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/fr/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.

The internship will be supervised by François Fages and Sylvain Soliman.

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 a 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 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 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 at a high-level of abstraction, without information on the kinetics of the reactions.

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

Main activities

Our previous work on this subject is described in


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...
implement the SSA.

The research will consist in experimenting further the
dynamic partitionning 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