

Process Calculi and Biology

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Concurrency theory, and particularly process algebras, are emerging as a suitable tool to provide formal foundations to systems biology. This field is enlarging day by day as witnessed by the large number of researchers interested in it and participating to the few related events.

The main idea is to model molecular processes as interaction/communicating systems with decentralized control and with incomplete knowledge of the execution environment. Furthermore strong localization of interactions and a huge number of interactive and competing partners characterize biological systems. The abstraction metaphor is to see biological components as concurrent processes and their interaction as process communication or process movement.

The recent attempts to use process algebra as modeling tools followed the adaptation strategy: calculi specifically designed to design concurrent, distributed and mobile systems have been tested against the new applicative domain of molecular biology. An open and challenging problem is the definition of a set basic and general primitives for modeling biological systems directly inspired by biological processes. The fallout of this approach can be twofold: better models and simulation of living phenomena and new model of computations that biologically inspired.

Quantitative aspects are essential to drive behavior in a physico-chemical world. This means that in the biological setting probabilistic/stochastic models are mandatory. We think that new semantics and new proposal should be directly considered at the design level of the new calculi above. Also in this case the approach followed to define stochastic process algebras as extensions of existing pure calculi does not seem to be fully adequate.

Many current approaches handle simulation aspects of biological phenomena, while others are mainly oriented to verification and analysis of properties. To build an in silico lab for biologists we definitely need to smoothly merge these alternative approaches and make any of them both a tuning and an information provider for the other.

The ultimate goal of systems biology is to predict the behavior of living matter. If we can devise process calculi that can predict behavior, then are on the right track. Ultimately, we want to understand the functioning of cells at useful levels of abstraction, and we want to be able to predict unknown behavior. Those achievement should then enable us to use biological matter as flexible information and material processing devices.

CLASSIFICATION: bioinformatics, modeling/simulation, semantics/specification, interdisciplinary.

KEYWORDS: process algebras, concurrency theory, molecular biology, systems biology, bio-inspired computations, predictive modeling, integration of simulation and verification.

