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Biological Processes & Petri Nets

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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.

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June 20, 2014 Monika Heiner
Cottbus

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