

Monika Heiner (Ed.)

# Biological Processes & Petri Nets

5th International Workshop BioPPN 2014

Tunis, 23 June 2014

Proceedings

CEUR Workshop Proceedings

Volume 1159

Editor:

Monika Heiner  
Brandenburg University of Technology Cottbus-Senftenberg  
Computer Science Institute  
Data Structures and Software Dependability  
03013 Cottbus, Germany  
[monika.heiner@b-tu.de](mailto:monika.heiner@b-tu.de)

Online available as CEUR Workshop Proceedings (ISSN 1613-0073), Volume 1159  
<http://CEUR-WS.org/Vol-1159/>

BIB<sub>T</sub>E<sub>X</sub> entry:

```
@proceedings{bioppn2014,  
  editor   = {Monika Heiner},  
  title    = {Proceedings of the 5th International Workshop on  
             Biological Processes & Petri Nets (BioPPN 2014),  
             satellite event of Petri Nets 2014, Tunis, Tunisia, June 23, 2014},  
  booktitle = {Biological Processes & Petri Nets},  
  location = {Tunis, Tunisia},  
  publisher = {CEUR-WS.org},  
  series   = {CEUR Workshop Proceedings},  
  volume   = {Vol-1159},  
  year     = {2014},  
  url      = {http://CEUR-WS.org/Vol-1159/}  
}
```

Copyright © 2014 for the individual papers by the papers' authors. Copying permitted for private and academic purposes. Re-publication of material from this volume requires permission by the copyright owners.

## Preface

This volume contains the peer-reviewed papers presented at BioPPN 2014 – the 5th International Workshop on *Biological Processes & Petri Nets* held on June 23, 2014 in Tunis as satellite event of PETRI NETS 2014.

The workshop had been organised to provide a platform for researchers aiming at fundamental research and real life applications of Petri nets in Systems and Synthetic Biology. Systems and Synthetic Biology are full of challenges and open issues, with adequate modelling and analysis techniques being one of them. The need for appropriate mathematical and computational modelling tools is widely acknowledged.

Petri nets offer a family of related models, which can be used as a kind of umbrella formalism – models may share the network structure, but vary in their kinetic details (quantitative information). This undoubtedly contributes to bridging the gap between different formalisms, and helps to unify diversity. Thus, Petri nets have proved their usefulness for the modelling, analysis, and simulation of a diversity of biological networks, covering qualitative, stochastic, continuous and hybrid models. The deployment of Petri nets to study biological applications has not only generated original models, but has also motivated research of formal foundations.

There were six submissions to the BioPPN workshop. One of the papers had been originally submitted to the PNSE workshop, and reviewed by the PNSE programme committee. Following the recommendation of these reviews, this paper has then been moved to the BioPPN workshop. In summary, each submission was reviewed by at least three, and on the average four, program committee members. The list of reviewers comprises 17 professionals of the field coming from 12 different countries and writing in total 28 reviews, most of them of substantial length.

The programme committees decided finally to accept five papers. The five accepted peer-reviewed papers (with an acceptance rate of 83%) involve 16 authors coming from seven different countries.

The program also includes one invited talk on *Mathematical models on cancer progression* given by Marco Beccuti from Università degli Studi di Torino. In summary, the workshop proceedings enclose theoretical contributions as well as biological applications, demonstrating the interdisciplinary nature of the topic.

For more details see the workshops website <http://www-dssz.informatik.tu-cottbus.de/BME/BioPPN2014>.

We acknowledge substantial support by the EasyChair management system, see <http://www.easychair.org>, during the reviewing process and the production of these proceedings.

June 20, 2014  
Cottbus

Monika Heiner

*This page is intentionally left blank.*

## Table of Contents

Mathematical models on cancer progression (invited talk) . . . . .	1
<i>Marco Beccuti</i>	
Overcoming unknown kinetic data for quantitative modelling of biological systems using fuzzy logic and Petri nets . . . . .	3
<i>Jure Bordon, Miha Moškon and Miha Mraz</i>	
A multi-scale extensive Petri net model of the bacterial-macrophage interaction . . . . .	15
<i>Rafael V. Carvalho, Jetty Kleijn and Fons Verbeek</i>	
Systemic approach for toxicity analysis . . . . .	30
<i>Cinzia Di Giusto, Hanna Klaudel and Franck Delaplace</i>	
Integrating a priori knowledge in automatic network reconstruction . . . . .	45
<i>Marie C.F. Favre, Wolfgang Marwan and Annegret Wagler</i>	
Coloured hybrid Petri nets for systems biology . . . . .	60
<i>Mostafa Herajy, Fei Liu and Christian Rohr</i>	

## Program Committee

Gianfranco Balbo	University of Torino, Computer Science Department, Italy
Rainer Breitling	University of Manchester, Manchester Institute of Biotechnology, UK
Claudine Chaouiya	Instituto Gulbenkian de Ciência, Oeiras, Network Modelling Group, Portugal
Ming Chen	Zhejiang University, College of Life Sciences, Department of Bioinformatics, China
David Gilbert	Brunel University, Centre for Systems and Synthetic Biology, UK
Simon Hardy	Université Laval, Institut universitaire en santé mentale de Québec, Canada
Monika Heiner	Brandenburg University of Technology Cottbus-Senftenberg, Computer Science Institute, Germany
Mostafa Herajy	Port Said University, Mathematics and Computer Science Department, Egypt
Peter Kemper	College of William and Mary, Department of Computer Science, USA
Sriram Krishnamachari	Indraprastha Institute of Information Technology (IIIT), India
Chen Li	Zhejiang University, School of Medicine, Center for Genetic & Genomic Medicine, China
Fei Liu	Harbin Institute of Technology, Control and Simulation Center, China
Wolfgang Marwan	Otto von Guericke University Magdeburg & Magdeburg Centre for Systems Biology, Germany
Hiroshi Matsuno	Yamaguchi University, Graduate School of Science and Engineering, Japan
P.S. Thiagarajan	National University of Singapore, School of Computing, Department of Computer Science, Singapore

## Author Index

<b>B</b>	
Beccuti, Marco	1
Bordon, Jure	3
<b>C</b>	
Carvalho, Rafael V.	15
<b>D</b>	
Delaplace, Franck	30
Di Giusto, Cinzia	30
<b>F</b>	
Favre, Marie C.F.	45
<b>H</b>	
Herajy, Mostafa	60
<b>K</b>	
Klaudel, Hanna	30
Kleijn, Jetty	15
<b>L</b>	
Liu, Fei	60
<b>M</b>	
Marwan, Wolfgang	45
Moškon, Miha	3
Mraz, Miha	3
<b>R</b>	
Rohr, Christian	60
<b>V</b>	
Verbeek, Fons	15
<b>W</b>	
Wagler, Annegret	45