

Lecture Notes in Bioinformatics

6575

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Transactions on Computational Systems Biology XIII

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Editor-in-Chief

Corrado Priami

The Microsoft Research - University of Trento

Centre for Computational and Systems Biology

Piazza Mancini, 17, 38050 Povo (TN), Italy

E-mail: priami@dit.unitn.it

Guest Editors

Ralph-Johan Back

Jon Petre

Åbo Akademi University

Department of Information Technologies

Joukohaisenkatu 3-5, 20520 Turku, Finland

E-mail: {backrj,ipetre}@abo.fi

Erik de Vink

Technische Universiteit Eindhoven

Den Dolech 2, Eindhoven, The Netherlands

E-mail: evink@win.tue.nl

ISSN 0302-9743 (LNCS)

e-ISSN 1611-3349 (LNCS)

ISSN 1861-2075 (TCSB)

e-ISSN 1861-2083 (TCSB)

ISBN 978-3-642-19747-5

e-ISBN 978-3-642-19748-2

DOI 10.1007/978-3-642-19748-2

Springer Heidelberg Dordrecht London New York

Library of Congress Control Number: 2011922750

CR Subject Classification (1998): J.3, F.1-2, F.4, I.6, I.2, C.1.3

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Typesetting: Camera-ready by author, data conversion by Scientific Publishing Services, Chennai, India

Printed on acid-free paper

Springer is part of Springer Science+Business Media (www.springer.com)

Preface

The many facets of life are reflected by the multitude of dimensions of systems biology research at present. Current modeling and analysis approaches to a systematic understanding of biological phenomena range from quantitative to qualitative, from discrete to continuous, from deterministic to stochastic, from concrete detailed biological case studies to abstract bio-inspired computing paradigms. 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 CompMod workshop that took place in Eindhoven, the Netherlands, on November 2, 2009. Previously held in Turku, Finland, the workshop was organized for the second time, now as a satellite event of the 16th International Symposium on Formal Methods, part of FMweek, running from November 2 to 6, 2009 in Eindhoven. The CompMod workshop aims to foster a platform gathering researchers in formal methods and related fields interested in the wealth of challenges and opportunities in systems 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 there has been an additional open call for paper submissions, with a separate peer-reviewing process.

The papers included illustrate the broad span of aspects of modeling and analysis of biological systems: evolution of a cell population with selection based on toxin resistance; a quantitative and tool-supported interpretation of flow abstraction in the Systems Biology Graphical Notation; an analytic approach to dynamic simulation of deformable biological structures; a new stochastic simulation algorithm reconsidering the delay-as-duration principle; a process algebraic case study on ammonium transport in plant-fungus symbiosis; iterative variable elimination for steady state equations using algebraic modules in the analysis of metabolic networks. From different points of view and following various approaches the papers cover a wide range of topics in Systems Biology, addressing the dynamics we begin to unravel and computational principles that we start to identify.

This issue also includes two regular papers by Wallace and Wallace on the heritability of complex diseases and by Paulevé et al. on the dynamics of gene regulatory networks.

December 2010

Ralph-Johan Back
Ion Petre
Corrado Priami
Erik de Vink

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Table of Contents

Evolutionary Dynamics of a Population of Cells with a Toxin Suppressor Gene	1
<i>Antti Häkkinen, Fred G. Biddle, Olli-Pekka Smolander, Olli Yli-Harja, and Andre S. Ribeiro</i>	
Translation from the Quantified Implicit Process Flow Abstraction in SBGN-PD Diagrams to Bio-PEPA Illustrated on the Cholesterol Pathway	13
<i>Laurence Loewe, Maria Luisa Guerriero, Steven Watterson, Stuart Moodie, Peter Ghazal, and Jane Hillston</i>	
Impulse-Based Dynamic Simulation of Deformable Biological Structures	39
<i>Rhys Goldstein and Gabriel Wainer</i>	
Delay Stochastic Simulation of Biological Systems: A Purely Delayed Approach	61
<i>Roberto Barbuti, Giulio Caravagna, Andrea Maggiolo-Schettini, and Paolo Milazzo</i>	
Modelling Ammonium Transporters in Arbuscular Mycorrhiza Symbiosis	85
<i>Mario Coppo, Ferruccio Damiani, Maurizio Drocco, Elena Grassi, Mike Guether, and Angelo Troina</i>	
Genetically Regulated Metabolic Networks: Gale-Nikaido Modules and Differential Inequalities.....	110
<i>Ovidiu Radulescu, Anne Siegel, Elisabeth Pécou, Clément Chatelain, and Sandrine Lagarrigue</i>	
Cultural Epigenetics: On the Heritability of Complex Diseases	131
<i>Rodrick Wallace and Deborah Wallace</i>	
Refining Dynamics of Gene Regulatory Networks in a Stochastic π -Calculus Framework	171
<i>Loïc Paulevé, Morgan Magnin, and Olivier Roux</i>	
Author Index	193