

Quantitative analysis of large stochastic systems Postdoctoral Fellowship

1. Context

The Lifeware team is an interdisciplinary research group whose aim is to better understand the functioning of cellular processes through the combination of quantitative experimental methods and computational approaches. With applications in synthetic biology, we develop approaches for the efficient design of large biomolecular systems performing a desired function in a robust manner.

2. Objectives

The objective of this work is to develop scalable analysis techniques for the design and analysis of large natural or artificial biological processes. In practice, because of their inherent noisiness, this amounts to analyze large stochastic systems. Typically one is interested in the computation of the probability for an event to happen, or in the case of an open system, in the search for an input profile that guarantees a specific behavior with a high probability. More specifically, we focus on the analysis of stochastic differential equation systems and define an abstraction of this system in the form of a large Markov chain. The latter can then be compactly represented as a dynamic Bayesian network and further analyzed. The central problem with this approach is the design of a proper abstraction. Indeed the abstraction employed should find a good balance between preserving the properties of the original system and providing an important simplification of the problem. In the case of an open system, this problem is even more challenging.

In this project, the postdoctoral researcher will be in charge of the three tasks. The first one is to apply existing abstraction methods to a model of apoptosis in mammalian cells. Apoptosis, or cell suicide, is a fundamental process that enables the maintenance of cell integrity within an organism. In the context of other projects, we study how to optimize drug treatments so as to minimize the appearance of resistant cells. Therefore, the abstraction should be constructed so as to preserve the cell behavior for various patterns of proapoptotic drug applications. The second task is to generalize the work done on the specific example of apoptosis and expand the theoretical framework on abstraction computation. The last step is to develop tools to automate these methodological developments.

3. Contacts

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