

## Workshop 4

### NETWORKS IN BIOLOGY: DISCOVERY, ANALYSIS AND MODELING

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#### **Abstract**

It is increasingly recognized that in order to understand the dynamics and function of a cell, as well as higher levels of biological organization, we need to know: 1) the components that constitute it; 2) the relations and interactions of these components, and 3) their dynamic behavior, i.e. how the biological entities behave over time under various conditions. Biological networks are defined to incorporate the first two ingredients and serve as the starting point for understanding the third. This tutorial will present three related topics at the intersection of network science and systems biology: network discovery (i.e. reconstructing the network of interactions among a set of biological entities), network analysis (i.e. mining the information content of the network), and dynamic network modeling (i.e. connecting the interaction network to the dynamic behavior of the system).

Cellular constituents such as DNA, RNA, proteins and small molecules interact on several levels, forming transcriptional regulatory-, protein interaction-, metabolic- and signal transduction networks. Genetic, biochemical and molecular biology techniques have been used for decades to identify biological interactions; newly-developed high-throughput methods now allow for the construction of genome-level interaction maps. In parallel, high-throughput expression data paired with computational algorithms can be used to discover (infer) networks of interactions and causal relationships capable of producing the observed experimental data.

Graph-theoretical measures (e.g. distances, degree distributions and network motifs) and network models are more and more frequently used to discern functional and evolutionary constraints in the organization of biological networks. Furthermore, network analysis enables specific biological discoveries such as novel interactions or predicted roles for proteins whose function is currently unknown.

The combination of interaction and expression information allows the formulation of quantitative and predictive dynamic models. A dynamic model that correctly captures experimentally observed normal behavior allows researchers to track the changes in the system's behavior due to perturbations. Dynamic network modeling allows the identification of key components (or subnetworks) and key parameters whose perturbation leads to drastic changes in the system's dynamics.

#### **Biography**

Réka Albert is currently Associate Professor in the Department of Physics of the Pennsylvania State University. She is also affiliated with the Department of Biology and the College of Information Sciences and Technology. She graduated from the Department of Physics of the Babes-Bolyai University (Cluj, Romania), working with Zoltán Nédá, and received her PhD in Physics from the University of Notre Dame, working on complex networks with Albert-László Barabási. Her career includes a post-doctoral fellowship in mathematical biology, with Hans Othmer, at the University of Minnesota. Reka Albert's research focuses on the modeling of biological networks. She is also committed to communicating the benefits of network science to biology through her teaching and her review articles in the *Journal of Cell Science*, *IET Systems Biology* and *Plant Cell*.