: Polyhedral compilation - Automatic parallelization - High-level synthesis

FUNCTIONAL DESCRIPTION: Dcc (Data-aware process network C compiler) analyzes a sequential regular program written in C and generates an equivalent architecture of parallel computer as a communicating process network (Data-aware Process Network, DPN). Internal communications (channels) and external communications (external memory) are automatically handled while fitting optimally the characteristics of the global memory (latency and throughput). The parallelism can be tuned. Dcc has been registered at the APP ("Agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria license.

- Participants: Alexandru Plesco and Christophe Alias
- Contact: Christophe Alias

5.2. PoCo

Polyhedral Compilation Library

KEYWORDS: Polyhedral compilation - Automatic parallelization

FUNCTIONAL DESCRIPTION: PoCo (Polyhedral Compilation Library) is a compilation framework allowing to develop parallelizing compilers for regular programs. PoCo features many state-of-the-art polyhedral program analysis and a symbolic calculator on execution traces (represented as convex polyhedra). PoCo has been registered at the APP ("agence de protection des programmes") and transferred to the XtremLogic start-up under an Inria licence.

- Participant: Christophe Alias
- Contact: Christophe Alias

5.3. MPPcodegen

Source-to-source loop tiling based on MPP

KEYWORDS: Source-to-source compiler - Polyhedral compilation

FUNCTIONAL DESCRIPTION: MPPcodegen applies a monoparametric tiling to a C program enriched with pragmas specifying the tiling and the scheduling function. The tiling can be generated by any convex polyhedron and translation functions, it is not necessarily a partition. The result is a C program depending on a scaling factor (the parameter). MPPcodegen relies on the MPP mathematical library to tile the iteration sets.

- Partner: Colorado State University
- Contact: Christophe Alias
- URL: http://foobar.ens-lyon.fr/mppcodegen/

CHROMA Project-Team

6. New Software and Platforms

6.1. Ground Elevation and Occupancy Grid Estimator (GEOG - Estimator)

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: GEOG-Estimator is a system of joint estimation of the shape of the ground, in the form of a Bayesian network of constrained elevation nodes, and the ground-obstacle classification of a pointcloud. Starting from an unclassified 3D pointcloud, it consists of a set of expectation-maximization methods computed in parallel on the network of elevation nodes, integrating the constraints of spatial continuity as well as the influence of 3D points, classified as ground-based or obstacles. Once the ground model is generated, the system can then construct a occupation grid, taking into account the classification of 3D points, and the actual height of these impacts. Mainly used with lidars (Velodyne64, Quanergy M8, IBEO Lux), the approach can be generalized to any type of sensor providing 3D pointclouds. On the other hand, in the case of lidars, free space information between the source and the 3D point can be integrated into the construction of the grid, as well as the height at which the laser passes through the area (taking into account the height of the laser in the sensor model). The areas of application of the system spread across all areas of mobile robotics, it is particularly suitable for unknown environments. GEOG-Estimator was originally developed to allow optimal integration of 3D sensors in systems using 2D occupancy grids, taking into account the orientation of sensors, and indefinite forms of grounds. The ground model generated can be used directly, whether for mapping or as a pre-calculation step for methods of obstacle recognition or classification. Designed to be effective (real-time) in the context of embedded applications, the entire system is implemented on Nvidia graphics card (in Cuda), and optimized for Tegra X2 embedded boards. To ease interconnections with the sensor outputs and other perception modules, the system is implemented using ROS (Robot Operating System), a set of opensource tools for robotics.

- Authors: Amaury Nègre, Lukas Rummelhard, Lukas Rummelhard, Jean-Alix David and Christian Laugier
- Contact: Christian Laugier

6.2. CMCDOT

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: CMCDOT is a Bayesian filtering system for dynamic occupation grids, allowing parallel estimation of occupation probabilities for each cell of a grid, inference of velocities, prediction of the risk of collision and association of cells belonging to the same dynamic object. Last generation of a suite of Bayesian filtering methods developed in the Inria eMotion team, then in the Inria Chroma team (BOF, HSBOF, ...), it integrates the managment of hybrid sampling methods (classical occupancy grids for static parts, particle sets for parts dynamics) into a Bayesian unified programming formalism , while incorporating elements resembling the Dempster-Shafer theory (state "unknown", allowing a focus of computing resources). It also offers a projection system of the estimated scene in the near future, to reference potential collisions with the ego-vehicle or any other element of the environment, as well as very low cost pre-segmentation of coherent dynamic spaces (taking into account speeds). It takes as input instantaneous occupation grids generated by sensor models for different sources, the system is composed of a ROS package, to manage the connectivity of I / O, which encapsulates the core of the embedded and optimized application on GPU Nvidia (Cuda), allowing real-time analysis of the direct environment on embedded boards (Tegra X1, X2). ROS (Robot Operating System) is a set of open source tools to develop software for robotics. Developed in an automotive setting, these techniques can be exploited in all areas of mobile robotics, and are particularly suited to highly dynamic and uncertain environment management (eg urban scenario, with pedestrians, cyclists, cars, buses, etc.).

- Authors: Amaury Nègre, Lukas Rummelhard, Jean-Alix David and Christian Laugier
- Partners: CEA - CNRS
- Contact: Christian Laugier

6.3. cuda_grid_fusion

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: This module, directly implemented in ROS / Cuda, performs the merge of occupancy grids, defined in the format proposed in CMCDOT (probabilities integrating the "visibility" information of the cell, via the coefficients "unknown") thanks to an original method, allowing not only consistency with the rest of the system, but also a nuanced consideration of confidence criteria towards the various sources of information.

- Authors: Lukas Rummelhard and Jean-Alix David
- Contact: Lukas Rummelhard

6.4. cuda_laser_grid

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: This module generates occupation grids from "almost" planar lidar. The sensor model, as well as the outputs, have been modified, in order to be fully consistent with the CMCDOT and grid fusion module formats.

- Authors: Amaury Nègre, Lukas Rummelhard and Jean-Alix David
- Contact: Lukas Rummelhard

6.5. Zoe Simulation

Simulation of Inria's Renault Zoe in Gazebo environment

KEYWORD: Simulation

FUNCTIONAL DESCRIPTION: This simulation represents the Renault Zoe vehicle considering the realistic physical phenomena (friction, sliding, inertia, ...). The simulated vehicle embeds sensors similar to the ones of the actual vehicle. They provide measurement data under the same format. Moreover the software input/output are identical to the vehicle's. Therefoe any program executed on the vehicle can be used with the simulation and reciprocally.

- Authors: Christian Laugier, Nicolas Turro and Thomas Genevois
- Contact: Christian Laugier

6.6. EKF Odom

EKF based localisation for vehicles

KEYWORDS: Localization - Autonomous Cars

FUNCTIONAL DESCRIPTION: This software fuses IMU data with wheel rotation or speed measurement inside an Extended Kalman Filter. It estimates the state position, orientation, speed, angular speed, acceleration.

- Authors: Thomas Genevois and Christian Laugier
- Contact: Christian Laugier
- URL: https://team.inria.fr/chroma/en/

6.7. Light Vehicle Simulation

Simulation of a light vehicle in Gazebo environment

KEYWORD: Simulation

FUNCTIONAL DESCRIPTION: This simulation represents a light vehicle considering the realistic physical phenomena (friction, sliding, inertia, ...). The simulated vehicle embeds sensors similar to the ones of the actual vehicle. They provide measurement data under the same format. Moreover the software input/output are identical to the vehicle's. Therefore any program executed on the vehicle can be used with the simulation and reciprocally.

- Authors: Thomas Genevois and Christian Laugier
- Contact: Christian Laugier
- URL: https://team.inria.fr/chroma/en/

6.8. CarHybridSim

Hybrid simulation for autonomous cars with high traffic

KEYWORDS: Simulation - Autonomous Cars

FUNCTIONAL DESCRIPTION: Open source tool for simulating autonomous vehicles in complex, high traffic, scenarios. The hybrid simulation fully integrates and synchronizes a microscopic, multi-modal traffic simulator and a complex 3D simulator.

- Contact: Mario Garzon Oviedo
- URL: https://github.com/marioney/hybrid_simulation

6.9. SimuDronesGR

Simultion of UAV fleets with Gazebo/ROS

KEYWORDS: Robotics - Simulation

FUNCTIONAL DESCRIPTION: The simulator includes the following functionality : 1) Simulation of the mechanical behavior of an Unmanned Aerial Vehicle : * Modeling of the body's aerodynamics with lift, drag and moment * Modeling of rotors' aerodynamics using the forces and moments' expressions from Philppe Martin's and Erwan Salaün's 2010 IEEE Conference on Robotics and Automation paper "The True Role of Accelerometer Feedback in Quadrotor Control". 2) Gives groundtruth informations : * Positions in East-North-Up reference frame * Linear velocity in East-North-Up and Front-Left-Up reference frames * Linear acceleration in East-North-Up and Front-Left-Up reference frames * Orientation from East-North-Up reference frame to Front-Left-Up reference frame (Quaternions) * Angular velocity of Front-Left-Up reference frame expressed in Front-Left-Up reference frame. 3) Simulation of the following sensors : * Inertial Measurement Unit with 9DoF (Accelerometer + Gyroscope + Orientation) * Barometer using an ISA model for the troposphere (valid up to 11km above Mean Sea Level) * Magnetometer with the earth magnetic field declination * GPS Antenna with a geodesic map projection.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Author: Vincent Le Doze
- Partner: Insa de Lyon
- Contact: Vincent Le Doze

6.10. cuda_US_grid

KEYWORDS: Robotics - Environment perception

FUNCTIONAL DESCRIPTION: This module generates occupation grids from data generated by an ultrasonic range sensor. The sensor model, as well as the outputs, have been modified, in order to be fully consistent with the CMCDOT and grid fusion module formats.

- Authors: Christian Laugier and Thomas Genevois
- Partner: CEA
- Contact: Christian Laugier

6.11. Embedded Perception

FUNCTIONAL DESCRIPTION: The method for computing occupancy grids from a stereoscopic sensor, developped in the e-motion team, has been implemented on GPU, using NVIDIA CUDA. This allows a real time implementation and an online processing within the Lexus experimental platform.

- Participants: Amaury Nègre, Christian Laugier and Mathias Perrollaz
- Contact: Christian Laugier

6.12. spank

Swarm Protocol And Navigation Kontrol

KEYWORD: Protocoles

FUNCTIONAL DESCRIPTION: Communication and distance measurement in an uav swarm

- Contact: Stéphane d'Alu
- URL: https://gitlab.inria.fr/dalu/spank

6.13. S-NAMO-SIM

S-NAMO Simulator

KEYWORDS: Simulation - Navigation - Robotics - Planning

FUNCTIONAL DESCRIPTION: 2D Simulator of NAMO algorithms (Navigation Among Movable Obstacles) ROS compatible

RELEASE FUNCTIONAL DESCRIPTION: Creation

- Contact: Benoit Renault

CONVECS Project-Team

6. New Software and Platforms

6.1. CADP

Construction and Analysis of Distributed Processes

KEYWORDS: Formal methods - Verification

FUNCTIONAL DESCRIPTION: CADP (*Construction and Analysis of Distributed Processes* – formerly known as *CAESAR/ALDEBARAN Development Package*) [5] is a toolbox for protocols and distributed systems engineering.

In this toolbox, we develop and maintain the following tools:

- CAESAR.ADT [34] is a compiler that translates LOTOS abstract data types into C types and C functions. The translation involves pattern-matching compiling techniques and automatic recognition of usual types (integers, enumerations, tuples, etc.), which are implemented optimally.

- CAESAR [40], [39] is a compiler that translates LOTOS processes into either C code (for rapid prototyping and testing purposes) or finite graphs (for verification purposes). The translation is done using several intermediate steps, among which the construction of a Petri net extended with typed variables, data handling features, and atomic transitions.

- OPEN/CAESAR [35] is a generic software environment for developing tools that explore graphs on the fly (for instance, simulation, verification, and test generation tools). Such tools can be developed independently of any particular high level language. In this respect, OPEN/CAESAR plays a central role in CADP by connecting language-oriented tools with model-oriented tools. OPEN/CAESAR consists of a set of 16 code libraries with their programming interfaces, such as:

  – CAESAR_GRAPH, which provides the programming interface for graph exploration,

  – CAESAR_HASH, which contains several hash functions,

  – CAESAR_SOLVE, which resolves Boolean equation systems on the fly,

  – CAESAR_STACK, which implements stacks for depth-first search exploration, and

  – CAESAR_TABLE, which handles tables of states, transitions, labels, etc.

A number of on-the-fly analysis tools have been developed within the OPEN/CAESAR environment, among which:

  – BISIMULATOR, which checks bisimulation equivalences and preorders,

  – CUNCTATOR, which performs steady-state simulation of continuous-time Markov chains,

  – DETERMINATOR, which eliminates stochastic nondeterminism in normal, probabilistic, or stochastic systems,

  – DISTRIBUTOR, which generates the graph of reachable states using several machines,

  – EVALUATOR, which evaluates MCL formulas,

  – EXECUTOR, which performs random execution,

  – EXHIBITOR, which searches for execution sequences matching a given regular expression,

  – GENERATOR, which constructs the graph of reachable states,

  – PROJECTOR, which computes abstractions of communicating systems,

- REDUCTOR, which constructs and minimizes the graph of reachable states modulo various equivalence relations,

- SIMULATOR, XSIMULATOR, and OCIS, which enable interactive simulation, and

- TERMINATOR, which searches for deadlock states.

- BCG (*Binary Coded Graphs*) is both a file format for storing very large graphs on disk (using efficient compression techniques) and a software environment for handling this format. BCG also plays a key role in CADP as many tools rely on this format for their inputs/outputs. The BCG environment consists of various libraries with their programming interfaces, and of several tools, such as:

  - BCG_CMP, which compares two graphs,

  - BCG_DRAW, which builds a two-dimensional view of a graph,

  - BCG_EDIT, which allows the graph layout produced by BCG_DRAW to be modified interactively,

  - BCG_GRAPH, which generates various forms of practically useful graphs,

  - BCG_INFO, which displays various statistical information about a graph,

  - BCG_IO, which performs conversions between BCG and many other graph formats,

  - BCG_LABELS, which hides and/or renames (using regular expressions) the transition labels of a graph,

  - BCG_MIN, which minimizes a graph modulo strong or branching equivalences (and can also deal with probabilistic and stochastic systems),

  - BCG_STEADY, which performs steady-state numerical analysis of (extended) continuous-time Markov chains,

  - BCG_TRANSIENT, which performs transient numerical analysis of (extended) continuous-time Markov chains, and

  - XTL (*eXecutable Temporal Language*), which is a high level, functional language for programming exploration algorithms on BCG graphs. XTL provides primitives to handle states, transitions, labels, *successor* and *predecessor* functions, etc.

    For instance, one can define recursive functions on sets of states, which allow evaluation and diagnostic generation fixed point algorithms for usual temporal logics (such as HML [43], CTL [32], ACTL [33], etc.) to be defined in XTL.

- PBG (*Partitioned BCG Graph*) is a file format implementing the theoretical concept of *Partitioned LTS* [38] and providing a unified access to a graph partitioned in fragments distributed over a set of remote machines, possibly located in different countries. The PBG format is supported by several tools, such as:

  - PBG_CP, PBG_MV, and PBG_RM, which facilitate standard operations (copying, moving, and removing) on PBG files, maintaining consistency during these operations,

  - PBG_MERGE (formerly known as BCG_MERGE), which transforms a distributed graph into a monolithic one represented in BCG format,

  - PBG_INFO, which displays various statistical information about a distributed graph.

- The connection between explicit models (such as BCG graphs) and implicit models (explored on the fly) is ensured by OPEN/CAESAR-compliant compilers, e.g.:

  - BCG_OPEN, for models represented as BCG graphs,

  - CAESAR.OPEN, for models expressed as LOTOS descriptions,

  - EXP.OPEN, for models expressed as communicating automata,

  - FSP.OPEN, for models expressed as FSP [45] descriptions,

  - LNT.OPEN, for models expressed as LNT descriptions, and

  - SEQ.OPEN, for models represented as sets of execution traces.

The CADP toolbox also includes TGV (*Test Generation based on Verification*), which has been developed by the VERIMAG laboratory (Grenoble) and Inria Rennes – Bretagne-Atlantique.

The CADP tools are well-integrated and can be accessed easily using either the EUCALYPTUS graphical interface or the SVL [36] scripting language. Both EUCALYPTUS and SVL provide users with an easy and uniform access to the CADP tools by performing file format conversions automatically whenever needed and by supplying appropriate command-line options as the tools are invoked.

- Participants: Hubert Garavel, Frédéric Lang, Radu Mateescu and Wendelin Serwe
- Contact: Hubert Garavel
- URL: http://cadp.inria.fr/

6.2. TRAIAN

KEYWORDS: Compilation - LOTOS NT

FUNCTIONAL DESCRIPTION: TRAIAN is a compiler for translating LOTOS NT descriptions into C programs, which will be used for simulation, rapid prototyping, verification, and testing.

The current version of TRAIAN, which handles LOTOS NT types and functions only, has useful applications in compiler construction [37], being used in all recent compilers developed by CONVECS.

- Participants: Hubert Garavel, Frédéric Lang and Wendelin Serwe
- Contact: Hubert Garavel
- URL: http://convecs.inria.fr/software/traian/

CORSE Project-Team

5. New Software and Platforms

5.1. Verde

KEYWORDS: Debug - Verification

FUNCTIONAL DESCRIPTION: Interactive Debugging with a traditional debugger can be tedious. One has to manually run a program step by step and set breakpoints to track a bug.

i-RV is an approach to bug fixing that aims to help developpers during their Interactive Debbugging sessions using Runtime Verification.

Verde is the reference implementation of i-RV.

- Participants: Kevin Pouget, Ylies Falcone, Raphael Jakse and Jean-François Méhaut
- Contact: Raphael Jakse
- Publication: Interactive Runtime Verification - When Interactive Debugging meets Runtime Verification
- URL: https://gitlab.inria.fr/monitoring/verde

5.2. Mickey

KEYWORDS: Dynamic Analysis - Performance analysis - Profiling - Polyhedral compilation

FUNCTIONAL DESCRIPTION: Mickey is a set of tools for profiling based performance debugging for compiled binaries. It uses a dynamic binary translator to instrument arbitrary programs as they are being run to reconstruct the control flow and track data dependencies. This information is then fed to a polyhedral optimizer that proposes structured transformations for the original code.

