

# Preface

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The fourth international workshop on *Computational Models for Cell Processes* (CompMod 2013) took place on June 11, 2013 at the Åbo Akademi University, Turku, Finland, in conjunction with *iFM 2013*. The first edition of the workshop (2008) took place in Turku, Finland, in conjunction with *Formal Methods 2008*, the second edition (2009) took place in Eindhoven, the Netherlands, in conjunction with *Formal Methods 2009*, and the third one took place in Aachen, Germany, in conjunction with *CONCUR 2013*. This volume contains the final versions of all contributions accepted for presentation at the workshop.

The goal of the CompMod workshop series is to bring together researchers in Computer Science and Mathematics (both discrete and continuous), interested in the opportunities and the challenges of Systems Biology. The Program Committee of CompMod 2013 selected 3 papers for presentation at the workshop (one was withdrawn). In addition, we had two invited talks and five other informal presentations. We thank the PC members for their excellent work in making this selection. The CompMod 2013 Program Committee consisted of:

- Oana Andrei (University of Glasgow, UK)
- Luca Bortolussi (University of Trieste, Italy)
- Lubos Brim (Masaryk University, Czech Republic)
- Eugen Czeizler (Aalto University, Finland)
- Jerome Feret (ENS, France)
- Vashti Galpin (University of Edinburgh, UK)
- Russ Harmer (University of Paris 7, France)
- Monika Heiner (Brandenburg University of Technology Cottbus, Germany)
- Ina Koch (Johann Wolfgang Goethe-University Frankfurt am Main, Germany)
- Andrzej Mizera (University of Luxembourg)
- Ion Petre (Åbo Akademi University, Finland) chair
- Corrado Priami (Microsoft Research – University of Trento, Centre for Computational and Systems Biology, Italy)
- David Safranek (Masaryk University, Czech Republic)
- Angelo Troina (Università di Torino)
- Erik de Vink (Eindhoven University of Technology, the Netherlands)
- Claudio Zandron (Università degli Studi di Milano-Bicocca, Italy)

The scientific program of the workshop spans an interesting mix of approaches to systems and even synthetic biology, encompassing several different modeling approaches, ranging from quantitative to qualitative techniques, from continuous to discrete mathematics, and from deterministic to stochastic methods. We thank our invited speakers

- Daniela Besozzi (Università degli Studi di Milano, Milano, Italy)
- Juho Rousu (Aalto University, Finland)

for accepting our invitation and for presenting some of their recent results at CompMod 2013. The technical contributions address the mathematical modeling of the PDGF signalling pathway, the canonical labelling of site graphs, rule-based modeling of polymerization reactions, rule-based modeling as a platform for the analysis of synthetic self-assembled nano-systems, robustness analysis of stochastic systems, an algebraic approach to gene assembly in ciliates, and large-scale text mining of biomedical literature.

We would also like to thank the editorial board of the *Electronic Proceedings in Theoretical Computer Science* (EPTCS) for accepting to publish these proceedings in their series.

*Ion Petre*

*Turku, Finland, May 2013*

*Workshop organizer and PC chair*