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.

Assignment

The chemical reaction network formalism (CRN) is used to model biological processes at the cellular level. They explain the complex phenotypes as resulting from elementary molecular interactions. A CRN has a hypergraph structure (that is, a bipartite species / reaction graph labeled by a rate function) and can be interpreted at different levels of abstraction with different dynamics: differential, stochastic, discrete Petri net or Boolean.

Visualization of the structure of CRNs is not a well-solved problem today, and the automatic drawing tools are far from being able to compete with the manual drawings that modelers make in publications, and which show much better “logic” of the network.

Before performing simulations, however, many static analyzers can provide information on network inputs and outputs, dependency graphs, and influences, as well as on dynamic properties, such as algebraic or place-invariant invariants of the network, Petri net (set of molecular species whose sum of concentrations is constant), transition-invariants (set of reactions forming a circuit), etc.

The aim of the internship is to try to use this static information (calculated by BIOCHAM) on the network structure so as to define drawing strategies and to set up the visualization tools of the interaction graph (GraphViz) so that he produces automatic drawings close to the manual drawings found in the publications.

Main activities

Our previous work on some BIOCHAM static analyzers is described in Sylvain Soliman. Invariants and Other Structural Properties of Biochemical Models as a Constraint Satisfaction Problem. Algorithms for Molecular Biology, 7 (15), 2012.

The work will involve using this information to design and experiment with different species placement strategies and reactions in the GraphViz visualization tool. The evaluation can be done on the BioModels model warehouse by comparing the results with the drawings of the corresponding publications.

Results may be published in the Systems Biology Graphical Notation (SBGN) community.
Skills
This subject requires common and basic knowledge in algorithmics, programming, graphs and graphics.
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