Mickey can handle both inter- and intra-procedural control and data flow in a unified way, thus enabling interprocedural structured transformations. It is based on QEMU to allow for portability, both in terms of targeted CPU architectures, but also in terms of programming environment and the use of third-party libraries for which no source code is available.

- Partner: STMicroelectronics
- Contact: Fabrice Rastello
- Publications: hal-02060796v1 - hal-01967828v2

5.3. GUS

KEYWORDS: CPU - Microarchitecture simulation - Performance analysis - Dynamic Analysis

FUNCTIONAL DESCRIPTION: GUS' goal is to detect performance bottlenecks at the very low level on monothread applications by the use of sensitivity analysis. It is coded as a QEMU plug-in in order to collect runtime information that are later treated by the generic CPU model.

- Contact: Nicolas Derumigny
- URL: https://gitlab.inria.fr/nderumig/gus

5.4. Pipedream

KEYWORDS: Performance analysis - CPU - Reverse engineering

SCIENTIFIC DESCRIPTION: Pipedream reverse engineers the following performance characteristics: - Instruction latency – The number of cycles an instruction requires to execute. - Peak micro-op retirement rate – How many fused micro-ops the CPU can retire per cycle. - Micro-fusion – The number of fused micro-ops an instruction decomposes into. - Micro-op decomposition and micro-op port usage – The list of unfused micro-ops every instruction decomposes into and the list of execution ports every one of these micro-ops can execute on.

The first step of the reverse engineering process consists of generating a number of microbenchmarks. Pipedream then runs these benchmark, measuring their performance using hardware counters. The latency, throughput, and micro-fusion of different instructions can then be read directly from these measurements.

The process of finding port mappings, i.e. micro-op decompositions and micro-op port usage, however, is more involved. For this purpose, we have defined a variation of the maximum flow problem which we call the "instruction flow problem". We have developed a linear program (LP) formulation of the instruction flow problem which can be used to calculate the peak IPC and micro-operations per cycle (MPC) a benchmark kernel can theoretically achieve with a given port mapping. The actual port mapping of the underlying hardware is then determined by finding the mapping for which the throughput predicted by instruction flow best matches the actual measured IPC and MPC.

FUNCTIONAL DESCRIPTION: Pipedream is a tool for measuring specific performance characteristics of CPUs It is used to build the performance model of another tool called Gus (https://gitlab.inria.fr/nderumig/gus). Pipedream finds measured performance characteristics such as the throughput and latency of instructions by running a large set of automatically generated microbenchmarks. The tool can also find port mappings, a model of part of the CPU instruction scheduler, by analysing performance measurements of specially crafted microkernels using a LP solver. We have used it to produce a port mapping for the Intel Skylake CPU architecture. Pipedream is able to find the port mappings for some instructions for which existing approaches fall back to manual analysis.

- Contact: Nicolas Derumigny
- URL: https://gitlab.inria.fr/fgruber/pipedream

5.5. Platforms

5.5.1. *Grid'5000*

Grid'5000 [0] is a large-scale and versatile testbed for experiment-driven research in all areas of computer science, with a focus on parallel and distributed computing including Cloud, HPC and Big Data. It provides access to a large amount of resources: 14828 cores, 829 compute-nodes grouped in homogeneous clusters located in 8 sites in France connected through a dedicated network (Renater), and featuring various technologies (GPU, SSD, NVMe, 10G and 25G Ethernet, Infiniband, Omni-Path) and advanced monitoring and measurement features for traces collection of networking and power consumption, providing a deep understanding of experiments. It is highly reconfigurable and controllable. Researchers can experiment with a fully customized software stack thanks to bare-metal deployment features, and can isolate their experiment at the networking layer advanced monitoring and measurement features for traces collection of networking and power consumption, providing a deep understanding of experiments designed to support Open Science and reproducible research, with full traceability of infrastructure and software changes on the testbed. Frédéric Desprez is director of the GRID5000 GIS.

5.5.2. *SILECS/SLICES*

Frédéric Desprez is co-PI with Serge Fdida (Université Sorbonne) of the SILECS [0] infrastructure (IR ministère) which goal is to provide an experimental platform for experimental computer Science (Internet of things, clouds, HPC, big data, IA, wireless technologies, ...). This new infrastructure is based on two existing infrastructures, Grid'5000 and FIT. A European infrastructure (SLICES) is also currently designed with other european partners (Spain, Cyprus, Greece, Netherland, Switzerland, Poland, ...).

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[0]https://www.grid5000.fr/
[0]https://www.silecs.net/

CTRL-A Project-Team

6. New Software and Platforms

6.1. Heptagon

KEYWORDS: Compilers - Synchronous Language - Controller synthesis

FUNCTIONAL DESCRIPTION: Heptagon is an experimental language for the implementation of embedded real-time reactive systems. It is developed inside the Synchronics large-scale initiative, in collaboration with Inria Rhones-Alpes. It is essentially a subset of Lucid Synchrone, without type inference, type polymorphism and higher-order. It is thus a Lustre-like language extended with hierchical automata in a form very close to SCADE 6. The intention for making this new language and compiler is to develop new aggressive optimization techniques for sequential C code and compilation methods for generating parallel code for different platforms. This explains much of the simplifications we have made in order to ease the development of compilation techniques.

The current version of the compiler includes the following features: - Inclusion of discrete controller synthesis within the compilation: the language is equipped with a behavioral contract mechanisms, where assumptions can be described, as well as an "enforce" property part. The semantics of this latter is that the property should be enforced by controlling the behaviour of the node equipped with the contract. This property will be enforced by an automatically built controller, which will act on free controllable variables given by the programmer. This extension has been named BZR in previous works. - Expression and compilation of array values with modular memory optimization. The language allows the expression and operations on arrays (access, modification, iterators). With the use of location annotations, the programmer can avoid unnecessary array copies.

- Participants: Adrien Guatto, Brice Gelineau, Cédric Pasteur, Eric Rutten, Gwenaël Delaval, Léonard Gérard and Marc Pouzet
- Partners: UGA - ENS Paris - Inria - LIG
- Contact: Gwenaël Delaval
- URL: http://heptagon.gforge.inria.fr

DANTE Project-Team

6. New Software and Platforms

6.1. GraSP

Graph Signal Processing

KEYWORDS: Matlab - LaTeX - Graph - Graph visualization - Signal processing - GNU Octave

FUNCTIONAL DESCRIPTION: Matlab / GNU Octave toolbox to manipulate and visualize signals on graphs. LaTeX package to draw signals.

- Contact: Benjamin Girault

6.2. IoT-LAB aggregation-tools

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB aggregation-tools allow aggregating data results from many nodes at a time. It connects to several tcp connections and handle the received data.

- Participant: Gaetan Harter
- Contact: Eric Fleury
- URL: https://github.com/iot-lab/aggregation-tools

6.3. IoT-LAB cli-tools

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB cli-tools provide a basic set of operations for managing IoT-LAB experiments from the command-line.

- Participants: Frederic Saint-Marcel and Gaetan Harter
- Contact: Eric Fleury
- URL: https://github.com/iot-lab/cli-tools

6.4. IoT-LAB gateway

KEYWORD: Internet of things

FUNCTIONAL DESCRIPTION: IoT-LAB software embedded on a IoT-LAB gateway node new generation provides the local management of the experiment on that node. It is a software bridge between the IoT-LAB server, the user open node and the control node.

- Contact: Frederic Saint-Marcel
- URL: https://github.com/iot-lab/iot-lab-gateway

6.5. IoT-LAB robots

KEYWORDS: Internet of things - Robotics

FUNCTIONAL DESCRIPTION: IoT-LAB robots is an embedded robot controler on a Turtlebot2 providing the IoT-LAB node mobility functionnality

- Partner: Université de Strasbourg
- Contact: Julien Vandaele
- URL: https://github.com/iot-lab/

6.6. Queueing Systems

FUNCTIONAL DESCRIPTION: This tool aims at providing a simple web interface to promote the use of our proposed solutions to numerically solve classical queueing systems.

- Participants: Alexandre Brandwajn and Thomas Begin
- Contact: Thomas Begin
- URL: http://queueing-systems.ens-lyon.fr/

6.7. WSNet

KEYWORD: Network simulator

FUNCTIONAL DESCRIPTION: WSNet is a modular event-driven simulator targeted to Wireless Sensor Networks. Its main goals are to offer scalabiliy, extensibility and modularity for the integration of new protocols/hardware models and a precise radio medium simulation. We still hope to find the proper resource to make WSNet evolve into a wireless capillary network simulator suitable for conducting simulations at the urban scale.

- Participants: Rodrigue Domga Komguem and Fabrice Valois
- Partner: CEA-LETI
- Contact: Guillaume Chelius
- URL: https://gforge.inria.fr/projects/wsnet-3/

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

6. New Software and Platforms

6.1. FlowVR

SCIENTIFIC DESCRIPTION: FlowVR adopts the "data-flow" paradigm, where your application is divided as a set of components exchanging messages (think of it as a directed graph). FlowVR enables to encapsulate existing codes in components, interconnect them through data channels, and deploy them on distributed computing resources. FlowVR takes care of all the heavy lifting such as application deployment and message exchange.

The base entity, called a module or component, is an autonomous process, potentially multi-threaded with tools like OpenMP, TBB, or deferring computations to a GPU or Xeon Phi. This module processes data coming from input ports and write data on output ports. A module has no global insight on where the data comes from or goes to. The programming interface is designed to limit code refactoring, easing turning an existing code into a FlowVR component. The three main functions are:

wait(): Blocking function call that waits for the availability of new messages on input ports. get(): Retrieve a handle to access the message received at the previous wait() call on a given input port. put(): Notify FlowVR that a new message on a given output port is ready for dispatch. FlowVR manages data transfers. Intra-node communications between two components take place through a shared memory segment, avoiding copies. Once the sender has prepared the data in a shared memory segment, it simply handles a pointer to the destination that can directly access them. Inter-node communications extend this mechanism, FlowVR taking care of packing and transferring the data from the source shared memory segment to the destination shared memory segment.

Assembling components to build an application consists in writing a Python script, instanciate it according to the target machine. FlowVR will process it and prepare everything so that in one command line you can deploy and start your application.

FUNCTIONAL DESCRIPTION: FlowVR adopts the "data-flow" paradigm, where your application is divided as a set of components exchanging messages (think of it as a directed graph). FlowVR enables to encapsulate existing codes in components, interconnect them through data channels, and deploy them on distributed computing resources. FlowVR takes care of all the heavy lifting such as application deployment and message exchange.

- Participants: Bruno Raffin, Clément Ménier, Emmanuel Melin, Jean Denis Lesage, Jérémie Allard, Jérémy Jaussaud, Matthieu Dreher, Sébastien Limet, Sophie Robert and Valérie Gourantou
- Contact: Bruno Raffin
- URL: http://flowvr.sf.net

6.2. OAR

KEYWORDS: HPC - Cloud - Clusters - Resource manager - Light grid

SCIENTIFIC DESCRIPTION: This batch system is based on a database (PostgreSQL (preferred) or MySQL), a script language (Perl) and an optional scalable administrative tool (e.g. Taktuk). It is composed of modules which interact mainly via the database and are executed as independent programs. Therefore, formally, there is no API, the system interaction is completely defined by the database schema. This approach eases the development of specific modules. Indeed, each module (such as schedulers) may be developed in any language having a database access library.

FUNCTIONAL DESCRIPTION: OAR is a versatile resource and task manager (also called a batch scheduler) for HPC clusters, and other computing infrastructures (like distributed computing experimental testbeds where versatility is a key).

- Participants: Bruno Bzeznik, Olivier Richard and Pierre Neyron
- Partners: LIG - CNRS - Grid'5000 - CIMENT
- Contact: Olivier Richard
- URL: http://oar.imag.fr

6.3. MELISSA

Modular External Library for In Situ Statistical Analysis

KEYWORD: Sensitivity Analysis

FUNCTIONAL DESCRIPTION: Melissa is an in situ solution for sensitivity analysis. It implements iterative algorithms to compute spatio-temporal statistic fields over results of large scale sensitivity studies. Melissa relies on a client/server architecture, composed of three main modules:

Melissa Server: an independent parallel executable. It receives data from the simulations, updates iterative statistics as soon as possible, then trow data away. Melissa API: a shared library to be linked within the simulation code. It mainly transmit simulation data to Melissa Server at each timestep. The simulations of the sensitivity analysis become the clients of Melissa Server. Melissa Launcher: A Python script in charge of generating and managing the whole global sensitivity analysis.

- Authors: Theophile Terraz, Bruno Raffin, Alejandro Ribes and Bertrand Iooss
- Partner: Edf
- Contact: Bruno Raffin
- Publications: In Situ Statistical Analysis for Parametric Studies - Melissa: Large Scale In Transit Sensitivity Analysis Avoiding Intermediate Files
- URL: https://melissa-sa.github.io

6.4. Platforms

6.4.1. *Grid'5000 (https://www.grid5000.fr/) and Meso Center Ciment (http://ciment.univ-grenoble-alpes.fr/)*

We have been very active in promoting the factorization of compute resources at a regional and national level. We have a three level implication, locally to maintain a pool of very flexible experimental machines (hundreds of cores), regionally through the CIMENT meso center (Equipex Grant), and nationally by contributing to the Grid'5000 platform, our local resources being included in this platform. Olivier Richard is member of Grid'5000 scientific committee and Pierre Neyron is member of the technical committee. The OAR scheduler in particular is deployed on both infrastructures. We are currently preparing proposals for the next generation machines within the context of the new university association (Univ. Grenoble-Alpes).

DATASPHERE Team

5. New Software and Platforms

5.1. DNS data analysis

Data analytics tools for DNS data analysis were developed in a cooperation with ICT, Chinese Academy of Sciences in the frame of the thesis of Jingxiu SU.

5.1.1. BGP Monitoring platform

An observatory of global BGP connectivity has been developed that is used to monitor and detect in real time BGP level attacks. In addition, a set of tools were developed to analyse the structure of information propagation over social networks.

5.1.2. Atlas of Data

A platform to visualize data flows over the planet is under construction. It can be accessed online at https://theatlasofdata.earth/.

5.1.3. Observatory of foreign influence on social media

This observatory is monitoring on twitter and facebook the evolution of foreign influence. It is based on a twitter collection platform that is using an extensive database of foreign actors to detect and monitor foreign interference.

DRACULA Project-Team

4. New Software and Platforms

4.1. CelDyn

KEYWORDS: Modeling - Bioinformatics - Biology

FUNCTIONAL DESCRIPTION: Software "Celdyn" is developed in order to model cell population dynamics for biological applications. Cells are represented either as soft spheres or they can have more complex structure. Cells can divide, move, interact with each other or with the surrounding medium. Different cell types can be introduced. When cells divide, the types of daughter cells are specified. A user interface is developed.

- Participants: Alen Tosenberger, Laurent Pujo-Menjouet, Nikolai Bessonov and Vitaly Volpert
- Contact: Vitaly Volpert

ELAN Project-Team

6. New Software and Platforms

6.1. Argus-distribution

KEYWORDS: Frictional contact - Cloth dynamics - Mesh adaptation

SCIENTIFIC DESCRIPTION: The Argus-distribution software exactly replicates all the results published in the SIGGRAPH 2018 paper entitled "An Implicit Frictional Contact Solver for Adaptive Cloth Simulation", by Li et al. This paper presents the first method able to account for cloth contact with exact Coulomb friction, treating both cloth self-contacts and contacts occurring between the cloth and an underlying character. The key contribution is to observe that for a nodal system like cloth, the frictional contact problem may be formulated based on velocities as primary variables, without having to compute the costly Delassus operator. Then, by reversing the roles classically played by the velocities and the contact impulses, conical complementarity solvers of the literature can be adapted to solve for compatible velocities at nodes. To handle the full complexity of cloth dynamics scenarios, this base algorithm has been extended in two ways: first, towards the accurate treatment of frictional contact at any location of the cloth, through an adaptive node refinement strategy, second, towards the handling of multiple constraints at each node, through the duplication of constrained nodes and the adding of pin constraints between duplicata. This method allows to handle the complex cloth-cloth and cloth-body interactions in full-size garments with an unprecedented level of realism compared to former methods, while maintaining reasonable computational timings.allows to simulate cloth dynamics subject to frictional contact.

FUNCTIONAL DESCRIPTION: Adaptive cloth simulation in the presence of frictional contact. Reference software for the paper "An Implicit Frictional Contact Solver for Adaptive Cloth Simulation", Li et al. 2018, ACM Transactions on Graphics (SIGGRAPH'18). The Argus-distribution code was awarded in 2019 the [Graphics Replicability stamp](http://www.replicabilitystamp.org/), which acknowledges its reproducibility.

- Participants: Jie Li, Gilles Daviet, Rahul Narain, Florence Bertails, Matthew Overby, George Brown and Laurence Boissieux
- Partners: Department of Computer Science and Engineering, University of Minnesota - IIT Delhi
- Contact: Florence Bertails
- Publication: An Implicit Frictional Contact Solver for Adaptive Cloth Simulation
- URL: http://www-users.cselabs.umn.edu/~lixx4611/contact_friction.html

6.2. Feel++

KEYWORDS: High order finite elements - Discontinuous Galerkin - High-Performance Computing

FUNCTIONAL DESCRIPTION: Feel++ is a high-performance C++ library for the resolution of general variational formulations, including continuous and discontinuous Galerkin methods, finite element or spectral element methods, reduced basis formulations, etc. It features a high-level domain specific embedded language (DSEL) for Galerkin methods, space dimension-agnostic computation kernels and seamless and automatic parallelism. It also includes applicative toolboxes to solve physics problems in fluid mechanics, solid mechanics, thermal conduction, and the corresponding multi-physics coupling.

- Partners: Université de Strasbourg - UGA - Inria
- Contact: Thibaut Metivet
- URL: http://www.feelpp.org

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ERABLE Project-Team

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5. New Software and Platforms

5.1. C3Part/Isofun

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: The C3PART / ISOFUN package implements a generic approach to the local alignment of two or more graphs representing biological data, such as genomes, metabolic pathways or protein-protein interactions, in order to infer a functional coupling between them.

