

# Lecture Notes in Bioinformatics

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Subseries of Lecture Notes in Computer Science

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# Transactions on Computational Systems Biology XIV

Special Issue on Computational Models  
for Cell Processes

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# Preface

The intricate and subtle interactions in biological systems (e.g., in terms of signaling, competition, synchronization, and regulation) enforce the need to represent them in formal models, with the goal of understanding the computational principles of their functioning. Current computational modeling approaches span a broad range from quantitative to qualitative, from discrete to continuous, from deterministic to stochastic, from detailed models to abstract interpretations. This special issue of the *Transactions on Computational Systems Biology* on *Computational Models for Cell Processes* also mirrors the rich variety of the field.

The volume is based on the *Computational Models for Cell Processes (CompMod)* workshop, which took place in Aachen, Germany, on September 10, 2011, in conjunction with *CONCUR 2011*. The first workshop (2008) took place in Turku, Finland, in conjunction with *Formal Methods 2008* and the second one (2009) took place in Eindhoven, the Netherlands, in conjunction with *Formal Methods 2009*.

The goal of the CompMod workshop series is to bring together researchers in Computer Science and Mathematics interested in the opportunities and the challenges of computational modeling in biology. A specific interest is expressed for papers discussing biological processes requiring special tools and techniques not investigated so far in the context of formal methods, as well as extensions of formal methods formalisms introduced to improve their applicability to biology. For this special issue of the *Transactions in Computational Systems Biology* there was an additional open call for paper submissions after CompMod 2011, with a separate peer-reviewing process.

The papers published in this volume cover various aspects of modeling and analysis of biological systems: Andrei and Calder show the advantage of stochastic model checking for population Markov chains with a stochastic logic that includes trend formulae. This way, both causality and pulsation can be studied in the setting of crosstalk between two signaling pathways. Angius et al. deal with state space explosion in the setting of chemical reaction networks. For the analysis of the Markov models involved, a computationally attractive approximation can be obtained by representation of transient behavior in a quasi-product form. Bartocci et al. present a case study of stabilization of bone tissue. Three complementary techniques are exploited to analyze quantitative aspects of the resulting model. Brim et al. study reachability in biochemical dynamical systems. By rectangular abstraction the system dynamics can be analyzed using a so-called quantitative discrete approximation automaton, balancing granularity and computational costs. Ehrenfeucht et al. contribute a fundamental study of minimality in the framework of reaction systems. In particular, characterizations of the update functions of reaction systems are given that are minimal in the

number of reactants, the number of inhibitors or the number of resources. Versari and Zavattaro, in a setting of rule-based modeling, propose to incorporate the structure of the complexes involved to have a finer control over reaction rates. The approach is illustrated for mass-dependent kinetics of polymer formation. Yuan et al. discuss stochastic model checking for the analysis of the PDGF signaling pathway. The in-silico model of the network makes it possible to analyze mutant dynamics and crosstalk reactions.

The papers, written from different points of view and following various approaches, cover a wide range of topics in the field. At the same time they address the computational principles that we are starting to identify and the dynamics we are beginning to unravel in computational systems biology.

The volume includes two regular submissions dealing with models of self-assembling systems and metabolic constraints on the evolution of genetic codes.

August 2012

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