



RESEARCH CENTER
Bordeaux - Sud-Ouest

FIELD

Activity Report 2018

Section Software

Edition: 2019-03-07

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AUCTUS Team

6. New Software and Platforms

6.1. HuMoSoft

Human Motion Analysis Software

KEYWORDS: Movement analysis - 3D movement

FUNCTIONAL DESCRIPTION: HuMoSoft is based on the ROS platform. The acquisition data can come from different depth sensors, for example Kinect, via the NuiTrack JDK. An extended Kalman filter has been implemented, and motion analysis uses the RULA method.

- Authors: Jessica Colombel and David Daney
- Contact: Sylvain Pion
- URL: <https://gitlab.inria.fr/auctus/kombos-server>

CAGIRE Project-Team

6. New Software and Platforms

6.1. AeroSol

KEYWORD: Finite element modelling

FUNCTIONAL DESCRIPTION: The AeroSol software is a high order finite element library written in C++. The code has been designed so as to allow for efficient computations, with continuous and discontinuous finite elements methods on hybrid and possibly curvilinear meshes. The work of the team CARDAMOM (previously Bacchus) is focused on continuous finite elements methods, while the team Cagire is focused on discontinuous Galerkin methods. However, everything is done for sharing the largest part of code we can. More precisely, classes concerning IO, finite elements, quadrature, geometry, time iteration, linear solver, models and interface with PaMPA are used by both of the teams. This modularity is achieved by mean of template abstraction for keeping good performances. The distribution of the unknowns is made with the software PaMPA , developed within the team TADAAM (and previously in Bacchus) and the team Castor.

NEWS OF THE YEAR: In 2018, the following points were addressed in AeroSol

* A 6 month CNRS contract, led by Vincent Perrier was obtained in the team Cagire, concentrated on the quality of the code. A two-year Inria Hub, led by H elo ise Beaugendre was obtained in the team Cardamom. On both of these contracts, Benjamin Lux was hired (January-June in Cagire team, and since October in Cardamom team). The library has kept on benefiting from the work of Florent Pruvost (Inria Hub HPCLib), on the continuous integration and packaging aspects.

* The CNRS contract, aiming at improving the code resulted in the successful porting from the inria gforge to the inria gitlab, with a functional pipeline of code assessment (based on Jenkins) and code quality assessment (based on sonarqube).

* Installation was simplified. A fully automatic installation script based on spack was developed.

* Development of a true documentation policy, based on a wiki. About half of the functional tests were documented and updated. Doxygen documentation was improved.

* An API was developed for the AeroSol library. The mesh reading, and parallel distribution was refactored.

* Update of the test case interface was updated by using this API for being more convenient. About half of the functional tests are now using this interface.

* Refactoring of the xml parameter file.

* Hyperbolized models, based on the hyperbolization of advection-diffusion models were added.

* Handling of nonconservative hyperbolic models.

* Improvement of mesh adaptation

* Beginning of implementation of droplet model for icing.

* Add the possibility of using several matrices, with a different number of variables

- Participants: Benjamin Lux, Damien Genet, Dragan Amenga Mbengoue, Hamza Belkhat Zougari, Mario Ricchiuto, Maxime Mog e, Simon Delmas and Vincent Perrier
- Contact: Vincent Perrier

CARDAMOM Project-Team

6. New Software and Platforms

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- Participants: Benjamin Lux, Damien Genet, Dragan Amenga Mbengoue, Hamza Belkhatat Zougari, Mario Ricchiuto, Maxime Mogé, Simon Delmas and Vincent Perrier
- Contact: Vincent Perrier

6.2. Crysa

KEYWORDS: Image analysis - 2D

FUNCTIONAL DESCRIPTION: Analyzes the organization of objects placed in a hexagonal grid in an image and the crystalline structure induced in this image.

- Participants: Cécile Dobrzynski and Jean Mercat
- Partners: LCTS (UMR 5801) - LCPO - ISM
- Contact: Cécile Dobrzynski

6.3. Cut-ANOVA

Cut-ANOVA Global Sensitivity Analysis

KEYWORDS: Stochastic models - Uncertainty quantification

SCIENTIFIC DESCRIPTION: An anchored analysis of variance (ANOVA) method is proposed to decompose the statistical moments. Compared to the standard ANOVA with mutually orthogonal component functions, the anchored ANOVA, with an arbitrary choice of the anchor point, loses the orthogonality if employing the same measure. However, an advantage of the anchored ANOVA consists in the considerably reduced number of deterministic solver's computations, which renders the uncertainty quantification of real engineering problems much easier. Different from existing methods, the covariance decomposition of the output variance is used in this work to take account of the interactions between non-orthogonal components, yielding an exact variance expansion and thus, with a suitable numerical integration method, provides a strategy that converges. This convergence is verified by studying academic tests. In particular, the sensitivity problem of existing methods to the choice of anchor point is analyzed via the Ishigami case, and we point out that covariance decomposition survives from this issue. Also, with a truncated anchored ANOVA expansion, numerical results prove that the proposed approach is less sensitive to the anchor point. The covariance-based sensitivity indices (SI) are also used, compared to the variance-based SI. Furthermore, we emphasize that the covariance decomposition can be generalized in a straightforward way to decompose higher-order moments. For academic problems, results show the method converges to exact solution regarding both the skewness and kurtosis. The proposed method can indeed be applied to a large number of engineering problems.

FUNCTIONAL DESCRIPTION: The Cut-ANOVA code (Fortran 90, MPI + OpenMP) is devoted to the stochastic analysis of numerical simulations. The method implemented is based on the spectral expansion of "anchored ANOVA", allowing the covariance-based sensitivity analysis. Compared to the conventional Sobol method, "Cut-ANOVA" provides three sensitivity indices instead of one, which allows a better analysis of the reliability of the numerical prediction. On the other hand, "Cut-ANOVA" is able to compute the higher order statistical moments such as the Skewness (3-rd order moment) and Kurtosis (4-th order moment). Several dimension reduction techniques have also been implemented to reduce the computational cost. Finally, thanks to the innovative method implemented into the Code Cut-ANOVA, one can obtain a similar accuracy for stochastic quantities by using a considerably less number of deterministic model evaluations, compared with the classical Monte Carlo method.

- Participants: Kunkun Tang and Pietro-Marco Congedo
- Contact: Kunkun Tang

6.4. Fmg

KEYWORD: Mesh adaptation

FUNCTIONAL DESCRIPTION: FMG is a library deforming an input/reference simplicial mesh w.r.t. a given smoothness error monitor (function gradient or Hessian), metric field, or given mesh size distribution. Displacements are computed by solving an elliptic Laplacian type equation with a continuous finite element method. The library returns an adapted mesh with a corresponding projected solution, obtained by either a second order projection, or by an ALE finite element remap. The addition of a new mass conservative approach developed ad-hoc for shallow water flows is under way.

NEWS OF THE YEAR: - Development of the Elasticity model to compute the nodes displacement. - Development of a new model to compute the nodes displacement. This mixed model takes the advantages of the Laplacian model and the Elasticity model: a refined mesh where the solution varies a lot and a smooth gradation of the edges size elsewhere. - Extension in three dimension

- Participants: Cécile Dobrzynski, Leo Nouveau, Luca Arpaia and Mario Ricchiuto
- Contact: Cécile Dobrzynski

6.5. Mmg

Mmg Platform

KEYWORDS: Mesh adaptation - Anisotropic - Mesh generation - Mesh - Isovalue discretization

SCIENTIFIC DESCRIPTION: The Mmg platform gathers open source software for two-dimensional, surface and volume remeshing. The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescriptions satisfaction.

The 3 softwares can be used by command line or using the library version (C, C++ and Fortran API) : - Mmg2d performs mesh generation and isotropic and anisotropic mesh adaptation. - Mmgs allows isotropic and anisotropic mesh adaptation for 3D surface meshes. - Mmg3d is a new version of the MMG3D4 software. It remesh both the volume and surface mesh of a tetrahedral mesh. It performs isotropic and anisotropic mesh adaptation and isovalue discretization of a level-set function.

The platform software allow to control the boundaries approximation: The "ideal" geometry is reconstruct from the piecewise linear mesh using cubic Bezier triangular patches. The surface mesh is modified to respect a maximal Hausdorff distance between the ideal geometry and the mesh.

Inside the volume, the software perform local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).

FUNCTIONAL DESCRIPTION: The Mmg platform gathers open source software for two-dimensional, surface and volume remeshing. It provides three applications : 1) mmg2d: generation of a triangular mesh , adaptation and optimization of a triangular mesh 2) mmgs: adaptation and optimization of a surface triangulation representing a piecewise linear approximation of an underlying surface geometry 3) mmg3d: adaptation and optimization of a tetrahedral mesh and isovalue discretization

The platform software perform local mesh modifications. The mesh is iteratively modified until the user prescription satisfaction.

NEWS OF THE YEAR: Release 5.3.0 improves: - the mmg3d algorithm for mesh adaptation (better convergence and edge lengths closest to 1) - the software behaviour in case of failure (warnings/error messages are printed only 1 time and there is no more exits in the code) - the mmg2d software that now uses the same structure than mmgs and mmg3d

It adds: - the -hsiz option for mmg2d/s/3d (that allows to generate a uniform mesh of size) - the -nosurf option for mmg2d (that allows to not modify the mesh boundaries) - the -opnbdy option for mmg3d (that allow to preserve an open boundary inside a volume mesh) - the possibility to provide meshes containing prisms to mmg3d (the prisms entities are preserved while the tetra ones are modified)

- Participants: Algiane Froehly, Cécile Dobrzynski, Charles Dapogny and Pascal Frey
- Partners: Université de Bordeaux - CNRS - IPB - UPMC
- Contact: Cécile Dobrzynski
- URL: <http://www.mmgtools.org>

6.6. MMG3D

Mmg3d

KEYWORDS: Mesh - Anisotropic - Mesh adaptation

SCIENTIFIC DESCRIPTION: Mmg3d is an open source software for tetrahedral remeshing. It performs local mesh modifications. The mesh is iteratively modified until the user prescriptions satisfaction.

Mmg3d can be used by command line or using the library version (C, C++ and Fortran API) : - It is a new version of the MMG3D4 software. It remesh both the volume and surface mesh of a tetrahedral mesh. It performs isotropic and anisotropic mesh adaptation and isovalue discretization of a level-set function.

Mmg3d allows to control the boundaries approximation: The "ideal" geometry is reconstructed from the piecewise linear mesh using cubic Bezier triangular patches. The surface mesh is modified to respect a maximal Hausdorff distance between the ideal geometry and the mesh.

Inside the volume, the software performs local mesh modifications (such as edge swap, pattern split, isotropic and anisotropic Delaunay insertion...).

FUNCTIONAL DESCRIPTION: Mmg3d is one of the software of the Mmg platform. It is dedicated to the modification of 3D volume meshes. It performs the adaptation and the optimization of a tetrahedral mesh and allows to discretize an isovalue.

Mmg3d performs local mesh modifications. The mesh is iteratively modified until the user prescription satisfaction.

- Participants: Algiane Froehly, Cécile Dobrzynski, Charles Dapogny and Pascal Frey
- Partners: Université de Bordeaux - CNRS - IPB - UPMC
- Contact: Cécile Dobrzynski
- URL: <http://www.mmgtools.org>

6.7. NOMESH

KEYWORDS: Mesh - Curved mesh - Tetrahedral mesh

FUNCTIONAL DESCRIPTION: NOMESH is a software allowing the generation of three order curved simplicial meshes. Starting from a "classical" mesh with straight elements composed by triangles and/or tetrahedra, we are able to curve the boundary mesh. Starting from a mesh with some curved elements, we can verify if the mesh is valid, that means there is no crossing elements and only positive jacobian. If the curved mesh is non valid, we modify it using linear elasticity equations until having a valid curved mesh.

- Participants: Algiane Froehly, Ghina El Jannoun and Cécile Dobrzynski
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: Cécile Dobrzynski

6.8. ORComp

FUNCTIONAL DESCRIPTION: The ORComp platform is a simulation tool permitting to design an ORC cycle. Starting from the solar radiation, this platform computes the cycle providing the best performance with optimal choices of the fluid and the operating conditions. It includes RobUQ, a simulation block of the ORC cycles, the RealfluidS code for the simulation of the turbine and of the heat exchanger, the software FluidProp (developed at the University of Delft) for computing the fluid thermodynamic properties.

- Participants: Maria-Giovanna Rodio and Pietro-Marco Congedo
- Contact: Maria-Giovanna Rodio
- URL: <https://github.com/Orcomp/Orcomp>

6.9. RealfluidS

KEYWORDS: Compressible flows - Finite element modelling - Residual distribution - Aeronautics

FUNCTIONAL DESCRIPTION: RealfuidS is a software dedicated to the simulation of inert or reactive flows. It is also able to simulate multiphase, multimaterial, MHD flows and turbulent flows (using the SA model). There exist 2D and 3D dimensional versions. The 2D version is used to test new ideas that are later implemented in the 3D one. This software implements the more recent residual distribution schemes. The code has been parallelized with and without overlap of the domains. The uncertainty quantification library RobUQ has been coupled to the software. A partitioning tool exists in the package, which uses Scotch . Recently, the code has been developed for taking into account real-gas effects, in order to use arbitrarily complex equations of state. Further developments concerning multiphase effects are under way.

- Participants: Cécile Dobrzynski, Héloïse Beaugendre, Leo Nouveau, Pietro-Marco Congedo and Quentin Viville
- Contact: Héloïse Beaugendre

6.10. SH-COMP

KEYWORDS: Finite element modelling - Multi-physics simulation - Chemistry - Incompressible flows - 2D
FUNCTIONAL DESCRIPTION: Numerical modelling of the healing process in ceramic matrix composites

- Participants: Gérard Vignoles, Gregory Perrot, Guillaume Couegnat, Mario Ricchiuto and Virginie Drean
- Partner: LCTS (UMR 5801)
- Contact: Guillaume Couegnat

6.11. SLOWS

Shallow-water fLOWS

KEYWORDS: Simulation - Free surface flows - Unstructured meshes

SCIENTIFIC DESCRIPTION: Three different approaches are available, based on conditionally depth-positivity preserving implicit schemes, or on conditionally depth-positivity preserving genuinely explicit discretizations, or on an unconditionally depth-positivity preserving space-time approach. Newton and frozen Newton loops are used to solve the implicit nonlinear equations. The linear algebraic systems arising in the discretization are solved with the MUMPS library. This year implicit and explicit (extrapolated) multistep higher order time integration methods have been implemented, and a mesh adaptation technique based on simple mesh deformation has been also included.

FUNCTIONAL DESCRIPTION: SLOWS is a C-platform allowing the simulation of free surface shallow water flows with friction. It can be used to simulate near shore hydrodynamics, wave transformations processes, etc.

- Participants: Andrea Filippini, Luca Arpaia, Maria Kazolea, Mario Ricchiuto and Nikolaos Pattakos
- Contact: Mario Ricchiuto

6.12. Sparse-PDD

Adaptive sparse polynomial dimensional decomposition for global sensitivity analysis

KEYWORDS: Stochastic models - Uncertainty quantification

SCIENTIFIC DESCRIPTION: The polynomial dimensional decomposition (PDD) is employed in this code for the global sensitivity analysis and uncertainty quantification (UQ) of stochastic systems subject to a moderate to large number of input random variables. Due to the intimate structure between the PDD and the Analysis of Variance (ANOVA) approach, PDD is able to provide a simpler and more direct evaluation of the Sobol' sensitivity indices, when compared to the Polynomial Chaos expansion (PC). Unfortunately, the number of PDD terms grows exponentially with respect to the size of the input random vector, which makes the computational cost of standard methods unaffordable for real engineering applications. In order to address the problem of the curse of dimensionality, this code proposes essentially variance-based adaptive strategies aiming to build a cheap meta-model (i.e. surrogate model) by employing the sparse PDD approach with its coefficients computed by regression. Three levels of adaptivity are carried out in this code: 1) the truncated dimensionality for ANOVA component functions, 2) the active dimension technique especially for second- and higher-order parameter interactions, and 3) the stepwise regression approach designed to retain only the most influential polynomials in the PDD expansion. During this adaptive procedure featuring stepwise regressions, the surrogate model representation keeps containing few terms, so that the cost to resolve repeatedly the linear systems of the least-square regression problem is negligible. The size of the finally obtained sparse PDD representation is much smaller than the one of the full expansion, since only significant terms are eventually retained. Consequently, a much less number of calls to the deterministic model is required to compute the final PDD coefficients.

FUNCTIONAL DESCRIPTION: This code allows an efficient meta-modeling for a complex numerical system featuring a moderate-to-large number of uncertain parameters. This innovative approach involves polynomial representations combined with the Analysis of Variance decomposition, with the objective to quantify the numerical output uncertainty and its sensitivity upon the variability of input parameters.

- Participants: Kunkun Tang and Pietro-Marco Congedo
- Contact: Kunkun Tang

6.13. TUCWave

KEYWORD: Physical simulation

SCIENTIFIC DESCRIPTION: A novel work that advances a step ahead the methodology of the solution of dispersive models. TUCWave uses a high-order well-balanced unstructured finite volume (FV) scheme on triangular meshes for modeling weakly nonlinear and weakly dispersive water waves over varying bathymetries, as described by the 2D depth-integrated extended Boussinesq equations of Nwogu (1993), rewritten in conservation law form. The FV scheme numerically solves the conservative form of the equations following the median dual node-centered approach, for both the advective and dispersive part of the equations. The code developed follows an efficient edge based structured technique. For the advective fluxes, the scheme utilizes an approximate Riemann solver along with a well-balanced topography source term up-winding. Higher order accuracy in space and time is achieved through a MUSCL-type reconstruction technique and through a strong stability preserving explicit Runge-Kutta time stepping. Special attention is given to the accurate numerical treatment of moving wet/dry fronts and boundary conditions. Furthermore, the model is applied to several examples of wave propagation over variable topographies and the computed solutions are compared to experimental data.

FUNCTIONAL DESCRIPTION: Fortran Planform which accounts for the study of near shore processes

- Participants: Argiris Delis, Ioannis Nikolos and Maria Kazolea
- Partner: CNRS
- Contact: Maria Kazolea

CARMEN Project-Team

5. New Software and Platforms

5.1. CEPS

Cardiac ElectroPhysiology Simulation

KEYWORDS: Simulation - Health - Mesh - Cardiac - 3D - Cardiac Electrophysiology

SCIENTIFIC DESCRIPTION: As compared to other existing softwares, CEPS aims at providing a more general framework of integration for new methods or models and a better efficiency in parallel. CEPS is designed to run on massively parallel architectures, and to make use of state-of-the-art and well known computing libraries to achieve realistic and complex heart simulations. CEPS also includes software engineering and validation tools.

FUNCTIONAL DESCRIPTION: CEPS is a numerical simulation tool focused on the modeling of cardiac electrophysiology. The goal of CEPS is to easily allow the development of new numerical methods and new physical models.

- Participants: Mehdi Juhoor, Nejib Zemzemi, Antoine Gerard, Charlie Douanla Lontsi, Pierre-Elliott Bécue, Marc Fuentes and Yves Coudière
- Partners: Université de Bordeaux - Fondation Bordeaux Université - CHU de Bordeaux - Inria
- Contact: Yves Coudière
- URL: <https://gforge.inria.fr/projects/ceps/>

5.2. Platforms

5.2.1. CEMPACK

CEMPACK is a new collection of software that was previously archived in different places. It includes the high-performance simulation code Propag and a suite of software for the creation of geometric models, preparing inputs for Propag, and analysing its outputs. In 2017 the code was collected in an archive on Inria's GitLab platform, and a public website was created for documentation (<http://cempack.gforge.inria.fr>). The main components of CEMPACK are the following.

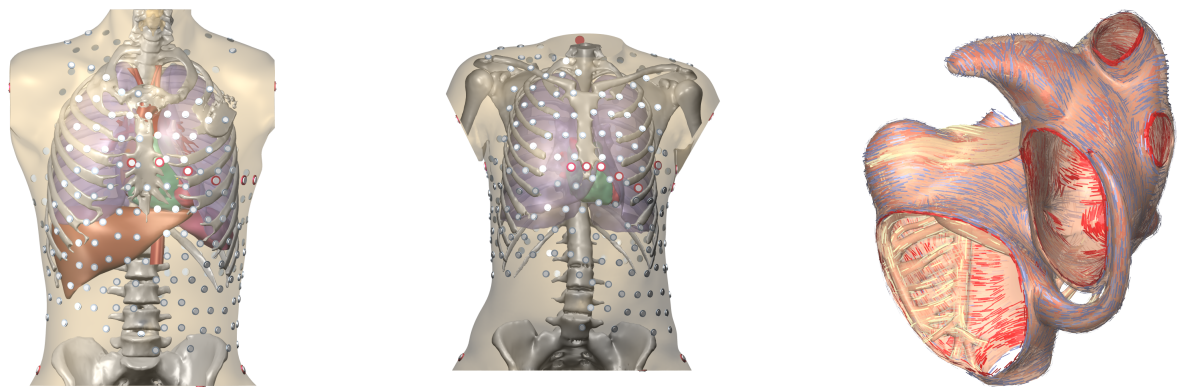
Propag-5.1 Applied modeling studies performed by the Carmen team in collaboration with IHU Liryc and foreign partners [7] [65], [56], [55], [53] rely on high-performance computations on the national supercomputers Irene, Occigen, and Turing. The Propag-5 code is optimized for these systems. It is the result of a decades-long development first at the *Université de Montréal* in Canada, then at Maastricht University in the Netherlands, and finally at the Institute of Computational Science of the *Università della Svizzera italiana* in Lugano, Switzerland. Since 2016 most of the development on Propag has been done by M. Potse at the Carmen team [27]. The code scales excellently to large core counts and, as it is controlled completely with command-line flags and configuration files, it can be used by non-programmers. It also features

- a plugin system for membrane models,
- a completely parallel workflow, including the initial anatomy input and mesh partitioning, which allows it to work with meshes of more than 10^9 nodes,
- a flexible output scheme allowing hundreds of different state variables and transient variables to be output to file, when desired, using any spatial and temporal subsampling,
- a configurable, LUSTRE-aware parallel output system in which groups of processes write HDF5/netCDF files, and
- CWEB documentation of the entire code base.

