Uncertainity in biological networks: Challenges, Solutions and Opportunities.

ABSTRACT

Biological networks of an organism show how different bio-chemical entities, such as enzymes or genes, interact with each other to perform vital functions for that organism. Each subnetwork within a network can perform various functions that it cannot do without interacting with other entities in the network. A common way to discover the physical interaction data is to use large scale experiments like yeast-two-hybrid and co-immunoprecipitation assays. These techniques produce high throughput results but they also introduce many false positives. The data produced are therefore uncertain. We call such networks with uncertain interactions probabilistic networks.

Dr. Kahveci's lab is focusing on developing computational methods that will help in understanding the functions of large scale biological networks. In this talk, we will discuss some of the recent research activities at Dr. Kahveci's lab. Particularly we will focus on the uncertainty in the topology of biological networks. We will start by describing the fundamental computational challenge introduced by the uncertainty which is the exponential growth in the number of deterministic network topologies. We will discuss our new mathematical model which represents probabilistic networks as collections of polynomials. We show that this is a powerful model that enables solving seemingly very tough computational problems on probabilistic networks efficiently and precisely. A careful design of these polynomials can transform complex problems on probabilistic networks into a simple evaluation of these polynomials. We will discuss the application of our model on three fundamental problems in analysis of biological networks, namely finding the degree distribution of a given network, aligning a pair of networks and finding whether an extracellular signal reaches from a membrane receptor to a reporter gene. Finally, we will briefly discuss a set of possible future applications of our polynomial model for probabilistic biological networks on various problems from different domains.