- Participants: Alain Viari, Anne Morgat, Frédéric Boyer, Marie-France Sagot and Yves-Pol Deniélou
- Contact: Alain Viari
- URL: http://www.inrialpes.fr/helix/people/viari/lxgraph/index.html

5.2. Cassis

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: Implements methods for the precise detection of genomic rearrangement breakpoints.

- Participants: Christian Baudet, Christian Gautier, Claire Lemaitre, Eric Tannier and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://pbil.univ-lyon1.fr/software/Cassis/

5.3. Coala

CO-evolution Assessment by a Likelihood-free Approach

KEYWORDS: Bioinformatics - Evolution

FUNCTIONAL DESCRIPTION:COALA stands for "COevolution Assessment by a Likelihood-free Approach". It is thus a likelihood-free method for the co-phylogeny reconstruction problem which is based on an Approximate Bayesian Computation (ABC) approach.

- Participants: Beatrice Donati, Blerina Sinaimeri, Catherine Matias, Christian Baudet, Christian Gautier, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinaimeri
- URL: http://coala.gforge.inria.fr/

5.4. CSC

KEYWORDS: Genomics - Algorithm

FUNCTIONAL DESCRIPTION: Given two sequences x and y, CSC (which stands for Circular Sequence Comparison) finds the cyclic rotation of x (or an approximation of it) that minimises the blockwise q-gram distance from y.

- Contact: Nadia Pisanti
- URL: https://github.com/solonas13/csc

5.5. Cycads

KEYWORDS: Systems Biology - Bioinformatics

FUNCTIONAL DESCRIPTION: Annotation database system to ease the development and update of enriched BIOCYC databases. CYCADS allows the integration of the latest sequence information and functional annotation data from various methods into a metabolic network reconstruction. Functionalities will be added in future to automate a bridge to metabolic network analysis tools, such as METEXPLORE. CYCADS was used to produce a collection of more than 22 arthropod metabolism databases, available at ACYPICYC (http://acypicyc.cycadsys.org) and ARTHROPODACYC (https://arthropodacyc.cycadsys.org). It will continue to be used to create other databases (newly sequenced organisms, Aphid biotypes and symbionts...).

- Participants: Augusto Vellozo, Hubert Charles, Marie-France Sagot and Stefano Colella
- Contact: Hubert Charles
- URL: http://www.cycadsys.org/

5.6. DBGWAS

KEYWORDS: Graph algorithmics - Genomics

FUNCTIONAL DESCRIPTION:DBGWAS is a tool for quick and efficient bacterial GWAS. It uses a compacted De Bruijn Graph (cDBG) structure to represent the variability within all bacterial genome assemblies given as input. Then cDBG nodes are tested for association with a phenotype of interest and the resulting associated nodes are then re-mapped on the cDBG. The output of DBGWAS consists of regions of the cDBG around statistically significant nodes with several informations related to the phenotypes, offering a representation helping in the interpretation. The output can be viewed with any modern web browser, and thus easily shared.

- Contact: Leandro Ishi Soares de Lima
- URL: https://gitlab.com/leoisl/dbgwas

5.7. Eucalypt

KEYWORDS: Bioinformatics - Evolution

FUNCTIONAL DESCRIPTION:EUCALYPT stands for "EnUmerator of Coevolutionary Associations in PoLYnomial-Time delay". It is an algorithm for enumerating all optimal (possibly time-unfeasible) mappings of a symbiont tree unto a host tree.

- Participants: Beatrice Donati, Blerina Sinaimeri, Christian Baudet, Marie-France Sagot and Pierluigi Crescenzi
- Contact: Blerina Sinaimeri
- URL: http://eucalypt.gforge.inria.fr/

5.8. Fast-SG

KEYWORDS: Genomics - Algorithm - NGS

FUNCTIONAL DESCRIPTION:FAST-SG enables the optimal hybrid assembly of large genomes by combining short and long read technologies.

- Participants: Alex Di Genova, Marie-France Sagot, Alejandro Maass and Gonzalo Ruz Heredia
- Contact: Alex Di Genova
- URL: https://github.com/adigenova/fast-sg

5.9. Gobbolino-Touché

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: Designed to solve the metabolic stories problem, which consists in finding all maximal directed acyclic subgraphs of a directed graph G whose sources and targets belong to a subset of the nodes of G, called the black nodes.

- Participants: Etienne Birmelé, Fabien Jourdan, Ludovic Cottret, Marie-France Sagot, Paulo Vieira Milreu, Pierluigi Crescenzi, Vicente Acuna Aguayo and Vincent Lacroix
- Contact: Marie-France Sagot
- URL: http://gforge.inria.fr/projects/gobbolino

5.10. HapCol

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: A fast and memory-efficient DP approach for haplotype assembly from long reads that works until 25x coverage and solves a constrained minimum error correction problem exactly.

- Contact: Nadia Pisanti
- URL: http://hapcol.algolab.eu/

5.11. HgLib

HyperGraph Library

KEYWORDS: Graph algorithmics - Hypergraphs

FUNCTIONAL DESCRIPTION: The open-source library hglib is dedicated to model hypergraphs, which are a generalisation of graphs. In an *undirected* hypergraph, an hyperedge contains any number of vertices. A *directed* hypergraph has hyperarcs which connect several tail and head vertices. This library, which is written in C++, allows to associate user defined properties to vertices, to hyperedges/hyperarcs and to the hypergraph itself. It can thus be used for a wide range of problems arising in operations research, computer science, and computational biology.

RELEASE FUNCTIONAL DESCRIPTION: Initial version

- Participants: Martin Wannagat, David P. Parsons, Arnaud Mary and Irene Ziska
- Contact: Arnaud Mary
- URL: https://gitlab.inria.fr/kirikomics/hglib

5.12. KissDE

KEYWORDS: Bioinformatics - NGS

FUNCTIONAL DESCRIPTION: KISSDE is an R Package enabling to test if a variant (genomic variant or splice variant) is enriched in a condition. It takes as input a table of read counts obtained from an NGS data pre-processing and gives as output a list of condition-specific variants.

RELEASE FUNCTIONAL DESCRIPTION: This new version improved the recall and made more precise the size of the effect computation.

- Participants: Camille Marchet, Aurélie Siberchicot, Audric Cologne, Clara Benoît-Pilven, Janice Kielbassa, Lilia Brinza and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kissDE/

5.13. KisSplice

KEYWORDS: Bioinformatics - Bioinfirmatics search sequence - Genomics - NGS

FUNCTIONAL DESCRIPTION: Enables to analyse RNA-seq data with or without a reference genome. It is an exact local transcriptome assembler, which can identify SNPs, indels and alternative splicing events. It can deal with an arbitrary number of biological conditions, and will quantify each variant in each condition.

RELEASE FUNCTIONAL DESCRIPTION: Improvements : The KissReads module has been modified and sped up, with a significant impact on run times. Parameters : –timeout default now at 10000: in big datasets, recall can be increased while run time is a bit longer. Bugs fixed : –Reads containing only 'N': the graph construction was stopped if the file contained a read composed only of 'N's. This is was a silence bug, no error message was produced. –Problems compiling with new versions of MAC OSX (10.8+): KisSplice is now compiling with the new default C++ compiler of OSX 10.8+.

KISSPLICE was applied to a new application field, virology, through a collaboration with the group of Nadia Naffakh at Institut Pasteur. The goal is to understand how a virus (in this case influenza) manipulates the splicing of its host. This led to new developments in KISSPLICE. Taking into account the strandedness of the reads was required, in order not to mis-interpret transcriptional readthrough. We now use BCALM instead of DBG-V4 for the de Bruijn graph construction and this led to major improvements in memory and time requirements of the pipeline. We still cannot scale to very large datasets like in cancer, the time limiting step being the quantification of bubbles.

- Participants: Alice Julien-Laferrière, Leandro Ishi Soares de Lima, Vincent Miele, Rayan Chikhi, Pierre Peterlongo, Camille Marchet, Gustavo Akio Tominaga Sacomoto, Marie-France Sagot and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/

5.14. KisSplice2RefGenome

KEYWORDS: Bioinformatics - NGS - Transcriptomics

FUNCTIONAL DESCRIPTION:KISSPLICE identifies variations in RNA-seq data, without a reference genome. In many applications however, a reference genome is available. KISSPLICE2REFGENOME enables to facilitate the interpretation of the results of KISSPLICE after mapping them to a reference genome.

- Participants: Audric Cologne, Camille Marchet, Camille Sessegolo, Alice Julien-Laferrière and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kiss2refgenome/

5.15. KisSplice2RefTranscriptome

KEYWORDS: Bioinformatics - NGS - Transcriptomics

FUNCTIONAL DESCRIPTION:KISSPLICE2REFTRANSCRIPTOME enables to combine the output of KISS-PLICE with the output of a full length transcriptome assembler, thus allowing to predict a functional impact for the positioned SNPs, and to intersect these results with condition-specific SNPs. Overall, starting from RNA-seq data only, we obtain a list of condition-specific SNPs stratified by functional impact.

- Participants: Helene Lopez Maestre, Mathilde Boutigny and Vincent Lacroix
- Contact: Vincent Lacroix
- URL: http://kissplice.prabi.fr/tools/kiss2rt/

5.16. MetExplore

KEYWORDS: Systems Biology - Bioinformatics

FUNCTIONAL DESCRIPTION: Web-server that allows to build, curate and analyse genome-scale metabolic networks. METEXPLORE is also able to deal with data from metabolomics experiments by mapping a list of masses or identifiers onto filtered metabolic networks. Finally, it proposes several functions to perform Flux Balance Analysis (FBA). The web-server is mature, it was developed in PHP, JAVA, Javascript and Mysql. METEXPLORE was started under another name during Ludovic Cottret's PhD in Bamboo, and is now maintained by the METEXPLORE group at the Inra of Toulouse.

- Participants: Fabien Jourdan, Hubert Charles, Ludovic Cottret and Marie-France Sagot
- Contact: Fabien Jourdan
- URL: https://metexplore.toulouse.inra.fr/index.html/

5.17. Mirinho

KEYWORDS: Bioinformatics - Computational biology - Genomics - Structural Biology

FUNCTIONAL DESCRIPTION: Predicts, at a genome-wide scale, microRNA candidates.

- Participants: Christian Gautier, Christine Gaspin, Cyril Fournier, Marie-France Sagot and Susan Higashi
- Contact: Marie-France Sagot
- URL: http://mirinho.gforge.inria.fr/

5.18. Momo

Multi-Objective Metabolic mixed integer Optimization

KEYWORDS: Metabolism - Metabolic networks - Multi-objective optimisation

FUNCTIONAL DESCRIPTION: MOMO is a multi-objective mixed integer optimisation approach for enumerating knockout reactions leading to the overproduction and/or inhibition of specific compounds in a metabolic network.

- Participants: Ricardo Luiz de Andrade Abrantes, Nuno Mira, Susana Vinga and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://momo-sysbio.gforge.inria.fr

5.19. Moomin

Mathematical explOration of Omics data on a MetabolIc Network

KEYWORDS: Metabolic networks - Transcriptomics

FUNCTIONAL DESCRIPTION: MOOMIN is a tool for analysing differential expression data. It takes as its input a metabolic network and the results of a DE analysis: a posterior probability of differential expression and a (logarithm of a) fold change for a list of genes. It then forms a hypothesis of a metabolic shift, determining for each reaction its status as "increased flux", "decreased flux", or "no change". These are expressed as colours: red for an increase, blue for a decrease, and grey for no change. See the paper for full details: https://doi.org/10.1093/bioinformatics/btz584

- Participants: Henri Taneli Pusa, Mariana Ferrarini, Ricardo Luiz de Andrade Abrantes, Arnaud Mary, Alberto Marchetti-Spaccamela, Leen Stougie and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: https://github.com/htpusa/moomin

5.20. MultiPus

KEYWORDS: Systems Biology - Algorithm - Graph algorithmics - Metabolic networks - Computational biology

FUNCTIONAL DESCRIPTION:MULTIPUS (for "MULTIple species for the synthetic Production of Useful biochemical Substances") is an algorithm that, given a microbial consortium as input, identifies all optimal sub-consortia to synthetically produce compounds that are either exogenous to it, or are endogenous but where interaction among the species in the sub-consortia could improve the production line.

- Participants: Alberto Marchetti-Spaccamela, Alice Julien-Laferrière, Arnaud Mary, Delphine Parrot, Laurent Bulteau, Leen Stougie, Marie-France Sagot and Susana Vinga
- Contact: Marie-France Sagot
- URL: http://multipus.gforge.inria.fr/

5.21. Pitufolandia

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: The algorithms in PITUFOLANDIA (PITUFO / PITUFINA / PAPAPITUFO) are designed to solve the minimal precursor set problem, which consists in finding all minimal sets of precursors (usually, nutrients) in a metabolic network that are able to produce a set of target metabolites.

- Participants: Vicente Acuna Aguayo, Paulo Vieira Milreu, Alberto Marchetti-Spaccamela, Leen Stougie, Martin Wannagat and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://gforge.inria.fr/projects/pitufo/

5.22. Sasita

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION:SASITA is a software for the exhaustive enumeration of minimal precursor sets in metabolic networks.

- Participants: Vicente Acuna Aguayo, Ricardo Luiz de Andrade Abrantes, Paulo Vieira Milreu, Alberto Marchetti-Spaccamela, Leen Stougie, Martin Wannagat and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://sasita.gforge.inria.fr/

5.23. Savage

KEYWORDS: Algorithm - Genomics

FUNCTIONAL DESCRIPTION: Reconstruction of viral quasi species without using a reference genome.

- Contact: Alexander Schonhuth
- URL: https://bitbucket.org/jbaaijens/savage

5.24. Smile

KEYWORDS: Bioinformatics - Genomic sequence

FUNCTIONAL DESCRIPTION: Motif inference algorithm taking as input a set of biological sequences.

- Participant: Marie-France Sagot
- Contact: Marie-France Sagot

5.25. Rime

KEYWORDS: Bioinformatics - Genomics - Sequence alignment

FUNCTIONAL DESCRIPTION: Detects long similar fragments occurring at least twice in a set of biological sequences.

- Participants: Nadia Pisanti and Marie-France Sagot
- Contact: Nadia Pisanti

5.26. Totoro & Kotoura

KEYWORDS: Bioinformatics - Graph algorithmics - Systems Biology

FUNCTIONAL DESCRIPTION: Both TOTORO and KOTOURA decipher the reaction changes during a metabolic transient state, using measurements of metabolic concentrations. These are called metabolic hyperstories. TOTORO (for TOpological analysis of Transient metabOlic RespOnse) is based on a qualitative measurement of the concentrations in two steady-states to infer the reaction changes that lead to the observed differences in metabolite pools in both conditions. In the currently available release, a pre-processing and a post-processing steps are included. After the post-processing step, the solutions can be visualised using DINGHY (http://dinghy.gforge.inria.fr). KOTOURA (for Kantitative analysis Of Transient metabOlic and regUlatory Response And control) infers quantitative changes of the reactions using information on measurement of the metabolite concentrations in two steady-states.

- Participants: Alice Julien-Laferrière, Ricardo Luiz de Andrade Abrantes, Arnaud Mary, Mariana Ferrarini, Susana Vinga, Irene Ziska and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: http://hyperstories.gforge.inria.fr/

5.27. VG-Flow

Viral haplotype reconstruction from contigs using variation graphs

KEYWORD: Haplotyping

FUNCTIONAL DESCRIPTION: The goal of haplotype-aware genome assembly is to reconstruct all individual haplotypes from a mixed sample and to provide corresponding abundance estimates. VG-FLOW provides a reference-genome-independent solution based on the construction of a variation graph, capturing all quasispecies diversity present in the sample. We solve the contig abundance estimation problem and propose a greedy algorithm to efficiently build full-length haplotypes. Finally, we obtain accurate frequency estimates for the reconstructed haplotypes through linear programming techniques.

- Contact: Alexander Schonhuth
- URL: https://bitbucket.org/jbaaijens/vg-flow

5.28. Virus-VG

Viral haplotype reconstruction from contigs using variation graphs

KEYWORD: Haplotyping

FUNCTIONAL DESCRIPTION: Viruses populate their hosts as a viral quasispecies: a collection of genetically related mutant strains. Viral quasispecies assembly refers to reconstructing the strain-specific haplotypes from read data, and predicting their relative abundances within the mix of strains, an important step for various treatment-related reasons. Reference-genome-independent (de novo) approaches have yielded benefits over reference-guided approaches, because reference-induced biases can become overwhelming when dealing with divergent strains. While being very accurate, extant de novo methods only yield rather short contigs. VIRUS-VG aims to reconstruct full-length haplotypes together with their abundances from such contigs, represented as a genome variation graph.

- Contact: Alexander Schonhuth
- URL: https://bitbucket.org/jbaaijens/virus-vg

5.29. Wengan

Making the path

KEYWORD: Genome assembly

FUNCTIONAL DESCRIPTION:WENGAN is a new genome assembler that unlike most of the current long-reads assemblers avoids entirely the all-vs-all read comparison. The key idea behind WENGAN is that long-read alignments can be inferred by building paths on a sequence graph. To achieve this, WENGAN builds a new sequence graph called the Synthetic Scaffolding Graph. The SSG is built from a spectrum of synthetic mate-pair libraries extracted from raw long-reads. Longer alignments are then built by performing a transitive reduction of the edges. Another distinct feature of WENGAN is that it performs self-validation by following the read information. WENGAN identifies miss-assemblies at differents steps of the assembly process.

- Participants: Alex Di Genova and Marie-France Sagot
- Contact: Marie-France Sagot
- URL: https://github.com/adigenova/wengan

5.30. WhatsHap

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION:WHATSHAP is a DP approach for haplotype assembly from long reads that works until 20x coverage and solves the minimum error correction problem exactly. pWHATSHAP is a parallelisation of the core dynamic programming algorithm of WHATSHAP.

- Contact: Nadia Pisanti
- URL: https://bitbucket.org/whatshap/whatshap

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

5. New Software and Platforms

5.1. WellFARE

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling

SCIENTIFIC DESCRIPTION: WellFARE is a Python library implementing linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. WellFARE form the computational core of the WellInverter web application.