The code has been stable and reliable for several years. It can be considered the workhorse for our HPC work until CEPS takes over.

Gepetto The Gepetto suite, named after a famous model maker, transforms a surface mesh of the heart into a set of (semi-)structured meshes for use by the Propag software or others. It creates the different fiber orientations in the model, including the transmurally rotating ventricular fibers and the various bundle structures in the atria (figure 2), and creates layers with possibly different electrophysiological properties across the wall. A practically important function is that it automatically builds the matching heart and torso meshes that Propag uses to simulate potentials in the torso (at a resolution of 1 mm) after projecting simulation results from the heart model (at 0.1 to 0.2 mm) on the coarser torso mesh [64]. Like Propag, the Gepetto software results from a long-term development that started in Montreal, Canada, around 2002. The code for atrial fiber structure was developed by our team.

Blender plugins Blender (<https://www.blender.org>) is a free software package for the production of 3-D models, renderings, and animations, comparable to commercial software such as Cinema4D. CEMPACK includes a set of plugins for Blender that facilitate the production of anatomical models and the visualization of measured and simulated data. It uses the MMG remeshing library, which is developed by the CARDAMOM team at Inria Bordeaux.



A **B** **C**
 Figure 2. **A and B:** Complete heart-torso geometries created with CEMPACK tools. **C:** Bundle structures and different layers of fiber orientation created by the Gepetto software.

5.2.2. MUSIC

MUSIC is a multimodal platform for cardiac imaging developed by the imaging team at IHU LIRYC in collaboration with the Inria team Asclepios (<https://bil.inria.fr/fr/software/view/1885/tab>). It is based on the medInria software also developed by the Asclepios team. MUSIC is a cross-platform software for segmentation of medical imaging data, meshing, and ultimately also visualization of functional imaging data and model results.

Several members of the Carmen team use MUSIC for their work, and the team contributes to the software through the IDAM project.

CQFD Project-Team

5. New Software and Platforms

5.1. biips

Bayesian Inference with Interacting Particle Systems

FUNCTIONAL DESCRIPTION: Biips is a software platform for automatic Bayesian inference with interacting particle systems. Biips allows users to define their statistical model in the probabilistic programming BUGS language, as well as to add custom functions or samplers within this language. Then it runs sequential Monte Carlo based algorithms (particle filters, particle independent Metropolis-Hastings, particle marginal Metropolis-Hastings) in a black-box manner so that to approximate the posterior distribution of interest as well as the marginal likelihood. The software is developed in C++ with interfaces with the softwares R, Matlab and Octave.

- Participants: Adrien Todeschini and François Caron
- Contact: Adrien Todeschini
- URL: <http://biips.gforge.inria.fr>

5.2. PCAmixdata

KEYWORD: Statistic analysis

FUNCTIONAL DESCRIPTION: Mixed data type arise when observations are described by a mixture of numerical and categorical variables. The R package PCAmixdata extends standard multivariate analysis methods to incorporate this type of data. The key techniques included in the package are PCAmix (PCA of a mixture of numerical and categorical variables), PCArot (rotation in PCAmix) and MFAmix (multiple factor analysis with mixed data within a dataset). The MFAmix procedure handles a mixture of numerical and categorical variables within a group - something which was not possible in the standard MFA procedure. We also included techniques to project new observations onto the principal components of the three methods in the new version of the package.

- Contact: Marie Chavent
- URL: <https://cran.r-project.org/web/packages/PCAmixdata/index.html>

5.3. QuantifQuantile

KEYWORD: Regression

FUNCTIONAL DESCRIPTION: QuantifQuantile is an R package that allows to perform quantization-based quantile regression. The different functions of the package allow the user to construct an optimal grid of N quantizers and to estimate conditional quantiles. This estimation requires a data driven selection of the size N of the grid that is implemented in the functions. Illustration of the selection of N is available, and graphical output of the resulting estimated curves or surfaces (depending on the dimension of the covariate) is directly provided via the plot function.

- Contact: Jérôme Saracco
- URL: <https://cran.r-project.org/web/packages/QuantifQuantile/index.html>

FLOWERS Project-Team

6. New Software and Platforms

6.1. 3rd hand infrastructure

KEYWORDS: Interaction - Robotics - Infrastructure software - Framework - Robot Operating System (ROS)

FUNCTIONAL DESCRIPTION: The infrastructure is predicate-based to handle relational actions and covers perception (scene description generation, human actions recognition), decision making (teleoperated, scripted or learning from demonstrations), interaction with end users (GUI, voice, gestures) and parallel executions of robotic actions (hold, pick, grasp, bring, ...).

- Contact: Yoan Mollard
- URL: https://github.com/3rdHand-project/thr_infrastructure

6.2. Aversive++

FUNCTIONAL DESCRIPTION: Aversive++ is a C++ library that eases micro-controller programming. Its aim is to provide an interface simple enough to be able to create complex applications, and optimized enough to enable small micro-controllers to execute these applications. The other aspect of this library is to be multiplatform. Indeed, it is designed to provide the same API for a simulator (named SASIAE) and for AVR-based and ARM-based micro-controllers.

- Contact: Loïc Dauphin
- URL: <https://github.com/AversivePlusPlus>

6.3. DMP-BBO

Black-Box Optimization for Dynamic Movement Primitives

KEYWORD: -

FUNCTIONAL DESCRIPTION: The DMP-BBO Matlab library is a direct consequence of the insight that black-box optimization outperforms reinforcement learning when using policies represented as Dynamic Movement Primitives. It implements several variants of the PIBB algorithm for direct policy search. The dmp-bbo C++ library has been extended to include the “unified model for regression”. The implementation of several of the function approximators have been made real-time compatible.

- Participant: Freek Stulp
- Partner: ENSTA
- Contact: Freek Stulp
- URL: <https://github.com/stulp/dmpbbo>

6.4. Explauto

an autonomous exploration library

KEYWORD: Exploration

SCIENTIFIC DESCRIPTION: An important challenge in developmental robotics is how robots can be intrinsically motivated to learn efficiently parametrized policies to solve parametrized multi-task reinforcement learning problems, i.e. learn the mappings between the actions and the problem they solve, or sensory effects they produce. This can be a robot learning how arm movements make physical objects move, or how movements of a virtual vocal tract modulates vocalization sounds. The way the robot will collect its own sensorimotor experience has a strong impact on learning efficiency because for most robotic systems the involved spaces are high dimensional, the mapping between them is non-linear and redundant, and there is limited time allowed for learning. If robots explore the world in an unorganized manner, e.g. randomly, learning algorithms will be often ineffective because very sparse data points will be collected. Data are precious due to the high dimensionality and the limited time, whereas data are not equally useful due to non-linearity and redundancy. This is why learning has to be guided using efficient exploration strategies, allowing the robot to actively drive its own interaction with the environment in order to gather maximally informative data to optimize the parametrized policies. In the recent year, work in developmental learning has explored various families of algorithmic principles which allow the efficient guiding of learning and exploration.

Explauto is a framework developed to study, model and simulate curiosity-driven learning and exploration in real and simulated robotic agents. Explauto's scientific roots trace back from Intelligent Adaptive Curiosity algorithmic architecture [122], which has been extended to a more general family of autonomous exploration architectures by [1] and recently expressed as a compact and unified formalism [113]. The library is detailed in [114]. In Explauto, interest models are implementing the strategies of active selection of particular problems / goals in a parametrized multi-task reinforcement learning setup to efficiently learn parametrized policies. The agent can have different available strategies, parametrized problems, models, sources of information, or learning mechanisms (for instance imitate by mimicking vs by emulation, or asking help to one teacher or to another), and chooses between them in order to optimize learning (a process called strategic learning [118]). Given a set of parametrized problems, a particular exploration strategy is to randomly draw goals/ RL problems to solve in the motor or problem space. More efficient strategies are based on the active choice of learning experiments that maximize learning progress using bandit algorithms, e.g. maximizing improvement of predictions or of competences to solve RL problems [122]. This automatically drives the system to explore and learn first easy skills, and then explore skills of progressively increasing complexity. Both random and learning progress strategies can act either on the motor or on the problem space, resulting in motor babbling or goal babbling strategies.

- Motor babbling consists in sampling commands in the motor space according to a given strategy (random or learning progress), predicting the expected effect, executing the command through the environment and observing the actual effect. Both the parametrized policies and interest models are finally updated according to this experience.
- Goal babbling consists in sampling goals in the problem space and to use the current policies to infer a motor action supposed to solve the problem (inverse prediction). The robot/agent then executes the command through the environment and observes the actual effect. Both the parametrized policies and interest models are finally updated according to this experience. It has been shown that this second strategy allows a progressive solving of problems much more uniformly in the problem space than with a motor babbling strategy, where the agent samples directly in the motor space [1].

FUNCTIONAL DESCRIPTION: This library provides high-level API for an easy definition of:

- Real and simulated robotic setups (Environment level),
- Incremental learning of parametrized policies (Sensorimotor level),
- Active selection of parametrized RL problems (Interest level).

The library comes with several built-in environments. Two of them corresponds to simulated environments: a multi-DoF arm acting on a 2D plan, and an under-actuated torque-controlled pendulum. The third one allows to control real robots based on Dynamixel actuators using the Pypot library. Learning parametrized policies involves machine learning algorithms, which are typically regression algorithms to learn forward models,

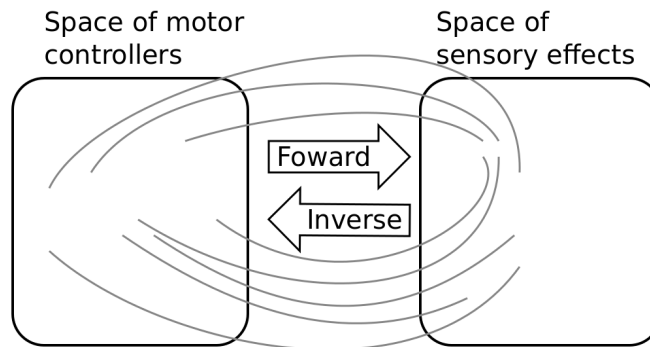


Figure 1. Complex parametrized policies involve high dimensional action and effect spaces. For the sake of visualization, the motor M and sensory S spaces are only 2D each in this example. The relationship between M and S is non-linear, dividing the sensorimotor space into regions of unequal stability: small regions of S can be reached very precisely by large regions of M , or large regions in S can be very sensitive to variations in M : s as well as a non-linear and redundant relationship. This non-linearity can imply redundancy, where the same sensory effect can be attained using distinct regions in M .

from motor controllers to sensory effects, and optimization algorithms to learn inverse models, from sensory effects, or problems, to the motor programs allowing to reach them. We call these sensorimotor learning algorithms sensorimotor models. The library comes with several built-in sensorimotor models: simple nearest-neighbor look-up, non-parametric models combining classical regressions and optimization algorithms, online mixtures of Gaussians, and discrete Lidstone distributions. Explauto sensorimotor models are online learning algorithms, i.e. they are trained iteratively during the interaction of the robot in the environment in which it evolves. Explauto provides also a unified interface to define exploration strategies using the InterestModel class. The library comes with two built-in interest models: random sampling as well as sampling maximizing the learning progress in forward or inverse predictions.

Explauto environments now handle actions depending on a current context, as for instance in an environment where a robotic arm is trying to catch a ball: the arm trajectories will depend on the current position of the ball (context). Also, if the dynamic of the environment is changing over time, a new sensorimotor model (Non-Stationary Nearest Neighbor) is able to cope with those changes by taking more into account recent experiences. Those new features are explained in Jupyter notebooks.

This library has been used in many experiments including:

- the control of a 2D simulated arm,
- the exploration of the inverse kinematics of a poppy humanoid (both on the real robot and on the simulated version),
- acoustic model of a vocal tract.

Explauto is cross-platform and has been tested on Linux, Windows and Mac OS. It has been released under the GPLv3 license.

- Contact: Sébastien Forestier
- URL: <https://github.com/flowersteam/explauto>

6.5. HiPi Board

FUNCTIONAL DESCRIPTION: Hipi is a board to control robots on Raspberry Pi. It is an extension of the Pixl board with the following features:

- A DC/DC power converter from 12V (motor) to 5V (Raspberry Pi) at 3A.
- A stereo audio amplifier 3W.
- A MPU9250 central motion unit .
- A RS232 and a RS485 bus connected to the Raspberry Pi by SPI for driving MX and RX Dynamixel motor series.

This board will be integrated soon in the new head of the Poppy Humanoid and Poppy Torso.

Using the Raspberry Pi for every Poppy robots will simplify the hardware complexity (we maintain 4 types of embedded boards, with different Linux kernel and configurations) and improve the usage and installation of new robots.

- Contact: Theo Segonds
- URL: <https://forum.poppy-project.org/t/poppy-1-1-hipi/2137>

6.6. IKPy

Inverse Kinematics Python Library

FUNCTIONAL DESCRIPTION: IKPy is a Python Inverse Kinematics library, designed to be simple to use and extend. It provides Forward and Inverse kinematics functionality, bundled with helper tools such as 3D plotting of the kinematics chains. Being written entirely in Python, IKPy is lightweight and is based on numpy and scipy for fast optimization. IKPy is compatible with many robots, by automatically parsing URDF files. It also supports other (such as DH-parameters) and custom representations. Moreover, it provides a framework to easily implement new Inverse Kinematics strategies. Originally developed for the Poppy project, it can also be used as a standalone library.

- Contact: Pierre Manceron
- URL: <https://github.com/Phylliade/ikpy>

6.7. KERAS-QR

KERAS with Quick Reset

KEYWORDS: Library - Deep learning

- Participant: Florian Golemo
- Contact: Florian Golemo
- URL: <https://github.com/fgolemo/keras>

6.8. KidBreath

FUNCTIONAL DESCRIPTION: KidBreath is a web responsive application composed by several interactive contents linked to asthma and displayed to different forms: learning activities with quiz, short games and videos. There are profil creation and personalization, and a part which describes historic and scoring of learning activities, to see evolution of Kidreath use. To test Kidlearn algorithm, it is iadapted and integrated on this platform. Development in PHP, HTML-5, CSS, MySQL, JQuery, Javascript. Hosting in APACHE, LINUX, PHP 5.5, MySQL, OVH.

- Partner: ItWell SAS
- Contact: Alexandra Delmas
- URL: <http://www.kidbreath.fr>

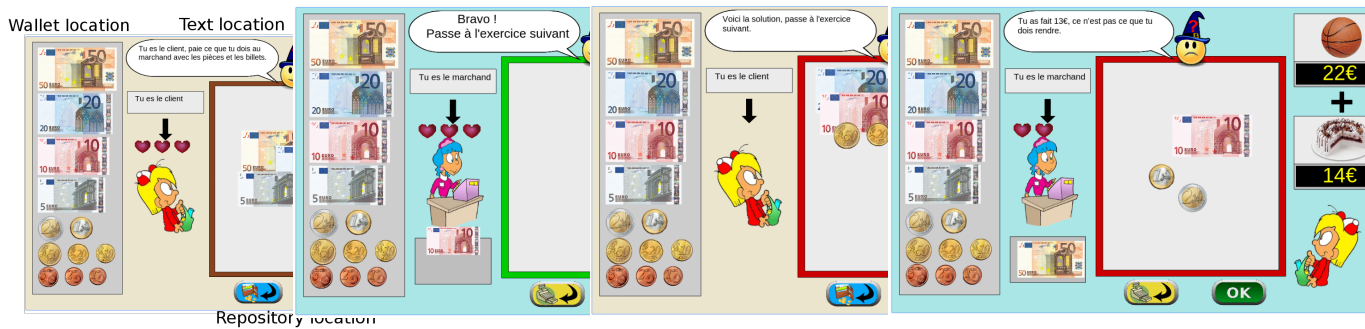


Figure 2. Four principal regions are defined in the graphical interface. The first is the wallet location where users can pick and drag the money items and drop them on the repository location to compose the correct price. The object and the price are present in the object location. Four different types of exercises exist: *M* : customer/one object, *R* : merchant/one object, *MM* : customer/two objects, *RM* : merchant/two objects.

6.9. Kidlearn: money game application

FUNCTIONAL DESCRIPTION: The game is instantiated in a browser environment where students are proposed exercises in the form of money/token games (see Figure 2). For an exercise type, one object is presented with a given tagged price and the learner has to choose which combination of bank notes, coins or abstract tokens need to be taken from the wallet to buy the object, with various constraints depending on exercises parameters. The games have been developed using web technologies, HTML5, javascript and Django.

- Contact: Benjamin Clement
- URL: <https://flowers.inria.fr/research/kidlearn/>

6.10. Kidlearn: script for Kidbreath use

FUNCTIONAL DESCRIPTION: A new way to test Kidlearn algorithms is to use them on Kidbreath Platform. The Kidbreath Platform use apache/PHP server, so to facilitate the integration of our algorithm, a python script have been made to allow PHP code to use easily the python library already made which include our algorithms.

Github link to explanation about it : <https://github.com/flowersteam/kidlearn/>.

- Contact: Benjamin Clement
- URL: <https://github.com/flowersteam/kidlearn/>

6.11. KidLearn

KEYWORD: Automatic Learning

FUNCTIONAL DESCRIPTION: KidLearn is a software which adaptively personalize sequences of learning activities to the particularities of each individual student. It aims at proposing to the student the right activity at the right time, maximizing concurrently his learning progress and its motivation.

- Participants: Benjamin Clement, Didier Roy, Manuel Lopes and Pierre Yves Oudeyer
- Contact: Pierre-Yves Oudeyer
- URL: <https://flowers.inria.fr/research/kidlearn/>

6.12. Kinect 2 Server

Kinect 2 server

KEYWORDS: Depth Perception - Speech recognition - Gesture recognition - Kinect

FUNCTIONAL DESCRIPTION: The server written in C# uses the Kinect SDK v2 to get the RGBD raw image, skeleton tracking information, recognized speech. It also uses the text-to-speech from Microsoft. Then it streams JSON data over the network using the Publisher/Subscriber pattern from the ZeroMQ network library. A Linux client has been written in Python but it can be written in any other language that is compatible with ZeroMQ. Features are controllable through a Graphical User Interface on Windows, or through the code from any Linux/Windows client. The clients can for instance enable features (speech recognition on, skeleton tracking off, ...) and parameters (set new speech to recognize, change language, ...) from remote.

- Contact: Yoan Mollard
- URL: https://github.com/baxter-flowers/kinect_2_server/

6.13. Multimodal

FUNCTIONAL DESCRIPTION: The python code provides a minimum set of tools and associated libraries to reproduce the experiments in [98], together with the choreography datasets. The code is primarily intended for reproduction of the multimodal learning experiment mentioned above. It has already been reused in several experimentations by other member of the team and is expected to play an important role in further collaborations. It is also expected that the public availability of the code encourages further experimentation by other scientists with data coming from other domains, thus increasing both the impact of the aforementioned publication and the knowledge on the algorithm behaviors.

- Participant: Olivier Mangin
- Contact: Olivier Mangin
- URL: <https://github.com/omangin/multimodal>

6.14. OptiTrack

FUNCTIONAL DESCRIPTION: This python library allows you to connect to an OptiTrack from NaturalPoint. This camera permits the tracking of 3D markers efficiently and robustly. With this library, you can connect to the Motive software used by the OptiTrack and retrieve the 3D position and orientation of all your tracked markers directly from python.

- Participant: Pierre Rouanet
- Contact: Pierre Rouanet
- URL: <http://www.optitrack.com/>

6.15. Pixl Board

FUNCTIONAL DESCRIPTION: Pixl is a tiny board used to create low cost robots based on Raspberry Pi board and Dynamixel XL-320 motors. This board has 2 main features:

- The power part, allowing the user to plug a 7.5V AC/DC converter or a battery directly into the Pixl. This power is distributed to all XL320 motors and is converted to 5V for the Raspberry Pi board.
- The communication part, which converts full duplex to half duplex and vice-versa. The half duplex part switch between RX and TX automatically. Another connector allows the user to connect his XL320 network.

The board is used in the Poppy Ergo Jr robot.

- Contact: Theo Segonds
- URL: <https://github.com/poppy-project/pixl>

6.16. Poppy

FUNCTIONAL DESCRIPTION: The Poppy Project team develops open-source 3D printed robots platforms based on robust, flexible, easy-to-use and reproduce hardware and software. In particular, the use of 3D printing and rapid prototyping technologies is a central aspect of this project, and makes it easy and fast not only to reproduce the platform, but also to explore morphological variants. Poppy targets three domains of use: science, education and art.

In the Poppy project we are working on the Poppy System which is a new modular and open-source robotic architecture. It is designed to help people create and build custom robots. It permits, in a similar approach as Lego, building robots or smart objects using standardized elements.

Poppy System is a unified system in which essential robotic components (actuators, sensors...) are independent modules connected with other modules through standardized interfaces:

- Unified mechanical interfaces, simplifying the assembly process and the design of 3D printable parts.
- Unified communication between elements using the same connector and bus for each module.
- Unified software, making it easy to program each module independently.

Our ambition is to create an ecosystem around this system so communities can develop custom modules, following the Poppy System standards, which can be compatible with all other Poppy robots.

- Participants: Jonathan Grizou, Matthieu Lapeyre, Pierre Rouanet and Pierre-Yves Oudeyer
- Contact: Pierre-Yves Oudeyer
- URL: <https://www.poppy-project.org/>

6.17. Poppy Ergo Jr

FUNCTIONAL DESCRIPTION: Poppy Ergo Jr is an open hardware robot developed by the Poppy Project to explore the use of robots in classrooms for learning robotic and computer science.

It is available as a 6 or 4 degrees of freedom arm designed to be both expressive and low-cost. This is achieved by the use of FDM 3D printing and low cost Robotis XL-320 actuators. A Raspberry Pi camera is attached to the robot so it can detect object, faces or QR codes.

