The internship is offered at Inria Saclay IdF (https://www.inria.fr/en/centre/saclay) in the LIFECWARE 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 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: CRNs can be interpreted 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 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 correctnes 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