

Dynamical Modeling of Biological Networks

Marianne Huebner, Ph.D.
Michigan State University

Abstract:

Experimental and computational approaches are beginning to define biological networks, for example those of interacting genes and their protein products, on a grander scale than previously imagined possible. When trying to understand complex biological phenomena, dynamical modeling is becoming increasingly important. Despite their importance in biological studies, biological networks are usually studied individually and are not jointly considered. However, different levels of networks are related and common characteristics exist among biological networks such as gene regulatory networks, protein interaction networks, metabolic networks, or ecological/epidemiological networks.

For example, ecological processes involve many levels, from environmental factors, to interacting populations, to genetic determinants. Computational models can help interpret the observed dynamics and guide the collection of data. Simulation studies can provide insights into the relative importance or interplay between factors. Experimental and computational approaches help identify network connections and analyze design principles, such as recurring motifs in *E.coli*.

This talk addresses only two levels of biological networks, namely gene regulatory networks and ecological/epidemiological networks. Design principles, dynamic properties, and problems encountered in the analysis of such networks are discussed.