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Preface

Matteo Cavaliere¹ · Alfonso Rodríguez-Patón²

Synthetic biology is concerned with the design and construction of new biological entities as well as with redesign of existing biological systems. Systems biology integrates experimental and computational research to study how the behaviour of a biological system results from the interactions of its components. Systems and synthetic biology are rapidly absorbing ideas and methodologies from Natural Computing leading to the development of novel applications and, at the same time, enhancing the notion of computation.

This special issue collects a selection of papers which cover theoretical, experimental and applied on-going research at the interface of these disciplines.

The work by Dalchau et al. focuses on the role of biological switches and clocks, discussing how these mechanisms can be used to extend the area of biological computing. The authors also present a more general historical perspective on biological computing.

The paper by Cunha et al. discusses the study of bacterial colonies as complex adaptive systems. The paper shows how simple individual cellular decision-making can lead to the formation of very complex bacterial colonies' actions.

In the paper by Bordihn et al. the authors investigate the computational power of a new variant of networks of splicing processors, a model which abstracts DNA

mutations in terms of formal languages and consider the computations which take place on abstract networks.

The review by Baskerville et al. discusses the role of cellular decision-making (and cellular computing) in the context of microbial communities, and suggests that a proper understanding of cellular information-processing can lead to a better and more quantitative understanding of microbial ecology.

The paper by Aman et al. presents a calculus which facilitates the modelling of covalent bonds between molecules, with the ultimate aim to model the dynamics of the interactions in biochemical systems. To demonstrate the calculus, the authors use a known software platform to simulate and verify specific properties of modelled chemical reactions.

The work by Xiang et al. discusses recent successful examples of distributed cellular computing implemented using cell consortia. In particular, the authors discuss the existing challenges and the potential solutions in building predictable large-scale circuits including modularity, context dependency and the effects of metabolic burden.

The editors would like to thank the authors for their contributions and the reviewers for their constructive and helpful feedback. We also thank Grzegorz Rozenberg, Joost Kok and the staff of Natural Computing for their meticulous precious help on assembling this special issue.