

New Systems Biology Course in Spring 2008

Course Number: CHBE 494/594 (under Special Topics, section B)*

Course Title: Systems Biology

Credit: 3 Hour (494); 4 hour (594)

Lecture Time: 10:30-11:50, TR

Classroom: TBD

Instructor: Nathan Price, ndprice@uiuc.edu

Course Description: This course will cover the process of reconstructing complex biochemical reaction networks in cells and mathematically simulating their behaviors. Topics covered will include: reconstruction of metabolic networks, regulatory networks and signaling networks; bottom-up and top-down approaches; principles underlying high-throughput experimental technologies and examples on how this data is used for network reconstruction, consistency checking, and validation; mathematical models of reconstructed reaction networks and simulation of their emergent properties; classical kinetic theory; and constraints-based models. Methods that are scalable and integrate multiple cellular processes will be emphasized. Existing genome-scale models will be described and computations performed. Emphasis will be on studying the genotype-phenotype relationship in an *in silico* model driven fashion, and comparisons with phenotypic data will be emphasized.

Course Goals: This course aims to introduce the student to the emerging field of systems biology – the intersection between high-throughput biological data integration and computational modeling. This course will focus primarily on the reconstruction and analysis of biochemical reaction networks (metabolic, regulatory, signaling) in cells as a basis for systems biology research and synthetic biology designs. By the end of this course, students will be expected to be able to:

1. Reconstruct biochemical networks of various types from biological data
2. Analyze the properties of these networks using a variety of techniques, including linear programming, convex analysis, SVD decomposition, Monte Carlo random sampling
3. Design mathematical models for a wide variety of biological processes and interpret the meaning of the network model simulations for the biological systems they represent

Main Topics:

1. Reconstruction of biochemical networks
2. Objective-based analyses of optimal network functions
3. Unbiased assessments of network capabilities
4. Alternate subspaces of network functions (fluxes, kinetics, and concentrations)

Questions: Contact Prof. N. Price at ndprice@uiuc.edu

***Note:** 494 is the undergrad version and 594 is the graduate version (taught concurrently). The graduate version will require a course project on a research topic in systems biology relevant to the course material and objectives.