SYBN 1 Biologische und Soziale Netzwerke I

Zeit: Montag 09:45–11:45 Raum: TU HE101

Hauptvortrag SYBN 1.1 Mo 09:45 TU HE101

Computation, evolution and tinkering in complex networks — •Ricard Sole — ICREA-Complex Systems Lab, Universitat Pompeu Fabra, Dr Aiguader 80, E-08003 Barcelona

Complex biological networks have very different origins than technologic ones. The latter involve extensive design and, as engineered structures, include a high level of optimization. The former involve (in principle) contingency and structural constraints, with new structures being incorporated through tinkering with previously evolved modules or units. However, the observation of the topological features of different biological nets suggests that nature can have a limited repertoire of "attractors"suggesting some common principles of evolution beyond their specific nature. A relevant link in this context involves the presence of computation, which is known to be robust in biological systems and fragile within the technological universe. Surprisingly, many relevant features of complex natural networks (some shared by artificial ones) are a consequence of evolutionary rules with weak relation to functionality. Conversely, when evolving artificial systems using bio-inspired rules, robustness to failure and heterogeneous topology seem to emerge as a byproduct of the evolutionary rules. These observations will help understanding the evolution of complexity in nature and reinventing the way technology is beign designed.

Hauptvortrag SYBN 1.2 Mo 10:15 TU HE101

Properties of attractors and relevant nodes in random Boolean networks — •Barbara Drossel — TU Darmstadt, Institut für Festkörperphysik, Hochschulstraße 6, 64289 Darmstadt

This talk gives an overview of the properties of random Boolean networks, based on recent work by several groups, and including a java applet to illustrate the properties of these networks. The focus is on critical networks with connectivity 1 or 2. After a general introduction to these models, the talk deals first with the relevant nodes, which determine the number and lengths of attractors. It will be shown that the number of relevant nodes increases with system size N as $N^{1/2}$ and $N^{1/3}$ for connectivity 1 and 2. Then, the properties of the attractors will be investigated. It will be argued that their mean number and length increase faster than any power law. Finally, the robustness of these findings with respect to modifications of the model will be discussed.

Hauptvortrag SYBN 1.3 Mo 10:45 TU HE101

Epidemic modeling: dealing with complex networks — •Alessandro Vespignani — School of Informatics and Department of Physics, Indiana University — Lab. Physique Theorique, Universite Paris Sud, Paris

The systematic study of population networks and their social/spatial structure has shown the ubiquitous presence of complexity features mathematically encoded in heavy-tailed statistical distributions, diverging fluctuations and emerging properties. Despite a variety of approaches have been developed in order to take into account the many complications and heterogeneities observed in the spread of epidemics, complexity is not the same as the sum of the merely complicated elements accounted for in sophisticate epidemic modeling. Indeed complex properties generally correspond to the breakdown of standard models. For instance this is the case of epidemic spreading in scale-free networks in which the lack of any intrinsic epidemic threshold generates a peculiar scenario with implications in immunization and containment policies. In this perspective we will provide a discussion of epidemic modeling that accounts for the presence of the network's complexity at various levels: connectivity pattern, traffic intensity, population heterogeneity. Finally, we will discuss to which extent the protection of populations, defined in the context of immunization policies designed to effectively reduce or prevent the large scale spreading of epidemics, is affected by the system's complexity.

Hauptvortrag SYBN 1.4 Mo 11:15 TU HE101

Traffic and Computation in Genetic Regulation — •Kim Sneppen — Nordita/Niels Bohr Institute, Blegdamsvej 17, 2100 Copenhagen Ø

I will discuss physics of biological regulatory mechanism from simple recruitment, to traffic on DNA and to analysis of genetic regulatory networks. The talk will discuss design principles found in regulation of bacterio-phages, using as examples the lambdoid family versus the P2 family of temperate phages. We will use these to empasize the parts of genetic regulative networks that deals with integrated computation, respectively the parts of the regulation that represents distributed signaling. We finally use the phage networks to teach us some basic lessons about how one can compare signaling networks of different organisms.