BMED 4477 Biological Networks and Genomics (Elective)

Catalog Description: BMED 4477 Bio Networks & Genomics (2-3-3)
Prerequisite(s): BMED 3520 and [ISYE/CEE 3770 or BMED 2400]
Introduction to modeling of biological networks involved in gene regulation, cell signaling and metabolism. Mathematical modeling of cellular processes, such as gene expression, using genomic data.

Textbook: Alon U., An Introduction to Systems Biology: Design Principles of Biological Circuits, Chapman and Hall, 2006

Prepared by: Mark Borodovsky

Topics Covered:

1. Introduction to OMICS data types and next generation data production techniques.
2. Machine learning methods for identification of "system parts" from genomic sequence
3. Examples of real life networks: transcriptional, protein-protein interaction, metabolic, signaling networks.
4. Experimental methods for discovery of network structure.
5. Random graph network models, structural patterns in random networks and in networks emerged as a result of biological evolution.
6. Use of conservation patterns in evolution of genome structure to infer elements of structure of metabolic networks.
7. Use of RNA-seq for measuring gene expression. Clustering of gene expression data. Identification of sets of co-expressed genes as modules of transcriptional networks
8. Global and local structure of transcriptional networks. Network motifs.
9. Dynamics of transcriptional regulation. Autoregulation.
10. Synthetic design of gene circuits. Binary and combinatorial regulation.

Course outcomes:

Students who complete this course will be able to:
Outcome 1: Understand research publications that apply machine learning techniques to infer new facts about biological networks relevant to modeling function of a particular gene or a set of genes of interest (Student Outcomes a, e, g, i, j, k)
Outcome 2: Apply standard computational techniques to analyze new experimental data on gene expression, such as RNA-Seq data from literature or from a lab experiment, and to infer sub-networks of co-regulated genes (Student Outcomes a, b, e, k)
Outcome 3: Apply standard data mining methods to retrieve information on the structure of metabolic, signal transduction pathway as well as protein-protein interaction networks related to a particular gene or protein of interest from existing databases (Student Outcomes a, b, e, k)
Outcome 4: Apply analytical and computational techniques to model dynamic of gene expression of a set of genes controlled by several regulators under various conditions. (Student Outcomes a, e, k)

Outcome 5: Understand principles of design of synthetic regulatory networks and come up with initial design of synthetic network using sets of binary or combinatorial regulators. (Student Outcomes c)

Correlation between course outcomes and student outcomes:

BMED 4477											
	Biomedical Engineering Student Outcomes										
Course outcomes	a	b	c	d	e	f	g	h	i	j	k
1	X				X		X		X	X	X
2	X	X			X						X
3	X	X			X						X
4	X				X						X
5			X								X

The Wallace H. Coulter Department of Biomedical Engineering Student Outcomes:

a. an ability to apply knowledge of mathematics, science, and engineering;
b. an ability to design and conduct experiments, as well as to analyze and interpret data;
c. an ability to design a system, component, or process to meet desired needs within realistic constraints such as economic, environmental, societal, political, ethical, health and safety, manufacturability, and sustainability;
d. an ability to function on multidisciplinary teams;
e. an ability to identify, formulate, and solve engineering problems;
f. an understanding of professional and ethical responsibility;
g. an ability to communicate effectively;
h. the broad education necessary to understand the impact of engineering solutions in a global, economic, environmental, and societal context;
i. a recognition of the need for, and an ability to engage in lifelong learning;
j. a knowledge of contemporary issues;
k. an ability to use the techniques, skills, and modern engineering tools necessary for engineering practice;