The practice 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 improve efficiency.

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]
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 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 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