

Guest Editors' Introduction to the Special Section on Computational Methods in Systems Biology

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THIS special section contains the second series of journal articles made from a selection of papers presented at the Ninth International Conference on Computational Methods in Systems Biology, CMSB 2011, held in cooperation with the ACM SIG Bioinformatics, at Institut Henri Poincaré, Paris, France, on 21-23 September 2011.

CMSB is an annual series of conferences, initiated in 2003, on the design of computational methods for modeling and analyzing biological systems, networks, data, and on their applications to study cases. The conference brings together computer scientists, biologists, mathematicians, engineers, and physicists interested in a system-level understanding of biological processes, their control by experimental or therapeutic means, or even their design or optimization by synthetic biology means.

The selection of CMSB 2011 is composed of eight papers, the first part of which has been published in *TCBB*, September/October 2012. This issue contains the second part which is composed of three papers.

The importance of noise in biomolecular systems has drained considerable interest for stochastic models in systems biology. However, stochastic simulations and Markov chain numerical methods are still computationally very expensive when compared to numerical methods for deterministic models. "The Propagation Approach for Computing Biochemical Reaction Networks" by Thomas A. Henzinger and Maria Mateescu revisits the chemical master equation, the rate equation and a combination of both, with the concepts of propagation models and propagation data type for abstracting from the further implementation choices made in simulators. This allows for threshold abstractions, deterministic approximations and hybrid analyses with better performance.

Such theoretical advances from the computer-aided verification community can also sometimes be coupled with technological developments from parallel computing, such as in the graphics processing community, to set the stage for fast simulation, powerful analysis, and accurate prediction of complex biological processes. This is nicely illustrated in "Curvature Analysis of Cardiac Excitation Wavefronts" by

Abhishek Murthy, Ezio Bartocci, Flavio H. Fenton, James Glimm, Richard A. Gray, Elizabeth M. Cherry, Scott A. Smolka, and Radu Grosu, which describes a parallel curvature analysis algorithm of cardiac excitation wavefronts. Given a series of frames generated by simulation or optical mapping, the algorithm running on a Graphical Processing Unit produces a curvature-based signature of waves and spirals which can be used for classifying and detecting different forms of arrhythmias.

Multiscale modeling is another crucial topic in systems biology for managing the complexity of biological processes in multicellular organisms. "Multiscale Modeling and Analysis of Planar Cell Polarity in the *Drosophila* Wing" by Qian Gao, David Gilbert, Monika Heiner, Fei Liu, Daniele Maccagnola, and David Tree proposes the use of Hierarchically Colored Petri Nets to develop models of tissues at different spatial scales. This is illustrated by a model of planar cell polarity signaling in an hexagonal grid of *drosophila* wing cells, and by the use of computer-aided verification methods to validate the model with respect to well-known gene mutations.

As guest editors of this special section, we would like to take the opportunity to thank the reviewers who did a very good job improving the quality of the papers by their constructive criticisms. We would also like to thank the sponsors of CMSB 2011 without who this kind of event would not be possible.

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Sylvain Soliman received the PhD degree in computer science in 2001 from the University Paris Diderot after graduating from the École Polytechnique in 1996. He worked for one and a half years for a DGA (French DoD) laboratory and was hired as a junior researcher at Inria in 2003, and promoted in 2005. He is responsible for the constraint programming course at Master Parisien de Recherche en Informatique, and is the former

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