FUNCTIONAL DESCRIPTION: As input, WellFARE reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various functions exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. WellFARE is the computational core of the web application WellInverter.

NEWS OF THE YEAR: Publication in BMC Bioinformatics describing the new version of WellFARE
- Participants: Delphine Ropers, Hans Geiselmann, Hidde de Jong, Michel Page, Valentin Zulkower and Yannick Martin
- Partner: UGA
- Contact: Hidde de Jong
- Publication: Robust reconstruction of gene expression profiles from reporter gene data using linear inversion
- URL: https://github.com/ibis-inria/wellfare

5.2. WellInverter

KEYWORDS: Bioinformatics - Statistics - Data visualization - Data modeling

SCIENTIFIC DESCRIPTION: WellInverter is a web application that implements linear inversion methods for the reconstruction of gene expression profiles from fluorescent or luminescent reporter gene data. WellInverter makes the methods available to a broad audience of biologists and bioinformaticians. In particular, we have put in place a parallel computing architecture with a load balancer to distribute the analysis queries over several back-end servers, redesigned the graphical user interface, and developed a plug-in system for defining high-level routines for parsing data files produced by microplate readers from different manufacturers.

FUNCTIONAL DESCRIPTION: As input, WellInverter reads the primary data file produced by a 96-well microplate reader, containing time-series measurements of the absorbance (optical density) as well as the fluorescence and luminescence intensities in each well (if available). Various modules exist to analyze the data, in particular for detecting outliers, subtracting background, estimating growth rates, promoter activities and protein concentrations, visualizing expression profiles, synchronizing replicate profiles, etc. The computational core of the web application consists of the Python library WellFARE.

NEWS OF THE YEAR: Deployment of WellInverter on an Inria server and on the new cloud of the French Institute for Bioinformatics (see the web page for details). Publication in BMC Bioinformatics describing the new version of the application.
- Participants: Delphine Ropers, Hans Geiselmann, Hidde de Jong, Johannes Geiselmann, Michel Page, Valentin Zulkower and Yannick Martin
- Partner: UGA
- Contact: Hidde de Jong
- Publication: Robust reconstruction of gene expression profiles from reporter gene data using linear inversion
- URL: https://team.inria.fr/ibis/wellinverter/

5.3. GNA

Genetic Network Analyzer

KEYWORDS: Model Checking - Bioinformatics - Gene regulatory networks - Qualitative simulation

SCIENTIFIC DESCRIPTION: Genetic Network Analyzer (GNA) is the implementation of methods for the qualitative modeling and simulation of gene regulatory networks developed in the IBIS project-team.

FUNCTIONAL DESCRIPTION: The input of GNA consists of a model of the regulatory network in the form of a system of piecewise-linear differential equations (PLDEs), supplemented by inequality constraints on the parameters and initial conditions. From this information, GNA generates a state transition graph summarizing the qualitative dynamics of the system. In order to analyze large graphs, GNA allows the user to specify properties of the qualitative dynamics of a network in temporal logic, using high-level query templates, and to verify these properties on the state transition graph by means of standard model-checking tools, either locally installed or accessible through a remote web server.

RELEASE FUNCTIONAL DESCRIPTION: (1) it supports the editing and visualization of regulatory networks, in an SBGN-compatible format, (2) it semi-automatically generates a prototype model from the network structure, thus accelerating the modeling process, and (3) it allows models to be exported in the SBML Qual standard.

NEWS OF THE YEAR: New mode of distribution from the IBIS web site. Tutorial on the use of the model formalism for analyzing synthetic genetic circuits.

- Participants: Hidde de Jong, Michel Page and Delphine Ropers
- Partner: UGA
- Contact: Hidde de Jong
- Publications: Genetic Network Analyzer: A Tool for the Qualitative Modeling and Simulation of Bacterial Regulatory Networks - Piecewise linear approximations to model the dynamics of adaptation to osmotic stress by food-borne pathogens
- URL: http://www-helix.inrialpes.fr/gna

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

6. New Software and Platforms

6.1. MyCF

My Corporis Fabrica

KEYWORDS: 3D modeling - Simulation - Health - Ontologies - Anatomy - Patientspecific - Medical imaging

FUNCTIONAL DESCRIPTION: Knowledge-based 3D anatomical modeling using MyCF The MyCF software eases the creation of 3D anatomical models for visualization and mechanical simulation. As input, the user provides a list of anatomical entities or functions to simulate, using keywords or navigating in reference 3D model. As output, she gets a 3D model ready to visualize, or to simulate.

- Participants: Ali Hamadi Dicko, Federico Ulliana, François Faure and Olivier Palombi
- Partner: Université Joseph-Fourier
- Contact: Olivier Palombi

6.2. Kino AI

Artificial intelligence for cinematography

KEYWORDS: Video analysis - Post-production

FUNCTIONAL DESCRIPTION: Kino AI is an implementation of the method described in our patent "automatic generation of cinematographic rushes using video processing". Starting from a single ultra high definitiion (UltraHD) recording of a live performance, we track and recognize all actors present on stage and generate one or more rushes suitable for cinematographic editing of a movie.

- Partner: IIIT Hyderabad
- Contact: Rémi Ronfard
- Publications: Multi-Clip Video Editing from a Single Viewpoint - Zooming On All Actors: Automatic Focus+Context Split Screen Video Generation

6.3. Platforms

6.3.1. RUMBA

RUMBA is a next-generation 3D animation software targeted to professional animation studios, developed jointly by Mercenaries Engineering, TEAMTO and IMAGINE. Development was funded in part by FUI projects COLLODI 1 and COLLODI 2. RUMBA has been used in production by TEAMTO since 2017. We are using RUMBA as a platform for developing new algorithms in sketch-based animation, based on our previous work during Martin Guay's PhD thesis. This includes many improvements to allow those methods to work in a professional workflow.

6.3.2. Sky Engine

Sky Engine is a realtime game engine developped by Maxime Garcia as part of his PhD thesis, which incorporates several shape modleing and animation tools developped within the team. It is hoped that it will supersede Expressive as a platform for future integration of research results of the team involving real-time, story-driven shape modeling, animation and cinematography.

MARACAS Team

6. New Software and Platforms

6.1. cortexlab-fftweb

KEYWORDS: Experimentation - Data visualization - SDR (Software Defined Radio)

FUNCTIONAL DESCRIPTION: fftweb is a real-time spectral (FFT) visualization of one or several signal, embedded in a web page. The FFT is computed in a GNURadio block, then sent to a gateway server, which serves the web page, associated javascripts, and signal websockets. The end user only has to use the GNURadio block and and the web page, and doesn't need to bother about the internal details of the system. fftweb has been developed specially for the CorteXlab testbed but with minor adaptations, it can be used in other contexts, and also can be used to draw more generic real-time graphs, not only FFTs. Technologies: GNURadio, python, python-gevent, Javascript, D3JS

- Contact: Matthieu Imbert

6.2. cortexlab-minus

KEYWORDS: Experimentation - SDR (Software Defined Radio)

FUNCTIONAL DESCRIPTION: Minus is an experiment control system able to control, the whole lifecycle of a radio experiment in CorteXlab or any other testbed inspired by it. Minus controls and automates the whole experiment process starting from node power cycling, experiment deployment, experiment start and stop, and results collection and transfer. Minus is also capable of managing multiple queues of experiments which are executed simultaneously in the testbed.

- Contact: Matthieu Imbert

6.3. cortexlab-webapp

KEYWORDS: Experimentation - SDR (Software Defined Radio)

FUNCTIONAL DESCRIPTION: User management module, which aims at easing platform usage and improving the metadata that we can associate with each experimenter and experiment. This metadata aims at improving the metrics we can gather about the platform's usage

- Partner: Insa de Lyon
- Contact: Pascal Girard

6.4. CorteXlab-IoT Framework

Framework for PHY-MAC layers Prototyping in Dense IoT Networks using CorteXlab Testbed

KEYWORDS: SDR (Software Defined Radio) - Iot - CorteXlab - GNU Radio

FUNCTIONAL DESCRIPTION: This framework was developed in the project "Enhanced Physical Layer for Cellular IoT" (EPHYL). It provides a customizable and open source design for IoT networks prototyping in a massive multi-user, synchronized and reproducible environment thanks to the hardware and software capabilities of the testbed.

- Author: Othmane Oubejja
- Contact: Othmane Oubejja
- Publication: Framework for PHY-MAC layers Prototyping in Dense IoT Networks using FIT/CorteXlab Testbed
- URL: https://github.com/CorteXlab/gr-ephyl

6.5. Platforms

6.5.1. FIT/CorteXlab

FIT (Future Internet of Things) is a french Equipex (Équipement d'excellence) which aims to develop an experimental facility, a federated and competitive infrastructure with international visibility and a broad panel of customers. FIT is be composed of four main parts: a Network Operations Center (FIT NOC), a set of IoT test-beds (FIT IoT-Lab), a set of wireless test-beds (FIT-Wireless) which includes the FIT/CorteXlab platform deployed previoulsy by the Socrate team and now managed by Maracas team in the Citi lab, and finally a set of Cloud test-beds (FIT-Cloud). In 2014 the construction of the room was done and SDR nodes have been installed in the room: 42 industrial PCs (Aplus Nuvo-3000E/P), 22 NI radio boards (usrp) and 18 Nutaq boards (PicoSDR, 2x2 and 4X4) can be programmed remotely, from internet now.

New features are under developments, and the platform is used or has been used by several research groups : i) Nokia Bell Labs - Inria common labs for research in machine learning, ii) ANR projects EPHYL and ARBURST for research on massive access for IoT, iii) ERC of prof. Michele Wigger, IMT Paris, for validating distributed coding strategies, iv) Nokia Bell Labs New Jersey for a proof of concept of wireless caching, Greentouch international consortium to develop a prototype of interference alignment.

Figure 3. FIT/CorteXlab facility

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

5. New Software and Platforms

5.1. GRATIN

FUNCTIONAL DESCRIPTION: Gratin is a node-based compositing software for creating, manipulating and animating 2D and 3D data. It uses an internal direct acyclic multi-graph and provides an intuitive user interface that allows to quickly design complex prototypes. Gratin has several properties that make it useful for researchers and students. (1) it works in real-time: everything is executed on the GPU, using OpenGL, GLSL and/or Cuda. (2) it is easily programmable: users can directly write GLSL scripts inside the interface, or create new C++ plugins that will be loaded as new nodes in the software. (3) all the parameters can be animated using keyframe curves to generate videos and demos. (4) the system allows to easily exchange nodes, group of nodes or full pipelines between people.

- Participants: Pascal Barla and Romain Vergne
- Partner: UJF
- Contact: Romain Vergne
- URL: http://gratin.gforge.inria.fr/

5.2. HQR

High Quality Renderer

KEYWORDS: Lighting simulation - Materials - Plug-in

FUNCTIONAL DESCRIPTION: HQR is a global lighting simulation platform. HQR software is based on the photon mapping method which is capable of solving the light balance equation and of giving a high quality solution. Through a graphical user interface, it reads X3D scenes using the X3DToolKit package developed at Maverick, it allows the user to tune several parameters, computes photon maps, and reconstructs information to obtain a high quality solution. HQR also accepts plugins which considerably eases the developpement of new algorithms for global illumination, those benefiting from the existing algorithms for handling materials, geometry and light sources.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: http://artis.imag.fr/~Cyril.Soler/HQR

5.3. libylm

LibYLM

KEYWORD: Spherical harmonics

FUNCTIONAL DESCRIPTION: This library implements spherical and zonal harmonics. It provides the means to perform decompositions, manipulate spherical harmonic distributions and provides its own viewer to visualize spherical harmonic distributions.

- Author: Cyril Soler
- Contact: Cyril Soler
- URL: https://launchpad.net/~csoler-users/+archive/ubuntu/ylm

5.4. ShwarpIt

KEYWORD: Warping

FUNCTIONAL DESCRIPTION: ShwarpIt is a simple mobile app that allows you to manipulate the perception of shapes in images. Slide the ShwarpIt slider to the right to make shapes appear rounder. Slide it to the left to make shapes appear more flat. The Scale slider gives you control on the scale of the warping deformation.

- Contact: Georges-Pierre Bonneau
- URL: http://bonneau.meylan.free.fr/ShwarpIt/ShwarpIt.html

5.5. Vrender

KEYWORDS: 3D - Vector graphics

FUNCTIONAL DESCRIPTION: The VRender library is a simple tool to render the content of an OpenGL window to a vectorial device such as Postscript, XFig, and soon SVG. The main usage of such a library is to make clean vectorial drawings for publications, books, etc.

In practice, VRender replaces the z-buffer based hidden surface removal of OpenGL by sorting the geometric primitives so that they can be rendered in a back-to-front order, possibly cutting them into pieces to solve cycles.

VRender is also responsible for the vectorial snapshot feature of the QGLViewer library.

- Participant: Cyril Soler
- Contact: Cyril Soler
- URL: http://maverick.inria.fr/Software/VRender/

5.6. X3D TOOLKIT

X3D Development pateform

KEYWORDS: X3D - Geometric modeling

FUNCTIONAL DESCRIPTION: X3DToolkit is a library to parse and write X3D files, that supports plugins and extensions.

- Participants: Gilles Debunne and Yannick Le Goc
- Contact: Cyril Soler
- URL: http://maverick.inria.fr/Software/X3D/

5.7. PLANTRAD

KEYWORDS: Bioinformatics - Biology

FUNCTIONAL DESCRIPTION: PlantRad is a software program for computing solutions to the equation of light equilibrium in a complex scene including vegetation. The technology used is hierarchical radiosity with clustering and instantiation. Thanks to the latter, PlantRad is capable of treating scenes with a very high geometric complexity (up to millions of polygons) such as plants or any kind of vegetation scene where a high degree of approximate self-similarity permits a significant gain in memory requirements.

- Participants: Cyril Soler, François Sillion and George Drettakis
- Contact: Cyril Soler

6. New Software and Platforms

6.1. BOLD model FIT

KEYWORDS: Functional imaging - FMRI - Health

SCIENTIFIC DESCRIPTION: Physiological and biophysical models have been proposed to link neuronal activity to the Blood Oxygen Level-Dependent (BOLD) signal in functional MRI (fMRI). Those models rely on a set of parameter values that are commonly estimated using gradient-based local search methods whose initial values are taken from the literature. In some applications, interesting insight into the brain physiology or physiopathology can be gained from an estimation of the model parameters from measured BOLD signals. In this work we focus on the extended Balloon model and propose the estimation of 15 parameters using seven different approaches: three versions of the Expectation Maximization Gauss-Newton (EM/GN) approach (the *de facto* standard in the neuroscientific community) and four metaheuristics (Particle Swarm Optimization (PSO), Differential Evolution (DE), Real-Coded Genetic Algorithms (GA), and a Memetic Algorithm (MA) combining EM/GN and DE). To combine both the ability to escape local optima and to incorporate prior knowledge, we derive the target function from Bayesian modeling. The general behavior of these algorithms is analyzed and compared, providing very promising results on challenging real and synthetic fMRI data sets involving rats with epileptic activity. These stochastic optimizers provided a better performance than EM/GN in terms of distance to the ground truth in 4 out of 6 synthetic data sets and a better signal fitting in 12 out of 12 real data sets. Non-parametric statistical tests showed the existence of statistically significant differences between the real data results obtained by DE and EM/GN. Finally, the estimates obtained from DE for these parameters seem both more realistic and more stable or at least as stable across sessions as the estimates from EM/GN. This is the largest comparison of optimizers for the estimation of biophysical parameters in BOLD fMRI

FUNCTIONAL DESCRIPTION: This Matlab toolbox performs the automatic estimation of biophysical parameters using the extended Balloon model and BOLD fMRI data. It takes as input a MAT file and provides as output the parameter estimates achieved by using stochastic optimization

NEWS OF THE YEAR: The main differences with our previous work: 1) we also use synthetic data, 2) we use stochastic GN and MCMC+DE, 3) We evaluate results not only in physiological terms but also comparing fitness function values. Also changes were made to allow running on the cluster via MPI

- Participants: Pablo Mesejo Santiago, Florence Forbes and Jan Warnking
- Partner: University of Granada, Spain
- Contact: Pablo Mesejo Santiago
- Publication: A differential evolution-based approach for fitting a nonlinear biophysical model to fMRI BOLD data
- URL: https://hal.archives-ouvertes.fr/hal-01221115v2/

6.2. PyHRF

KEYWORDS: Medical imaging - Health - Brain - IRM - Neurosciences - Statistic analysis - FMRI

SCIENTIFIC DESCRIPTION: Functional Magnetic Resonance Imaging (fMRI) is a neuroimaging technique that allows the non-invasive study of brain function. It is based on the hemodynamic variations induced by changes in cerebral synaptic activity following sensory or cognitive stimulation. The measured signal depends on the variation of blood oxygenation level (BOLD signal) which is related to brain activity: a decrease in deoxyhemoglobin concentration induces an increase in BOLD signal. The BOLD signal is delayed with respect to changes in synaptic activity, which can be modeled as a convolution with the Hemodynamic Response Function (HRF) whose exact form is unknown and fluctuates with various parameters such as age, brain region or physiological conditions. In this work we propose to analyze fMRI data using a Joint Detection-Estimation (JDE) approach. It jointly detects cortical activation and estimates the HRF. In contrast to existing tools, PyHRF estimates the HRF instead of considering it as a given constant in the entire brain.

FUNCTIONAL DESCRIPTION: As part of fMRI data analysis, PyHRF provides a set of tools for addressing the two main issues involved in intra-subject fMRI data analysis : (i) the localization of cerebral regions that elicit evoked activity and (ii) the estimation of the activation dynamics also referenced to as the recovery of the Hemodynamic Response Function (HRF). To tackle these two problems, PyHRF implements the Joint Detection-Estimation framework (JDE) which recovers parcel-level HRFs and embeds an adaptive spatio-temporal regularization scheme of activation maps.

NEWS OF THE YEAR: The framework to perform software tests has been further developed. Some unitary tests have been set.