The Ergo Jr is controlled by the Pypot library and runs on a Raspberry pi 2 or 3 board. Communication between the Raspberry Pi and the actuators is made possible by the Pixl board we have designed.

The Poppy Ergo Jr robot has several 3D printed tools extending its capabilities. There are currently the lampshade, the gripper and a pen holder.

With the release of a new Raspberry Pi board early 2016, the Poppy Ergo Jr disk image was updated to support Raspberry Pi 2 and 3 boards. The disk image can be used seamlessly with a board or the other.

- Contact: Theo Segonds
- URL: <https://github.com/poppy-project/poppy-ergo-jr>

6.18. Poppy Ergo Jr Installer

FUNCTIONAL DESCRIPTION: An alternative way to install the Ergo Jr robot software is made available using containers.

Users can own their own operating system installation, then add the Ergo Jr required software in a sandboxed environment. This results in a non-intrusive installation on the host system.

Docker containers implementation were used, and image is hosted at Docker Hub.

- Contact: Damien Caselli
- URL: <https://hub.docker.com/r/poppycommunity/ergo-jr/>

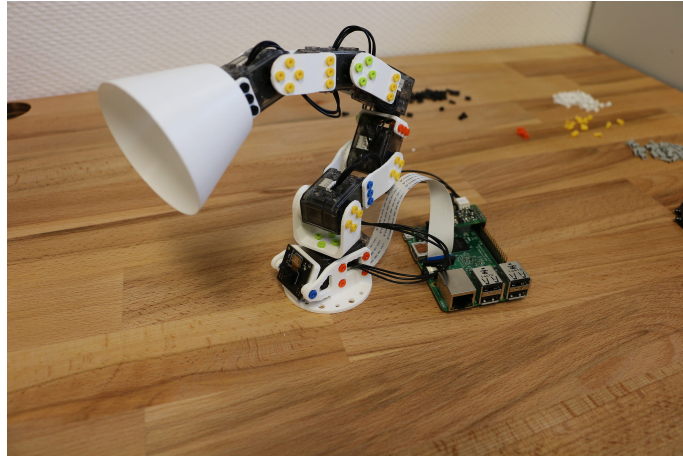


Figure 3. Poppy Ergo Jr, 6-DoFs arm robot for education

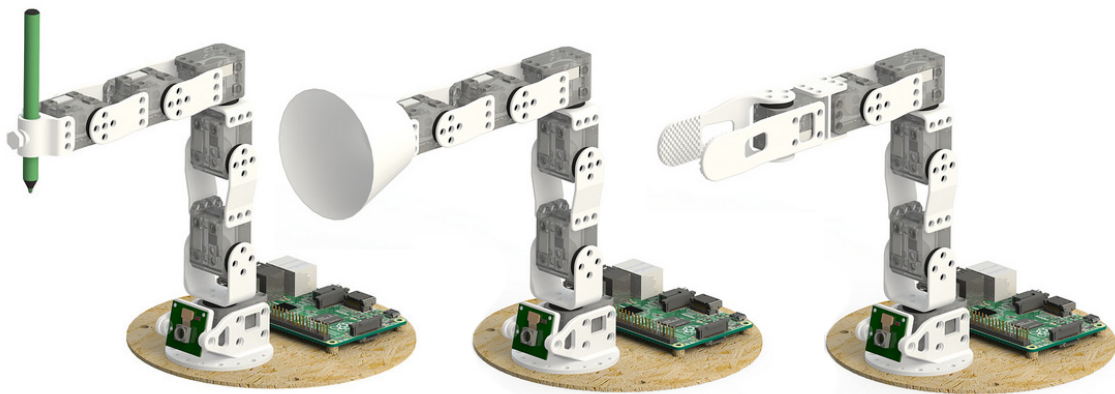


Figure 4. The available Ergo Jr tools: a pen holder, a lampshade and a gripper

6.19. Poppy Ergo Jr Simulator

FUNCTIONAL DESCRIPTION: Poppy Project, through Poppy Education, wants users to get used to robotics, even without owning a physical robot.

For that purpose, Poppy Project team created a dummy robot in Pypot that is meant to be used in conjunction with a consumer application. We choose to develop a web hosted application using a 3D engine (Threejs) to render the robot.

Our ambition is to have a completely standalone simulated robot with physics. Some prototypes were created to benchmark possible solutions.

- Contact: Damien Caselli
- URL: <https://github.com/poppy-project/poppy-simu>

6.20. ProMP

Probabilistic Movement Primitives

KEYWORDS: Interaction - Robotics - Probability - Motion model - Robot Operating System (ROS)

FUNCTIONAL DESCRIPTION: Joint-space primitives with a task-space constraint: The primitives are stored in joint-space but demonstrations are provided both in joint space and task space, context. Thanks to this context, task-space goals can be requested to these joint-space primitives. The benefit is that requesting a new task-space goal does not require to call an IK method which would return demonstrations-agnostic joint configurations.

Vocal interactive learning and clustering: This work includes an interactive learning aspect which allows to automatically cluster motor primitives based on the standard deviation of their demonstrations. A new primitive is created automatically if the provided demonstration is out of 2 standard deviation of the existing primitives, otherwise the demonstration is distributed to an existing one.

- Contact: Yoan Mollard
- URL: <https://github.com/baxter-flowers/promplib>

6.21. PyPot

SCIENTIFIC DESCRIPTION: Pypot is a framework developed to make it easy and fast to control custom robots based on Dynamixel motors. This framework provides different levels of abstraction corresponding to different types of use. Pypot can be used to:

- control Robotis motors through a USB2serial device,
- define the structure of a custom robot and control it through high-level commands,
- define primitives and easily combine them to create complex behavior.

Pypot is part of the Poppy project. It is the core library used by the Poppy robots. This abstraction layer allows to seamlessly switch from a given Poppy robot to another. It also provides a common set of tools, such as forward and inverse kinematics, simple computer vision, recording and replaying moves, or easy access to the autonomous exploration library Explauto.

To extend pypot application domains and connection to outside world, it also provides an HTTP API. On top of providing an easy way to connect to smart sensors or connected devices, it is notably used to connect to Snap!, a variant of the well-known Scratch visual programming language.

FUNCTIONAL DESCRIPTION: Pypot is entirely written in Python to allow for fast development, easy deployment and quick scripting by non-expert developers. It can also benefit from the scientific and machine learning libraries existing in Python. The serial communication is handled through the standard library and offers high performance (10ms sensorimotor loop) for common Poppy uses. It is cross-platform and has been tested on Linux, Windows and Mac OS.

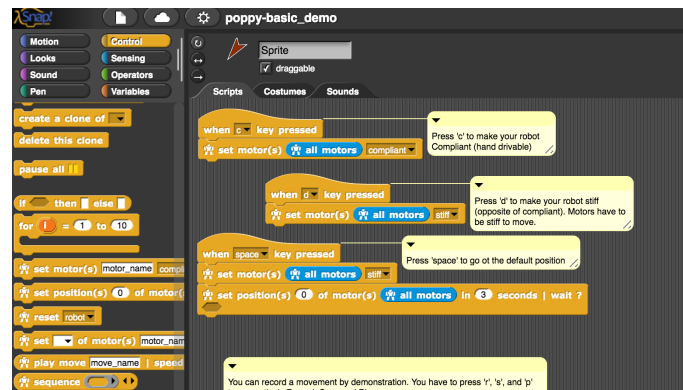


Figure 5. Example of using pypot to program a robot to reproduce a drawn shape

Pypot is also compatible with the V-REP simulator. This allows the transparent switch from a real robot to its simulated equivalent with a single code base.

Finally, it has been developed to be easily and quickly extended for other types of motors and sensors.

It works with Python 2.7 or Python 3.3 or later, and has also been adapted to the Raspberry Pi board.

Pypot has been connected to Snap!, a variant of the famous Scratch visual language, developed to teach computer science to children. It is based on a drag-and-drop blocks interface to write scripts by assembling those blocks.

Thanks to the Snap! HTTP block, a connection can be made to pypot allowing users to directly control robots through their visual interfaces. A set of dedicated Snap! blocks have been designed, such as *set motor position* or *get motor temperature*. Thanks to the Snap! HTTP block, users can control robots through this visual interfaces connecting to Pypot. A set of dedicated Snap! blocks has been designed, such as *set motor position* or *get motor temperature*.

Snap! is also used as a tool to program the robot by demonstration. Using the *record* and *play* blocks, users can easily trigger kinesthetic recording of the whole robot or only a specific subpart, such as an arm. These records can then be played or "mixed" - either played in sequence or simultaneously - with other recordings to compose complex choreographies. The moves are encoded as a model of mixture of gaussians (GMM) which allows the definition of clean mathematical operators for combining them.

This recording tool has been developed and used in collaboration with artists who show interest in the concept of robotic moves.

- Participants: Damien Caselli, Matthieu Lapeyre, Pierre Rouanet, Steve Nguyen and Theo Segonds
- Contact: Theo Segonds
- URL: <https://github.com/poppy-project/pypot>

6.22. PyQMC

Python library for Quasi-Metric Control

FUNCTIONAL DESCRIPTION: PyQMC is a python library implementing the control method described in <http://dx.doi.org/10.1371/journal.pone.0083411> It allows to solve discrete markovian decision processes by computing a Quasi-Metric on the state space. This model based method has the advantage to be goal independant and thus can produce a policy for any goal with relatively few recomputation. New addition to this method is the possibility of online learning of the transition model and the Quasi-Metric.



Figure 6. Using Snap! to program a robot by demonstration and create complex choreographies

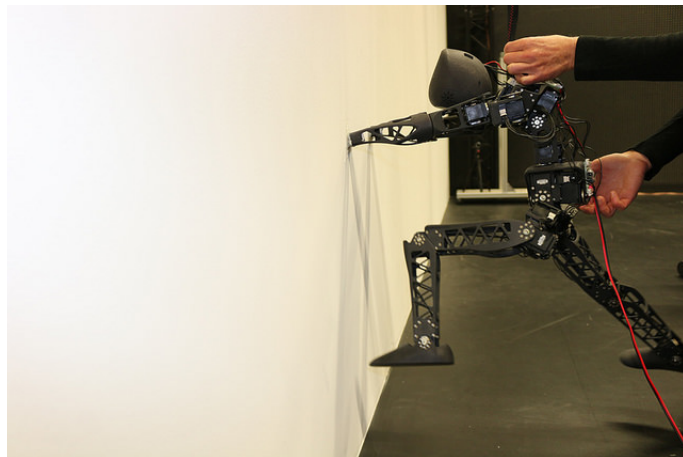


Figure 7. Artistic project exploring the concept of robotic move.

- Participant: Steve Nguyen
- Contact: Steve Nguyen
- URL: <https://github.com/SteveNguyen/pyqmc>

6.23. ROS Optitrack Publisher

KEYWORDS: Target tracking - Robot Operating System (ROS)

FUNCTIONAL DESCRIPTION: This package allows to publish optitrack markers declared as rigid bodies as TF transforms. Data is gathered through the embedded VRPN server of Motive/Arena. Only rigid bodies are requested to the server, thus single points in 2D/3D are ignored. VRPN server can be enable in View > Data streaming in Motive.

- Contact: Yoan Mollard
- URL: https://github.com/baxter-flowers/optitrack_publisher

6.24. ThifloNet

KEYWORDS: Deep learning - Policy Learning

SCIENTIFIC DESCRIPTION: We created a software architecture that combines a state-of-the-art computer vision system with a policy learning framework. This system is able to perceive a visual scene, given by a still image, extract facts (“predicates”), and propose an optimal action to achieve a given goal. Both systems are chained into a pipeline that is trained by presenting images and demonstrating an optimal action. By providing this information, both the predicate recognition model and the policy learning model are updated.

Our architecture is based on the recent works of Lerer, A., Gross, S., & Fergus, R., 2016 ("Learning Physical Intuition of Block Towers by Example"). They created a large network able to identify physical properties of stacked blocks. Analogously our vision system utilizes the same network layout (without the image prediction auxiliary output), with an added output layer for predicates, based on the expected number and arity of predicates. The vision subsystem is not trained with a common cross-entropy or MSE loss function, but instead receives its loss form the policy learning subsystem. The policy learning module calculates the loss as optimal combination of predicates for the given expert action.

By using this combination of systems, the architecture as a whole requires significantly fewer data samples than other systems (which exclusively utilize neural networks). This makes the approach more feasible to real-life application with actual live demonstration.

FUNCTIONAL DESCRIPTION: The neural network consists of ResNet-50 (the currently best-performing computer vision system), with 50 layers, 2 layers for converting the output of ResNet to predicates and a varying amount of output neurons, corresponding to the estimated number of n-arity predicates. The network was pretrained on the ImageNet dataset. The policy learning module incorporates the ACE tree learning tool and a wrapper in Prolog.

Our example domain consists of 2-4 cubes colored in red, blue, green, and yellow and randomly stacked on top of each other in a virtual 3D environment. The dataset used for training and testing contains a total of 30000 elements, each with an image of the scene, the correct predicates, a list of blocks that are present and the corresponding expert action, that would lead to stacking the blocks to a tower.

- Participants: Florian Golemo, Manuel Lopes and Thibaut Munzer
- Contact: Florian Golemo

6.25. S-RL Toolbox

Reinforcement Learning (RL) and State Representation Learning (SRL) for Robotics

KEYWORDS: Machine learning - Robotics

FUNCTIONAL DESCRIPTION: This repository was made to evaluate State Representation Learning methods using Reinforcement Learning. It integrates (automatic logging, plotting, saving, loading of trained agent) various RL algorithms (PPO, A2C, ARS, ACKTR, DDPG, DQN, ACER, CMA-ES, SAC, TRPO) along with different SRL methods (see SRL Repo) in an efficient way (1 Million steps in 1 Hour with 8-core cpu and 1 Titan X GPU).

- Partner: ENSTA
- Contact: David Filliat
- URL: <https://github.com/araffin/robotics-rl-srl>

6.26. Sets

KEYWORD: Data structures

FUNCTIONAL DESCRIPTION: The sets library allow to manipulate and operate on sets.

Those can be simple sets: + Empty: + Singleton: 'a' + Finite: 'a', 'b' + Integer subset: $[1, 10]$ + Reals subset: $[1, \text{inf}]$ Or, they can be cartesian product of sets: + 'a', 'b' x $[0, 10]$ x $]-\text{inf}, \text{inf}[$ Or, they can be incomplete unions of sets: + 'a', 'b' x $[0, 5]$ U 'c' x $]-[0, 10]$

In particular, every set is hashable. This operation is non-trivial in the case of an incomplete union (equivalent to an orthogonal polyhedron). An extreme vertices representations, corresponding to the state-of-the-art, is used to implement it.

Various operations are available: + Product (Cartesian) + Measure + Partition + Belonging test + Subset test (Proper) + Equality test + Union + Intersection + Exclusion

- Contact: Alexandre Pere

6.27. Deep-Explauto

KEYWORDS: Deep learning - Unsupervised learning - Learning - Experimentation

FUNCTIONAL DESCRIPTION: Until recently, curiosity driven exploration algorithms were based on classic learning algorithms, unable to handle large dimensional problems (see explauto). Recent advances in the field of deep learning offer new algorithms able to handle such situations.

Deep explauto is an experimental library, containing reference implementations of curiosity driven exploration algorithms. Given the experimental aspect of exploration algorithms, and the low maturity of the libraries and algorithms using deep learning, proposing black-box implementations of those algorithms, enabling a blind use of those, seem unrealistic.

Nevertheless, in order to quickly launch new experiments, this library offers an set of objects, functions and examples, allowing to kickstart new experiments.

- Contact: Alexandre Pere

6.28. Orchestra

KEYWORD: Experimental mechanics

FUNCTIONAL DESCRIPTION: Orchestra is a set of tools meant to help in performing experimental campaigns in computer science. It provides you with simple tools to:

+ Organize a manual experimental workflow, leveraging git and lfs through a simple interface. + Collaborate with other peoples on a single experimental campaign. + Execute pieces of code on remote hosts such as clusters or clouds, in one line. + Automate the execution of batches of experiments and the presentation of the results through a clean web ui.

A lot of advanced tools exists on the net to handle similar situations. Most of them target very complicated workflows, e.g. DAGs of tasks. Those tools are very powerful but lack the simplicity needed by newcomers. Here, we propose a limited but very simple tool to handle one of the most common situation of experimental campaigns: the repeated execution of an experiment on variations of parameters.

In particular, we include three tools: + `expegit`: a tool to organize your experimental campaign results in a git repository using `git-lfs` (large file storage). + `runaway`: a tool to execute code on distant hosts parameterized with easy to use file templates. + `orchestra`: a tool to automate the use of the two previous tools on large campaigns.

- Contact: Alexandre Pere

GEOSTAT Project-Team

6. New Software and Platforms

6.1. Fluex

KEYWORDS: Signal - Signal processing

SCIENTIFIC DESCRIPTION: Fluex is a package consisting of the Microcanonical Multiscale Formalism for 1D, 2D 3D and 3D+t general signals.

FUNCTIONAL DESCRIPTION: Fluex is a C++ library developed under Gforge. Fluex is a library in nonlinear signal processing. Fluex is able to analyze turbulent and natural complex signals, Fluex is able to determine low level features in these signals that cannot be determined using standard linear techniques.

- Participants: Hussein Yahia and Rémi Paties
- Contact: Hussein Yahia
- URL: <http://fluex.gforge.inria.fr/>

6.2. FluidExponents

KEYWORDS: Signal processing - Wavelets - Fractal - Spectral method - Complexity

FUNCTIONAL DESCRIPTION: FluidExponents is a signal processing software dedicated to the analysis of complex signals displaying multiscale properties. It analyzes complex natural signals by use of nonlinear methods. It implements the multifractal formalism and allows various kinds of signal decomposition and reconstruction. One key aspect of the software lies in its ability to evaluate key concepts such as the degree of unpredictability around a point in a signal, and provides different kinds of applications. The software can be used for times series or multidimensional signals.

- Participants: Antonio Turiel and Hussein Yahia
- Contact: Hussein Yahia
- URL: <svn+ssh://fluidexponents@scm.gforge.inria.fr/svn/fluidexponents/FluidExponents>

6.3. classifemo

KEYWORDS: Classification - Audio

FUNCTIONAL DESCRIPTION: Classifies vocal audio signals. Classifemo extracts characteristics from vocal audio signals. These characteristics are extracted from signals of different type: initially these were emotion databases, but it can also process signals recorded from patients with motor speech disorders. The software can train usual classifiers (SVM, random forests, etc) on these databases as well as classify new signals.

- Participants: Khalid Daoudi and Nicolas Brodu
- Contact: Khalid Daoudi
- URL: <https://allgo.inria.fr/app/emotionclassifierprototype>

6.4. superres

Super-Resolution of multi-spectral and multi-resolution images

KEYWORD: Multiscale

SCIENTIFIC DESCRIPTION: This resolution enhancement method is designed for multispectral and multiresolution images, such as these provided by the Sentinel-2 satellites (but not only). Starting from the highest resolution bands, band-dependent information (reflectance) is separated from information that is common to all bands (geometry of scene elements). This model is then applied to unmix low-resolution bands, preserving their reflectance, while propagating band-independent information to preserve the sub-pixel details.

FUNCTIONAL DESCRIPTION: This super-resolution software for multi-spectral images consists of: - A core C++ library, which can be used directly - A Python module interface to this library - A Java JNI interface to the library - An end-user Python script for super-resolving Sentinel-2 images - An end-user plugin for the widely used SNAP software of the ESA.

- Participant: Nicolas Brodu
- Contact: Nicolas Brodu
- URL: <http://nicolas.brodu.net/recherche/superres/index.html>

6.5. EdgeReconstruct

Edge Reconstruction With UPM Manifold

KEYWORDS: 2D - Fractal - Signal processing

FUNCTIONAL DESCRIPTION: EdgeReconstruct is a software that reconstructs a complex signal from the computation of most unpredictable points in the framework of the Microcanonical Multifractal Formalism. The quality of the reconstruction is also evaluated. The software is a companion of a paper published in 2013: <https://hal.inria.fr/hal-00924137>.

- Contact: Suman Kumar Maji
- URL: <https://geostat.bordeaux.inria.fr/index.php/downloads.html>

6.6. ProximalDenoising

KEYWORDS: 2D - Image filter - Filtering - Minimizing overall energy - Noise - Signal processing - Image reconstruction - Image processing

SCIENTIFIC DESCRIPTION: Image filtering is contemplated in the form of a sparse minimization problem in a non-convex setting. Given an input image I , one seeks to compute a denoised output image u such that u is close to I in the L_2 norm. To do so, a minimization term is added which favors sparse gradients for output image u . Imposing sparse gradients lead to a non-convex minimization term: for instance a pseudo-norm L_p with $0 < p < 1$ or a Cauchy or Welsh function. Half-quadratic algorithm is used by adding a new variable in the minimization functional which leads to two sub-problems, the first sub-problem is non-convex and solved by use of proximal operators. The second sub-problem can be written in variational form, and is best solved in Fourier space: it takes the form of a deconvolution operator whose kernel can be approximated by a finite sum of separable filters. This solution method produces excellent computation times even on big images.

FUNCTIONAL DESCRIPTION: Use of proximal and non quadratic minimization. GPU implementation.

RELEASE FUNCTIONAL DESCRIPTION: This software implements H. Badri PhD thesis results.

- Authors: Marie Martin, Chiheb Sakka, Hussein Yahia, Nicolas Brodu, Gabriel Augusto Zebadua Garcia and Khalid Daoudi
- Partner: Innovative Imaging Solutions I2S
- Contact: Hussein Yahia
- URL: https://gitlab.inria.fr/marmarti/i2s_geostat_C

HIEPACS Project-Team

6. New Software and Platforms

6.1. Chameleon

KEYWORDS: Runtime system - Task-based algorithm - Dense linear algebra - HPC - Task scheduling

SCIENTIFIC DESCRIPTION: Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

We expect advances in three directions based first on strong and closed interactions between the runtime and numerical linear algebra communities. This initial activity will then naturally expand to more focused but still joint research in both fields.

