

Predictive modeling of biological networks

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All organisms have a remarkable capacity to process complex changes and adjust behavior to best suit their environment. The cascade of events from sensing an environmental change and triggering a response constitute many layers of intricate information processing pathways such as signal transduction, pre- and post-transcriptional regulation, post-translation regulation, and allosteric modulation of enzyme function. Information is propagated in a controlled manner through all of these complex layers to effect a systemic change in cell behavior. I am interested in developing and applying systems approaches to reverse engineer the architecture of the regulatory networks and mathematically model their dynamics to fully understand how these complex processes operate. One of my longer term goals is to establish foundational theory to use these systems scale models to rationally re-engineer designer circuits for a variety of biotechnological applications related to bioenergy, bioremediation and medicine.

In addition, I am interested in using the systems approach I have described above to answer fundamental questions regarding evolution of biological networks:

1. How does biological complexity arise through expansion of gene families?
2. How is memory encoded in microbes? How do they use this memory to anticipate environmental changes? What is the adaptive learning process?