- Participants: Aina Frau Pascual, Christine Bakhous, Florence Forbes, Jaime Eduardo Arias Almeida, Laurent Risser, Lotfi Chaari, Philippe Ciuciu, Solveig Badillo, Thomas Perret and Thomas Vincent
- Partners: CEA - NeuroSpin
- Contact: Florence Forbes
- Publications: Flexible multivariate hemodynamics fMRI data analyses and simulations with PyHRF - Fast joint detection-estimation of evoked brain activity in event-related fMRI using a variational approach - A Bayesian Non-Parametric Hidden Markov Random Model for Hemodynamic Brain Parcellation
- URL: http://pyhrf.org

6.3. xLLiM

High dimensional locally linear mapping

KEYWORDS: Clustering - Regression

SCIENTIFIC DESCRIPTION: Building a regression model for the purpose of prediction is widely used in all disciplines. A large number of applications consists of learning the association between responses and predictors and focusing on predicting responses for the newly observed samples. In this work, we go beyond simple linear models and focus on predicting low-dimensional responses using high-dimensional covariates when the associations between responses and covariates are non-linear.

FUNCTIONAL DESCRIPTION: This is an R package available on the CRAN at https://cran.r-project.org/web/packages/xLLiM/index.html

XLLiM provides a tool for non linear mapping (non linear regression) using a mixture of regression model and an inverse regression strategy. The methods include the GLLiM model (Deleforge et al (2015)) based on Gaussian mixtures and a robust version of GLLiM, named SLLiM (see Perthame et al (2016)) based on a mixture of Generalized Student distributions.

NEWS OF THE YEAR: A new Hierarchical version of GLLiM has been developed in collaboration with University of Michigan, USA.

- Participants: Antoine Deleforge, Emeline Perthame and Florence Forbes
- Partner: University of Michigan, Ann Arbor, USA
- Contact: Florence Forbes

- Publications: Inverse regression approach to robust nonlinear high-to-low dimensional mapping - High-Dimensional Regression with Gaussian Mixtures and Partially-Latent Response Variables
- URL: https://cran.r-project.org/web/packages/xLLiM/index.html

6.4. MMST

Mixtures of Multiple Scaled Student T distributions

KEYWORDS: Health - Statistics - Brain MRI - Medical imaging - Robust clustering

SCIENTIFIC DESCRIPTION: A new family of multivariate heavy-tailed distributions that allow variable marginal amounts of tailweight is proposed and implemented. The originality comes from introducing multidimensional instead of univariate scale variables for the mixture of scaled Gaussian family of distributions. In contrast to most existing approaches, the derived distributions can account for a variety of shapes and have a simple tractable form with a closed-form probability density function whatever the dimension. We provide maximum likelihood estimation of the parameters and illustrate their modelling flexibility.

FUNCTIONAL DESCRIPTION: The package implements mixtures of so-called multiple scaled Student distributions, which are generalisation of multivariate Student T distribution allowing different tails in each dimension. Typical applications include Robust clustering to analyse data with possible outliers. In this context, the model and package have been used on large data sets of brain MRI to segment and identify brain tumors. Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

RELEASE FUNCTIONAL DESCRIPTION: Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

NEWS OF THE YEAR: Recent additions include a Markov random field implementation to account for spatial dependencies between observations, and a Bayesian implementation that can be used to select the number of mixture components automatically.

- Participants: Alexis Arnaud, Darren Wraith, Florence Forbes, Steven Quinito Masnada and Stéphane Despréaux
- Partner: Institut des Neurosciences Grenoble
- Contact: Florence Forbes
- Publications: A new family of multivariate heavy-tailed distributions with variable marginal amounts of tailweights: Application to robust clustering - Fully Automatic Lesion Localization and Characterization: Application to Brain Tumors Using Multiparametric Quantitative MRI Data
- URL: https://team.inria.fr/mistis/software/

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

5. New Software and Platforms

5.1. Lazylav

Lazy lavender

KEYWORDS: Reproducibility - Multi-agent - Simulation

SCIENTIFIC DESCRIPTION: Lazy lavender aims at supporting mOeX's research on simulating knowledge evolution. It is not a general purpose simulator. However, it features some methodological innovations in term of facilitating publication, recording, and replaying of experiments.

FUNCTIONAL DESCRIPTION: Lazy Lavender is a simulation environment for cultural knowledge evolution, i.e. running randomised experiments with agent adjusting their knowledge while attempting to communicate. It can generate detailed report and data from the experiments and directions to repeat them.

NEWS OF THE YEAR: In 2019, we implemented facilities for dealing with population of agents and designed several synchronisation approaches. This led to seriously refactor the code.

- Participant: Jérôme Euzenat
- Contact: Jérôme Euzenat
- Publications: Crafting ontology alignments from scratch through agent communication - Interaction-based ontology alignment repair with expansion and relaxation - First experiments in cultural alignment repair (extended version)
- URL: http://lazylav.gforge.inria.fr

5.2. Alignment API

KEYWORDS: Ontologies - Alignment - Ontology engineering - Knowledge representation

SCIENTIFIC DESCRIPTION: The api itself is a Java description of tools for accessing the common format. It defines five main interfaces (OntologyNetwork, Alignment, Cell, Relation and Evaluator).

We provide an implementation for this api which can be used for producing transformations, rules or bridge axioms independently from the algorithm that produced the alignment. The proposed implementation features: - a base implementation of the interfaces with all useful facilities, - a library of sample matchers, - a library of renderers (XSLT, RDF, SKOS, SWRL, OWL, C-OWL, SPARQL), - a library of evaluators (various generalisation of precision/recall, precision/recall graphs), - a flexible test generation framework that allows for generating evaluation data sets, - a library of wrappers for several ontology APIs , - a parser for the format.

To instanciate the API , it is sufficient to refine the base implementation by implementing the align() method. Doing so, the new implementation will benefit from all the services already implemented in the base implementation.

FUNCTIONAL DESCRIPTION: Using ontologies is the privileged way to achieve interoperability among heterogeneous systems within the Semantic web. However, as the ontologies underlying two systems are not necessarily compatible, they may in turn need to be reconciled. Ontology reconciliation requires most of the time to find the correspondences between entities (e.g. classes, objects, properties) occurring in the ontologies. We call a set of such correspondences an alignment.

NEWS OF THE YEAR: Link keys are fully supported by the EDOAL language. In particular it can transform them into SPARQL queries.

- Participants: Armen Inants, Chan Le Duc, Jérôme David, Jérôme Euzenat, Jérôme Pierson, Luz Maria Priego-Roche and Nicolas Guillouet
- Contact: Jérôme Euzenat
- Publications: An API for ontology alignment - The Alignment API 4.0
- URL: http://alignapi.gforge.inria.fr/

<div align="center">

MORPHEO Project-Team

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6. New Software and Platforms

6.1. Lucy Viewer

KEYWORDS: Data visualization - 4D - Multi-Cameras

SCIENTIFIC DESCRIPTION: Lucy Viewer is an interactive viewing software for 4D models, i.e, dynamic three-dimensional scenes that evolve over time. Each 4D model is a sequence of meshes with associated texture information, in terms of images captured from multiple cameras at each frame. Such data is available from the 4D repository website hosted by Inria Grenoble.

With Lucy Viewer, the user can use the mouse to zoom in onto the 4D models, zoom out, rotate, translate and view from an arbitrary angle as the 4D sequence is being played. The texture information is read from the images at each frame in the sequence and applied onto the meshes. This helps the user visualize the 3D scene in a realistic manner. The user can also freeze the motion at a particular frame and inspect a mesh in detail. Lucy Viewer lets the user to also select a subset of cameras from which to apply texture information onto the meshes. The supported formats are meshes in .OFF format and associated images in .PNG or .JPG format.

FUNCTIONAL DESCRIPTION: Lucy Viewer is an interactive viewing software for 4D models, i.e, dynamic three-dimensional scenes that evolve over time. Each 4D model is a sequence of meshes with associated texture information, in terms of images captured from multiple cameras at each frame.

- Participants: Edmond Boyer, Jean-Sébastien Franco, Matthieu Armando and Eymeric Amselem
- Contact: Edmond Boyer
- URL: https://kinovis.inria.fr/lucyviewer/

6.2. Shape Tracking

FUNCTIONAL DESCRIPTION: We are developing a software suite to track shapes over temporal sequences. The motivation is to provide temporally coherent 4D Models, i.e. 3D models and their evolutions over time , as required by motion related applications such as motion analysis. This software takes as input a temporal sequence of 3D models in addition to a template and estimate the template deformations over the sequence that fit the observed 3D models.

- Contact: Edmond Boyer

6.3. QuickCSG V2

KEYWORDS: 3D modeling - CAD - 3D reconstruction - Geometric algorithms

SCIENTIFIC DESCRIPTION: See the technical report "QuickCSG: Arbitrary and Faster Boolean Combinations of N Solids", Douze, Franco, Raffin.

The extension of the algorithm to self-intersecting meshes is described in "QuickCSG with self-intersections", a document inside the package.

FUNCTIONAL DESCRIPTION: QuickCSG is a library and command-line application that computes Boolean operations between polyhedra. The basic algorithm is described in the research report "QuickCSG: Arbitrary and Faster Boolean Combinations of N Solids", Douze, Franco, Raffin. The input and output polyhedra are defined as indexed meshes. In version 2, that was developed in the context of a software transfer contract, the meshes can be self-intersecting, in which case the inside and outside are defined by the non-zero winding rule. The operation can be any arbitrary Boolean function, including one that is defined as a CSG tree. The focus of QuickCSG is speed. Robustness to degeneracies is obtained by carefully applied random perturbations.

- Authors: Matthys Douze, Jean-Sébastien Franco and Bruno Raffin
- Contact: Jean-Sébastien Franco
- URL: https://kinovis.inria.fr/quickcsg/

6.4. CVTGenerator

KEYWORDS: Mesh - Centroidal Voronoi tessellation - Implicit surface

FUNCTIONAL DESCRIPTION: CVTGenerator is a program to build Centroidal Voronoi Tessellations of any 3D meshes and implicit surfaces.

- Partner: INP Grenoble
- Contact: Li WANG
- URL: http://cvt.gforge.inria.fr/

6.5. Adaptive mesh texture

KEYWORDS: 3D - Geometry Processing - Texturing

FUNCTIONAL DESCRIPTION: Tool for computing appearance information on a 3D scene acquired with a multi-view stereo (MVS) pipeline. Appearance information is sampled in an adaptive way so as to maximize the entropy of stored information. This is made possible through a homemade representation of appearance, different from the more traditional texture maps. This tool laso includes a compression module, so as to optimize disk space.

RELEASE FUNCTIONAL DESCRIPTION: 1st version

- Authors: Matthieu Armando, Edmond Bover, Jean-Sébastien Franco and Vincent Leroy
- Partner: Microsoft
- Contact: Matthieu Armando
- URL: https://gitlab.inria.fr/marmando/adaptive-mesh-texture

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

5. New Software and Platforms

5.1. cellcomplex

KEYWORDS: Polyhedral meshes - 3D

FUNCTIONAL DESCRIPTION: The cellcomplex library is a Python library that allows manipulating 2D or 3D multicellular complexes, with the study of plant tissues as a main application. It is mostly structured around a data structure that is used to represent such complexes as incidence graphs of dimension 2 or 3, and provides several key functionalities:

* The creation of structures from more basic representation (polygons of points for instance), from some geometrical primitives (2D or 3D) and the generation of synthetic regular or irregular grids, allowing notably the simulation of tissues.

* The computation of topological and geometrical properties on the multicellular complex structures, including notably useful computations on triangle meshes, a specific case of complexes with simplicial faces (areas, normals, triangle eccentricity, curvature estimator).

* The edition of structures by local topological operations, notably in th case of triangle meshes (edge flip, subdivision, vertex insertion) and multi-criteria geometrical optimization processes and isotropic remeshing.

* The import and export in various standard file formats for geometries (.obj, .ply, .msh) and notably in the standard formad defined by the community of plant tissue modelling (PLY, Saisnbury Computational Workshop 2015).

RELEASE FUNCTIONAL DESCRIPTION: * Major restructuration involving a change of namespace and a simplification of module architecture. * Inclusion of 3D visualization functionalities based on VTK.

- Participant: Guillaume Cerutti
- Contact: Guillaume Cerutti

5.2. draco_stem

DRACO-STEM : Dual Reconstruction by Adjacency Complex Optimization & SAM Tissue Enhanced Mesh

KEYWORDS: Meshing - Image segmentation - Computational biology - Optimization

FUNCTIONAL DESCRIPTION: Draco-stem provides a computational pipeline that allows going from multi-label segmented images of living tissue (typically resulting from a watershed segmentation of 3D microscopy image stacks) to topologically consistent, FEM-ready triangular meshes of all cell interfaces in the tissue.

It relies on an original topological optimization method that aims at reconstructing the simplicial complex of cellular adjacencies from the image, and on dualization and geometrical optimization to obtain a triangle mesh that satisfies simultaneously several quality criteria (triangle regularity, adequation to image, biological priors). The library provides implementations for 3D tissue reconstruction, single-layer 2.5D reconstruction and advanced 2D reconstruction.

RELEASE FUNCTIONAL DESCRIPTION: * Major refactoring, python3 compatibility * Addition of Draco2D functionalities

- Contact: Guillaume Cerutti
- Publication: DRACO-STEM: An Automatic Tool to Generate High-Quality 3D Meshes of Shoot Apical Meristem Tissue at Cell Resolution
- URL: https://gitlab.inria.fr/mosaic/draco_stem.git

5.3. Gnomon

KEYWORDS: 4D - Modelization and numerical simulations - Finite element modelling - Computational biology - Data visualization

SCIENTIFIC DESCRIPTION: Gnomon is a user-friendly computer platform developed by the Mosaic team for seamless simulation of form development in silico. It is intended to be a major tool for the team members to develop, integrate and share their models, algorithms and tools. In Gnomon, a developing form is represented at any time by a central data-structure that contains topological, geometric, genetic and physiological information and that represents the state of the growing form. Flexible components (plugins) make it possible to up-load or to create such data-structures, to program their development, to analyze, visualize them and interact with them in 3D+time.

FUNCTIONAL DESCRIPTION: Gnomon is a plugin-based computational platform for the analysis and simulation of morphogenesis. It relies on a scalable software architecture based on the dtk kernel developed by the group of software engineers (SED) from the Sophia-Antipolis Inria Center. The development of Gnomon aims at answering four main challenges:

* Provide an easily accessible computational tool for the exploration of morphogenesis, by focusing on the deployability of the software (using conda), on the ergonomics of the user interface and the availability of the documentation.

* Give access to powerful tools for the exploration of dynamical forms, through an interactive visualization framework allowing the exploration in space in time and the access to algorithmic resources developed by the team for image sequences of multicellular tissues or collections of branching forms.

* Ensure the interoperability of computational libraries within the platform and its extensibility by a generalized plugin-based architecture (facilitated by the dtk framework) for algorithms, visualizations and data structures, enabling the members of the team and future users to feed the platform with their own C++ and Python libraries.

* Bridge the gap between experimental data and computational simulations by offering the possibility to go from one to the other in the same platform in a nearly transparent way, thanks to a common dynamical system framework integrated to the core of the platform.

Gnomon project organization: * Project leader: Christophe Godin * Software development coordinator: Guillaume Cerutti * DTK coordinators: Julien Wintz, Thibaud Kloczko * Plugin coordinators: Jonathan Legrand, Romain Azais, Olivier Ali, Frédéric Boudon. * Diffusion coordinator: Teva Vernoux

This work is part of the Gnomon ADT project supported by the Inria centers of Grenoble Rhône-Alpes and Sophia-Antipolis Méditerranée.

RELEASE FUNCTIONAL DESCRIPTION: A major technical update has been carried out on the Gnomon platform with the switch of the platform core to dtk2, implying an upgrade of all involved Python code to python 3.6+. The newer version 0.13 displays a clearer and more customizable interface and all functionalities from the version 0.9. In terms of functionalities, a major effort has been put on recovering former applications of the team (LPy and PlantGL) and including them in a robust way in the scope of the platform. A release of the version 1.0 is planned for early 2020 including validated algorithms for the quantitative analysis of 3D images of tissue, a much more robust user interface and an extensive user and developer documentation made available online.

- Participants: Olivier Ali, Frédéric Boudon, Guillaume Cerutti, Florian Gacon, Christophe Godin, Jonathan Legrand and Grégoire Malandain
- Contact: Christophe Godin

5.4. MorphoNet

KEYWORDS: 3D web - Morphogenesis - Big data - 3D reconstruction

FUNCTIONAL DESCRIPTION: MorphoNet is an open-source web-based morphological browser. It consists of a web application, exploiting the Unity3D gaming engine, which offers the user a comprehensive palette of interactions with the data, in order to explore the structure, the dynamics and the variability of biological systems. Users can also project quantitative and genetic properties onto the morphological scaffold, allowing for instance to easily explore the correlation between shape dynamics and gene expression patterns. On top of that, datasets and associated information can be shared with other selected users or with entire groups. This possibility of directly sharing results within and between research communities, together with the use of a unified, human readable format, makes MorphoNet a unique tool for multidisciplinary research. Its web-based, user-friendly and open-source structure is also ideal for science dissemination and teaching.

- Partner: CRBM - Centre de Recherche en Biologie cellulaire de Montpellier
- Contact: Emmanuel Faure
- URL: http://www.morphonet.org

5.5. TimageTK

Tissue Image ToolKit

KEYWORDS: 3D - Image segmentation - Fluorescence microscopy - Image registration - Image processing - Image filter

FUNCTIONAL DESCRIPTION: TimageTK (Tissue Image Toolkit) is a Python package dedicated to image processing of multicellular architectures such as plants or animals and is intended for biologists and modelers. It provides grayscale or labeled image filtering and mathematical morphology algorithms, as well as image registration and segmentation methods.

- Contact: Jonathan Legrand
- URL: https://mosaic.gitlabpages.inria.fr/timagetk/index.html

5.6. treex

KEYWORDS: Graph algorithmics - Data structures - Combinatorics - Machine learning

SCIENTIFIC DESCRIPTION: Trees form an expanded family of combinatorial objects that offers a wide range of application fields, especially in biology, from plant modeling to blood vessels network analysis through study of lineages. Consequently, it is crucial for the team to develop numerical tools and algorithms for processing tree data, in particular to answer questions about the representation of biological organisms and their forms in silico.

treex is a Python 3 library dedicated to the manipulation of tree objects, whatever they are ordered or not, with or without quantitative or qualitative labels.

