

BMED 4477 Biological Networks and Genomics

Credit: 2-3-3

Prerequisites: ECE 2025 and BMED 3600 and [ISYE/MATH/CEE 3770 or BMED 2400]

Catalog Description

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.

Text

Selected journal papers

Objectives

The overall objective of this course is to introduce students to physical, mathematical and computational aspects of modeling of biological networks as important part of fundamental theoretical concepts of biomedical engineering.

Outcomes

At the end of the course students will be able to:

1. apply analytical and computational machine learning techniques to determine the structure of a gene regulatory network relevant to a particular gene or a set of genes of interest in a given cell based on literature or new experimental data. (Program Outcomes 1 and 2)
2. apply analytical and computational techniques to infer the structure of a protein-protein interaction network (or the set of components of a protein complex) based on literature or new experimental data. (Program Outcomes 1 and 2)
3. apply analytical and computational techniques to derive the structure of a metabolic pathway based on literature or new experimental data. (Program Outcomes 1 and 2)
4. apply analytical and computational techniques to parameterize a gene regulatory network by using data on gene expression, and proceed further with modeling the gene regulation for various conditions. (Program Outcomes 1 and 2)
5. apply analytical and computational techniques to identify function of a gene or protein in a network from comparative analysis of genomes and proteomes of other species and detection of network conservation patterns. (Program Outcomes 1 and 2)

Topical Outline

1. Examples of real life networks: social networks, computer networks, molecular networks, etc.
2. Network properties: degree distribution, clustering coefficient, distance related measures,

3. Random and special network models: random graph, exponential random graph, geometric random graph, generalized random graph, small world model; scale free model, hierarchical model, network motifs, feed forward loop, motif conservation and evolution, noise in real life networks.
4. Transcriptional networks: transcription regulation molecules and signals, promoters and transcription factor binding sites, cis-regulatory modules, integration of sequence information and microarray analysis, de-novo motif finding, EM algorithm and Gibbs sampling, MEME algorithm
5. Gene expression network model: co-expression, clustering, cost functions and algorithms (K-means), biclustering (SAMBA), expression correlation, interlogs.
6. Cellular signal transduction networks: basic components and mechanisms, integration with gene expression networks.
7. Protein-protein interactions: protein complexes, probabilistic models, scoring schemes, confidence assignment, RoC curves, assigning reliabilities to individual interactions
8. Functional annotation: module based inference of function, maximizing intra-class interactions.
9. Network alignment: PathBLAST, Path search in PathBLAST, identifying conserved protein complexes, protein complex scoring and validation, orthology mapping, conservation index, multiple network alignment.
10. Metabolic networks: constraint-based modeling, kinetic models, convex solution space, flux balance analysis, energy balance, application of linear programming
11. Genetic interaction networks: interaction arrays, high order genetic interactions, module finding, interrelation with PPI data, reconstruction of genetic networks from expression data
12. Network integration: phenotype clustering, pathway reconstruction, network dynamics.
13. Network robustness and evolution: failure vs attack, essentiality and centrality, party vs date hubs, essentiality and hubs; growth and preferential attachment, link dynamics, rates of interaction gain and loss, duplication vs link dynamics