Course Proposal: CMSC 703 - Network Analysis and modeling of Biological Systems

September 2015
Computational Biology Field Committee

Motivation and background

Recent technological advances in biomedical research have been generating tremendous amounts of data. This calls for the development of novel rigorous computational methods to extract the potential significant information that is embedded in this data to fully capitalize on the large investments and revolutionary breakthroughs that are being made in collecting the data. This information is composed of many biological modalities that are analyzed by numerous computational tools, as encompassed in the different CNSC70* courses offered. The current course will survey network based approaches that analyze post-genomic data, including transcriptional, regulatory, proteomic and metabolomics data. The lion’s share of the course will focus on genome scale metabolic modeling, as this is currently the only approach where we can begin to advance on the ‘holy grail’ challenge of whole cell modeling of human cells in silico.

Course Description

The course will focus on the computational network analysis and modeling of biological systems focusing on transcriptional, protein, signaling and metabolic networks (with primary emphasis on integrating the former within the latter). Computational methods studied for this type of analysis include: network and graph algorithms, network-based machine learning approaches, modeling dynamical systems, numerical optimization (linear, integer and quadratic programming) and a variety of other methods used to solve constraint based problems (primarily in the context of studying metabolic networks). These methods are complementary to those studied in CMSC701 and CMSC702.

Prerequisites

Computer Science or Applied Mathematics student or permission of instructor.

No knowledge of biology required.

Textbooks:

There is currently no single textbook that covers all the topics presented in the course. The following textbooks contain a number of topics discussed and will be listed as recommended reading. The relevant material from these books will be made available to the students as handouts.

**Tentative Syllabus**

1. **Introduction (1-2 weeks):**
   - Biomedicine 101 for computer scientists
   - Introduction to systems biology – the research questions and the experimental methods; cellular networks and an overview of computational approaches for modeling them

2. **Genome scale modeling of cellular metabolism (8 weeks):**
   - Introduction to metabolism and metabolic networks, from bacteria to plants to humans.
   - Constraint based modeling of metabolism: Linear, quadratic, mixed-integer and mixed-integer quadratic programming.
   - Methods for modeling cell growth, cellular response to genetic and environmental perturbations, estimating network activity and flux distributions, maximizing cellular objectives, and biotechnological applications of metabolic modeling.
   - Methods for integrating molecular data to infer likely network states, to build compartmentalized models, and build cell-specific and tissue-specific models.
   - Methods for studying metabolic alterations accompanying human diseases, the prediction of drug targets and biomarkers, and the prediction of clinical phenotypes and drug side effects.
   - Integrating regulatory information within metabolic models
   - Targeting metabolic alterations in cancer, aging, and neurodegenerative disorders.

3. **Analysis and modeling Protein-Protein Interaction (PPI) networks (2 weeks):**
   - Network measures and random network models
   - PPI networks – construction and network motifs
   - PPI networks in disease and drug development and repurposing
• 4. Towards whole cell modeling  (2 weeks)
• Recap