FUNCTIONAL DESCRIPTION: The package provides a data structure for rooted trees as well as the following main functionalities: - Random generation algorithms - DAG compression for ordered or not, labeled or not, trees - Approximation algorithms for unordered trees - Edit distance for unordered labeled trees - Kernels for ordered or not, labeled or not, trees - Computation of coding processes (Harris path, Lukasiewicz walk and height process) - Visualization algorithms in Matplotlib or in LaTeX

RELEASE FUNCTIONAL DESCRIPTION: In 2019, treex has been published in JOSS (Journal of Open Source Software). The subtree kernel has been released to accompany an article submitted to Journal of Machine Learning Research. In addition, the DAG class and the kernel class have been extensively redesigned to be more user-friendly.

- Participants: Romain Azais, Guillaume Cerutti, Didier Gemmerle and Florian Ingels
- Contact: Romain Azais
- Publication: treex: a Python package for manipulating rooted trees
- URL: https://gitlab.inria.fr/azais/treex

NANO-D Team

5. New Software and Platforms

5.1. Knodle

KNOwledge-Driven Ligand Extractor

KEYWORDS: Bioinformatics - Machine learning

FUNCTIONAL DESCRIPTION: KNOwledge-Driven Ligand Extractor is a software library for the recognition of atomic types, their hybridization states and bond orders in the structures of small molecules. Its prediction model is based on nonlinear Support Vector Machines. The process of bond and atom properties perception is divided into several steps. At the beginning, only information about the coordinates and elements for each atom is available :

Connectivity is recognized. A search of rings is performed to find the Smallest Set of Smallest Rings (SSSR). Atomic hybridizations are predicted by the corresponding SVM model. Bond orders are predicted by the corresponding SVM model. Aromatic cycles are found. Atomic types are set in obedience to the functional groups. Some bonds are reassigned during this stage.

- Participants: Maria Kadukova and Sergei Grudinin
- Partner: MIPT Moscow
- Contact: Sergei Grudinin
- Publication: Knodle: A Support Vector Machines-Based Automatic Perception of Organic Molecules from 3D Coordinates
- URL: https://team.inria.fr/nano-d/software/Knodle/

5.2. DeepSymmetry

KEYWORDS: Bioinformatics - 3D modeling - Machine learning - Neural networks

FUNCTIONAL DESCRIPTION: DeepSymmetry is a method based on three-dimensional (3D) convolutional networks that detects structural repetitions in proteins and their density maps. It identifies tandem repeat proteins, proteins with internal symmetries, their symmetry order, and also the corresponding symmetry axes.

- Participants: Guillaume Pages and Sergei Grudinin
- Contact: Sergei Grudinin
- Publication: DeepSymmetry : Using 3D convolutional networks for identification of tandem repeats and internal symmetries in protein structures
- URL: https://team.inria.fr/nano-d/software/deepsymmetry/

5.3. Ananas

Analytical Analyzer of Symmetries

KEYWORDS: Bioinformatics - Structural Biology

FUNCTIONAL DESCRIPTION: Analytical Analyzer of Symmetries is a software for detection and assessment of the quality of symmetry in a protein assembly.

This software can : Detect the best axes of symmetry for any symmetry group in an assembly containing the right amount of chains, Provide the symmetry-aware RMSD for these axes, Detect the best axis of symmetry for cyclic assemblies with missing subunits, Compute the axes of symmetry with user-provided correspondences.

RELEASE FUNCTIONAL DESCRIPTION: Version 0.7 from 3 Sep 2018: mmCIF support added. A file can be gzipped. Version 0.8 from 30 July 2019: Checks the similarity between chains. Explicitly output when an incomplete assembly is detected as symmetric. Version 0.9 from 8 Nov 2019: Added lists of excluded chains for both PDB and CIF formats.

- Participants: Guillaume Pages and Sergei Grudinin
- Contact: Sergei Grudinin
- Publications: Analytical symmetry detection in protein assemblies. I. Cyclic symmetries - Analytical symmetry detection in protein assemblies. II. Dihedral and Cubic symmetries
- URL: https://team.inria.fr/nano-d/software/ananas/

5.4. Pepsi-SAXS

KEYWORDS: Bioinformatics - Structural Biology - Data modeling

FUNCTIONAL DESCRIPTION: Pepsi-SAXS (PEPSI stands for Polynomial Expansions of Protein Structures and Interactions) is new implementation of the multipole-based scheme initially proposed by Stuhrmann (Stuhrmann, 1970). Overall, our method is significantly faster with a similar accuracy compared to Crysol, FoXS, and the 3D-Zernike implementation from the SAStbx package.

RELEASE FUNCTIONAL DESCRIPTION: Version 1.0 from 6th March 2018: Added computation of P(r). Version 1.1 from 19th April 2018: Excluded solvent radii updated. Many more ions added. Version 1.2 from 24th April 2018: Added automatic identification of labile and nonlabile explicit hydrogens. Added bulk SLD option. Version 1.3 from 30th July 2018: Added initial prototype of 2D dcattering images. Version 1.4 from 1st August 2018: Added docking module. Version 2.0 from January 2019: Added flexible optimization of conformations. A bug with absolute contrast fixed. Default behaiviour of Pepsi-SAXS changed, now it reads all the hydrogen atoms if the –hyd flag is set. Otherwise, it reads only explicit hydrogens on non-standard residues. Version 2.1 from February 2019: First implimentation of the multi-structure fitting.

- Participant: Sergei Grudinin
- Partner: MIPT Moscow
- Contact: Sergei Grudinin
- Publication: Pepsi-SAXS : an adaptive method for rapid and accurate computation of small-angle X-ray scattering profiles
- URL: https://team.inria.fr/nano-d/software/pepsi-saxs/

5.5. NOLB

NOn-Linear rigid Block NMA method

KEYWORDS: Structural Biology - Bioinformatics - Elasticity - Proteins - Motion analysis

FUNCTIONAL DESCRIPTION: It's a new conceptually simple and computationally efficient method for non-linear normal mode analysis of macromolecules.

RELEASE FUNCTIONAL DESCRIPTION: Version 1.2 from January 2019: Exclusion interaction list added. Version 1.3 from April 2019: Sequence and structural alignment fixed thanks to Guillaume Pages. More advanced iterative structural alignment added. Version 1.4 from June 2019: Firt version of domain identification added. Please use the "–nDomains" option Version 1.5 from July 2019: Rigid block format updated. JSON and Text output formats added. Version 1.6 from December 2019: Added initial Voronota support.

- Participants: Sergei Grudinin and Alexandre Hoffmann
- Contact: Sergei Grudinin
- Publications: NOLB: Nonlinear Rigid Block Normal Mode Analysis Method - RapidRMSD: Rapid determination of RMSDs corresponding to motions of flexible molecules
- URL: https://team.inria.fr/nano-d/software/nolb-normal-modes/

5.6. SBROD

KEYWORDS: Bioinformatics - Machine learning

FUNCTIONAL DESCRIPTION: Smooth orientation-dependent scoring function (SBROD) for coarse-grained protein quality assessment uses only the conformation of the protein backbone, and hence it can be applied to scoring the coarse-grained protein models.

The workflow of SBROD consists in two stages. First, the method extracts features from each protein model in the dataset. Then, the scoring function assigns a score to each processed protein model depending on its features extracted at the first stage. Figure above schematically shows the workflow of SBROD. Here, four types of inter-atomic interactions, described in details below, are taken into account when extracting the features. After these features have been extracted and preprocessed, a Ridge Regression model is trained on them to predict the GDT-TS of protein models.

- Participants: Mikhail Karasikov, Guillaume Pages and Sergei Grudinin
- Contact: Sergei Grudinin
- Publication: Smooth orientation-dependent scoring function for coarse-grained protein quality assessment
- URL: https://team.inria.fr/nano-d/software/sbrod/

5.7. Ornate

KEYWORDS: Bioinformatics - Machine learning - Neural networks

FUNCTIONAL DESCRIPTION: Oriented Routed Neural network with Automatic Typing is a method for protein quality assessment. Ornate is a residue-wise scoring method. It first constructs a three dimensional map representing the structure of the residue, and its neighborhood.

- Participants: Guillaume Pages, Benoit Charmettant and Sergei Grudinin
- Contact: Sergei Grudinin
- Publication: Protein model quality assessment using 3D oriented convolutional neural networks
- URL: https://team.inria.fr/nano-d/software/ornate/

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NECS Team

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6. New Software and Platforms

6.1. GTL

Grenoble Traffic Lab

FUNCTIONAL DESCRIPTION: The Grenoble Traffic Lab (GTL) initiative, led by the NeCS team, is a real-time traffic data Center (platform) that collects traffic road infrastructure information in real-time with minimum latency and fast sampling periods. The main elements of the GTL are: a real-time data-base, a show room, and a calibrated micro-simulator of the Grenoble South Ring. Sensed information comes from a dense wireless sensor network deployed on Grenoble South Ring, providing macroscopic traffic signals such as flows, velocities, densities, and magnetic signatures. This sensor network was set in place in collaboration with Inria spin-off Karrus-ITS, local traffic authorities (DIR-CE, CG38, La Metro), and specialized traffic research centers. In addition to real data, the project also uses simulated data, in order to validate models and to test the ramp-metering, the micro-simulator is a commercial software (developed by TSS AIMSUN ©). More details at http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php

- Participants: Alain Kibangou, Andres Alberto Ladino Lopez, Anton Andreev, Carlos Canudas-de-Wit, Dominik Pisarski, Enrico Lovisari, Fabio Morbidi, Federica Garin, Hassen Fourati, Iker Bellicot, Maria Laura Delle Monache, Paolo Frasca, Pascal Bellemain, Pietro Grandinetti, Remi Piotaix, Rohit Singhal and Vadim Bertrand
- Contact: Carlos Canudas-de-Wit
- URL: http://necs.inrialpes.fr/pages/grenoble-traffic-lab.php

6.2. Benchmarks Attitude Smartphones

KEYWORDS: Experimentation - Motion analysis - Sensors - Performance analysis - Smartphone

SCIENTIFIC DESCRIPTION: We investigate the precision of attitude estimation algorithms in the particular context of pedestrian navigation with commodity smartphones and their inertial/magnetic sensors. We report on an extensive comparison and experimental analysis of existing algorithms. We focus on typical motions of smartphones when carried by pedestrians. We use a precise ground truth obtained from a motion capture system. We test state-of-the-art attitude estimation techniques with several smartphones, in the presence of magnetic perturbations typically found in buildings. We discuss the obtained results, analyze advantages and limits of current technologies for attitude estimation in this context. Furthermore, we propose a new technique for limiting the impact of magnetic perturbations with any attitude estimation algorithm used in this context. We show how our technique compares and improves over previous works.

- Participants: Hassen Fourati, Nabil Layaïda, Pierre Genevès and Thibaud Michel
- Partner: GIPSA-Lab
- Contact: Pierre Genevès
- URL: http://tyrex.inria.fr/mobile/benchmarks-attitude/

<p align="center">**NUMED Project-Team**</p>

4. New Software and Platforms

4.1. Bingham flows

FUNCTIONAL DESCRIPTION: A 1D and 2D code with a new method for the computation of viscoplatic flows with free-surface. It essentially couples Optimization methods and Well-Balanced Finite-Volumes schemes for viscous shallow-water equations (induced by the viscoplastic nature of the fluid). Currently applied to avalanches of dense snow, it is a private code currently actively developed (in C++). One of the key feature is that its well-balanced property allows to obtained the stationary states which are linked to the stopping of the snow avalanche for this highly non-linear type of fluid.

- Contact: Emmanuel Grenier

4.2. OptimChemo

FUNCTIONAL DESCRIPTION: OptimChemo is a userfriendly software designed to study numerically the effect of multiple chemotherapies on simple models of tumour growth and to optimize chemotherapy schedules.

- Participants: Ehouarn Maguet, Emmanuel Grenier, Paul Vigneaux and Violaine Louvet
- Contact: Emmanuel Grenier

4.3. SETIS

KEYWORDS: Health - DICOM - Medical imaging - Drug development

FUNCTIONAL DESCRIPTION: SETIS software is a GUI allowing to treat DICOM medical images to extract pathological data. These data can then be exported and used in a SAEM software (including Monolix (Inria & Lixoft)) for the parameters' estimation of models in the context of population approaches. As an example SETIS can be used to segment and compute the tumor size of a patients from MRI scans taken at different times. The software is sufficiently general to be used in various situations by clinicians (already done by colleagues in Lyon Hospital).

- Participants: Ehouarn Maguet and Paul Vigneaux
- Partner: ENS Lyon
- Contact: Paul Vigneaux

4.4. SIMPHYT

KEYWORDS: Bioinformatics - Cancer - Drug development

FUNCTIONAL DESCRIPTION: SimPHyt is an implementation in Python of the low grad glioma model. The aim is to predict the evolution of the glioma size of patients.

- Participant: Benjamin Ribba
- Contact: Benjamin Ribba

4.5. SITLOG

- Participants: Benjamin Ribba and Morgan Martinet
- Contact: Emmanuel Grenier

4.6. VAXSIMSTAB

KEYWORDS: Bioinformatics - Health - Drug development

FUNCTIONAL DESCRIPTION: VAXSIMSTAB is a modeler stability prediction of vaccine software.

- Participants: Benjamin Ribba, Emmanuel Grenier and Vincent Calvez
- Contact: Benjamin Ribba

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PERCEPTION Project-Team

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5. New Software and Platforms

5.1. NaoLab

Distributed middleware architecture for interacting with NAO

FUNCTIONAL DESCRIPTION: This software provides a set of librairies and tools to simply the control of NAO robot from a remote machine. The main challenge is to make easy prototuping applications for NAO ising C++ and Matlab programming environments. Thus NaoLab provides a prototyping-friendly interface to retrieve sensor date (video and sound streams, odometric data...) and to control the robot actuators (head, arms, legs...) from a remote machine.This interface is available on Naoqi SDK, developed by Aldebarab company, Naoqi SDK is needed as it provides the tools to acess the embedded NAO services (low-level motor command, sensor data access...)

- Authors: Fabien Badeig, Quentin Pelorson and Radu Horaud
- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/research/naolab/

5.2. Associations of Audio Cues with 3D locations library

FUNCTIONAL DESCRIPTION: Library to associate some auditory cues with 3D locations (points). It provides an estimation of the emitting state of each of the input locations. There are two main assumptions : 1 - The 3D locations are valid during the acquisition interval related to the audio cues 2 - The 3D locations are the only possible locations for the sound sources, no new locations will be created in this module

The software provides also a multimodal fusion library

- Participants: Antoine Deleforge, Jordi Sanchez-Riera, Radu Horaud and Xavier Alameda-pineda
- Contact: Radu Horaud

5.3. Audio Cue Extractor Library

FUNCTIONAL DESCRIPTION: This module extracts auditory cues from the raw audio streams. The interaural time difference (ITD) is estimated using cross-correlation methods.

- Participants: Antoine Deleforge, Radu Horaud and Soraya Arias
- Contact: Soraya Arias

5.4. Audiovisual Robots and Heads

FUNCTIONAL DESCRIPTION: The team has developed two audiovisual (AV) robot heads: the POPEYE head and the NAO stereo head. Both are equipped with a binocular vision system and with four microphones. The software modules comprise stereo matching and reconstruction, sound-source localization and audio-visual fusion. POPEYE has been developed within the European project POP in collaboration with the project-team MISTIS and with two other POP partners: the Speech and Hearing group of the University of Sheffield and the Institute for Systems and Robotics of the University of Coimbra. The NAO stereo head was developed under the European project HUMAVIPS in collaboration with Aldebaran Robotics (which manufactures the humanoid robot NAO) and with the University of Bielefeld, the Czech Technical Institute, and IDIAP. The software modules that we develop are compatible with both these robot heads.

- Contact: Radu Horaud
- URL: https://team.inria.fr/perception/popeye/

5.5. GLLiM

Gaussian Locally Linear Mapping

KEYWORDS: Regression - Machine learning - Gaussian mixture

SCIENTIFIC DESCRIPTION: GLLiM is a flexible tool for probabilistic non-linear regression using Gaussian mixtures. Using an inverse regression strategy with a reduced number of parameters, it is particularly suited for high- to low-dimensional regression tasks. It also enables the modeling of additional unobserved non-linear effects on input data. The method was published in [Deleforge et al., IJNS 2015]. The toolbox include an example of application to head pose estimation from synthetic images.

- Participant: Antoine Deleforge
- Contact: Antoine Deleforge
- Publication: hal-00863468, version 3
- URL: https://team.inria.fr/perception/gllim_toolbox/

5.6. Litbot

Live together with robots

KEYWORDS: Speaker Localization - Audio tracking - Visual tracking - NAO Robot - Computer vision - Signal processing

SCIENTIFIC DESCRIPTION: Litbot stands for "Live together with robots". This library aims to provide algorithms and associated software packages to perform audio-visual speaker localization and tracking with a consumer robot (in particular a NAO robot). The scope of this project is two-fold. The first is to develop the robust speaker localization and tracking algorithm in the presence of other audio-visual sources like TV. The second is to modify or optimize the original algorithm to be fit into real-time system. This library benefits from the work done with Online Multiple Sound-Source Localization package developed by X. Li.

FUNCTIONAL DESCRIPTION: This project develops algorithms and associated software packages to perform audio-visual speaker localization and tracking with a consumer robot. This version of the litbot library provides new functions to integrate the Samsung robotic platform to handle ROS middleware (robotic defacto standard) and modifies and optimizes tracking and audio localization processes (better handling of the residual noise signals, performance improved to match real time).

- Participants: Xiaofei Li, Yutong Ban, Soraya Arias, Radu Horaud, Guillaume Sarrazin and Bastien Mourgue
- Contact: Radu Horaud

5.7. Online Multiple Sound-Source Localization

KEYWORDS: Audio signal processing - Multiple sound-source localization - Matlab - Direct-path RTF

FUNCTIONAL DESCRIPTION: This project tackles multiple sound-source localization in noisy and reverberant environments, using binaural recordings of an acoustic scene. It provides Matlab routines to estimate multiple sound source (such as speakers) locations based on direct-path relative transfer function (DP-RTF) estimation.