1. Fine interaction between linear algebra and runtime systems. On parallel machines, HPC applications need to take care of data movement and consistency, which can be either explicitly managed at the level of the application itself or delegated to a runtime system. We adopt the latter approach in order to better keep up with hardware trends whose complexity is growing exponentially. One major task in this project is to define a proper interface between HPC applications and runtime systems in order to maximize productivity and expressivity. As mentioned in the next section, a widely used approach consists in abstracting the application as a DAG that the runtime system is in charge of scheduling. Scheduling such a DAG over a set of heterogeneous processing units introduces a lot of new challenges, such as predicting accurately the execution time of each type of task over each kind of unit, minimizing data transfers between memory banks, performing data prefetching, etc. Expected advances: In a nutshell, a new runtime system API will be designed to allow applications to provide scheduling hints to the runtime system and to get real-time feedback about the consequences of scheduling decisions.

2. Runtime systems. A runtime environment is an intermediate layer between the system and the application. It provides low-level functionality not provided by the system (such as scheduling or management of the heterogeneity) and high-level features (such as performance portability). In the framework of this proposal, we will work on the scalability of runtime environment. To achieve scalability it is required to avoid all centralization. Here, the main problem is the scheduling of the tasks. In many task-based runtime environments the scheduler is centralized and becomes a bottleneck as soon as too many cores are involved. It is therefore required to distribute the scheduling decision or to compute a data distribution that impose the mapping of task using, for instance the so-called “owner-compute” rule. Expected advances: We will design runtime systems that enable an efficient and scalable use of thousands of distributed multicore nodes enhanced with accelerators.

3. Linear algebra. Because of its central position in HPC and of the well understood structure of its algorithms, dense linear algebra has often pioneered new challenges that HPC had to face. Again, dense linear algebra has been in the vanguard of the new era of petascale computing with the design of new algorithms that can efficiently run on a multicore node with GPU accelerators. These algorithms are called “communication-avoiding” since they have been redesigned to limit the amount of communication between processing units (and between the different levels of memory hierarchy). They are expressed through Direct Acyclic Graphs (DAG) of fine-grained tasks that are dynamically scheduled. Expected advances: First, we plan to investigate the impact of these principles in the case of sparse applications (whose algorithms are slightly more complicated but often rely on dense kernels). Furthermore, both in the dense and sparse cases, the scalability on thousands of nodes is still limited, new numerical approaches need to be found. We will specifically design sparse hybrid direct/iterative methods that represent a promising approach.

Overall end point. The overall goal of the MORSE associate team is to enable advanced numerical algorithms to be executed on a scalable unified runtime system for exploiting the full potential of future exascale machines.

FUNCTIONAL DESCRIPTION: Chameleon is a dense linear algebra software relying on sequential task-based algorithms where sub-tasks of the overall algorithms are submitted to a Runtime system. A Runtime system such as StarPU is able to manage automatically data transfers between not shared memory area (CPUs-GPUs, distributed nodes). This kind of implementation paradigm allows to design high performing linear algebra algorithms on very different type of architecture: laptop, many-core nodes, CPUs-GPUs, multiple nodes. For example, Chameleon is able to perform a Cholesky factorization (double-precision) at 80 TFlop/s on a dense matrix of order 400 000 (e.i. 4 min).

RELEASE FUNCTIONAL DESCRIPTION: Chameleon includes the following features:

- BLAS 3, LAPACK one-sided and LAPACK norms tile algorithms - Support QUARK and StarPU runtime systems and PaRSEC since 2018 - Exploitation of homogeneous and heterogeneous platforms through the use of BLAS/LAPACK CPU kernels and cuBLAS/MAGMA CUDA kernels - Exploitation of clusters of interconnected nodes with distributed memory (using OpenMPI)

- Participants: Cédric Castagnede, Samuel Thibault, Emmanuel Agullo, Florent Pruvost and Mathieu Faverge
- Partners: Innovative Computing Laboratory (ICL) - King Abdulla University of Science and Technology - University of Colorado Denver
- Contact: Emmanuel Agullo
- URL: <https://gitlab.inria.fr/solverstack/chameleon>

6.2. Fabulous

Fast Accurate Block Linear krylOv Solver

KEYWORDS: Numerical algorithm - Block Krylov solver

SCIENTIFIC DESCRIPTION: Versatile and flexible numerical library that implements Block Krylov iterative schemes for the solution of linear systems of equations with multiple right-hand sides

FUNCTIONAL DESCRIPTION: Versatile and flexible numerical library that implements Block Krylov iterative schemes for the solution of linear systems of equations with multiple right-hand sides. The library implements block variants of minimal norm residual variants with partial convergence management and spectral information recycling. The package already implements regular block-GMRES (BGMRES), Inexact Breakdown BGMRES (IB-BMGRES), Inexact Breakdown BGMRES with Deflated Restarting (IB-BGMRES-DR), Block Generalized Conjugate Residual with partial convergence management. The C++ library relies on call-back mechanisms to implement the calculations (matrix-vector, dot-product, ...) that depend on the parallel data distribution selected by the user.

- Participants: Emmanuel Agullo, Luc Giraud and Cyrille Piacibello
- Contact: Luc Giraud
- Publication: [Block GMRES method with inexact breakdowns and deflated restarting](#)
- URL: <https://gitlab.inria.fr/solverstack/fabulous/>

6.3. HIPS

Hierarchical Iterative Parallel Solver

KEYWORDS: Simulation - HPC - Parallel calculation - Hybrid direct iterative method

SCIENTIFIC DESCRIPTION: The key point of the methods implemented in HIPS is to define an ordering and a partition of the unknowns that relies on a form of nested dissection ordering in which cross points in the separators play a special role (Hierarchical Interface Decomposition ordering). The subgraphs obtained by nested dissection correspond to the unknowns that are eliminated using a direct method and the Schur complement system on the remaining of the unknowns (that correspond to the interface between the subgraphs viewed as sub-domains) is solved using an iterative method (GMRES or Conjugate Gradient at the time being). This special ordering and partitioning allows for the use of dense block algorithms both in the direct and iterative part of the solver and provides a high degree of parallelism to these algorithms. The code provides a hybrid method which blends direct and iterative solvers. HIPS exploits the partitioning and multistage ILU techniques to enable a highly parallel scheme where several subdomains can be assigned to the same process. It also provides a scalar preconditioner based on the multistage ILUT factorization.

HIPS can be used as a standalone program that reads a sparse linear system from a file, it also provides an interface to be called from any C, C++ or Fortran code. It handles symmetric, unsymmetric, real or complex matrices. Thus, HIPS is a software library that provides several methods to build an efficient preconditioner in almost all situations.

FUNCTIONAL DESCRIPTION: HIPS (Hierarchical Iterative Parallel Solver) is a scientific library that provides an efficient parallel iterative solver for very large sparse linear systems.

- Participants: Jérémie Gaidamour, Pascal Hénon and Yousef Saad
- Contact: Pierre Ramet
- URL: <https://gitlab.inria.fr/solverstack/hips>

6.4. MAPHYS

Massively Parallel Hybrid Solver

KEYWORD: Parallel hybrid direct/iterative solution of large linear systems

FUNCTIONAL DESCRIPTION: MaPHyS is a software package that implements a parallel linear solver coupling direct and iterative approaches. The underlying idea is to apply to general unstructured linear systems domain decomposition ideas developed for the solution of linear systems arising from PDEs. The interface problem, associated with the so called Schur complement system, is solved using a block preconditioner with overlap between the blocks that is referred to as Algebraic Additive Schwarz. A fully algebraic coarse space is available for symmetric positive definite problems, that insures the numerical scalability of the preconditioner.

The parallel implementation is based on MPI+thread. Maphys relies on state-of-the art sparse and dense direct solvers.

MaPHyS is essentially a preconditioner that can be used to speed-up the convergence of any Krylov subspace method and is coupled with the ones implemented in the Fabulous package.

- Participants: Emmanuel Agullo, Luc Giraud, Matthieu Kuhn, Gilles Marait and Louis Poirel
- Contact: Emmanuel Agullo
- Publications: [Hierarchical hybrid sparse linear solver for multicore platforms - Robust coarse spaces for Abstract Schwarz preconditioners via generalized eigenproblems](#)
- URL: <https://gitlab.inria.fr/solverstack/maphys>

6.5. MetaPart

KEYWORDS: High performance computing - HPC - Parallel computing - Graph algorithmics - Graph - Hypergraph

FUNCTIONAL DESCRIPTION: MetaPart is a framework for graph or hypergraph manipulation that addresses different problems, like partitioning, repartitioning, or co-partitioning, ... MetaPart is made up of several projects, such as StarPart, LibGraph or CoPart. StarPart is the core of the MetaPart framework. It offers a wide variety of graph partitioning methods (Metis, Scotch, Zoltan, Patoh, ParMetis, Kahip, ...), which makes it easy to compare these different methods and to better adjust the parameters of these methods. It is built upon the LibGraph library, that provides basic graph and hypergraph routines. The Copart project is a library used on top of StarPart, that provides co-partitioning algorithms for the load-blancing of parallel coupled simulations.

- Participant: Aurélien Esnard
- Contact: Aurélien Esnard
- URL: <https://gitlab.inria.fr/metapart>

6.6. MPICPL

MPI CouPLing

KEYWORDS: MPI - Coupling software

FUNCTIONAL DESCRIPTION: MPICPL is a software library dedicated to the coupling of parallel legacy codes, that are based on the well-known MPI standard. It proposes a lightweight and comprehensive programming interface that simplifies the coupling of several MPI codes (2, 3 or more). MPICPL facilitates the deployment of these codes thanks to the mpicplrun tool and it interconnects them automatically through standard MPI intercommunicators. Moreover, it generates the universe communicator, that merges the world communicators of all coupled-codes. The coupling infrastructure is described by a simple XML file, that is just loaded by the mpicplrun tool.

- Participant: Aurélien Esnard
- Contact: Aurélien Esnard
- URL: <https://gitlab.inria.fr/esnard/mpicpl>

6.7. OptiDis

KEYWORDS: Dislocation dynamics simulation - Fast multipole method - Large scale - Collision

FUNCTIONAL DESCRIPTION: OptiDis is a new code for large scale dislocation dynamics simulations. Its purpose is to simulate real life dislocation densities (up to 5.1022 dislocations/m²) in order to understand plastic deformation and study strain hardening. The main application is to observe and understand plastic deformation of irradiated zirconium. Zirconium alloys are the first containment barrier against the dissemination of radioactive elements. More precisely, with neutron irradiated zirconium alloys we are talking about channeling mechanism, which means to stick with the reality, more than tens of thousands of induced loops, i. e. 100 million degrees of freedom in the simulation. The code is based on Numodis code developed at CEA Saclay and the ScalFMM library developed in HiePACS project. The code is written in C++ language and using the last features of C++11/14. One of the main aspects is the hybrid parallelism MPI/OpenMP that gives the software the ability to scale on large cluster while the computation load rises. In order to achieve that, we use different levels of parallelism. First of all, the simulation box is distributed over MPI processes, then we use a thinner level for threads, dividing the domain by an Octree representation. All these parts are controlled by the ScalFMM library. On the last level, our data are stored in an adaptive structure that absorbs the dynamics of this type of simulation and manages the parallelism of tasks..

- Participant: Olivier Coulaud
- Contact: Olivier Coulaud
- URL: <http://optidis.gforge.inria.fr/>

6.8. PaStiX

Parallel Sparse matrix package

KEYWORDS: Linear algebra - High-performance calculation - Factorisation - Sparse Matrices - Linear Systems Solver

SCIENTIFIC DESCRIPTION: PaStiX is based on an efficient static scheduling and memory manager, in order to solve 3D problems with more than 50 million of unknowns. The mapping and scheduling algorithm handle a combination of 1D and 2D block distributions. A dynamic scheduling can also be applied to take care of NUMA architectures while taking into account very precisely the computational costs of the BLAS 3 primitives, the communication costs and the cost of local aggregations.

FUNCTIONAL DESCRIPTION: PaStiX is a scientific library that provides a high performance parallel solver for very large sparse linear systems based on block direct and block ILU(k) methods. It can handle low-rank compression techniques to reduce the computation and the memory complexity. Numerical algorithms are implemented in single or double precision (real or complex) for LLt, LDLt and LU factorization with static pivoting (for non symmetric matrices having a symmetric pattern). The PaStiX library uses the graph partitioning and sparse matrix block ordering packages Scotch or Metis.

The PaStiX solver is suitable for any heterogeneous parallel/distributed architecture when its performance is predictable, such as clusters of multicore nodes with GPU accelerators or KNL processors. In particular, we provide a high-performance version with a low memory overhead for multicore node architectures, which fully exploits the advantage of shared memory by using an hybrid MPI-thread implementation.

The solver also provides some low-rank compression methods to reduce the memory footprint and/or the time-to-solution.

- Participants: Grégoire Pichon, Mathieu Faverge and Pierre Ramet
- Partners: Université Bordeaux 1 - INP Bordeaux
- Contact: Pierre Ramet
- URL: <https://gitlab.inria.fr/solverstack/pastix>

6.9. ScalFMM

Scalable Fast Multipole Method

KEYWORDS: N-body - Fast multipole method - Parallelism - MPI - OpenMP

SCIENTIFIC DESCRIPTION: ScalFMM is a software library to simulate N-body interactions using the Fast Multipole Method. The library offers two methods to compute interactions between bodies when the potential decays like $1/r$. The first method is the classical FMM based on spherical harmonic expansions and the second is the Black-Box method which is an independent kernel formulation (introduced by E. Darve @ Stanford). With this method, we can now easily add new non oscillatory kernels in our library. For the classical method, two approaches are used to decrease the complexity of the operators. We consider either matrix formulation that allows us to use BLAS routines or rotation matrix to speed up the M2L operator.

ScalFMM intends to offer all the functionalities needed to perform large parallel simulations while enabling an easy customization of the simulation components: kernels, particles and cells. It works in parallel in a shared/distributed memory model using OpenMP and MPI. The software architecture has been designed with two major objectives: being easy to maintain and easy to understand. There is two main parts:

the management of the octree and the parallelization of the method the kernels. This new architecture allow us to easily add new FMM algorithm or kernels and new paradigm of parallelization.

FUNCTIONAL DESCRIPTION: Compute N-body interactions using the Fast Multipole Method for large number of objects

- Participants: Bramas Bérenger and Olivier Coulaud
- Contact: Olivier Coulaud
- URL: <https://gitlab.inria.fr/solverstack/ScalFMM>

6.10. VITE

Visual Trace Explorer

KEYWORDS: Visualization - Execution trace

FUNCTIONAL DESCRIPTION: ViTE is a trace explorer. It is a tool made to visualize execution traces of large parallel programs. It supports Pajé, a trace format created by Inria Grenoble, and OTF and OTF2 formats, developed by the University of Dresden and allows the programmer a simpler way to analyse, debug and/or profile large parallel applications.

- Participant: Mathieu Faverge
- Contact: Mathieu Faverge
- URL: <http://vite.gforge.inria.fr/>

6.11. PlaFRIM

Plateforme Fédérative pour la Recherche en Informatique et Mathématiques

KEYWORDS: High-Performance Computing - Hardware platform

FUNCTIONAL DESCRIPTION: PlaFRIM is an experimental platform for research in modeling, simulations and high performance computing. This platform has been set up from 2009 under the leadership of Inria Bordeaux Sud-Ouest in collaboration with computer science and mathematics laboratories, respectively Labri and IMB with a strong support in the region Aquitaine.

It aggregates different kinds of computational resources for research and development purposes. The latest technologies in terms of processors, memories and architecture are added when they are available on the market. It is now more than 1,000 cores (excluding GPU and Xeon Phi) that are available for all research teams of Inria Bordeaux, Labri and IMB. This computer is in particular used by all the engineers who work in HiePACS and are advised by F. Rue from the SED.

- Contact: Olivier Coulaud
- URL: <https://www.plafrim.fr/en/home/>

LFANT Project-Team

5. New Software and Platforms

5.1. APIP

Another Pairing Implementation in PARI

KEYWORDS: Cryptography - Computational number theory

SCIENTIFIC DESCRIPTION: Apip , Another Pairing Implementation in PARI, is a library for computing standard and optimised variants of most cryptographic pairings.

The following pairings are available: Weil, Tate, ate and twisted ate, optimised versions (à la Vercauteren–Hess) of ate and twisted ate for selected curve families.

The following methods to compute the Miller part are implemented: standard Miller double-and-add method, standard Miller using a non-adjacent form, Boxall et al. version, Boxall et al. version using a non-adjacent form.

The final exponentiation part can be computed using one of the following variants: naive exponentiation, interleaved method, Avanzi–Mihalescu’s method, Kato et al.’s method, Scott et al.’s method.

Part of the library has been included into Pari/Gp proper.

FUNCTIONAL DESCRIPTION: APIP is a library for computing standard and optimised variants of most cryptographic pairings.

- Participant: Jérôme Milan
- Contact: Andreas Enge
- URL: <http://www.lix.polytechnique.fr/~milanj/apip/apip.xhtml>

5.2. AVIsogenies

Abelian Varieties and Isogenies

KEYWORDS: Computational number theory - Cryptography

FUNCTIONAL DESCRIPTION: AVIsogenies is a Magma package for working with abelian varieties, with a particular emphasis on explicit isogeny computation.

Its prominent feature is the computation of (l,l)-isogenies between Jacobian varieties of genus-two hyperelliptic curves over finite fields of characteristic coprime to l, practical runs have used values of l in the hundreds.

It can also be used to compute endomorphism rings of abelian surfaces, and find complete addition laws on them.

- Participants: Damien Robert, Gaëtan Bisson and Romain Cosset
- Contact: Damien Robert
- URL: <http://avisogenies.gforge.inria.fr/>

5.3. CM

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: The Cm software implements the construction of ring class fields of imaginary quadratic number fields and of elliptic curves with complex multiplication via floating point approximations. It consists of libraries that can be called from within a C program and of executable command line applications.

RELEASE FUNCTIONAL DESCRIPTION: Features - Precisions beyond 300000 bits are now supported by an addition chain of variable length for the `-function`. Dependencies - The minimal version number of Mpfr has been increased to 3.0.0, that of Mpc to 1.0.0 and that of Pari to 2.7.0.

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: <http://www.multiprecision.org/cm/home.html>

5.4. CMH

Computation of Igusa Class Polynomials

KEYWORDS: Mathematics - Cryptography - Number theory

FUNCTIONAL DESCRIPTION: Cmh computes Igusa class polynomials, parameterising two-dimensional abelian varieties (or, equivalently, Jacobians of hyperelliptic curves of genus 2) with given complex multiplication.

- Participants: Andreas Enge, Emmanuel Thomé and Regis Dupont
- Contact: Emmanuel Thomé
- URL: <http://cmh.gforge.inria.fr>

5.5. CUBIC

KEYWORD: Number theory

FUNCTIONAL DESCRIPTION: Cubic is a stand-alone program that prints out generating equations for cubic fields of either signature and bounded discriminant. It depends on the Pari library. The algorithm has quasi-linear time complexity in the size of the output.

- Participant: Karim Belabas
- Contact: Karim Belabas
- URL: <http://www.math.u-bordeaux.fr/~belabas/research/software/cubic-1.2.tgz>

5.6. Euclid

KEYWORD: Number theory

FUNCTIONAL DESCRIPTION: Euclid is a program to compute the Euclidean minimum of a number field. It is the practical implementation of the algorithm described in [38]. Some corresponding tables built with the algorithm are also available. Euclid is a stand-alone program depending on the PARI library.

- Participants: Jean-Paul Cerri and Pierre Lezowski
- Contact: Jean-Paul Cerri
- URL: <http://www.math.u-bordeaux1.fr/~plezowsk/euclid/index.php>

5.7. KleinianGroups

KEYWORDS: Computational geometry - Computational number theory

FUNCTIONAL DESCRIPTION: KleinianGroups is a Magma package that computes fundamental domains of arithmetic Kleinian groups.

- Participant: Aurel Page
- Contact: Aurel Page
- URL: <http://www.normalesup.org/~page/Recherche/Logiciels/logiciels-en.html>

5.8. GNU MPC

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: Mpc is a C library for the arithmetic of complex numbers with arbitrarily high precision and correct rounding of the result. It is built upon and follows the same principles as Mpfr. The library is written by Andreas Enge, Philippe Théveny and Paul Zimmermann.

RELEASE FUNCTIONAL DESCRIPTION: Fixed mp_pow, see <http://lists.gforge.inria.fr/pipermail/mpc-discuss/2014-October/001315.html> - \#18257: Switched to libtool 2.4.5.

- Participants: Andreas Enge, Mickaël Gastineau, Paul Zimmermann and Philippe Théveny
- Contact: Andreas Enge
- URL: <http://www.multiprecision.org/>

5.9. MPFR CX

KEYWORD: Arithmetic

FUNCTIONAL DESCRIPTION: Mpfr cx is a library for the arithmetic of univariate polynomials over arbitrary precision real (Mpfr) or complex (Mpc) numbers, without control on the rounding. For the time being, only the few functions needed to implement the floating point approach to complex multiplication are implemented. On the other hand, these comprise asymptotically fast multiplication routines such as Toom-Cook and the FFT.

RELEASE FUNCTIONAL DESCRIPTION: - new function `prod_an_hecke` - improved memory consumption for unbalanced FFT multiplications

- Participant: Andreas Enge
- Contact: Andreas Enge
- URL: <http://www.multiprecision.org/mpfr cx/home.html>

5.10. PARI/GP

KEYWORD: Computational number theory

FUNCTIONAL DESCRIPTION: Pari/Gp is a widely used computer algebra system designed for fast computations in number theory (factorisation, algebraic number theory, elliptic curves, modular forms ...), but it also contains a large number of other useful functions to compute with mathematical entities such as matrices, polynomials, power series, algebraic numbers, etc., and many transcendental functions.

