

TALK ANNOUNCEMENT

Seminar Series: The Science of Complex Networks (description below)

Speaker: Professor John J. Tyson, Department of Biological Sciences & Virginia Bioinformatics Institute.

Title: Network Dynamics and Cell Physiology

Abstract: Please see below.

Date & Time: Monday, January 30, 2006. 4:00-5:00 PM

Location: Virginia Tech Corporate Research Center, Building XV, Conference room 2018

Web: <http://ndssl.vbi.vt.edu/seminars>

Abstract

Complex networks of interacting proteins control the physiological properties of a cell (metabolism, reproduction, motility, signaling, etc.). Intuitive reasoning about these networks is often sufficient to guide the next experiment, and a cartoon drawing of a network can be useful in codifying the results of hundreds of observations. But what tools are available for understanding the rich dynamical repertoire of such control systems? Why does a control system behave the way it does? What other behaviors are possible? How do these behaviors depend on the genetic and biochemical parameters of the system (gene dosage, enzymatic rate constants, equilibrium binding constants, etc)? Using basic principles of biochemical kinetics, we convert network diagrams into sets of ordinary differential equations and then explore their solutions by analytical and computational methods. We illustrate this approach with a mathematical model of cell cycle transitions in eukaryotes, based on a molecular network controlling the activity of cyclin-dependent kinase (Cdk). In this model, arrest points in the cell cycle correspond to stable steady states of the control system. As biochemical parameters of the control system change, these arrest points are imposed or lifted by transitions called "bifurcations." During normal growth and division, cell size is the critical parameter that drives progression from G1 to S/G2 to M phase and back to G1. Simple diagrams, which correlate Cdk activity with cell growth, give a new way of thinking about cell cycle control, particularly the role of checkpoint pathways in arresting the cycle. The method is generally applicable to any complex gene-protein network that regulates some behavior of a living cell.

References:

- ▶ Tyson, Chen & Novak (2001) *Nature Rev. Mol. Cell Biol.* 2:908-916
 - ▶ Tyson, Csikasz-Nagy & Novak (2002) *BioEssays* 24:1095-1109
 - ▶ Tyson, Chen & Novak (2003) *Curr. Opin. Cell Biol.* 15:221-231
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Seminar Series: "The Science of Complex Networks"

A new seminar series titled "The Science of Complex Networks" is being started. It is organized by the group NDSSL at VBI, on the web at <http://ndssl.vbi.vt.edu>. The theme of the seminar is mathematical and computational aspects of dynamics over large graphs. Examples include the dynamics on networks in communication, urban traffic systems, and networks arising in biological systems such as the molecular networks in the genome and the immune system.

The systems and network models that come from these various areas describe very different phenomena and dynamics and may seem to have little in common. Contrary to this intuition, there are large classes of models with fundamental similarities in both structure and dynamics. This common and generic structure has already motivated research, and is an extremely active area of current research.

The seminars will have a formal flavor, and at least proof ideas and outlines will be encouraged. Presentations of experimental data and findings displaying interesting phenomena that point to possible general results are also welcome.