- Participants: Xiaofei Li and Radu Horaud
- Contact: Radu Horaud
- Publications: Multiple-Speaker Localization Based on Direct-Path Features and Likelihood Maximization with Spatial Sparsity Regularization - Estimation of the Direct-Path Relative Transfer Function for Supervised Sound-Source Localization

5.8. RMP

RoMPers

KEYWORDS: Middleware - Robotics - NAO Robot

SCIENTIFIC DESCRIPTION: Robot Middleware developed by Perception. It follows the development done on RobotHandler and NAOLab. Its goal is to provide an abstraction which allows an easy access to robot sensors. In the same time, this high level access is independant of the robot.

FUNCTIONAL DESCRIPTION: Robot Middleware developed by Perception. It follows the development done on RobotHandler and NAOLab. Its goal is to provide an abstraction which allows an easy access to robot sensors. In the same time, this high level access is independant of the robot. And it also provides tools for sensor calibration (audio, video), video annotation, etc

- Participant: Guillaume Sarrazin
- Contact: Soraya Arias

5.9. SE-VAE-alpha-stable

KEYWORDS: Audio signal processing - Speech processing - Deep learning - Neural networks

FUNCTIONAL DESCRIPTION: This software provides an iterative algorithm for enhancing a speech signal in a noisy monophonic recording. The algorithm is detailed in the following paper: "Speech enhancement with variational autoencoders and alpha-stable distributions" Simon Leglaive, Umut Simsekli, Antoine Liutkus, Laurent Girin, Radu Horaud IEEE International Conference on Acoustics Speech and Signal Processing (ICASSP), Brighton, UK, May 2019

- Contact: Simon Leglaive

5.10. Sound recognition library

FUNCTIONAL DESCRIPTION: This recognition module is based on supervised learning.

- Participants: Maxime Janvier and Radu Horaud
- Contact: Radu Horaud

5.11. SE-VAE-NMF

KEYWORDS: Audio signal processing - Speech processing - Deep learning - Neural networks

FUNCTIONAL DESCRIPTION: This software provides an iterative algorithm for enhancing a speech signal in a noisy monophonic recording. The algorithm is detailed in the following paper: "A variance modeling framework based on variational autoencoders for speech enhancement" Simon Leglaive, Laurent Girin, Radu Horaud Proc. of the IEEE International Workshop on Machine Learning for Signal Processing (MLSP), Aalborg, Denmark, September 2018

- Contact: Simon Leglaive
- Publication: hal-01832826v1

PERVASIVE Project-Team (section vide)

POLARIS Project-Team

6. New Software and Platforms

6.1. Framesoc

FUNCTIONAL DESCRIPTION: Framesoc is the core software infrastructure of the SoC-Trace project. It provides a graphical user environment for execution-trace analysis, featuring interactive analysis views as Gantt charts or statistics views. It provides also a software library to store generic trace data, play with them, and build other analysis tools (e.g., Ocelotl).

- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Guillaume Huard
- URL: http://soctrace-inria.github.io/framesoc/

6.2. GameSeer

FUNCTIONAL DESCRIPTION: GameSeer is a tool for students and researchers in game theory that uses Mathematica to generate phase portraits for normal form games under a variety of (user-customizable) evolutionary dynamics. The whole point behind GameSeer is to provide a dynamic graphical interface that allows the user to employ Mathematica's vast numerical capabilities from a simple and intuitive front-end. So, even if you've never used Mathematica before, you should be able to generate fully editable and customizable portraits quickly and painlessly.

- Contact: Panayotis Mertikopoulos
- URL: http://mescal.imag.fr/membres/panayotis.mertikopoulos/

6.3. marmoteCore

Markov Modeling Tools and Environments - the Core

KEYWORDS: Modeling - Stochastic models - Markov model

FUNCTIONAL DESCRIPTION: marmoteCore is a C++ environment for modeling with Markov chains. It consists in a reduced set of high-level abstractions for constructing state spaces, transition structures and Markov chains (discrete-time and continuous-time). It provides the ability of constructing hierarchies of Markov models, from the most general to the particular, and equip each level with specifically optimized solution methods.

This software is developed within the ANR MARMOTE project: ANR-12-MONU-00019.

- Participants: Alain Jean-Marie, Hlib Mykhailenko, Benjamin Briot, Franck Quessette, Issam Rabhi, Jean-Marc Vincent and Jean-Michel Fourneau
- Partner: UVSQ
- Contact: Alain Jean-Marie
- Publications: marmoteCore: a Markov Modeling Platform - marmoteCore: a software platform for Markov modeling
- URL: http://marmotecore.gforge.inria.fr/

6.4. Moca

Memory Organisation Cartography and Analysis

KEYWORDS: High-Performance Computing - Performance analysis
- Contact: David Beniamine
- URL: https://github.com/dbeniamine/MOCA

6.5. Ocelotl

Multidimensional Overviews for Huge Trace Analysis

FUNCTIONAL DESCRIPTION: Ocelotl is an innovative visualization tool, which provides overviews for execution trace analysis by using a data aggregation technique. This technique enables to find anomalies in huge traces containing up to several billions of events, while keeping a fast computation time and providing a simple representation that does not overload the user.
- Participants: Arnaud Legrand and Jean-Marc Vincent
- Contact: Jean-Marc Vincent
- URL: http://soctrace-inria.github.io/ocelotl/

6.6. PSI

Perfect Simulator

FUNCTIONAL DESCRIPTION: Perfect simulator is a simulation software of markovian models. It is able to simulate discrete and continuous time models to provide a perfect sampling of the stationary distribution or directly a sampling of functional of this distribution by using coupling from the past. The simulation kernel is based on the CFTP algorithm, and the internal simulation of transitions on the Aliasing method.
- Contact: Jean-Marc Vincent
- URL: http://psi.gforge.inria.fr/

6.7. SimGrid

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

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

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

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

NEWS OF THE YEAR: There were 3 major releases in 2019: Python bindings were introduced, SMPI now partially supports some of the MPI/IO functions, a new model for Wifi networks was proposed, and the API for the simulation of storage resources was completely revisited. We also pursued our efforts to improve the documentation of the software, simplified the web site, and made a lot of bug fixing and code refactoring.
- Participants: Adrien Lèbre, Arnaud Legrand, Augustin Degomme, Florence Perronnin, Frédéric Suter, Jean-Marc Vincent, Jonathan Pastor, Luka Stanisic and Martin Quinson
- Partners: CNRS - ENS Rennes
- Contact: Martin Quinson
- URL: https://simgrid.org/

6.8. Tabarnac

Tool for Analyzing the Behavior of Applications Running on NUMA ArChitecture

KEYWORDS: High-Performance Computing - Performance analysis - NUMA

- Contact: David Beniamine
- URL: https://dbeniamine.github.io/Tabarnac/

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

5. New Software and Platforms

5.1. FECFRAME

FEC Framework following RFC 6363 specifications (https://datatracker.ietf.org/doc/rfc6363/)

KEYWORDS: Error Correction Code - Content delivery protocol - Robust transmission

FUNCTIONAL DESCRIPTION: This sofware implements the FECFRAME IETF standard (RFC 6363) co-authored by V. Roca, and is compliant with 3GPP specifications for mobile terminals. It enables the simultaneous transmission of multimedia flows to one or several destinations, while being robust to packet erasures that happen on wireless networks (e.g., 4G or Wifi). This software relies on the OpenFEC library (the open-source http://openfec.org version or the commercial version) that provides the erasure correction codes (or FEC) and thereby offer robustness in front of packet erasures.

- Participant: Vincent Roca
- Contact: Vincent Roca

5.2. Wombat

Wi-Fi tracking system for testing and demonstrational purpose

KEYWORDS: Wi-Fi - Privacy - Multimodal tracking of human activity - Wireless network

FUNCTIONAL DESCRIPTION: Wombat is a fully functional Wi-Fi tracking platform supporting three main features: collection, storage/processing, query/output. These three features are implemented through a distributed infrastructure composed of:

Sensor nodes: small devices with wireless monitoring capabilities. They collect information sent on wireless channels and forward it to the server. Central server: the central entity of the system. It receives data sent by sensor nodes and then stores it in an internal data structure. It is also in charge of answering queries related to the stored data.

To ensure communication between the sensor nodes and the server, the Wombat system relies on a wired network (Ethernet). In addition, Wombat can be enriched with a user interface and an opt-out node:

User interface: a device in charge of displaying detailed information about one or several tracked devices (see figure below). The device to display can be specified manually by its MAC address or through proximity detection. Opt-out node: an element in charge of implementing an opt-out mechanism for users refusing to be tracked by the system.

The system is made to work on a dedicated network (the server includes a DHCP server). Nodes can be switched off at any time (they function in read-only mode to be crash-proof).

- Partner: Insa de Lyon
- Contact: Mathieu Cunche
- URL: https://github.com/Perdu/wombat

5.3. Cookie glasses

KEYWORDS: GDPR - Cookie - Consent

SCIENTIFIC DESCRIPTION: In the paper Do Cookie Banners Respect my Choice? Measuring Legal Compliance of Banners from IAB Europe's Transparency and Consent Framework, we show that Consent Management Providers (CMPs) of IAB Europe's Transparency & Consent Framework (TCF) do not always respect user's choice. This extension allows users to verify that their consent is stored appropriately by themselves.

This extension for Firefox and Chrome queries CMPs of IAB Europe's TCF in the same position as a third-party advertiser, making it possible to see consent set by CMPs in real time. In other words, you can see whether consent registered by cookie banners is actually the consent you gave. Will only work with cookie banners of IAB Europe's TCF.

We also added a functionality to manually decode a so-called "consent string" of the framework.

- Participants: Célestin Matte and Nataliia Bielova
- Contact: Alain Prette

5.4. BELL

Browser fingerprinting via Extensions and Login-Leaks

KEYWORDS: Browser Extensions - Security and Privacy in Web Services - Social Networks Security and Privacy

FUNCTIONAL DESCRIPTION: Recent studies show that users can be tracked based on their web browser properties. This software is designed to conduct an experiment on such kinds of user tracking. In this experiment, we demonstrate that a Web user can also be tracked by

- her browser extensions (such as AdBlock, Pinterest, or Ghostery), and

- the websites she has logged in (such as Facebook, Gmail, or Twitter).

In the experiment, we collect user's browser fingerprint, together with the browser extensions installed and a list of websites she has logged in. We only collect anonymous data during the experiment (more details in our Privacy Policy [0]), we will securely store the data on an Inria server, use it only for research purposes and not share it with anyone outside of Inria.

- Contact: Gabor Gulyas
- URL: https://extensions.inrialpes.fr/

5.5. SWIF-codec

An open-source sliding window FEC codec

KEYWORD: Error Correction Code

FUNCTIONAL DESCRIPTION: This development is done in the context of the "Coding for Efficient Network Communications" IRTF Research Group (NWCRG, [https://datatracker.ietf.org/rg/nwcrg]) and IETF hackathon.

This work has strong relationships with the Generic API I-D [https://datatracker.ietf.org/doc/draft-roca-nwcrg-generic-fec-api/] and RFC 8681 on RLC codes [https://www.rfc-editor.org/rfc/rfc8681] as examples of sliding window codes.

- Authors: Vincent Roca, Cédric Adjih, Oumaima Attia and François Michel
- Contact: Vincent Roca
- URL: https://github.com/irtf-nwcrg/swif-codec

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[0] https://extensions.inrialpes.fr/privacy.php

ROMA Project-Team

6. New Software and Platforms

6.1. MUMPS

A MUltifrontal Massively Parallel Solver

KEYWORDS: High-Performance Computing - Direct solvers - Finite element modelling

FUNCTIONAL DESCRIPTION: MUMPS is a software library to solve large sparse linear systems (AX=B) on sequential and parallel distributed memory computers. It implements a sparse direct method called the multifrontal method. It is used worldwide in academic and industrial codes, in the context numerical modeling of physical phenomena with finite elements. Its main characteristics are its numerical stability, its large number of features, its high performance and its constant evolution through research and feedback from its community of users. Examples of application fields include structural mechanics, electromagnetism, geophysics, acoustics, computational fluid dynamics. MUMPS has been developed by INPT(ENSEEIHT)-IRIT, Inria, CERFACS, University of Bordeaux, CNRS and ENS Lyon. Since January 2019, it is developed and licensed by Mumps Technologies SAS.

NEWS OF THE YEAR: In June 2019, a new version of MUMPS, MUMPS 5.2.1, was released by Mumps Technologies.

- Participants: Gilles Moreau, Abdou Guermouche, Alfredo Buttari, Aurélia Fevre, Bora Uçar, Chiara Puglisi, Clément Weisbecker, Emmanuel Agullo, François-Henry Rouet, Guillaume Joslin, Jacko Koster, Jean-Yves L'Excellent, Marie Durand, Maurice Brémond, Mohamed Sid-Lakhdar, Patrick Amestoy, Philippe Combes, Stéphane Pralet, Theo Mary and Tzvetomila Slavova

- Partners: Université de Bordeaux - CNRS - CERFACS - ENS Lyon - INPT - IRIT - Université de Lyon - Université de Toulouse - LIP - Mumps Technologies SAS

- Contact: Jean-Yves L'Excellent

- URL: http://mumps-solver.org/

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

4. New Software and Platforms

4.1. FloPoCo

Floating-Point Cores, but not only

KEYWORD: Synthesizable VHDL generator

FUNCTIONAL DESCRIPTION: The purpose of the open-source FloPoCo project is to explore the many ways in which the flexibility of the FPGA target can be exploited in the arithmetic realm.

- Participants: Florent de Dinechin and Luc Forget
- Partners: CNRS - ENS Lyon - UCBL Lyon 1 - UPVD
- Contact: Florent de Dinechin
- URL: http://flopoco.gforge.inria.fr/

4.2. Sytare

KEYWORDS: Embedded systems - Operating system - Non volatile memory

FUNCTIONAL DESCRIPTION: Sytare is an embedded operating system targeting tiny platforms with intermittent power. In order to make power failures transparent for the application, the system detects imminent failures and saves a checkpoint of program state to non-volatile memory. Hardware peripherals are also made persistent without requiring developer attention.

- Authors: Tristan Delizy, Gautier Berthou, Guillaume Salagnac, Kevin Marquet and Tanguy Risset
- Contact: Guillaume Salagnac
- Publication: Peripheral State Persistence For Transiently Powered Systems
- URL: https://hal.inria.fr/hal-01460699

4.3. NanoTracer

KEYWORDS: Embedded systems - Power monitoring - Low power consumption

FUNCTIONAL DESCRIPTION: NanoTracer is a high performance ammeter dedicated to power measurements for small devices. The system measures currents between 100nA and 100mA (gain is audo-adjusted dynamically) with a sampling frequency of 2Msps. Data is streamed to a PC over USB which enables long-running experiments, or just real-time visualization of data.

- Contact: Guillaume Salagnac
- URL: https://gitlab.inria.fr/nanotracer/

4.4. marto

Modern Arithmetic Tools

KEYWORDS: High-level synthesis - Arithmetic - FPGA

FUNCTIONAL DESCRIPTION: Marto provides C++ headers to implement custom sized arithmetic operators such as:

Custom sized posits and their environment (including the quire) Custom sized IEEE-754 numbers Custom sized Kulisch accumulators (and sums of products)

- Participants: Yohann Uguen, Florent de Dinechin and Luc Forget
- Contact: Yohann Uguen
- Publication: hal-02130912v4
- URL: https://gitlab.inria.fr/lforget/marto

4.5. hint

High-level synthesis Integer Library

KEYWORD: High-level synthesis

FUNCTIONAL DESCRIPTION: Hint is an header-only arbitrary size integer API with strong semantics for C++. Multiple backends are provided using various HLS libraries, allowing a user to write one operator and synthetize it using the main vendor tools.

- Participants: Yohann Uguen, Florent de Dinechin and Luc Forget
- Contact: Luc Forget
- Publication: hal-02131798v2
- URL: https://github.com/yuguen/hint

SPADES Project-Team

5. New Software and Platforms

5.1. pyCPA_TWCA

Analysis tool for weakly-hard real-time systems

KEYWORDS: Real time - Scheduling analyses

FUNCTIONAL DESCRIPTION: pyCPA_TWCA is a pyCPA plugin for Typical Worst-Case Analysis. pyCPA is an open-source Python implementation of Compositional Performance Analysis developed at TU Braunschweig, which allows in particular response-time analysis. pyCPA_TWCA is an extension of that tool that is co-developed by Sophie Quinton and Zain Hammadeh at TU Braunschweig. It allows in particular the computation of weakly-hard guarantees for real-time tasks, i.e. number of deadline misses out of a sequence of executions. So far, pyCPA_TWCA is restricted to uniprocessor systems of independent tasks. pyCPA_TWCA can handle the following scheduling policies: Fixed Priority Preemptive, Fixed Priority Non-Preemptive, Weighted Round-Robin, Earliest Deadline First.

- Contact: Sophie Quinton

5.2. CertiCAN

Certifier of CAN bus analysis results

KEYWORDS: Certification - CAN bus - Real time - Static analysis

FUNCTIONAL DESCRIPTION: CertiCAN is a tool, produced using the Coq proof assistant, allowing the formal certification of the correctness of CAN bus analysis results. Result certification is a process that is lightweight and flexible compared to tool certification, which makes it a practical choice for industrial purposes. The analysis underlying CertiCAN, which is based on a combined use of two well-known CAN analysis techniques, is computationally efficient. Experiments demonstrate that CertiCAN is able to certify the results of RTaW-Pegase, an industrial CAN analysis tool, even for large systems. Furthermore, CertiCAN can certify the results of any other RTA tool for the same analysis and system model (periodic tasks with offsets in transactions).

- Contact: Xiaojie Guo

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STEEP Project-Team

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5. New Software and Platforms

5.1. USAT

Urban Sprawl Analysis Toolkit

KEYWORDS: Urban sprawl - Urban planning

FUNCTIONAL DESCRIPTION: This software allows to calculate and analyse indices of urban sprawl from open data (OpenStreetMap), aimed to be used by urban scientists and urban planners. A spatialized version of indices measuring the accessibility, dispersion and land use mix is calculated. The implemented methods are described in [15].

NEWS OF THE YEAR: In 2019 we started a refactoring of this software, together with an overhaul of the associated web service USAT-WEB.