- Participants: Andreas Enge, Hamish Ivey-Law, Henri Cohen and Karim Belabas
- Partner: CNRS
- Contact: Karim Belabas
- URL: <http://pari.math.u-bordeaux.fr/>

MAGIQUE-3D Project-Team

5. New Software and Platforms

5.1. Elasticus

KEYWORDS: Discontinuous Galerkin - Acoustic equation - Elastodynamic equations - Elastoacoustic - 2D - 3D - Time Domain

SCIENTIFIC DESCRIPTION: Elasticus simulate acoustic and elastic wave propagation in 2D and in 3D, using Discontinuous Galerkin Methods. The space discretization is based on two kind of basis functions, using Lagrange or Jacobi polynomials. Different kinds of fluxes (upwind and centered) are implemented, coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION: Elasticus is a sequential library, independent of Total platform and developed in Fortran, to simulate wave propagation in geophysical environment, based on a DG method. It is meant to help PhD students and post-doctoral fellows to easily implement their algorithms in the library. Thus, readability of the code is privileged to optimization of its performances. Developed features should be easily transferred in the computing platform of Total. Elasticus manages arbitrary orders for the spatial discretization with DG method.

NEWS OF THE YEAR: In 2018, we implemented the coupling between hexahedra and tetrahedra and the coupling between Discontinuous Galerkin methods and Spectral Element methods in 2D and in 3D. We also introduced Perfectly Matched layers in the Spectral Element kernel.

- Participants: Julien Diaz, Lionel Boillot and Simon Ettouati
- Contact: Julien Diaz
- Publications: [Spectral Element Method and Discontinuous Galerkin approximation for elasto-acoustic problems](#) - [Hybrid space discretization to solve elasto-acoustic coupling](#) - [On the coupling of Spectral Element Method with Discontinuous Galerkin approximation for elasto-acoustic problems](#) - [SEM-DG Approximation for elasto-acoustics](#)

5.2. Hou10ni

KEYWORDS: 2D - 3D - Elastodynamic equations - Acoustic equation - Elastoacoustic - Frequency Domain - Time Domain - Discontinuous Galerkin

SCIENTIFIC DESCRIPTION: Hou10ni simulates acoustic and elastic wave propagation in time domain and in harmonic domain, in 2D and in 3D. It is also able to model elasto acoustic coupling. It is based on the second order formulation of the wave equation and the space discretization is achieved using Interior Penalty Discontinuous Galerkin Method. Recently, the harmonic domain solver has been extended to handle Hybridizable Discontinuous Galerkin Methods.

FUNCTIONAL DESCRIPTION: This software simulates the propagation of waves in heterogeneous 2D and 3D media in time-domain and in frequency domain. It is based on an Interior Penalty Discontinuous Galerkin Method (IPDGM) and allows for the use of meshes composed of cells of various order (p-adaptivity in space).

NEWS OF THE YEAR: In 2018, we have finished scalability tests and performance comparison of Hou10ni/Mumps vs Hou10ni/Maphys on Plafrim, in the framework of the european project HPC4E. The code is now being ported on Turing, in order to extend the scalability tests to the time-domain problem.

- Participants: Conrad Hillairet, Elodie Estecahandy, Julien Diaz, Lionel Boillot and Marie Bonnasse Gahot
- Contact: Julien Diaz
- Publications: [Hybridizable discontinuous Galerkin method for the two-dimensional frequency-domain elastic wave equations](#) - [Convergence of seismic full waveform inversion and extension to Cauchy data](#) - [Convergence Analysis for Seismic Full Waveform Inversion](#) - [Stability and convergence analysis for seismic depth imaging using FWI](#) - [On the use of a laser ablation as a laboratory seismic source](#) - [Towards Energy-Efficient Storage Servers](#) - [Equivalent Robin Boundary Conditions for Acoustic and Elastic Media](#) - [Comparison of solvers performance when solving the 3D Helmholtz elastic wave equations over the Hybridizable Discontinuous Galerkin method](#) - [Comparison of solvers performance when solving the 3D Helmholtz elastic wave equations using the Hybridizable Discontinuous Galerkin method](#) - [Resolution strategy for the Hybridizable Discontinuous Galerkin system for solving Helmholtz elastic wave equations](#) - [Seismic imaging in laboratory trough laser Doppler vibrometry](#) - [Absorbing Boundary Conditions for 3D Elastic TTI Modeling, Application to Time-Based and Time-Harmonic Simulations](#) - [Shape and material parameter reconstruction of an isotropic or anisotropic solid immersed in a fluid](#) - [Modelling and advanced simulation of wave propagation phenomena in 3D geophysical media.](#) - [Multi-level explicit local time-stepping methods for second-order wave equations](#) - [Absorbing Boundary Conditions for 3D elastic TTI modeling](#) - [Modeling of elastic Helmholtz equations by hybridizable discontinuous Galerkin method \(HDG\) for geophysical applications](#) - [Performance Assessment on Hybridizable Dg Approximations for the Elastic Wave Equation in Frequency Domain](#) - [High-Order IPDG Approximations for Elasto-Acoustic Problems](#) - [High-order Discontinuous Galerkin approximations for elasto-acoustic scattering problems](#) - [Modelling of seismic waves propagation in harmonic domain by hybridizable discontinuous Galerkin method \(HDG\)](#) - [Absorbing Boundary Conditions for 3D Tilted Transverse Isotropic media](#) - [Performance comparison between hybridizable DG and classical DG methods for elastic waves simulation in harmonic domain](#) - [Polynomial speeds in a Discontinuous Galerkin code](#) - [Hybridizable Discontinuous Galerkin method for the simulation of the propagation of the elastic wave equations in the frequency domain](#) - [Discontinuous Galerkin methods for the simulation of the propagation of the elastic wave equations in the frequency domain](#) - [High order discontinuous Galerkin methods for time-harmonic elastodynamics](#) - [Hybridizable discontinuous Galerkin method for the two-dimensional frequency-domain elastic wave equations](#) - [Efficient DG-like formulation equipped with curved boundary edges for solving elasto-acoustic scattering problems](#) - [Numerical schemes for the simulation of seismic wave propagation in frequency domain](#) - [Performance analysis of DG and HDG methods for the simulation of seismic wave propagation in harmonic domain](#) - [Hybridizable Discontinuous Galerkin method for solving Helmholtz elastic wave equations](#) - [Discontinuous Galerkin methods for solving Helmholtz elastic wave equations for seismic imaging](#) - [Performance comparison of HDG and classical DG method for the simulation of seismic wave propagation in harmonic domain](#) - [Contributions to the mathematical modeling and to the parallel algorithmic for the optimization of an elastic wave propagator in anisotropic media](#) - [Contribution to the mathematical analysis and to the numerical solution of an inverse elasto-acoustic scattering problem](#)
- URL: <https://team.inria.fr/magique3d/software/hou10ni/>

5.3. MONTJOIE

KEYWORDS: High order finite elements - Edge elements - Aeroacoustics - High order time schemes

SCIENTIFIC DESCRIPTION: Montjoie is designed for the efficient solution of time-domain and time-harmonic linear partial differential equations using high-order finite element methods. This code is mainly written for quadrilateral/hexahedral finite elements, partial implementations of triangular/tetrahedral elements are provided. The equations solved by this code, come from the "wave propagation" problems, particularly acoustic, electromagnetic, aeroacoustic, elastodynamic problems.

FUNCTIONAL DESCRIPTION: Montjoie is a code that provides a C++ framework for solving partial differential equations on unstructured meshes with finite element-like methods (continuous finite element, discontinuous Galerkin formulation, edge elements and facet elements). The handling of mixed elements (tetrahedra, prisms, pyramids and hexahedra) has been implemented for these different types of finite elements methods. Several applications are currently available : wave equation, elastodynamics, aeroacoustics, Maxwell's equations.

- Participants: Gary Cohen, Juliette Chabassier, Marc Duruflé and Morgane Bergot
- Contact: Marc Duruflé
- URL: <http://montjoie.gforge.inria.fr/>

5.4. tmodeling-DG

Time-domain Wave-equation Modeling App

KEYWORDS: 2D - 3D - Elastoacoustic - Elastodynamic equations - Discontinuous Galerkin - Time Domain

SCIENTIFIC DESCRIPTION: tmodeling-DG simulate acoustic and elastic wave propagation in 2D and in 3D, using Discontinuous Galerkin Methods. The space discretization is based on two kind of basis functions, using Lagrange or Jacobi polynomials. Different kinds of fluxes (upwind and centered) are implemented, coupled with RK2 and RK4 time schemes.

FUNCTIONAL DESCRIPTION: tmodelling-DG is the follow up to DIVA-DG that we develop in collaboration with our partner Total. Its purpose is more general than DIVA-DG and should contains various DG schemes, basis functions and time schemes. It models wave propagation in acoustic media, elastic (isotropic and TTI) media and elasto-acoustic media, in two and three dimensions.

NEWS OF THE YEAR: In 2018, we have coupled the code with a Reverse Time Migration algorithm.

- Participants: Julien Diaz, Lionel Boillot, Simon Ettouati and H el ene Barucq
- Partner: TOTAL
- Contact: Julien Diaz

5.5. OpenWind

Open Wind Instrument Design

KEYWORDS: Wave propagation - Inverse problem - Experimental mechanics - Image processing

FUNCTIONAL DESCRIPTION: -Computes resonating pipes' impedance using one-dimensional finite element method and the transfer matrix method -sound synthesis in the time domain (FDTD and FEM in space) -informatic interface for the usage of an input impedance measurement setup. -instrument bore extraction using tomographical image processing -inverse problem solving

- Contact: Juliette Chabassier

5.6. ffwi

Frequency-domain Full Waveform Inversion

KEYWORDS: 2D - 3D - Discontinuous Galerkin - Inverse problem - Frequency Domain - Acoustic equation - Elasticity

FUNCTIONAL DESCRIPTION: ffwi is developed in partnership with Total in the context of the Depth Imaging Partnership (DIP). It is devoted to perform seismic imaging using the Full Waveform Inversion method, in the frequency domain. It is based upon the software Fmodeling, which is itself dedicated to the forward problem. In FWI, the forward problem is solved using Hybridizable Discontinuous Galerkin Methods. The reconstruction of medium parameter is conducted with an iterative minimization scheme, which uses gradient descent techniques. The software can work with acoustic and elastic media, in two and three dimensions.

- Partner: TOTAL
- Contact: Florian Faucher

MANAO Project-Team

6. New Software and Platforms

6.1. Eigen

KEYWORD: Linear algebra

FUNCTIONAL DESCRIPTION: Eigen is an efficient and versatile C++ mathematical template library for linear algebra and related algorithms. In particular it provides fixed and dynamic size matrices and vectors, matrix decompositions (LU, LLT, LDLT, QR, eigenvalues, etc.), sparse matrices with iterative and direct solvers, some basic geometry features (transformations, quaternions, axis-angles, Euler angles, hyperplanes, lines, etc.), some non-linear solvers, automatic differentiations, etc. Thanks to expression templates, Eigen provides a very powerful and easy to use API. Explicit vectorization is performed for the SSE, AltiVec and ARM NEON instruction sets, with graceful fallback to non-vectorized code. Expression templates allow to perform global expression optimizations, and to remove unnecessary temporary objects.

RELEASE FUNCTIONAL DESCRIPTION: In 2017, we released three revisions of the 3.3 branch with few fixes of compilation and performance regressions, some doxygen documentation improvements, and the addition of transpose, adjoint, conjugate methods to SelfAdjointView to ease writing generic code.

- Participant: Gaël Guennebaud
- Contact: Gaël Guennebaud
- URL: <http://eigen.tuxfamily.org/>

6.2. Elasticity Skinning

KEYWORD: 3D animation

FUNCTIONAL DESCRIPTION: Geometric skinning techniques are very popular in the industry for their high performances, but fail to mimic realistic deformations. With elastic implicit skinning the skin stretches automatically (without skinning weights) and the vertices distribution is more pleasing. Our approach is more robust, for instance the angle's range of joints is larger than implicit skinning.

This software has been ported as a plugin for the Modo software (The Foundry) in collaboration with Toulouse Tech Transfer. This plugin has been bought by The Foundry, which maintains and sells it.

- Participants: Brian Wyvill, Damien Rohmer, Florian Canezin, Gaël Guennebaud, Loïc Barthe, Marie-Paule Cani, Mathias Paulin, Olivier Gourmel and Rodolphe Vaillant
- Partners: Université de Bordeaux - CNRS - INP Bordeaux - Université de Toulouse - Institut Polytechnique de Grenoble - Ecole Supérieure de Chimie Physique Electronique de Lyon
- Contact: Gaël Guennebaud
- URL: <https://www.irit.fr/~Loic.Barthe/transfer.php>

MEMPHIS Project-Team

6. New Software and Platforms

6.1. COCOFLOW

KEYWORDS: 3D - Elasticity - MPI - Compressible multimaterial flows

FUNCTIONAL DESCRIPTION: The code is written in fortran 95 with a MPI parallelization. It solves equations of conservation modeling 3D compressible flows with elastic models as equation of state.

- Contact: Florian Bernard
- URL: <https://gforge.inria.fr/projects/cocoflow>

6.2. KOPPA

Kinetic Octree Parallel PolyAtomic

FUNCTIONAL DESCRIPTION: KOPPA is a C++/MPI numerical code solving a large range of rarefied flows from external to internal flows in 1D, 2D or 3D. Different kind of geometries can be treated such as moving geometries coming from CAO files or analytical geometries. The models can be solved on Octree grids with dynamic refinement.

- Participant: Florian Bernard
- Contact: Florian Bernard
- URL: <https://git.math.cnrs.fr/gitweb/?p=plm/fbernard/KOPPA.git;a=summary>

6.3. NaSCar

Navier-Stokes Cartesian

KEYWORDS: HPC - Numerical analyse - Fluid mechanics - Langage C - PETSc

SCIENTIFIC DESCRIPTION: NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.

FUNCTIONAL DESCRIPTION: This code is devoted to solve 3D-flows in around moving and deformable bodies. The incompressible Navier-Stokes equations are solved on fixed grids, and the bodies are taken into account thanks to penalization and/or immersed boundary methods. The interface between the fluid and the bodies is tracked with a level set function or in a Lagrangian way. The numerical code is fully second order (time and space). The numerical method is based on projection schemes of Chorin-Temam's type. The code is written in C language and use Petsc library for the resolution of large linear systems in parallel.

NaSCar can be used to simulate both hydrodynamic bio-locomotion as fish like swimming and aerodynamic flows such wake generated by a wind turbine.

- Participant: Michel Bergmann
- Contact: Michel Bergmann
- URL: <https://gforge.inria.fr/projects/nascar/>

6.4. NS-penal

Navier-Stokes-penalization

KEYWORDS: 3D - Incompressible flows - 2D

FUNCTIONAL DESCRIPTION: The software can be used as a black box with the help of a data file if the obstacle is already proposed. For new geometries the user has to define them. It can be used with several boundary conditions (Dirichlet, Neumann, periodic) and for a wide range of Reynolds numbers.

- Partner: Université de Bordeaux
- Contact: Charles-Henri Bruneau

MNEMOSYNE Project-Team

6. New Software and Platforms

6.1. DANA

Distributed Asynchronous Numerical and Adaptive computing framework

KEYWORD: Neural networks

FUNCTIONAL DESCRIPTION: DANA is a python framework whose computational paradigm is grounded on the notion of a unit that is essentially a set of time dependent values varying under the influence of other units via adaptive weighted connections. The evolutions of a unit's value are defined by a set of differential equations expressed in standard mathematical notation which greatly ease their definition. The units are organized into groups that form a model. Each unit can be connected to any other unit (including itself) using a weighted connection. The DANA framework offers a set of core objects needed to design and run such models. The modeler only has to define the equations of a unit as well as the equations governing the training of the connections. The simulation is completely transparent to the modeler and is handled by DANA. This allows DANA to be used for a wide range of numerical and distributed models as long as they fit the proposed framework (e.g. cellular automata, reaction-diffusion system, decentralized neural networks, recurrent neural networks, kernel-based image processing, etc.).

- Participant: Nicolas Rougier
- Contact: Nicolas Rougier
- URL: <http://dana.loria.fr/>

6.2. Virtual Enaction

KEYWORDS: Neurosciences - Simulation - Health

FUNCTIONAL DESCRIPTION: VirtualEnaction: A Platform for Systemic Neuroscience Simulation. The computational models studied in this project have applications that extend far beyond what is possible to experiment yet in human or non-human primate subjects. Real robotics experimentations are also impaired by rather heavy technological constraints, for instance, it is not easy to dismantle a given embedded system in the course of emerging ideas. The only versatile environment in which such complex behaviors can be studied both globally and at the level of details of the available modeling is a virtual environment, as in video games. Such a system can be implemented as "brainy-bot" (a programmed player based on our knowledge of the brain architecture) which goal is to survive in a complete manipulable environment.

In order to attain this rather ambitious objective we both (i) deploy an existing open-source video game middleware in order to be able to shape the survival situation to be studied and (ii) revisit the existing models in order to be able to integrate them as an effective brainy-bot. It consists of a platform associated to a scenario that is the closest possible to a survival situation (foraging, predator-prey relationship, partner approach to reproduction) and in which it is easy to integrate an artificial agent with sensory inputs (visual, touch and smell), emotional and somatosensory cues (hunger, thirst, fear, ..) and motor outputs (movement, gesture, ..) connected to a "brain" whose architecture will correspond to the major anatomical regions involved in the issues of learning and action selection (cortex areas detailed here, basal ganglia, hippocampus, and areas dedicated to sensorimotor processes). The internal game clock can be slowed down enough to be able to run non trivial brainy-bot implementations. This platform has already being used by two students of the team and is now a new deliverable of the KEOpS project.

- Participants: André Garenne, Frédéric Alexandre, Nicolas Rougier and Thierry Viéville
- Contact: Frédéric Alexandre

6.3. Mnemonas

KEYWORDS: Recurrent network - Manifold

FUNCTIONAL DESCRIPTION: This source bundle provides source files of the: - Manifold representation of ontology for machine learning (in progress). - Recurrent neural network weight estimation though backward tuning publication.

- Contact: Thierry Viéville

6.4. ReservoirPy

KEYWORDS: Recurrent network - Artificial intelligence - Reservoir Computing - Multi-label classification - Timeseries Prediction - Time Series - Machine learning - Classification

FUNCTIONAL DESCRIPTION: This toolbox provides a class of Echo State Networks that can be used with Python and its scientific libraries like Numpy, Scipy and Matplotlib. It includes useful expertise to train recurrent neural networks of ESN architecture kind.

ESN is a particular kind of recurrent neural network (RNN) with or without leaky neurons. The input stream is projected to a random recurrent layer and a linear output layer (called "read-out") is modified by learning (which can also be done in an online fashion).

Compared to other RNNs, the input layer and the recurrent layer (called "reservoir") do not need to be trained. For other RNNs, the structure of the recurrent layer evolves in most cases by gradient descent algorithms like Backpropagation-Through-Time, which is not biologically plausible and is adapted iteratively to be able to hold a representation of the input sequence. In contrast, the random weights of the ESN's reservoir are not trained, but adapted to possess the "Echo State Property" (ESP) or at least suitable dynamics (e.g. 'edge of chaos') to generalize, which includes a non-linear transformation of the input that can be learned by a linear classifier. The weights are adapted by scaling the weights based on the maximum absolute eigenvalue (also called spectral radius), which is a hyperparameter specific to the task. The states of the reservoir are linearly separable and can be mapped to the output layer by a computationally cheap linear regression, as no gradient descent is necessary. The weights of the input layer can be scaled by the input scaling hyperparameter, which also depends on the nature of the inputs.

- Partners: Université de Hamburg - University of Hamburg
- Contact: Xavier Hinaut
- URL: <https://github.com/neuronalX/reservoirpy>

MONC Project-Team

6. New Software and Platforms

6.1. Nenuphar

KEYWORDS: Modeling - Oncologie - Cancer - Partial differential equation - Medical - Medical imaging

FUNCTIONAL DESCRIPTION: The goal of project is to evaluate the aggressiveness of a tumor or its response to therapy. For that purpose, we use a mathematical model based on a set of nonlinear partial differential equations. This model is calibrated on patient data using a longitudinal sequence of CT Scan or MRI of the patient. This approach has been validated on about 35 clinical cases of lung metastases from various primary tumors (kidney, bladder, thyroid). Using two initial images showing the targeted lesion, we recover the patient-specific parameters of the model. The evolution of the disease is then predicted by letting the model run for later times with these parameters.

- Partners: CNRS - INP Bordeaux - Université Bordeaux 1
- Contact: Olivier Saut
- URL: <https://team.inria.fr/monc/software/>

6.2. papriK

KEYWORDS: Medical imaging - DICOM - Image registration - Image segmentation - 2D - 3D - Image analysis - Image processing - Medical applications - Radiomics

SCIENTIFIC DESCRIPTION: PapriK is the team toolkit devoted to processing and analyzing medical images. It currently wraps VTK and ITK and contains our own algorithms as well : - images input/output (including DICOM) - filtering, rescaling, resampling - segmentation/registration - radiomics computation: histogram, texture, shape

NEWS OF THE YEAR: - add python3 support - work on registration - simplify the library - fix bugs

- Participants: Cynthia Perier, Olivier Saut and Erwan Le Masson
- Partners: Institut Bergonié - Université de Bordeaux
- Contact: Cynthia Perier
- Publications: [T2-based MRI Delta-Radiomics Improve Response Prediction in Soft-Tissue Sarcomas Treated by Neoadjuvant Chemotherapy - Pre-treatment magnetic resonance-based texture features as potential imaging biomarkers for predicting event free survival in anal cancer treated by chemoradiotherapy](#)
- URL: <https://team.inria.fr/monc/software/>

6.3. NENUCORE

KEYWORDS: Image segmentation - Biomedical imaging - Image processing - Real-time rendering

SCIENTIFIC DESCRIPTION: Standalone application for visualization, manipulation and segmentation of 2D and 3D images. The software has been developed for application to medical imaging. The visualization is done in real time and the segmentation can be manual or semi-automatic. The software contains a database including medical images of patients, the segmentation data of these images as well as the associated meta-data.

