Editorial

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This special issue of Theory in Biosciences is devoted to contributions from ECCS07, the annual European Conference on Complex Systems that in 2007 took place in Dresden. As the name indicates, this conference is interdisciplinary in character and brings together scientists from a wide range of fields. Among those, the biological sciences play an important role, from two perspectives in fact:

• On one hand, many experimental findings in the entire range of biological sciences, from the molecular to the behavioral, neurobiological or even to the population and biosystems levels, and actually many simulation results as well, pose the challenge of developing formal models that can account for them. Also, biology is in need of systematic theoretical concepts. Therefore, many scientists from the theoretical fields, including mathematics, physics, and computer science are drawn to biological problems and test their range of methods and concepts on biological questions. This range is wide, and so then is the one of the biological problems addressed. One can model and conceptualize general mechanisms of evolution, or one can treat concrete biophysical problems or analyze large sets of biological data. Nevertheless, certain aspects are characteristic of biological structures in particular and complex systems in general. They include the relation between a system and its constituents, elements or parts. Another instance is the dynamical interaction of different spatial and temporal scales. Also, nonlinear effects like sudden bifurcations or phase transitions when some crucial parameter reaches a critical threshold play an important role. Moreover, for the investigation of a complex system, the identification of those, sometimes relatively few, variables that determine the important qualitative features of the system is fundamental. In other words, in order not to get lost in an overwhelming amount of complicated details, one needs to understand how the system as a whole constrains the local degrees of freedom in the dynamics of the elements and parts and their interactions.

• On the other hand, over the long span of time that evolution could operate, biological systems have found strategies for solving many problems, and this in turn provides ideas for a wide range of optimization schemes for technical and infrastructural problems. This goes under the name of bio-inspired computing or modelling and includes
  – Evolutionary and genetic algorithms for population based search strategies in high dimensional spaces,
– swarm algorithms that utilize local interactions between cooperating agents to find good solutions for tasks where the transition from the local contributions to the global goal is combinatorially complicated or even intransparent, or
– neural networks that employ the parallel activity of synaptically coupled units, called neurons, to build implicit associations instead of explicit rules.

All these schemes depend on the distributed activity of local units or agents without central coordination and thereby illustrate a paradigm of self-organization.

In a certain sense, the conference has also been following this approach: from a wide range of contributions that were developed by individual scientists or groups without any central guidance, we hope that in the end a more global perspective on complex systems will emerge. In that sense, the contributions that, in an additional strict evaluation process, have been selected for this special issue span a wide range of topics. When taken together, they may reflect the general structure of the interplay between biological structures and problems on one hand and formal methods and concepts on the other hand. With this in mind, let us now briefly describe the articles in this issue: naturally, they range from the molecular to the population level, and from concrete physical mechanisms to abstract theoretical issues, but they often link these aspects or span many different biological scales:

1. Starting with the smallest scale, Sadovsky and Putintseva define an information capacity measure for sequences and apply it to nucleotide sequences and evaluate it for several data sets.
2. Poudret et al. develop topological models to understand and test the spatial structure and the dynamics of the Golgi apparatus in the cell.
3. Tero et al. model how an amoeba reconfigures an internal tubular network for the transportation of signals and materials in response to specific conditions which may suggest a new biologically inspired computational scheme for network optimization.
4. Barat et al. model the release of proteins from their bioerodible capsules, which is important for the design of drug delivery systems.
5. Sbano and Kirkilionis develop a systematic mathematical theory for the multiscale analysis of reaction networks, to study the interplay between concentration and conformation changes of molecules. These are processes that occur on different temporal scales and necessitate different types of approximation.

6. Tournier and Gouzé systematically develop the method of hierarchical analysis of piecewise affine systems and utilize them as models of gene regulatory networks.
7. Gutkin et al. detect and investigate a new stochastic mechanism in coupled neurons. They find that in contrast to the enhancing effect of large noise, small noise can disrupt cooperative firing patterns, both in excitatory and in oscillatory neuron models.
8. Baptista and Costa develop and investigate a model for the emergence of circadian rhythms by the adaptation of agents to external cycles.
9. Scheidler et al. come up with a scheme for task partitioning between agents inspired by ant queues.
10. Bernadet et al. propose a neurobiologically plausible system of how animals find their way back to their point of departure after exploring its vicinity, that is, about storing and retrieving direction and distance information. They test their model against simulated and behavioral data from ants.
11. Sumpter et al. analyze local interaction models about how animal flocks maintain cohesive directional motion while making rapid changes in direction. They then evaluate the phase transitions and bifurcations predicted by the models on data from locusts and pidgeons.
12. Inden develops a new neuroevolution system, that is, a system for the evolution of developmental processes for neural networks, thus linking three fundamental biological mechanisms, evolution by selection, ontogenesis, and neural information processing. The performance of his model is demonstrated at well-known simulated benchmark tests.
13. Finally, Kaneko and Furusawa address an abstract issue that is relevant in many areas of biology. They propose a consistency principle between different levels of organization in a biological system and discuss applications to the relations between molecule proliferation and cell reproduction, between cell reproduction and growth of cell ensembles (leading to a chaotic mechanism for stem cell differentiation), and between genotype and phenotype.

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