- Participants: Luciano Gervasoni, Serge Fenet, Peter Sturm and Roger Pissard-Gibollet
- Partner: LIRIS
- Contact: Peter Sturm
- URL: https://github.com/lgervasoni/urbansprawl

5.2. USAT WEB

Urban Sprawl Analysis Toolkit Web-service

KEYWORDS: Urban planning - Urban sprawl

FUNCTIONAL DESCRIPTION: This is a web-service on top of the software USAT described above. The web-service will allow any user to select a region of interest and to launch the calculation and display of sprawl indices using USAT. It is in the process of being hosted on the HPC platform of IN2P3, after which it will be made open to the public. The source code for this web-service is already available at the below site.

The web-service is described in [21].

NEWS OF THE YEAR: In 2019 we started a complete overhaul of this software, together with a factorization of the underlying computation core (USAT).

- Participants: Lucas Rezakhanlou, Peter Sturm, Luciano Gervasoni, Serge Fenet and Roger Pissard-Gibollet
- Contact: Peter Sturm
- Publication: USAT (Urban Sprawl Analysis Toolkit) : une plateforme web d'analyse de l'étalement urbain à partir de données massives ouvertes
- URL: https://gitlab.inria.fr/lrezakha/usat-web

5.3. LUM_OSM

Land Use Mix calculation from OpenStreepMap data

KEYWORD: Urban sprawl

FUNCTIONAL DESCRIPTION: The software uses Mapzen Metro Extracts to retrieve the OpenStreetMap data of a given region in the PostgreSQL format. Afterwards, a continuous representation of residential and activity land uses is created. Finally, a GIS output containing the degree of land use mixture is calculated by means of using the land uses maps. The implemented approach is documented in the paper "A framework for evaluating urban land use mix from crowd-sourcing data", http://hal.inria.fr/hal-01396792

- Participants: Luciano Gervasoni, Marti Bosch Padros, Peter Sturm, Serge Fenet and Roger Pissard-Gibollet
- Partners: EPFL - Ecole Polytechnique Fédérale de Lausanne - LIRIS
- Contact: Peter Sturm
- URL: http://github.com/martibosch/landusemix

5.4. Comptabilité Ecologique

FUNCTIONAL DESCRIPTION: Databases, database handling tools and data visualization tools (on the web-site). Databases include socio-economic and environmental datasets. Visualization tools include interactive piecharts, maps and Sankey diagrams.

- Participants: Jean-Yves Courtonne and Pierre-Yves Longaretti
- Contact: Jean-Yves Courtonne
- URL: http://www.eco-data.fr

5.5. REDEM

REDuction Of EMission

KEYWORD: Climate change

FUNCTIONAL DESCRIPTION: REDEM soft is a tool designed for the benchmarking of national GHG emission reduction trajectories. The actual version of the software is implemented in Visual Basic under Microsoft Excel in order to facilitate handling and diffusion to climate/energy economists.

NEWS OF THE YEAR: In 2019, the database underlying REDEM was updated with recent national emission trajectory information.

- Participants: Constantin Ilasca, Hélène Benveniste, Olivier Boucher, Patrick Criqui and Roger Pissard-Gibollet
- Partners: EDDEN - IPSL
- Contact: Emmanuel Prados
- URL: http://redem.gforge.inria.fr/

5.6. REDEM web

REDEM Web

KEYWORDS: Benchmarking - Climate change - Global warming - Greenhouse gas emissions

FUNCTIONAL DESCRIPTION: Python Library of REDEM model and its web application.

- Participants: Constantin Ilasca, Emmanuel Prados, Hélène Benveniste, Nicolas Assouad, Olivier Boucher, Patrick Criqui and Roger Pissard-Gibollet
- Partners: UPMC - EDDEN
- Contact: Emmanuel Prados
- URL: http://redem.inria.fr/

THOTH Project-Team

6. New Software and Platforms

6.1. LCR-Net

Localization-Classification-Regression Network for Human Pose

KEYWORDS: Object detection - Recognition of human movement

FUNCTIONAL DESCRIPTION: We propose an end-to-end architecture for joint 2D and 3D human pose estimation in natural images. Key to our approach is the generation and scoring of a number of pose proposals per image, which allows us to predict 2D and 3D pose of multiple people simultaneously. Our architecture contains 3 main components: 1) the pose proposal generator that suggests potential poses at different locations in the image, 2) a classifier that scores the different pose proposals , and 3) a regressor that refines pose proposals both in 2D and 3D.

- Participants: Grégory Rogez, Philippe Weinzaepfel and Cordelia Schmid
- Partner: Naver Labs Europe
- Contact: Nicolas Jourdan
- Publication: LCR-Net: Localization-Classification-Regression for Human Pose
- URL: https://thoth.inrialpes.fr/src/LCR-Net/

6.2. CKN-seq

Convolutional Kernel Networks for Biological Sequences

KEYWORD: Bioinformatics

SCIENTIFIC DESCRIPTION: The growing amount of biological sequences available makes it possible to learn genotype-phenotype relationships from data with increasingly high accuracy. By exploiting large sets of sequences with known phenotypes, machine learning methods can be used to build functions that predict the phenotype of new, unannotated sequences. In particular, deep neural networks have recently obtained good performances on such prediction tasks, but are notoriously difficult to analyze or interpret. Here, we introduce a hybrid approach between kernel methods and convolutional neural networks for sequences, which retains the ability of neural networks to learn good representations for a learning problem at hand, while defining a well characterized Hilbert space to describe prediction functions. Our method outperforms state-of-the-art convolutional neural networks on a transcription factor binding prediction task while being much faster to train and yielding more stable and interpretable results.

FUNCTIONAL DESCRIPTION: D. Chen, L. Jacob, and J. Mairal. Biological Sequence Modeling with Convolutional Kernel Networks. Bioinformatics, volume 35, issue 18, pages 3294-3302, 2019.

- Participants: Laurent Jacob, Dexiong Chen and Julien Mairal
- Partners: CNRS - UGA
- Contact: Julien Mairal
- Publication: Biological Sequence Modeling with Convolutional Kernel Networks
- URL: https://gitlab.inria.fr/dchen/CKN-seq

6.3. LVO

Learning Video Object Segmentation with Visual Memory

KEYWORD: Video analysis

FUNCTIONAL DESCRIPTION: This is a public implementation of the method described in the following paper: Learning Video Object Segmentation with Visual Memory [ICCV 2017] (https://hal.archives-ouvertes.fr/hal-01511145v2/document).

This paper addresses the task of segmenting moving objects in unconstrained videos. We introduce a novel two-stream neural network with an explicit memory module to achieve this. The two streams of the network encode spatial and temporal features in a video sequence respectively, while the memory module captures the evolution of objects over time. The module to build a "visual memory" in video, i.e., a joint representation of all the video frames, is realized with a convolutional recurrent unit learned from a small number of training video sequences. Given a video frame as input, our approach assigns each pixel an object or background label based on the learned spatio-temporal features as well as the "visual memory" specific to the video, acquired automatically without any manually-annotated frames. The visual memory is implemented with convolutional gated recurrent units, which allows to propagate spatial information over time. We evaluate our method extensively on two benchmarks, DAVIS and Freiburg-Berkeley motion segmentation datasets, and show state-of-the-art results. For example, our approach outperforms the top method on the DAVIS dataset by nearly 6%. We also provide an extensive ablative analysis to investigate the influence of each component in the proposed framework.

- Participants: Karteek Alahari, Cordelia Schmid and Pavel Tokmakov
- Contact: Pavel Tokmakov
- Publication: hal-01511145v2
- URL: http://lear.inrialpes.fr/research/lvo/

6.4. SURREAL

Learning from Synthetic Humans

KEYWORDS: Synthetic human - Segmentation - Neural networks

FUNCTIONAL DESCRIPTION: The SURREAL dataset consisting of synthetic videos of humans, and models trained on this dataset are released in this package. The code for rendering synthetic images of people and for training models is also included in the release.

- Participants: Gül Varol, Xavier Martin, Ivan Laptev and Cordelia Schmid
- Contact: Gül Varol
- Publication: Learning from Synthetic Humans
- URL: http://www.di.ens.fr/willow/research/surreal/

6.5. attn2d

Pervasive Attention

KEYWORDS: NLP - Deep learning - Machine translation

SCIENTIFIC DESCRIPTION: Pervasive attention : 2D Convolutional Networks for Sequence-to-Sequence Prediction

FUNCTIONAL DESCRIPTION: An open source PyTorch implementation of the pervasive attention model described in: Maha Elbayad, Laurent Besacier, and Jakob Verbeek. 2018. Pervasive Attention: 2D Convolutional Networks for Sequence-to-Sequence Prediction. In Proceedings of the 22nd Conference on Computational Natural Language Learning (CoNLL 2018)

- Participants: Maha Elbayad and Jakob Verbeek
- Contact: Maha Elbayad
- Publication: Pervasive Attention: 2D Convolutional Neural Networks for Sequence-to-Sequence Prediction
- URL: https://github.com/elbayadm/attn2d

6.6. Cyanure

Cyanure: An Open-Source Toolbox for Empirical Risk Minimization

KEYWORD: Machine learning

FUNCTIONAL DESCRIPTION: Cyanure is an open-source C++ software package with a Python interface. The goal of Arsenic is to provide state-of-the-art solvers for learning linear models, based on stochastic variance-reduced stochastic optimization with acceleration mechanisms and Quasi-Newton principles. Arsenic can handle a large variety of loss functions (logistic, square, squared hinge, multinomial logistic) and regularization functions (l2, l1, elastic-net, fused Lasso, multi-task group Lasso). It provides a simple Python API, which is very close to that of scikit-learn, which should be extended to other languages such as R or Matlab in a near future.

RELEASE FUNCTIONAL DESCRIPTION: version initiale

- Participant: Julien Mairal
- Contact: Julien Mairal
- URL: http://thoth.inrialpes.fr/people/mairal/arsenic/welcome.html

TRIPOP Project-Team

5. New Software and Platforms

5.1. SICONOS

Participants: Vincent Acary, Maurice Brémond, Olivier Huber, Franck Pérignon.

In the framework of the FP5 European project Siconos (2002-2006), Bipop was the leader of the Work Package 2 (WP2), dedicated to the numerical methods and the software design for nonsmooth dynamical systems. This has given rise to the platform SICONOS which is the main software development task in the team. The aim of this work is to provide a common platform for the simulation, modeling, analysis and control of abstract nonsmooth dynamical systems. Besides usual quality attributes for scientific computing software, we want to provide a common framework for various scientific fields, to be able to rely on the existing developments (numerical algorithms, description and modeling software), to support exchanges and comparisons of methods, to disseminate the know-how to other fields of research and industry, and to take into account the diversity of users (end-users, algorithm developers, framework builders) in building expert interfaces in Python and end-user front-end through Scilab.

After the requirement elicitation phase, the Siconos Software project has been divided into 5 work packages which are identified to software products:

1. SICONOS/NUMERICS This library contains a set of numerical algorithms, already well identified, to solve non smooth dynamical systems. This library is written in low-level languages (C,F77) in order to ensure numerical efficiency and the use of standard libraries (Blas, Lapack, ...)

2. SICONOS/KERNEL This module is an object-oriented structure (C++) for the modeling and the simulation of abstract dynamical systems. It provides the users with a set of classes to describe their nonsmooth dynamical system (dynamical systems, intercations, nonsmooth laws, ...) and to perform a numerical time integration and solving.

3. SICONOS/FRONT-END. This module is mainly an auto-generated wrapper in Python which provides a user-friendly interface to the Siconos libraries. A scilab interface is also provided in the Front-End module.

4. SICONOS/CONTROL This part is devoted to the implementation of control strategies of non smooth dynamical systems.

5. SICONOS/MECHANICS. This part is dedicated to the modeling and the simulation of multi-body systems with 3D contacts, impacts and Coulomb's friction. It uses the Siconos/Kernel as simulation engine but relies on a industrial CAD library (OpenCascade and pythonOCC) to deal with complex body geometries and to compute the contact locations and distances between B-Rep description and on Bullet for contact detection between meshes.

Further informations may be found at http://siconos.gforge.inria.fr/

<p align="center">**TYREX Project-Team**</p>

5. New Software and Platforms

5.1. SPARQLGX

KEYWORDS: RDF - SPARQL - Distributed computing

SCIENTIFIC DESCRIPTION: SPARQL is the W3C standard query language for querying data expressed in RDF (Resource Description Framework). The increasing amounts of RDF data available raise a major need and research interest in building efficient and scalable distributed SPARQL query evaluators.

In this context, we propose and share SPARQLGX: our implementation of a distributed RDF datastore based on Apache Spark. SPARQLGX is designed to leverage existing Hadoop infrastructures for evaluating SPARQL queries. SPARQLGX relies on a translation of SPARQL queries into executable Spark code that adopts evaluation strategies according to (1) the storage method used and (2) statistics on data. Using a simple design, SPARQLGX already represents an interesting alternative in several scenarios.

FUNCTIONAL DESCRIPTION: This software system is an implementation of a distributed evaluator of SPARQL queries. It makes it possible to evaluate SPARQL queries on billions of triples distributed across multiple nodes in a cluster, while providing attractive performance figures.

RELEASE FUNCTIONAL DESCRIPTION: - Faster load routine which widely improves this phase perfomances by reading once the initial triple file and by partitioning data in the same time into the correct predicate files. - Improving the generated Scala-code of the translation process with mapValues. This technic allows not to break the partitioning of KeyValueRDD while applying transformations to the values instead of the traditional map that was done prior. - Merging and cleaning several scripts in bin/ such as for example sgx-eval.sh and sde-eval.sh - Improving the compilation process of compile.sh - Cleaner test scripts in tests/ - Offering the possibility of an easier deployment using Docker.

- Participants: Damien Graux, Thomas Calmant, Louis Jachiet, Nabil Layaïda and Pierre Genevès
- Contact: Pierre Genevès
- Publications: Optimizing SPARQL query evaluation with a worst-case cardinality estimation based on statistics on the data - The SPARQLGX System for Distributed Evaluation of SPARQL Queries
- URL: https://github.com/tyrex-team/sparqlgx

5.2. musparql

KEYWORDS: SPARQL - RDF - Property paths

FUNCTIONAL DESCRIPTION: reads a SPARQL request and translates it into an internal algebra. Rewrites the resulting term into many equivalent versions, then choses one of them and executes it on a graph.

- Participant: Louis Jachiet
- Contact: Nabil Layaïda
- Publication: Extending the SPARQL Algebra for the optimization of Property Paths
- URL: https://gitlab.inria.fr/tyrex/musparql

5.3. MRB

Mixed Reality Browser

KEYWORDS: Augmented reality - Geolocation - Indoor geolocalisation - Smartphone

FUNCTIONAL DESCRIPTION: MRB displays PoI (Point of Interest) content remotely through panoramics with spatialized audio, or on-site by walking to the corresponding place, it can be used for indoor-outdoor navigation, with assistive audio technology for the visually impaired. It is the only browser of geolocalized data to use XML as a native format for PoIs, panoramics, 3D audio and to rely on HTML5 both for the iconic and full information content of PoIs. Positioning in MRB is based on a PDR library, written in C++ and Java and developed by the team, which provides the user's location in real time based on the interpretation of sensors. Three main modules have been designed to build this positioning system: (i) a pedometer that estimates the distance the user has walked and his speed, (ii) a motion manager that enables data set recording and simulation but also the creation of virtual sensors or filters (e.g gyroscope drift compensation, linear acceleration, altimeter), and (iii) a map-matching algorithm that provides a new location based on a given OpenStreetMap file description and the current user's trajectory.

- Participant: Thibaud Michel
- Contact: Nabil Layaïda
- Publications: On Mobile Augmented Reality Applications based on Geolocation - Attitude Estimation for Indoor Navigation and Augmented Reality with Smartphones
- URL: http://tyrex.inria.fr/projects/mrb.html

5.4. Benchmarks Attitude Smartphones

KEYWORDS: Experimentation - Motion analysis - Sensors - Performance analysis - Smartphone

SCIENTIFIC DESCRIPTION: We investigate the precision of attitude estimation algorithms in the particular context of pedestrian navigation with commodity smartphones and their inertial/magnetic sensors. We report on an extensive comparison and experimental analysis of existing algorithms. We focus on typical motions of smartphones when carried by pedestrians. We use a precise ground truth obtained from a motion capture system. We test state-of-the-art attitude estimation techniques with several smartphones, in the presence of magnetic perturbations typically found in buildings. We discuss the obtained results, analyze advantages and limits of current technologies for attitude estimation in this context. Furthermore, we propose a new technique for limiting the impact of magnetic perturbations with any attitude estimation algorithm used in this context. We show how our technique compares and improves over previous works.

- Participants: Hassen Fourati, Nabil Layaïda, Pierre Genevès and Thibaud Michel
- Partner: GIPSA-Lab
- Contact: Pierre Genevès
- URL: http://tyrex.inria.fr/mobile/benchmarks-attitude/

5.5. MedAnalytics

KEYWORDS: Big data - Predictive analytics - Distributed systems

FUNCTIONAL DESCRIPTION: We implemented a method for the automatic detection of at-risk profiles based on a fine-grained analysis of prescription data at the time of admission. The system relies on an optimized distributed architecture adapted for processing very large volumes of medical records and clinical data. We conducted practical experiments with real data of millions of patients and hundreds of hospitals. We demonstrated how the various perspectives of big data improve the detection of at-risk patients, making it possible to construct predictive models that benefit from volume and variety. This prototype implementation is described in the 2017 preprint available at: https://hal.inria.fr/hal-01517087/document.

- Participants: Pierre Genevès and Thomas Calmant
- Partner: CHU Grenoble
- Contact: Pierre Genevès
- Publication: Scalable Machine Learning for Predicting At-Risk Profiles Upon Hospital Admission

5.6. MuIR

Mu Intermediate Representation

KEYWORDS: Optimizing compiler - Querying

FUNCTIONAL DESCRIPTION: This is a prototype of an intermediate language representation, i.e. an implementation of algebraic terms, rewrite rules, query plans, cost model, query optimizer, and query evaluators (including a distributed evaluator of algebraic terms using Apache Spark).

- Contact: Pierre Genevès