- Participants: Benjamin Taton, Boris Raymond, Jean Mercat and Vivien Pianet
- Contact: Boris Raymond

6.4. metamats_burden

KEYWORDS: Metastasis - Cancer - Data assimilation - Regression - Biostatistics - Mechanistic modeling - Simulation

SCIENTIFIC DESCRIPTION: This Matlab software is a minimal code for fitting simultaneously primary tumor growth and metastatic burden data using nonlinear mixed-effects modeling.

FUNCTIONAL DESCRIPTION: Set of functions for calibration of models of metastatic burden and primary tumor growth to empirical population data

NEWS OF THE YEAR: Submission to the French agency of software protection (APP). Inclusion of a new model for pre-operative anti-angiogenic treatment. Validation of the previous models on large databases (400+ animals)

- Participants: Sébastien Benzekry and Chiara Nicolo
- Partner: Roswell Park Comprehensive Cancer Center
- Contact: Sébastien Benzekry
- Publications: [Modeling Spontaneous Metastasis following Surgery: An In Vivo-In Silico Approach - Computational Modelling of Metastasis Development in Renal Cell Carcinoma](#)
- URL: <http://metamats.bordeaux.inria.fr/>

6.5. metamats_core

KEYWORDS: Metastasis - Cancer - Mechanistic modeling - Simulation - Modeling

SCIENTIFIC DESCRIPTION: This code is devoted to the simulation of partial differential equation (PDE) based models for the time development of a population of secondary tumors (metastases).

FUNCTIONAL DESCRIPTION: Metamats_core simulates a partial differential equation (PDE)-based model for the time development of a population of secondary tumors (metastases).

NEWS OF THE YEAR: Submission to the French agency of software protection (APP)

- Participant: Sébastien Benzekry
- Contact: Sébastien Benzekry
- Publications: [Modeling Spontaneous Metastasis following Surgery: An In Vivo-In Silico Approach - Passing to the limit 2D-1D in a model for metastatic growth - Mathematical analysis of a two-dimensional population model of metastatic growth including angiogenesis - Modeling the impact of anticancer agents on metastatic spreading - Global Dormancy of Metastases due to Systemic Inhibition of Angiogenesis](#)
- URL: <http://benzekry.perso.math.cnrs.fr/>

6.6. IRENA

Numerical Assessment of IRreversible Electroporation ablation

KEYWORDS: Cancer - Numerical electroporation

SCIENTIFIC DESCRIPTION: The C++ software IRENA developed by O. Gallinato and C. Pognard within the Inria team Monc enable to compute the static electric field distribution in the clinical configuration of IRE ablation of liver tumors. The code is based on the finite volume method on Cartesian grid. The needles and the liver boundary are determined as the zero of a level-set function. Close to the boundaries, the first and second order derivatives are computed with the standard Ghost Fluid Method. The equivalent conductivities at half points are computed thanks to harmonic mean (additivity law of resistivity). In order to maintain a reasonable computation time, the refinement is low enough (1 mm³ grid voxels). As the mesh does not pick up the very fine needles, the Dirichlet conditions imposed on the active parts of the electrodes and the Neumann conditions imposed on the insulated parts are changed into Robin conditions on the first layer of points around the needles, thanks to a second order development. This results in a numerical scheme, which is computationally efficient and accurate enough.

FUNCTIONAL DESCRIPTION: Digital simulation tool for the assessment of irreversible electroporation clinical process

- Authors: Olivier Gallinato and Clair Poinard
- Contact: Clair Poinard

6.7. metamats_size

Fitting longitudinal data of size and number of metastases using mechanistic models

KEYWORDS: Cancer - Mechanistic modeling - Metastasis - Regression - Simulation - Data assimilation

SCIENTIFIC DESCRIPTION: This software fits models of metastatic development to longitudinal data of metastatic sizes and provides simulation and visualization tools for metastatic modeling.

NEWS OF THE YEAR: Establishment of a first clean and minimal version. Validation of the software on clinical data of brain metastases from non-small cell lung cancer. Submission to the French agency of software protection (APP).

- Participants: Sébastien Benzekry and Mariia Bilous
- Partners: Centre de Recherches en Cancérologie de Marseille - Institut Bergonié - Assistance Publique - Hôpitaux de Marseille
- Contact: Sébastien Benzekry
- Publication: [Computational modeling reveals dynamics of brain metastasis in non-small cell lung cancer and provides a tool for personalized therapy](#)
- URL: <http://metamats.bordeaux.inria.fr/>

6.8. Carcinom

Computer-Assisted Research about Cancer growth and INSights on Oncological Mechanisms

KEYWORDS: Cancer - Regression - Tumor growth

SCIENTIFIC DESCRIPTION: This software is primarily designed to perform a modeling analysis of tumor growth kinetics. Given a data set of longitudinal measurements of tumor size in a population, it fits multiple models of tumor growth (either user-defined or selected from a library of classical models), computes goodness-of-fit statistical metrics, identifies the parameters of the models and estimates associated standard errors. Fits of the data can be performed either individual per individual or using a population approach (nonlinear mixed-effects).

FUNCTIONAL DESCRIPTION: Software for modeling and fitting tumor growth kinetics. Given a data set of longitudinal measurements of tumor size in a population, it fits multiple models of tumor growth (either user-defined or selected from a library of classical models), computes goodness-of-fit statistical metrics, identifies the parameters of the models and estimates associated standard errors. Fits of the data can be performed either on an individual basis or using a population approach (nonlinear mixed-effects).

Graphical and statistical tools of use when analyzing growth curves are also included.

NEWS OF THE YEAR: Submission to the French agency of software protection (APP). Development of a python module for interaction with Monolix.

- Participants: Simon Evain, Vivien Pianet and Cristina Vaghi
- Partner: Roswell Park Comprehensive Cancer Center
- Contact: Sébastien Benzekry
- Publication: [Classical Mathematical Models for Description and Forecast of Experimental Tumor Growth](#)
- URL: <https://team.inria.fr/monc/software/>

6.9. Platforms

6.9.1. Transport Equation Solver v1

Submission to the French agency of software protection of the software "Transport Equation Solver v1".

Ce logiciel répond aux besoins liés à l'analyse fonctionnelle de la vascularisation d'un organe par imagerie dynamique et en particulier il concerne l'analyse de la vascularisation placentaire qui est destinée au diagnostic d'anomalies d'invasion placentaire par échographie dynamique de contraste. De manière plus précise, ce logiciel permet, à partir d'un modèle physique d'écoulement des fluides, d'estimer et de quantifier le transport du produit de contraste injecté lors d'une imagerie par échographie dynamique de contraste.

PHOENIX-POST Team

5. New Software and Platforms

5.1. Allen

The Allen DSL for online context detection over binary sensors

KEYWORDS: DSL - Contextual service - Iot - Sensors - Data stream

SCIENTIFIC DESCRIPTION: There is a large variety of binary sensors in use today, and useful context-aware services can be defined using such binary sensors. However, the currently available approaches for programming context-aware services do not conveniently support binary sensors. Indeed, no existing approach simultaneously supports a notion of state, central to binary sensors, offers a complete set of operators to compose states, allows to define reusable abstractions by means of such compositions, and implements efficient online processing of these operators.

The Allen language proposes a new approach for event processing specifically targeted to binary sensors. The central contributions of this language are a native notion of state and semi-causal operators for temporal state composition including: Allen logic's interval relations generalized for handling multiple intervals, and temporal filters for handling delays. Compared to other approaches such as CEP (complex event processing), our language provides less discontinued information, allows less restricted compositions, and supports reusable abstractions. We implemented a compiler for our language and applied it to successfully rewrite a full set of real Ambient Assisted Living services. The performance of our prototype interpreter has been shown to compete well with a commercial CEP engine when expressing the same services.

FUNCTIONAL DESCRIPTION: Main concepts and features: * Signal: formalized as a boolean function of (discrete) time. A signal models either the current state of a physical sensor or a higher-level context depending on such sensors. The "states" of a signal are the time intervals where the signal is 1. * Precise semantics of an Allen program: based on the above model. Allows checking domain properties. * Operators: allow to combine signals for deriving more complex signals. Each operator takes a given number of signals and produces a signal. For instance, the logic operators "and", "or", "not" have their usual meaning, at each time point, unary operators up(s) and down(s) produces the starting/ending events of signal s. Binary operator during(p,q) produces a signal containing the states of p entirely contained in some state of q. * Parameterized operators: take, besides a given number of signals, a given number of scalar (numeric) parameters, such as temporal delays. For instance, the unary operators gt[T](s) and lt[T](s) produces signals containing only the states of s which are longer/shorter than some delay T. * Language constructs for defining new operators. For instance, "def up(s) = gt[1](s)" allows defining operator "up" above, based on the more primitive operator "gt". This feature enables the construction of user-defined abstractions, and thus creating layers of reusable pieces of context logic. * Online context detection: the computation in real time of contexts based on incoming streams of events produces by sensors.

RELEASE FUNCTIONAL DESCRIPTION: First public version.

- Author: Eugène Volanschi
- Contact: Eugène Volanschi
- URL: <https://github.com/NicVolanschi/Allen>

PLEIADE Team

6. New Software and Platforms

6.1. Magus

KEYWORDS: Bioinformatics - Genomic sequence - Knowledge database

SCIENTIFIC DESCRIPTION: MAGUS can be used on small installations with a web server and a relational database on a single machine, or scaled out in clusters or elastic clouds using Apache Cassandra for NoSQL data storage and Apache Hadoop for Map-Reduce.

FUNCTIONAL DESCRIPTION: The MAGUS genome annotation system integrates genome sequences and sequences features, in silico analyses, and views of external data resources into a familiar user interface requiring only a Web navigator. MAGUS implements annotation workflows and enforces curation standards to guarantee consistency and integrity. As a novel feature the system provides a workflow for simultaneous annotation of related genomes through the use of protein families identified by in silico analyses this has resulted in a three-fold increase in curation speed, compared to one-at-a-time curation of individual genes. This allows us to maintain standards of high-quality manual annotation while efficiently using the time of volunteer curators.

NEWS OF THE YEAR: Magus is now available as a Docker image, and can be integrated with other containerized services using Pleiade's Alcyone system.

- Participants: David Sherman, Florian Lajus, Natalia Golenetskaya, Pascal Durrens and Xavier Calcas
- Partners: Université de Bordeaux - CNRS - INRA
- Contact: David James Sherman
- Publication: [High-performance comparative annotation](#)
- URL: <http://magus.gforge.inria.fr>

6.2. Mimoza

KEYWORDS: Systems Biology - Bioinformatics - Biotechnology

FUNCTIONAL DESCRIPTION: Mimoza uses metabolic model generalization and cartographic paradigms to allow human experts to explore a metabolic model in a hierarchical manner. Mimoza generalizes genome-scale metabolic models, by factoring equivalent reactions and metabolites while preserving reaction consistency. The software creates a zoomable representation of a model submitted by the user in SBML format. The most general view represents the compartments of the model, the next view shows the visualization of generalized versions of reactions and metabolites in each compartment, and the most detailed view visualizes the initial model with the generalization-based layout (where similar metabolites and reactions are placed next to each other). The resulting map can be explored on-line, or downloaded in a COMBINE archive. The zoomable representation is implemented using the Leaflet JavaScript library for mobile-friendly interactive maps. Users can click on reactions and compounds to see the information about their annotations.

NEWS OF THE YEAR: Mimoza is now available as a Docker image, and can be integrated with other containerized services using Pleiade's Alcyone system.

- Participants: Anna Zhukova and David James Sherman
- Contact: David James Sherman
- Publications: [Knowledge-based generalization of metabolic models - Knowledge-based zooming for metabolic models - Knowledge-based generalization of metabolic networks: a practical study](#)
- URL: <http://mimoza.bordeaux.inria.fr/>

6.3. Declic

FUNCTIONAL DESCRIPTION: Declic is a Python library that provides several tools for data analysis in the domains of multivariate data analysis, machine learning, and graph based methods. It can be used to study in-depth the accuracy of the dictionary between molecular based and morphological based taxonomy.

Declic includes an interpreter for a Domain Specific Language (DSL) to make its Python library easy to use for scientists familiar with environments such as R.

- Partner: INRA
- Contact: Alain Franc

6.4. Diagno-Syst

diagno-syst: a tool for accurate inventories in metabarcoding

KEYWORDS: Biodiversity - Clustering - Ecology

FUNCTIONAL DESCRIPTION: Diagno-syst builds accurate inventories for biodiversity. It performs supervised clustering of reads obtained from a next-generation sequencing experiment, mapping onto an existing reference database, and assignment of taxonomic annotations.

- Participants: Alain Franc, Jean-Marc Frigerio, Philippe Chaumeil and Franck Salin
- Partner: INRA
- Contact: Alain Franc
- Publication: [diagno-syst: a tool for accurate inventories in metabarcoding](#)

6.5. Alcyone

Alcyone instantiates bioinformatics environments from specifications committed to a Git repository

KEYWORDS: Docker - Orchestration - Bioinformatics - Microservices - Versioning

SCIENTIFIC DESCRIPTION: Alcyone conceives the user's computing environment as a microservices architecture, where each bioinformatics tool in the specification is a separate containerized Docker service. Alcyone builds a master container for the specified environment that is responsible for building, updating, deploying and stopping these containers, as well as recording and sharing the environment in a Git repository. The master container can be manipulated using a command-line interface.

FUNCTIONAL DESCRIPTION: Alcyone defines a file structure for the specifying bioinformatics analysis environments, including tool choice, interoperability, and sources of raw data. These specifications are recorded in a Git repository. Alcyone compiles a specification into a master Docker container that deploys and orchestrates containers for each of the component tools. Alcyone can restore any version of an environment recorded in the Git repository.

NEWS OF THE YEAR: Alcyone was designed and implemented this year.

- Participants: Louise-Amelie Schmitt and David Sherman
- Contact: David Sherman
- URL: <https://team.inria.fr/pleiade/alcyone/>

6.6. family-3d

KEYWORDS: Biodiversity - Point cloud - 3D modeling

SCIENTIFIC DESCRIPTION: The method statistically selects a subset of pairwise distances between proteins in the family, constructs a weighted graph, and lays it out using an adaptation of the three-dimensional extension of the Kamada-Kawai force-directed layout.

FUNCTIONAL DESCRIPTION: Family-3D lays out high-dimension protein family point clouds in 3D space. The resulting lower-dimension forms can be printed, so that they can be explored and compared manually. They can also be explored interactively or stereographically.

Comparison of the 3D forms reveals classes of structurally similar families, whose characteristic shapes correspond to different evolutionary scenarios. Some of these scenarios are: neofunctionalization, subfunctionalization, founder gene effect, ancestral family.

To facilitate curator training, Family-3D includes an interactive terminal containing a microcontroller, an RFID reader, and an LED ring. A set of shapes that fall in predetermined classes is printed, with a unique RFID tag in each shape. Trainees classify family shapes by manual inspection and submit their classes to the terminal, which evaluates the proposed class and provides visual feedback.

- Participant: David Sherman
- Contact: David Sherman
- URL: <https://gitlab.inria.fr/pleiade/family-3d>

6.7. magecal

KEYWORD: Genomics

SCIENTIFIC DESCRIPTION: Magecal independently runs training and prediction steps for Augustus, Conrad, GeneID, GeneMark, and Snap. The results are cleaned and integrated into a common format. Jigsaw is trained and used for model reconciliation. Consistency constraints are applied to ensure that phase and intron structure are biologically plausible.

FUNCTIONAL DESCRIPTION: Magecal predicts a set of protein coding genes in fungal genomic sequences, using different de novo prediction algorithms, and reconciling the predictions with the aid of comparative data. Magecal applies consistency constraints to guarantee that the predicted genes are biologically valid.

RELEASE FUNCTIONAL DESCRIPTION: Dockerization and compatibility with Alcyone

- Participants: Pascal Durrens and David Sherman
- Contact: David Sherman
- URL: <https://gitlab.inria.fr/magecal/magecal>

6.8. AsebaHub

Turn-key bridging of Aseba mobile robots to wifi networks

KEYWORD: Robotics

SCIENTIFIC DESCRIPTION: Aseba is an open-source modular architecture for event-based control of multi-microcontroller robots, used in the Thymio-II educational robot, and integrated into development environments for teaching robotics programming to 8-18 year old children. Since 2014 Inria has contributed several modules to Aseba, including mDNS-sd support for discovering TCP/IP connections, an HTTP bridge that allows Aseba robots to be used with the Scratch programming environment, and photo-realistic 2D simulation.

Thymio-II robots only communicate through USB connections from a host computer, so until now it has been necessary to install Aseba software on that computer. This is not always possible in schools.

AsebaHub is a firmware image for wifi routers that takes responsibility for USB communication with Aseba robots. Each robot is exposed as a TCP/IP target, advertised using mDNS-sd. AsebaHub can group robots together in ad hoc Aseba networks. It provides HTTP access to robots so that they can be used with Scratch or Snap!. These services work out of the box, without any host configuration or software installation.

AsebaHub can operate as a wifi Access Point, or as a network Bridge to an existing local-area network. A slide switch on the side of the router seamlessly switches between these configurations.

AsebaHub is implemented by compiling Aseba software for the OpenWrt/LEDE open source router platform, adding interfacing code that automatically associates new robots, starts and stops the corresponding network services, and provides a web-based administrative interface.

FUNCTIONAL DESCRIPTION: AsebaHub is a small device with a USB port for connecting Aseba robots, single or with a USB hub. Every robot is made available as a network target on the wifi and wired local-area networks, where they can be discovered using mDNS-sd (Zeroconf/Bonjour). No network or user configuration is necessary.

AsebaHub works out of the box with the Aseba Studio and VPL programming environments. AsebaHub can be configured to also provide an HTTP service that is compatible with Scratch or other environments.

AsebaHub acts as either a wireless Access Point to which users may connect, or as a Bridge to an existing local-area network. Either configuration can be chosen seamlessly with the flick of a switch.

- Participants: David Sherman and Louise-Amelie Schmitt
- Contact: David Sherman

POTIOC Project-Team

6. New Software and Platforms

6.1. Aïana

KEYWORD: Multimedia player

FUNCTIONAL DESCRIPTION: This software aims to make accessible the playing of a MOOC composed of various information flows (boards, videos, subtitles ...). It is not intended to be "reserved" for people with disabilities but rather to be open to as many as possible by allowing each user to adapt the interface, and therefore the use, to its users own capabilities and needs.

- Authors: Damien Caselli, Pierre-Antoine Cinquin, Pascal Guitton and H el ene Sauz eon
- Partner: Universit e de Bordeaux
- Contact: Pascal Guitton
- Publications: [Towards Truly Accessible MOOCs for Persons with Cognitive Disabilities: Design and Field Assessment - Online e-learning and cognitive disabilities: A systematic review](#)

6.2. HybridOptics : Hybrid Optical Platform

KEYWORDS: Augmented reality - Education - Tangible interface

FUNCTIONAL DESCRIPTION: The software platform - gets the values of the sensors - computes in real-time the result of the simulation - generates pedagogical supports that are directly linked to the simulation (projected on the work table) - allows the user to control several parameters from a dedicated application on a tablet

- Participants: Beno t Coulais, Lionel Canioni, Bruno Bousquet, Martin Hachet and Jean-Paul Guillet
- Contact: Martin Hachet
- URL: <https://project.inria.fr/hobit/>

6.3. Platforms

6.3.1. HOBIT

In 2018, we have continued working on the HOBIT platform dedicated to teaching and training of Optics at University. We have notably improved the hardware side, as illustrated in Figure 3 .

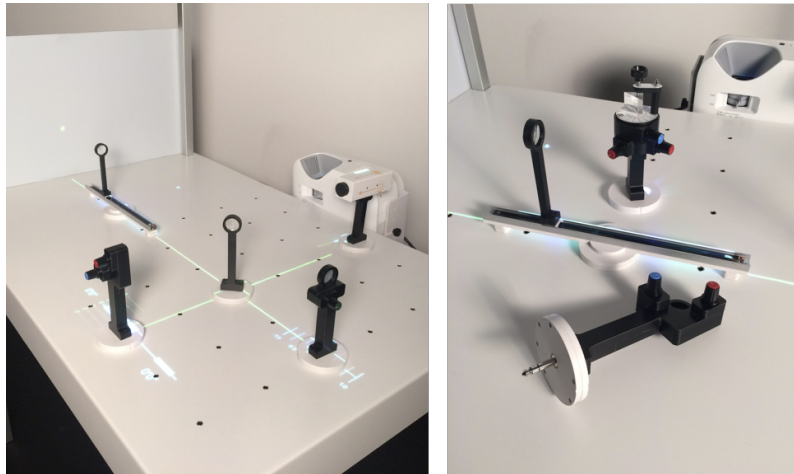


Figure 3. The new version of HOBIT. Users can easily plug fake optical components (e.g. source lights, mirrors and lens) anywhere on the table to build their optical experiment.

REALOPT Project-Team

6. New Software and Platforms

6.1. BaPCod

A generic Branch-And-Price-And-Cut Code

KEYWORDS: Column Generation - Branch-and-Price - Branch-and-Cut - Mixed Integer Programming - Mathematical Optimization - Benders Decomposition - Dantzig-Wolfe Decomposition - Extended Formulation

FUNCTIONAL DESCRIPTION: BaPCod is a prototype code that solves Mixed Integer Programs (MIP) by application of reformulation and decomposition techniques. The reformulated problem is solved using a branch-and-price-and-cut (column generation) algorithms, Benders approaches, network flow and dynamic programming algorithms. These methods can be combined in several hybrid algorithms to produce exact or approximate solutions (primal solutions with a bound on the deviation to the optimum).

