Network biology is an emerging discipline that studies complex cellular processes by modeling them as networks of interactions between molecules. The analysis of biological networks presents exciting graph-theoretic and statistical problems with important applications in biology. The course will review the state-of-the-art algorithms and analysis techniques in the field, and demonstrate their applications to the study of real biological networks.

The course requires no prior knowledge in biology. All background will be provided in the lectures.

The course is open to all graduate students in computer science. Interested undergraduate students, as well as non-CS students, should contact the instructor.

Course Outline

- Introduction: basic biological and graph theoretic concepts.
- Network properties: degree sequence, connectivity, clustering coefficient.
- Network models: random graph, degree-preserving graph, scale-free graph, geometric model.
- Components of a network: motifs and modules.
- Algorithms for network searches: greedy, color coding, branch and bound, bicluster analysis.
- Evolution of networks: conservation analysis, network queries.
- Protein-protein interaction networks.
- Metabolic networks: constraint based modeling.
- Regulatory networks: promoter sequence analysis.
- Advanced topics: integration of networks, network robustness.
**Prerequisites:**

“Efficiency of Computations (Algorithms)” (mandatory),
“Computational Genomics” (recommended).