The practical work of this internship is to implement (in Prolog) in BIOCHAM-4 the dynamic strategy described in this paper, using both the differential integrator and the event mechanism as a mean to combining both simulation algorithms with general criteria ensuring both correctness and maximum efficiency.

Main activities

Our previous work on this subject is described in Hui-Ju Chiang, François Fages, Jie-Hong Jiang, Sylvain Soliman. Hybrid Simulations of Heterogeneous Biochemical Models in SBML. ACM Transactions on Modeling and Computer Simulation (TOMACS), 25(2):14:1–14:22, 2015. [preprint]

About the research centre or Inria department

Located at the heart of the main national research and higher education cluster, member of the Université Paris Saclay, a major actor in the French Investments for the Future Programme (Idex, LabEx, IRT, Equipex) and partner of the main establishments present on the plateau, the centre is particularly active in three major areas: data and knowledge; safety, security and reliability; modelling, simulation and optimisation (with priority given to energy).

The 450 researchers and engineers from Inria and its partners who work in the research centre’s 31 teams, the 100 research support staff members, the high-level equipment at their disposal (image walls, high-performance computing clusters, sensor networks), and the privileged relationships with prestigious industrial partners, all make Inria Saclay Île-de-France a key research centre in the local landscape and one that is oriented towards Europe and the world.

Context

This research internship is offered at Inria Saclay IdF (https://www.inria.fr/en/centre/saclay) in the LIFEWARE project-team (http://lifeware.inria.fr). This team works in computational systems biology and develops the Biochemical Abstract Machine (BIOCHAM http://lifeware.inria.fr/biocham4) software for modeling, analyzing and now synthesizing biochemical reaction networks (CRNs) using methods from fundamental computer science and mathematics. The software developments are expected to be integrated in BIOCHAM.

Assignment

The formalism of chemical reaction networks (CRNs) is used to model biological processes at the cellular level. They explain complex phenotypes as the result of elementary molecular interactions. A CRN has an hypergraph structure (i.e. a bipartite graph species/reactions labelled with rate functions) and can be interpreted at different levels of abstraction in a hierarchy of different dynamics: differential, stochastic, Petri net or Boolean. The differential and stochastic simulations can make quantitative predictions, while the Petri net and Boolean interpretation can serve analysis purposes.

The stochastic simulation algorithm (SSA) provides a numerical integration of the chemical master equation (continuous-time Markov chain). The ordinary differential equation associated to a CRN is a differential, stochastic, Petri net or Boolean. The differential and stochastic simulations can make quantitative predictions, while the Petri net and Boolean interpretation can serve analysis purposes at a high-level of abstraction, without information on the kinetics of the reactions.

The stochastic simulation algorithm (SSA) provides a numerical integration of the chemical master equation (continuous-time Markov chain). The ordinary differential equation associated to a CRN is a first-order approximation of the mean stochastic behavior which is much more efficient to compute by numerical integration (using implicit methods for stiff systems) but which is not correct for small numbers of molecules.

Hybrid stochastic-differential simulations aim at providing automatic dynamic strategies for combining both simulation algorithms with general criteria ensuring both correctness and maximum efficiency.

General Information

- Theme/Domain: Numerical schemes and simulations
- Scientific computing (BAP E)
- Town/City: PALAISEAU
- Inria Center: CRI Saclay - Île-de-France
- Starting date: 2019-04-01
- Duration of contract: 6 months
- Deadline to apply: 2019-03-31

Contacts

- Inria Team: LIFEWARE
- Recruiter: Fages François / Francois.Fages@inria.fr

About Inria

Inria is the French national research institute dedicated to digital science and technology. It employs 2,600 people. Its 200 agile project teams, generally run jointly with academic partners, include more than 3,500 scientists and engineers working to meet the challenges of digital technology, often at the interface with other disciplines. The Institute also employs numerous talents in over forty different professions. 900 research support staff contribute to the preparation and development of scientific and entrepreneurial projects that have a worldwide impact.

The keys to success

We are seeking a highly talented and motivated candidate not afraid by crossing disciplinary frontiers.

Instruction to apply

Send an e-mail with CV + cover letter to Mr François Fages : francois.fages@inria.fr

Defence Security:

This position is likely to be situated in a restricted area (ZRR), as defined in Decree No. 2011-1425 relating to the protection of national scientific and technical potential (PPST). Authorisation to enter an area is granted by the director of the unit, following a favourable Ministerial decision, as defined in the decree of 3 July 2012 relating to the PPST. An unfavourable Ministerial decision in respect of a position situated in a ZRR would result in the cancellation of the appointment.

Recruitment Policy:

As part of its diversity policy, all Inria positions are accessible to people with disabilities.

Warning: you must enter your e-mail address in order to save your application to Inria. Applications must be submitted online on the Inria website. Processing of applications sent from other channels is not guaranteed.
implement the SSA.

The research will consist in experimenting further the dynamic partitioning strategies described in the paper and evaluate them on the repository of models BioModels.

Theoretical work on this subject is possible concerning the correctness criteria, as well as for instance the search of correctness criteria weaker than approximation in all time points.

The expected results aim to lead to both an international publication and an integration in the next release of BIOCHAM-4 to be routinely used for stochastic simulation of CRNs in BIOCHAM commands for sensitivity and robustness analysis, parameter search in high-dimension, artificial evolution of CRNs, and machine learning CRNs from data.

Skills
This subject requires common and basic knowledge in algorithmics, programming, and in numerical integration methods for ordinary differential equations.

Specific knowledge of the the Prolog programming language or of Computational Systems Biology will be a plus.

Benefits package
- Subsidised catering service
- Partially-reimbursed public transport
- Social security
- Paid leave
- Flexible working hours
- Sports facilities

Remuneration
500 euros/month