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Preface

Biology is witnessing a transformation towards a more quantitative science, based on the major technological breakthroughs of the past decade. In this transformation, biology is incorporating mathematical modeling techniques and computational approaches towards numerical simulations, model analysis, and quantitative predictions. An important goal is to formalize and analyze the ever-changing inter-connections between components (often on different time and space scales), their influence on one another, regulatory patterns, alternative pathways, etc. Formal reasoning rather than empirical observations is the main driving force in this new type of biological research. At the same time, computer science and applied mathematics are faced with considerable methodological challenges in handling an unprecedented level of concurrency, stochastic effects, a mix of large and small populations, combinatorial explosions in the state space, model refinement, and model (de)composition, etc.

This special issue of *Transactions on Computational Systems Biology on Computational Models for Cell Processes* is based on a workshop with the same name that took place in Turku, Finland, on May 27, 2008. The workshop was organized as a satellite event of *the 15th International Symposium on Formal Methods* that took place in Turku in the period May 28-31, 2008. This special issue however had an open call for paper submissions, with a separate peer-review process. The accepted papers span an interesting mix of approaches to systems biology, ranging from quantitative to qualitative techniques, from continuous to discrete mathematics, from deterministic to stochastic methods, from computational models for biology to computing paradigms inspired by biology. Overall, they give a good glimpse into some of the exciting current research avenues in computational systems biology.

This volume also contains three regular submissions that deal with the relationships between ODEs and stochastic concurrent constraint programming (by Bertolussi and Policriti), with the equilibrium points of genetic regulatory networks (by Chesi), and with probability models describing how epigenetic context affects gene expression and organismal development (by Wallace and Wallace).

July 2009

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