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Preface

The Computational Methods in Systems Biology (CMSB) workshop series was established in 2003 by Corrado Priami. The purpose of the workshop series is to help catalyze the convergence between computer scientists interested in language design, concurrency theory, software engineering or program verification, and physicists, mathematicians and biologists interested in the systems-level understanding of cellular processes. Systems biology was perceived as being increasingly in search of sophisticated modeling frameworks whether for representing and processing system-level dynamics or for model analysis, comparison and refinement. One has here a clear-cut case of a must-explore field of application for the formal methods developed in computer science in the last decade.

This proceedings consists of papers from the CMSB 2003 workshop. A good third of the 24 papers published here have a distinct formal methods origin; we take this as a confirmation that a synergy is building that will help solidify CMSB as a forum for cross-community exchange, thereby opening new theoretical avenues and making the field less of a potential application and more of a real one. Publication in Springer's new Lecture Notes in Bioinformatics (LNBI) offers particular visibility and impact, which we gratefully acknowledge.

Our keynote speakers, Alfonso Valencia and Trey Ideker, gave challenging and somewhat humbling lectures: they made it clear that strong applications to systems biology are still some way ahead. We thank them all the more for accepting the invitation to speak and for the clarity and excitement they brought to the conference. We also wish to thank René Thomas for his keynote lecture on recent mathematical advances in the qualitative analysis of genetic regulation networks. As one can tell from the proceedings, his work has inspired many recent applications of formal methods to the engineering of biological models.

We are glad to take here the opportunity to express our gratitude to the members of the program committee and to the referees for their effort in the paper selection process and for their willingness to participate in the open-minded debate needed given the interdisciplinary nature of the area of computational systems biology. We would also like to thank the authors for their interest in the workshop and for their high-quality submissions and communications.

Finally, we wish to extend our warmest thanks to Monique Meugnier, Catherine Sarlande and Serge Smidtas for their invaluable help in organizing the workshop, and to the participating institutions, Genoscope, Genopole, CNRS, University of Paris 7, and the BioPathways Consortium, which provided financial support.

Conference web-site: <http://www.biopathways.org/CMSB04/>

Vincent Danos
Vincent Schachter

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