- Participants: Artur Alves Pessoa, Boris Detienne, Eduardo Uchoa Barboza, Franck Labat, François Clautiaux, François Vanderbeck, Halil Sen, Issam Tahiri, Michael Poss, Pierre Pesneau, Romain Leguay and Ruslan Sadykov
- Partners: Université de Bordeaux - CNRS - IPB - Universidade Federal Fluminense
- Contact: François Vanderbeck
- URL: <https://wiki.bordeaux.inria.fr/realopt/pmwiki.php/Project/BaPCod>

6.2. WineryPlanning

- Participants: Agnes Le Roux, Alexis Toullat, François Vanderbeck, Issam Tahiri and Ruslan Sadykov
- Contact: François Vanderbeck

6.3. ORTOJ

Operation Research Tools Under Julia

KEYWORDS: Modeling - Processing - Dashboard

FUNCTIONAL DESCRIPTION: This set of tools currently includes : 1) BlockJuMP.jl: extension of JuMP to model decomposable mathematical programs (using either Benders or Dantzig-Wolfe decomposition paradigm) 2) Scanner.jl: a default data parser to ease the reading of the input data in the form that they are often encountered in operational research. 3) BenchmarkUtils.jl: Tools to ease the setup of numerical experiments to benchmark algorithmic feature performances. The test automation permits to quickly calibrate the parameters of an arbitrary algorithm control function.

- Participants: François Vanderbeck, Guillaume Marques, Issam Tahiri and Ruslan Sadykov
- Contact: Issam Tahiri

6.4. pmtool

KEYWORDS: Scheduling - Task scheduling - StarPU - Heterogeneity - GPGPU - Performance analysis

FUNCTIONAL DESCRIPTION: Analyse post-mortem the behavior of StarPU applications. Provide lower bounds on makespan. Study the performance of different schedulers in a simple context. Provide implementations of many scheduling algorithms from the literature

NEWS OF THE YEAR: Included many new algorithms, in particular online algorithms Better integration with StarPU by accepting .rec files as input

- Participant: Lionel Eyraud-Dubois
- Contact: Lionel Eyraud-Dubois
- Publications: [Approximation Proofs of a Fast and Efficient List Scheduling Algorithm for Task-Based Runtime Systems on Multicores and GPUs - Fast Approximation Algorithms for Task-Based Runtime Systems](#)
- URL: <https://gitlab.inria.fr/eyrauddu/pmtool>

6.5. Platforms

6.5.1. Bapcod

We have developed a stabilized Benders' decomposition in our generic library BapCod. This allowed to produce state-of-the-art results for an energy production planning.

SISTM Project-Team

6. New Software and Platforms

6.1. marqLevAlg

KEYWORDS: Optimization - Biostatistics

FUNCTIONAL DESCRIPTION: An R package for function optimization. Available on CRAN, this package performs a minimization of function based on the Marquardt-Levenberg algorithm. This package is really useful when the surface to optimize is non-strictly convex or far from a quadratic function. A new convergence criterion, the relative distance to maximum (RDM), allows the user to have a better confidence in the stopping points, other than basic algorithm stabilization.

- Contact: Melanie Prague
- URL: <https://cran.r-project.org/web/packages/marqLevAlg/index.html>

6.2. VSURF

Variable Selection Using Random Forests

KEYWORDS: Classification - Statistics - Machine learning - Regression

FUNCTIONAL DESCRIPTION: An R package for Variable Selection Using Random Forests. Available on CRAN, this package performs an automatic (meaning completely data-driven) variable selection procedure. Originally designed to deal with high dimensional data, it can also be applied to standard datasets.

- Contact: Robin Genuer
- URL: <https://github.com/robingenuer/VSURF>

6.3. NPflow

Bayesian Nonparametrics for Automatic Gating of Flow-Cytometry Data

KEYWORDS: Bayesian estimation - Bioinformatics - Biostatistics

FUNCTIONAL DESCRIPTION: Dirichlet process mixture of multivariate normal, skew normal or skew t-distributions modeling oriented towards flow-cytometry data pre-processing applications.

- Contact: Boris Hejblum
- URL: <https://cran.r-project.org/web/packages/NPflow/>

6.4. COVVSURF

Combination of Clustering Of Variables and Variable Selection Using Random Forests

KEYWORDS: Classification - Statistics - Cluster - Machine learning - Regression

- Contact: Robin Genuer
- URL: <https://github.com/robingenuer/CoVVSURF>

6.5. clogitLasso

KEYWORDS: Biostatistics - Bioinformatics - Machine learning - Regression

FUNCTIONAL DESCRIPTION: R package to fit a sequence of conditional logistic regression models with lasso, for small to large sized samples.

RELEASE FUNCTIONAL DESCRIPTION: Optimisation

- Partner: DRUGS-SAFE
- Contact: Marta Avalos Fernandez
- URL: <https://cran.r-project.org/web/packages/clogitLasso/index.html>

6.6. TcGSA

Time-course Gene Set Analysis

KEYWORDS: Bioinformatics - Genomics

FUNCTIONAL DESCRIPTION: An R package for the gene set analysis of longitudinal gene expression data sets. This package implements a Time-course Gene Set Analysis method and provides useful plotting functions facilitating the interpretation of the results.

- Contact: Boris Hejblum
- URL: <https://cran.r-project.org/web/packages/TcGSA/index.html>

6.7. NIMROD

Normal approximation Inference in Models with Random effects based on Ordinary Differential equations

KEYWORDS: Ordinary differential equations - Statistical modeling

FUNCTIONAL DESCRIPTION: We have written a specific program called NIMROD for estimating parameter of ODE based population models.

- Contact: Melanie Prague
- URL: <http://etudes.isped.u-bordeaux2.fr/BIOSTATISTIQUE/NIMROD/documentation/html/index.html>

6.8. tcgsaseq

Time-Course Gene Set Analysis for RNA-Seq Data

KEYWORDS: Genomics - Biostatistics - Statistical modeling - RNA-seq - Gene Set Analysis

FUNCTIONAL DESCRIPTION: Gene set analysis of longitudinal RNA-seq data with variance component score test accounting for data heteroscedasticity through precision weights.

- Contact: Boris Hejblum
- URL: <https://cran.r-project.org/web/packages/tcgsaseq/index.html>

6.9. cytometree

KEYWORDS: Clustering - Biostatistics - Bioinformatics

FUNCTIONAL DESCRIPTION: Given the hypothesis of a bimodal distribution of cells for each marker, the algorithm constructs a binary tree, the nodes of which are subpopulations of cells. At each node, observed cells and markers are modeled by both a family of normal distributions and a family of bimodal normal mixture distributions. Splitting is done according to a normalized difference of AIC between the two families.

- Contact: Boris Hejblum
- URL: <https://cran.r-project.org/web/packages/cytometree/index.html>

6.10. CRTgeeDR

KEYWORDS: Missing data - Statistics - Regression

FUNCTIONAL DESCRIPTION: The CRTgeeDR package allows you to estimate parameters in a regression model (with possibly a link function). It allows treatment augmentation and IPW for missing outcome. It is particularly of use when the goal is to estimate the intervention effect of a prevention strategy against epidemics in cluster randomised trials.

- Contact: Melanie Prague
- URL: <https://cran.r-project.org/web/packages/CRTgeeDR/index.html>

6.11. ludic

KEYWORDS: Probability - Biostatistics

FUNCTIONAL DESCRIPTION: An R package to perform probabilistic record Linkage Using only Diagnosis Codes without direct identifiers, using C++ code to speed up computations. Available on CRAN, development version on github.

- Contact: Boris Hejblum
- URL: <https://cran.r-project.org/web/packages/ludic/index.html>

6.12. CoDaPCA

KEYWORDS: Unsupervised learning - PCA

FUNCTIONAL DESCRIPTION: R functions associated to the article Avalos et al. Representation Learning of Compositional Data. NeurIPS 2018 <http://papers.nips.cc/paper/7902-representation-learning-of-compositional-data>

- Contact: Marta Avalos Fernandez
- URL: <https://github.com/sistm/CoDa-PCA>

6.13. Left-censored Lasso

KEYWORDS: Biostatistics - Machine learning

FUNCTIONAL DESCRIPTION: R function associated to the article Soret et al. Lasso regularization for left-censored Gaussian outcome and high-dimensional predictors. BMC Medical Research Methodology (2018) 18:159 <https://doi.org/10.1186/s12874-018-0609-4>

RELEASE FUNCTIONAL DESCRIPTION: <https://github.com/psBiostat/left-censored-Lasso>

- Contact: Marta Avalos Fernandez

6.14. dd-sPLS

Data-Driven Sparse PLS

KEYWORDS: Marker selection - Classification - Regression - Missing data - Multi-Block - High Dimensional Data - PLS - SVD

FUNCTIONAL DESCRIPTION: Allows to build Multi-Data-Driven Sparse PLS models. Multi-blocks with high-dimensional settings are particularly sensible to this. Whatsmore it deals with missing samples (entire lines missing per block) thanks to the Koh-Lanta algorithm. SVD decompositions permit to offer a fast and controlled method.

- Contact: Hadrien Lorenzo
- URL: <https://hadrienlorenzo.netlify.com/projects/ddspl/>

6.15. kernscr

KEYWORDS: Genomics - Biostatistics

FUNCTIONAL DESCRIPTION: An R package to perform KERNel machine score test for pathway analysis in the presence of Semi-Competing Risks

- Contact: Boris Hejblum
- URL: <https://CRAN.R-project.org/package=kernscr>

6.16. phenotypr

KEYWORDS: Phenotyping - Automatic labelling - Automatic Learning

FUNCTIONAL DESCRIPTION: Machine learning prediction algorithm for predicting a clinical phenotype from structured diagnostic data and CUI occurrence data collected from medical reports, previously processed by NLP approaches.

- Contact: Boris Hejblum
- URL: <https://github.com/borishejblum/phenotypr>

6.17. R2GUESS

Graphical processing Unit Evolutionary Stochastic Search

FUNCTIONAL DESCRIPTION: R2GUESS package is a wrapper of the GUESS (Graphical processing Unit Evolutionary Stochastic Search) program. GUESS is a computationally optimised C++ implementation of a fully Bayesian variable selection approach that can analyse, in a genome-wide context, single and multiple responses in an integrated way. The program uses packages from the GNU Scientific Library (GSL) and offers the possibility to re-route computationally intensive linear algebra operations towards the Graphical Processing Unit (GPU) through the use of proprietary CULA-dense library.

- Contact: Rodolphe Thiebaut

STORM Project-Team

6. New Software and Platforms

6.1. Chameleon

KEYWORDS: Runtime system - Task-based algorithm - Dense linear algebra - HPC - Task scheduling

SCIENTIFIC DESCRIPTION: Chameleon is part of the MORSE (Matrices Over Runtime Systems @ Exascale) project. The overall objective is to develop robust linear algebra libraries relying on innovative runtime systems that can fully benefit from the potential of those future large-scale complex machines.

We expect advances in three directions based first on strong and closed interactions between the runtime and numerical linear algebra communities. This initial activity will then naturally expand to more focused but still joint research in both fields.

1. Fine interaction between linear algebra and runtime systems. On parallel machines, HPC applications need to take care of data movement and consistency, which can be either explicitly managed at the level of the application itself or delegated to a runtime system. We adopt the latter approach in order to better keep up with hardware trends whose complexity is growing exponentially. One major task in this project is to define a proper interface between HPC applications and runtime systems in order to maximize productivity and expressivity. As mentioned in the next section, a widely used approach consists in abstracting the application as a DAG that the runtime system is in charge of scheduling. Scheduling such a DAG over a set of heterogeneous processing units introduces a lot of new challenges, such as predicting accurately the execution time of each type of task over each kind of unit, minimizing data transfers between memory banks, performing data prefetching, etc. Expected advances: In a nutshell, a new runtime system API will be designed to allow applications to provide scheduling hints to the runtime system and to get real-time feedback about the consequences of scheduling decisions.

2. Runtime systems. A runtime environment is an intermediate layer between the system and the application. It provides low-level functionality not provided by the system (such as scheduling or management of the heterogeneity) and high-level features (such as performance portability). In the framework of this proposal, we will work on the scalability of runtime environment. To achieve scalability it is required to avoid all centralization. Here, the main problem is the scheduling of the tasks. In many task-based runtime environments the scheduler is centralized and becomes a bottleneck as soon as too many cores are involved. It is therefore required to distribute the scheduling decision or to compute a data distribution that impose the mapping of task using, for instance the so-called “owner-compute” rule. Expected advances: We will design runtime systems that enable an efficient and scalable use of thousands of distributed multicore nodes enhanced with accelerators.

3. Linear algebra. Because of its central position in HPC and of the well understood structure of its algorithms, dense linear algebra has often pioneered new challenges that HPC had to face. Again, dense linear algebra has been in the vanguard of the new era of petascale computing with the design of new algorithms that can efficiently run on a multicore node with GPU accelerators. These algorithms are called “communication-avoiding” since they have been redesigned to limit the amount of communication between processing units (and between the different levels of memory hierarchy). They are expressed through Direct Acyclic Graphs (DAG) of fine-grained tasks that are dynamically scheduled. Expected advances: First, we plan to investigate the impact of these principles in the case of sparse applications (whose algorithms are slightly more complicated but often rely on dense kernels). Furthermore, both in the dense and sparse cases, the scalability on thousands of nodes is still limited, new numerical approaches need to be found. We will specifically design sparse hybrid direct/iterative methods that represent a promising approach.

Overall end point. The overall goal of the MORSE associate team is to enable advanced numerical algorithms to be executed on a scalable unified runtime system for exploiting the full potential of future exascale machines.

FUNCTIONAL DESCRIPTION: Chameleon is a dense linear algebra software relying on sequential task-based algorithms where sub-tasks of the overall algorithms are submitted to a Runtime system. A Runtime system such as StarPU is able to manage automatically data transfers between not shared memory area (CPUs-GPUs, distributed nodes). This kind of implementation paradigm allows to design high performing linear algebra algorithms on very different type of architecture: laptop, many-core nodes, CPUs-GPUs, multiple nodes. For example, Chameleon is able to perform a Cholesky factorization (double-precision) at 80 TFlop/s on a dense matrix of order 400 000 (e.i. 4 min).

RELEASE FUNCTIONAL DESCRIPTION: Chameleon includes the following features:

- BLAS 3, LAPACK one-sided and LAPACK norms tile algorithms - Support QUARK and StarPU runtime systems and PaRSEC since 2018 - Exploitation of homogeneous and heterogeneous platforms through the use of BLAS/LAPACK CPU kernels and cuBLAS/MAGMA CUDA kernels - Exploitation of clusters of interconnected nodes with distributed memory (using OpenMPI)

- Participants: Cédric Castagnede, Samuel Thibault, Emmanuel Agullo, Florent Pruvost and Mathieu Faverge
- Partners: Innovative Computing Laboratory (ICL) - King Abdullha University of Science and Technology - University of Colorado Denver
- Contact: Emmanuel Agullo
- URL: <https://gitlab.inria.fr/solverstack/chameleon>

6.2. hwloc

Hardware Locality

KEYWORDS: NUMA - Multicore - GPU - Affinities - Open MPI - Topology - HPC - Locality

FUNCTIONAL DESCRIPTION: Hardware Locality (hwloc) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices. It builds a widely-portable abstraction of these resources and exposes it to applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

hwloc targets many types of high-performance computing applications, from thread scheduling to placement of MPI processes. Most existing MPI implementations, several resource managers and task schedulers, and multiple other parallel libraries already use hwloc.

- Participants: Brice Goglin and Samuel Thibault
- Partners: Open MPI consortium - Intel - AMD
- Contact: Brice Goglin
- Publications: [hwloc: a Generic Framework for Managing Hardware Affinities in HPC Applications](#) - [Managing the Topology of Heterogeneous Cluster Nodes with Hardware Locality \(hwloc\)](#) - [A Topology-Aware Performance Monitoring Tool for Shared Resource Management in Multicore Systems](#) - [Exposing the Locality of Heterogeneous Memory Architectures to HPC Applications](#) - [Towards the Structural Modeling of the Topology of next-generation heterogeneous cluster Nodes with hwloc](#) - [On the Overhead of Topology Discovery for Locality-aware Scheduling in HPC](#)
- URL: <http://www.open-mpi.org/projects/hwloc/>

6.3. KaStORS

The KaStORS OpenMP Benchmark Suite

KEYWORDS: Benchmarking - HPC - Task-based algorithm - Task scheduling - OpenMP - Data parallelism

FUNCTIONAL DESCRIPTION: The KaStORS benchmarks suite has been designed to evaluate implementations of the OpenMP dependent task paradigm, introduced as part of the OpenMP 4.0 specification.

- Participants: François Broquedis, Nathalie Furmento, Olivier Aumage, Philippe Virouleau, Pierrick Brunet, Samuel Thibault and Thierry Gautier
- Contact: Thierry Gautier
- URL: <http://kastors.gforge.inria.fr/#!/index.md>

6.4. KStar

The KStar OpenMP Compiler

KEYWORDS: Source-to-source compiler - OpenMP - Task scheduling - Compilers - Data parallelism

FUNCTIONAL DESCRIPTION: The KStar software is a source-to-source OpenMP compiler for languages C and C++. The KStar compiler translates OpenMP directives and constructs into API calls from the StarPU runtime system or the XKaapi runtime system. The KStar compiler is virtually fully compliant with OpenMP 3.0 constructs. The KStar compiler supports OpenMP 4.0 dependent tasks and accelerated targets.

- Participants: Nathalie Furmento, Olivier Aumage, Philippe Virouleau and Samuel Thibault
- Contact: Olivier Aumage
- Publications: [Bridging the gap between OpenMP and task-based runtime systems for the fast multipole method](#) - [Bridging the gap between OpenMP 4.0 and native runtime systems for the fast multipole method](#) - [Evaluation of OpenMP Dependent Tasks with the KASTORS Benchmark Suite](#)
- URL: <http://kstar.gforge.inria.fr/#!/index.md>

6.5. MAQAO

SCIENTIFIC DESCRIPTION: MAQAO relies on binary codes for Intel x86 and ARM architectures. For x86 architecture, it can insert probes for instrumentation directly inside the binary. There is no need to recompile. The static/dynamic approach of MAQAO analysis is the main originality of the tool, combining performance model with values collected through instrumentation.

MAQAO has a static performance model for x86 and ARM architectures. This model analyzes performance of the codes on the architectures and provides some feed-back hints on how to improve these codes, in particular for vector instructions.

The dynamic collection of data in MAQAO enables the analysis of thread interactions, such as false sharing, amount of data reuse, runtime scheduling policy, ...

FUNCTIONAL DESCRIPTION: MAQAO is a performance tuning tool for OpenMP parallel applications. It relies on the static analysis of binary codes and the collection of dynamic information (such as memory traces). It provides hints to the user about performance bottlenecks and possible workarounds.

- Participants: Christopher Haine, Denis Barthou, James Tombi A Mba and Olivier Aumage
- Contact: Denis Barthou

6.6. StarPU

The StarPU Runtime System

KEYWORDS: Multicore - GPU - Scheduling - HPC - Performance

SCIENTIFIC DESCRIPTION: Traditional processors have reached architectural limits which heterogeneous multicore designs and hardware specialization (eg. coprocessors, accelerators, ...) intend to address. However, exploiting such machines introduces numerous challenging issues at all levels, ranging from programming models and compilers to the design of scalable hardware solutions. The design of efficient runtime systems for these architectures is a critical issue. StarPU typically makes it much easier for high performance libraries or compiler environments to exploit heterogeneous multicore machines possibly equipped with GPGPUs or Cell processors: rather than handling low-level issues, programmers may concentrate on algorithmic concerns. Portability is obtained by the means of a unified abstraction of the machine. StarPU offers a unified offloadable task abstraction named "codelet". Rather than rewriting the entire code, programmers can encapsulate existing functions within codelets. In case a codelet may run on heterogeneous architectures, it is possible to specify one function for each architectures (eg. one function for CUDA and one function for CPUs). StarPU takes care to schedule and execute those codelets as efficiently as possible over the entire machine. In order to relieve programmers from the burden of explicit data transfers, a high-level data management library enforces memory coherency over the machine: before a codelet starts (eg. on an accelerator), all its data are transparently made available on the compute resource. Given its expressive interface and portable scheduling policies, StarPU obtains portable performances by efficiently (and easily) using all computing resources at the same time. StarPU also takes advantage of the heterogeneous nature of a machine, for instance by using scheduling strategies based on auto-tuned performance models.

StarPU is a task programming library for hybrid architectures

The application provides algorithms and constraints: - CPU/GPU implementations of tasks - A graph of tasks, using either the StarPU's high level GCC plugin pragmas or StarPU's rich C API

StarPU handles run-time concerns - Task dependencies - Optimized heterogeneous scheduling - Optimized data transfers and replication between main memory and discrete memories - Optimized cluster communications

Rather than handling low-level scheduling and optimizing issues, programmers can concentrate on algorithmic concerns!

FUNCTIONAL DESCRIPTION: StarPU is a runtime system that offers support for heterogeneous multicore machines. While many efforts are devoted to design efficient computation kernels for those architectures (e.g. to implement BLAS kernels on GPUs), StarPU not only takes care of offloading such kernels (and implementing data coherency across the machine), but it also makes sure the kernels are executed as efficiently as possible.

