

Introduction to Special Issue ECCS'10 in Theory in Biosciences

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Published online: 19 June 2012
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The European Conference on Complex Systems 2010 (ECCS'10) took place in September 2010 and was located at Lisbon in an excellent conference environment. The conference attracted more than 500 participants from a whole range of scientists having a joint interest in complex systems science. Two major tracks of the conference were devoted to biological systems on different scales, ranging from molecular to ecological interactions. Biological systems created an important motivation to study complex systems right from the beginning of the movement. But it becomes increasingly clear that both fields—complex and biological systems—become even more entangled as complex systems deliver new ways to understand biological complexity, and the more the biological systems are investigated it becomes apparent that evolution has already invented numerous ways to tackle ‘complexity’ in the wider sense. In the spirit of design, it is always worth first looking at the answer of the question: ‘how has nature solved the problem’?

The papers collected in this special issue of *Theory in Biosciences* represent a part of the research presented during ECCS'10. Complex systems research is surely at the innovation boundary of modern inter- and multi-disciplinary science. The journal *Theory in Biosciences* has

supported this process for quite some time, and we are pleased to add another ECCS contribution with this special issue.

Network theory is one of the current major branches of complex systems science. The contribution of Susan Khor on structural characteristics of protein residue networks takes the subject of linking proteins much further: now the aspect of protein folding is included. The first protein networks available in the literature have been constructed on experimental binding evidence only. Unfortunately, the assays used proved unreliable in certain cases for certain proteins, making the results and their implications to some degree doubtful. Finding the structural reasons why proteins can connect or bind to each other provides much needed additional information on the reliability of such protein binding data. Moreover, the analysis gives some insight in the true reasons why certain proteins can bind to each other, and others do not.

The special issue contains two contributions on molecular kinetics. Reaction systems are generally important for complex systems, as they can be compared with agent-based models which are equally based on rules, i.e. events like reactions. Moreover, they are generic models to study the action of feedback loops and stochastic noise. In their contribution A. Lindo, B. Faria and F. de Abreu study a model of molecular tunable kinetic proofreading, which is based on the actions of feedback loops. The second contribution by A. Filisetti, A. Graudenzi, R. Serra, M. Villani, R.M. Füchslin, N. Packard, S.A. Kauffman and I. Poli on stochastic autocatalytic reaction systems extends the originally deterministic theory of autocatalytic cycles by Stuart Kauffman to a new stochastic setting. The paper is at the end of some extensions based on early criticisms of Kauffman's model, making the whole framework more robust.

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Finally, we were able to cover two more important fields of complex systems research in one paper: genetic regulation and data integration. The data fitting problem is already under normal circumstances a mathematically challenging situation, and even more so for a complex system like a gene regulatory network. This is especially true as dynamic data points in genetics are hard to obtain, and there are only a few reliable longer time series of gene expression data available. The article by A. Sirbu, H.J. Ruskin and M. Crane on ‘Integrating heterogeneous gene expression data for gene regulatory network modelling’

investigates how well the information contained in different heterogeneous time series can be fitted to the same standard model of genetic regulation, all with the help of the latest fitting technology including the help of wavelets used to show that the models display limited noise overfitting.

We hope the reader will enjoy this special issue which shows the complex systems community is very active in biological research. Moreover, we aim to deliver equally inspiring contributions at future ECCS conferences.