- Participants: Corentin Salingue, Andra Hugo, Benoît Lize, Cédric Augonnet, Cyril Roelandt, François Tessier, Jérôme Clet-Ortega, Ludovic Courtes, Ludovic Stordeur, Marc Sergent, Mehdi Juhoor, Nathalie Furmento, Nicolas Collin, Olivier Aumage, Pierre-André Wacrenier, Raymond Namyst, Samuel Thibault, Simon Archipoff, Xavier Lacoste, Terry Cojean, Yanis Khorsi, Philippe Virouleau, LOïc JOUANS and Leo Villeveygoux
- Contact: Olivier Aumage
- Publications: [Achieving High Performance on Supercomputers with a Sequential Task-based Programming Model](#) - [The StarPU Runtime System at Exascale ?](#) - [Analyzing Dynamic Task-Based Applications on Hybrid Platforms: An Agile Scripting Approach](#) - [Resource aggregation for task-based Cholesky Factorization on top of heterogeneous machines](#) - [Resource aggregation in task-based applications over accelerator-based multicore machines](#) - [Controlling the Memory Subscription of Distributed Applications with a Task-Based Runtime System](#) - [Exploiting Two-Level Parallelism by Aggregating Computing Resources in Task-Based Applications Over Accelerator-Based Machines](#) - [Exploiting Two-Level Parallelism by Aggregating Computing Resources in Task-Based Applications Over Accelerator-Based Machines](#) - [Achieving High Performance on Supercomputers with a Sequential Task-based Programming Model](#) - [Bridging the gap between OpenMP 4.0 and native runtime systems for the fast multipole method](#) - [Scalability of a task-based runtime system for dense linear algebra applications](#) - [Faithful Performance Prediction of a Dynamic Task-Based Runtime](#)

System for Heterogeneous Multi-Core Architectures - Towards seismic wave modeling on heterogeneous many-core architectures using task-based runtime system - Bridging the Gap between Performance and Bounds of Cholesky Factorization on Heterogeneous Platforms - Composing multiple StarPU applications over heterogeneous machines: A supervised approach - Evaluation of OpenMP Dependent Tasks with the KASTORS Benchmark Suite - A runtime approach to dynamic resource allocation for sparse direct solvers - Modeling and Simulation of a Dynamic Task-Based Runtime System for Heterogeneous Multi-Core Architectures - Toward OpenCL Automatic Multi-Device Support - Harnessing clusters of hybrid nodes with a sequential task-based programming model - Taking advantage of hybrid systems for sparse direct solvers via task-based runtimes - Modulariser les ordonnanceurs de tâches : une approche structurelle - Overview of Distributed Linear Algebra on Hybrid Nodes over the StarPU Runtime - StarPU-MPI: Task Programming over Clusters of Machines Enhanced with Accelerators - Modeling and Simulation of a Dynamic Task-Based Runtime System for Heterogeneous Multi-Core Architectures - Taking advantage of hybrid systems for sparse direct solvers via task-based runtimes - Adaptive Task Size Control on High Level Programming for GPU/CPU Work Sharing - Composing multiple StarPU applications over heterogeneous machines: a supervised approach - Implementation of FEM Application on GPU with StarPU - Le problème de la composition parallèle : une approche supervisée - Support exécutif scalable pour les architectures hybrides distribuées - SOCL: An OpenCL Implementation with Automatic Multi-Device Adaptation Support - C Language Extensions for Hybrid CPU/GPU Programming with StarPU - Programming Models and Runtime Systems for Heterogeneous Architectures - Programmation unifiée multi-accélérateur OpenCL - StarPU-MPI: Task Programming over Clusters of Machines Enhanced with Accelerators - Parallelization on Heterogeneous Multicore and Multi-GPU Systems of the Fast Multipole Method for the Helmholtz Equation Using a Runtime System - High-Level Support for Pipeline Parallelism on Many-Core Architectures - Programmability and Performance Portability Aspects of Heterogeneous Multi-/Manycore Systems - Programmation des architectures hétérogènes à l'aide de tâches divisibles - StarPU: a unified platform for task scheduling on heterogeneous multicore architectures - PEPPIER: Efficient and Productive Usage of Hybrid Computing Systems - The PEPPIER Approach to Programmability and Performance Portability for Heterogeneous many-core Architectures - Flexible runtime support for efficient skeleton programming on hybrid systems - LU Factorization for Accelerator-based Systems - QR Factorization on a Multicore Node Enhanced with Multiple GPU Accelerators - Programmation multi-accélérateurs unifiée en OpenCL - Détection optimale des coins et contours dans des bases d'images volumineuses sur architectures multicœurs hétérogènes - Association de modèles de programmation pour l'exploitation de clusters de GPUs dans le calcul intensif - Programming heterogeneous, accelerator-based multicore machines: current situation and main challenges - Scheduling Tasks over Multicore machines enhanced with accelerators: a Runtime System's Perspective - Composabilité de codes parallèles sur architectures hétérogènes - Data-Aware Task Scheduling on Multi-Accelerator based Platforms - Dynamically scheduled Cholesky factorization on multicore architectures with GPU accelerators. - StarPU: a Runtime System for Scheduling Tasks over Accelerator-Based Multicore Machines - StarPU : un support exécutif unifié pour les architectures multicœurs hétérogènes - Automatic Calibration of Performance Models on Heterogeneous Multicore Architectures - StarPU: A Unified Platform for Task Scheduling on Heterogeneous Multicore Architectures - Exploiting the Cell/BE architecture with the StarPU unified runtime system - Bridging the gap between OpenMP and task-based runtime systems for the fast multipole method

- URL: <http://starpu.gforge.inria.fr/>

6.7. PARCOACH

PARallel Control flow Anomaly CHecker

KEYWORDS: High-Performance Computing - Program verification - Debug - MPI - OpenMP - Compilation

SCIENTIFIC DESCRIPTION: PARCOACH verifies programs in two steps. First, it statically verifies applications with a data- and control-flow analysis and outlines execution paths leading to potential deadlocks. The code is then instrumented, displaying an error and synchronously interrupting all processes if the actual scheduling leads to a deadlock situation.

FUNCTIONAL DESCRIPTION: Supercomputing plays an important role in several innovative fields, speeding up prototyping or validating scientific theories. However, supercomputers are evolving rapidly with now millions of processing units, posing the questions of their programmability. Despite the emergence of more widespread and functional parallel programming models, developing correct and effective parallel applications still remains a complex task. As current scientific applications mainly rely on the Message Passing Interface (MPI) parallel programming model, new hardware designed for Exascale with higher node-level parallelism clearly advocate for an MPI+X solutions with X a thread-based model such as OpenMP. But integrating two different programming models inside the same application can be error-prone leading to complex bugs - mostly detected unfortunately at runtime. PARallel Control flow Anomaly CHEcker aims at helping developers in their debugging phase.

- Participants: Emmanuelle Saillard, Denis Barthou and Pierre Huchant
- Partner: CEA
- Contact: Emmanuelle Saillard
- URL: <https://esaillar.github.io/PARCOACH/>

6.8. AFF3CT

A Fast Forward Error Correction Toolbox

KEYWORDS: High-Performance Computing - Signal processing - Error Correction Code

FUNCTIONAL DESCRIPTION: AFF3CT proposes high performance Error Correction algorithms for Polar, Turbo, LDPC, RSC (Recursive Systematic Convolutional), Repetition and RA (Repeat and Accumulate) codes. These signal processing codes can be parameterized in order to optimize some given metrics, such as Bit Error Rate, Bandwidth, Latency, ...using simulation. For the designers of such signal processing chain, AFF3CT proposes also high performance building blocks so to develop new algorithms. AFF3CT compiles with many compilers and runs on Windows, Mac OS X, Linux environments and has been optimized for x86 (SSE, AVX instruction sets) and ARM architectures (NEON instruction set).

- Authors: Adrien Cassagne, Bertrand Le Gal, Camille Leroux, Denis Barthou and Olivier Aumage
- Partner: IMS
- Contact: Adrien Cassagne
- URL: <https://aff3ct.github.io/>

6.9. MORSE

KEYWORDS: High performance computing - Matrix calculation - Fast multipole method - Runtime system

FUNCTIONAL DESCRIPTION: MORSE (Matrices Over Runtime Systems @ Exascale) is a scientific project, its objectives are to solve matrix problems on complex architectures, using runtime systems. More specifically, the goal is to write codes that reach a high level of performance for all architectures. The algorithms are written independently of the architecture, and the runtime system dispatches the different computational parts to the different computing units. This methodology has been validated on three classes of problems: dense linear algebra, sparse and dense, and fast multipole methods. The corresponding codes have been incorporated into several softwares, MAGMA, Pastix and ScalFMM.

- Contact: Emmanuel Agullo
- URL: <http://icl.cs.utk.edu/morse/>

6.10. SwLoc

Software Contexts for Locality

KEYWORDS: HPC - Locality - Contexts - Multicore - GPU

FUNCTIONAL DESCRIPTION: SwLoc is a library for flexible and generic partitioning of computing resources (processors, accelerators) to be able to co-execute confined parallel regions which can rely on different runtime systems (e.g. OpenMP, Intel TBB, StarPU, etc.). With all different hypervisor strategies, It is possible to adapt dynamically the computing resources of each context, in order to match each parallel region's need as closely as possible.

- Contact: Corentin Salingue
- URL: <http://swloc.gforge.inria.fr/>

6.11. VITE

Visual Trace Explorer

KEYWORDS: Visualization - Execution trace

FUNCTIONAL DESCRIPTION: ViTE is a trace explorer. It is a tool made to visualize execution traces of large parallel programs. It supports Pajé, a trace format created by Inria Grenoble, and OTF and OTF2 formats, developed by the University of Dresden and allows the programmer a simpler way to analyse, debug and/or profile large parallel applications.

- Participant: Mathieu Faverge
- Contact: Mathieu Faverge
- URL: <http://vite.gforge.inria.fr/>

TADAAM Project-Team

6. New Software and Platforms

6.1. Hsplit

Hierarchical communicators split

KEYWORDS: MPI communication - Topology - Hardware platform

SCIENTIFIC DESCRIPTION: Hsplit is a library that implements an abstraction allowing the programmer using MPI in their parallel applications to access the underlying hardware structure through a hierarchy of communicators. Hsplit is based on the MPI_Comm_split_type routine and provides a new value for the split_type argument that specifically creates a hierarchy of subcommunicators where each new subcommunicator corresponds to a meaningful hardware level. The important point is that only the structure of the hardware is exploited and the number of levels or the levels names are not fixed so as to propose a solution independent from future hardware evolutions (such as new levels for instance). Another flavor of this MPI_Comm_split_type function is provided that creates a roots communicator at the same time a subcommunicator is produced, in order to ease the collective communication and/or synchronization among subcommunicators.

FUNCTIONAL DESCRIPTION: Hsplit implements an abstraction that allows the programmer using MPI in their parallel applications to access the underlying hardware structure through a hierarchy of communicators. Hsplit is based on the MPI_Comm_split_type routine and provides a new value for the split_type argument that specifically creates a hierarchy of subcommunicators where each new subcommunicator corresponds to a meaningful hardware level. The important point is that only the structure of the hardware is exploited and the number of levels or the levels names are not fixed so as to propose a solution independent from future hardware evolutions (such as new levels for instance). Another flavor of this MPI_Comm_split_type function is provided that creates a roots communicator at the same time a subcommunicator is produced, in order to ease the collective communication and/or synchronization among subcommunicators.

NEWS OF THE YEAR: A new working group in the MPI Forum to champion the integration of this proposal in the MPI standard has been created. This working group includes Inria, CEA, Atos/Bull, Paratools, the University of Tennessee - Knoxville and many other institutions/companies are interested to join in.

- Participants: Guillaume Mercier, Brice Goglin, Emmanuel Jeannot and Farouk Mansouri
- Contact: Guillaume Mercier
- Publications: [A hierarchical model to manage hardware topology in MPI applications - A Hierarchical Model to Manage Hardware Topology in MPI Applications](#)
- URL: <http://mpi-topology.gforge.inria.fr/>

6.2. hwloc

Hardware Locality

KEYWORDS: NUMA - Multicore - GPU - Affinities - Open MPI - Topology - HPC - Locality

FUNCTIONAL DESCRIPTION: Hardware Locality (hwloc) is a library and set of tools aiming at discovering and exposing the topology of machines, including processors, cores, threads, shared caches, NUMA memory nodes and I/O devices. It builds a widely-portable abstraction of these resources and exposes it to applications so as to help them adapt their behavior to the hardware characteristics. They may consult the hierarchy of resources, their attributes, and bind task or memory on them.

hwloc targets many types of high-performance computing applications, from thread scheduling to placement of MPI processes. Most existing MPI implementations, several resource managers and task schedulers, and multiple other parallel libraries already use hwloc.

- Participants: Brice Goglin and Samuel Thibault
- Partners: Open MPI consortium - Intel - AMD
- Contact: Brice Goglin
- Publications: [hwloc: a Generic Framework for Managing Hardware Affinities in HPC Applications](#) - [Managing the Topology of Heterogeneous Cluster Nodes with Hardware Locality \(hwloc\)](#) - [A Topology-Aware Performance Monitoring Tool for Shared Resource Management in Multicore Systems](#) - [Exposing the Locality of Heterogeneous Memory Architectures to HPC Applications](#) - [Towards the Structural Modeling of the Topology of next-generation heterogeneous cluster Nodes with hwloc](#) - [On the Overhead of Topology Discovery for Locality-aware Scheduling in HPC](#)
- URL: <http://www.open-mpi.org/projects/hwloc/>

6.3. NetLoc

Network Locality

KEYWORDS: Topology - Locality - Distributed networks - HPC - Parallel computing - MPI communication

FUNCTIONAL DESCRIPTION: netloc (Network Locality) is a library that extends hwloc to network topology information by assembling hwloc knowledge of server internals within graphs of inter-node fabrics such as Infiniband, Intel OmniPath or Cray networks.

Netloc builds a software representation of the entire cluster so as to help applications properly place their tasks on the nodes. It may also help communication libraries optimize their strategies according to the wires and switches.

Netloc targets the same challenges as hwloc but focuses on a wider spectrum by enabling cluster-wide solutions such as process placement. It interoperates with the Scotch graph partitioner to do so.

Netloc is distributed within hwloc releases starting with hwloc 2.0.

- Participants: Brice Goglin, Clement Foyer and Cyril Bordage
- Contact: Brice Goglin
- Publications: [netloc: Towards a Comprehensive View of the HPC System Topology](#) - [Netloc: a Tool for Topology-Aware Process Mapping](#)
- URL: <http://www.open-mpi.org/projects/netloc/>

6.4. NewMadeleine

NewMadeleine: An Optimizing Communication Library for High-Performance Networks

KEYWORDS: High-performance calculation - MPI communication

FUNCTIONAL DESCRIPTION: NewMadeleine is the fourth incarnation of the Madeleine communication library. The new architecture aims at enabling the use of a much wider range of communication flow optimization techniques. Its design is entirely modular: drivers and optimization strategies are dynamically loadable software components, allowing experimentations with multiple approaches or on multiple issues with regard to processing communication flows.

The optimizing scheduler SchedOpt targets applications with irregular, multi-flow communication schemes such as found in the increasingly common application conglomerates made of multiple programming environments and coupled pieces of code, for instance. SchedOpt itself is easily extensible through the concepts of optimization strategies (what to optimize for, what the optimization goal is) expressed in terms of tactics (how to optimize to reach the optimization goal). Tactics themselves are made of basic communication flows operations such as packet merging or reordering.

The communication library is fully multi-threaded through its close integration with PIOMan. It manages concurrent communication operations from multiple libraries and from multiple threads. Its MPI implementation MadMPI fully supports the MPI_THREAD_MULTIPLE multi-threading level.

- Participants: Alexandre Denis, Clement Foyer, Nathalie Furmento, Raymond Namyst and ADRIEN GUILBAUD
- Contact: Alexandre Denis
- Publications: [NewMadeleine: a Fast Communication Scheduling Engine for High Performance Networks](#) - [Ordonnancement et qualité de service pour réseaux rapides](#) - [Improving Reactivity and Communication Overlap in MPI using a Generic I/O Manager](#) - [PIOMan : un gestionnaire d'entrées-sorties générique](#) - [A multithreaded communication engine for multicore architectures](#) - [A multicore-enabled multirail communication engine](#) - [About the interactions between communication and thread scheduling in clusters of multicore machines](#) - [An analysis of the impact of multi-threading on communication performance](#) - [A scalable and generic task scheduling system for communication libraries](#) - [A Generic and High Performance Approach for Fault Tolerance in Communication Library](#) - [A High-Performance Superpipeline Protocol for InfiniBand](#) - [A sampling-based approach for communication libraries auto-tuning](#) - [High performance checksum computation for fault-tolerant MPI over InfiniBand](#) - [pioman: a Generic Framework for Asynchronous Progression and Multithreaded Communications](#) - [pioman: a pthread-based Multithreaded Communication Engine](#) - [Updating MadMPI to MPI-3: Remote Memory Access](#) - [Portage de StarPU sur la bibliothèque de communication NewMadeleine](#)
- URL: <http://pm2.gforge.inria.fr/newmadeleine/>

6.5. PaMPA

Parallel Mesh Partitioning and Adaptation

KEYWORDS: Dynamic load balancing - Unstructured heterogeneous meshes - Parallel remeshing - Subdomain decomposition - Parallel numerical solvers

SCIENTIFIC DESCRIPTION: PaMPA is a parallel library for handling, redistributing and remeshing unstructured meshes on distributed-memory architectures. PaMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes. It provides solver writers with a distributed mesh abstraction and an API to: - describe unstructured and possibly heterogeneous meshes, on the form of a graph of interconnected entities of different kinds (e.g. elements, faces, edges, nodes), - attach values to the mesh entities, - distribute such meshes across processing elements, with an overlap of variable width, - perform synchronous or asynchronous data exchanges of values across processing elements, - describe numerical schemes by means of iterators over mesh entities and their connected neighbors of a given kind, - redistribute meshes so as to balance computational load, - perform parallel dynamic remeshing, by applying adequately a user-provided sequential remesher to relevant areas of the distributed mesh.

PaMPA runs concurrently multiple sequential remeshing tasks to perform dynamic parallel remeshing and redistribution of very large unstructured meshes. E.g., it can remesh a tetrahedral mesh from 43Melements to more than 1Belements on 280 Broadwell processors in 20 minutes.

FUNCTIONAL DESCRIPTION: Parallel library for handling, redistributing and remeshing unstructured, heterogeneous meshes on distributed-memory architectures. PaMPA dramatically eases and speeds-up the development of parallel numerical solvers for compact schemes.

NEWS OF THE YEAR: PaMPA has been used to remesh an industrial mesh of a helicopter turbine combustion chamber, up to more than 1 billion elements.

- Participants: Cécile Dobrzynski, Cedric Lachat and François Pellegrini
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: François Pellegrini
- URL: <http://project.inria.fr/pampa/>

6.6. TreeMatch

KEYWORDS: Intensive parallel computing - High-Performance Computing - Hierarchical architecture - Placement

SCIENTIFIC DESCRIPTION: TreeMatch embeds a set of algorithms to map processors/cores in order to minimize the communication cost of the application.

Important features are : the number of processors can be greater than the number of applications processes , it assumes that the topology is a tree and does not require valuation of the topology (e.g. communication speeds) , it implements different placement algorithms that are switched according to the input size.

Some core algorithms are parallel to speed-up the execution. Optionally embeds scotch for fix-vertex mapping. enable exhaustive search if required. Several metric mapping are computed. Allow for oversubscribing of ressources. multithreaded.

TreeMatch is integrated into various software such as the Charm++ programming environment as well as in both major open-source MPI implementations: Open MPI and MPICH2.

FUNCTIONAL DESCRIPTION: TreeMatch is a library for performing process placement based on the topology of the machine and the communication pattern of the application.

- Participants: Adele Villiermet, Emmanuel Jeannot, François Tessier, Guillaume Mercier and Pierre Celor
- Partners: Université de Bordeaux - CNRS - IPB
- Contact: Emmanuel Jeannot
- URL: <http://treematch.gforge.inria.fr/>

6.7. SCOTCH

KEYWORDS: Mesh partitioning - Domain decomposition - Graph algorithmics - High-performance calculation - Sparse matrix ordering - Static mapping

FUNCTIONAL DESCRIPTION: Scotch is a graph partitioner. It helps optimise the division of a problem, by means of a graph, into a set of independent sub-problems of equivalent sizes. These sub-problems can also be solved in parallel.

RELEASE FUNCTIONAL DESCRIPTION: Version 6.0 offers many new features:

sequential graph repartitioning

sequential graph partitioning with fixed vertices

sequential graph repartitioning with fixed vertices

new, fast, direct k-way partitioning and mapping algorithms

multi-threaded, shared memory algorithms in the (formerly) sequential part of the library

exposure in the API of many centralized and distributed graph handling routines

embedded pseudo-random generator for improved reproducibility

and even more...

- Participants: François Pellegrini, Sébastien Fourestier, Jun-Ho Her and Cédric Chevalier
- Partners: Université de Bordeaux - IPB - CNRS - Region Aquitaine
- Contact: François Pellegrini
- Publications: [Process Mapping onto Complex Architectures and Partitions Thereof](#) - [Multi-criteria Graph Partitioning with Scotch](#) - [Adaptation au repartitionnement de graphes d'une méthode d'optimisation globale par diffusion](#) - [Contributions au partitionnement de graphes parallèle multi-niveaux](#) - [A parallelisable multi-level banded diffusion scheme for computing balanced partitions with smooth boundaries](#) - [PT-Scotch: A tool for efficient parallel graph ordering](#) - [Design and implementation of efficient tools for parallel partitioning and distribution of very large numerical problems](#) - [Improvement of the Efficiency of Genetic Algorithms for Scalable Parallel Graph Partitioning in a Multi-Level Framework](#) - [PT-Scotch : Un outil pour la renumérotation parallèle efficace de grands graphes dans un contexte multi-niveaux](#) - [PT-Scotch: A tool for efficient parallel graph ordering](#)
- URL: <http://www.labri.fr/~pelegrin/scotch/>

6.8. disk-revolve

KEYWORDS: Automatic differentiation - Gradients - Machine learning

FUNCTIONAL DESCRIPTION: This software provides several algorithms (Disk-Revolve, 1D-Revolve, Periodic-Disk-Revolve,...) computing the optimal checkpointing strategy when executing a adjoint chain with limited memory. The considered architecture has a level of limited memory that is free to access (writing and reading costs are negligible) and a level of unlimited memory with non-negligible access costs. The algorithms describe which data should be saved in the memory to minimize the number of re-computation during the execution.

- Authors: Guillaume Aupy and Julien Herrmann
- Contact: JULIEN HERRMANN
- Publications: [Periodicity in optimal hierarchical checkpointing schemes for adjoint computations](#) - [Optimal Multistage Algorithm for Adjoint Computation](#)
- URL: <https://gitlab.inria.fr/adjoint-computation/disk-revolve-public>