

Syllabus for Columbia University Course: *Computational Biology II: Proteins, Networks, Function*

Teachers: Dennis Vitkup & Burkhard Rost

CONTACT: Dennis Vitkup (dv2121@columbia.edu); TAs: Lifeng Chen lc2071@columbia.edu; Chani Weinreb chani.weinreb@dbmi.columbia.edu

PLACE: Columbia University: Medical Campus: Irving Cancer Research Center 121B (the Irving Cancer Center is located at the corner of St. Nicholas and 166/167th streets; room 121B is on the first floor).

Week	Date	Topic	Teacher
Proteomics:			
1	Wed Jan 26, 1:30-2:30	Introduction / Lecture: Sequence alignments: from simple pairwise to profile-profile alignments	Rost
1	Fri Jan 28, 1:30-3:00	Continuation of lecture: Sequence alignments	Rost
2	Wed Feb 2, 1:30-2:30	Structure prediction: methods that predict protein structure in 1D, 2D and 3D	Rost
2	Fri Feb 4, 1:30-3:00	Continuation of lecture: Structure prediction	Rost
3	Wed Feb 9, 1:30-2:30	Prediction of protein function from sequence and through homology	Rost
3	Fri Feb 11, 1:30-3:00	Continuation of lecture: Function prediction	Rost
4	Wed Feb 16, 1:30-2:30	Prediction of protein function: examples I	Punta
4	Fri Feb 18, 1:30-3:00	Prediction of protein function: examples II	Punta
5	Wed Feb 23, 1:30-2:30	Annotating entire proteomes	Rost
5	Fri Feb 25, 1:30-3:00	Discussion/Student Paper Presentation	
Network Biology:			
6	Wed Mar 2, 1:30-2:30	Overview of cellular biological networks. Metabolic, Signaling, Regulatory, Protein-protein interaction networks. The basic topological and structural properties of cellular networks. Network modules and motifs. Comparison with non-biological networks	Vitkup
6	Fri Mar 4, 1:30-3:00	Discussion/Student Paper Presentation	
7	Wed Mar 9, 1:30-2:30	Computational methods used to reconstruct cellular networks. Comparative genomics, text-based approaches, context-based approaches, expression-based approaches, data integration	Vitkup
7	Fri Mar 11, 1:30-3:00	Discussion/Student Paper Presentation	
8	Wed Mar 16, 1:30-2:30	NO COURSE - spring-break	
8	Fri Mar 18, 1:30-3:00	NO COURSE - spring-break	
9	Wed Mar 23, 1:30-2:30	NO COURSE - break	
9	Fri Mar 25, 1:30-3:00	NO COURSE - break	
10	Wed Mar 30, 1:30-2:30	Evolution of biological networks. Basic evolutionary laws, duplication and preferential attachment. Network robustness.	Vitkup
10	Fri Apr 1, 1:30-3:00	Discussion/Student Paper Presentation	
11	Wed Apr 6, 1:30-2:30	Network simulation and analysis (metabolic networks). Metabolic control analysis, differential equations,	Vitkup

11	Fri Apr 8, 1:30-3:00	constrained-based approaches Discussion/Student Paper Presentation	
12	Wed Apr 13, 1:30-2:30	Network simulation and analysis (signaling and regulatory networks). Differential equations, stochastic methods, Spatial methods.	Vitkup
12	Fri Apr 15, 1:30-3:00	Discussion/Student Paper Presentation	
Student Projects:			
13	Wed Apr 20, 1:30-2:30	Discussion/Student Paper presentation	
13	Fri Apr 22, 1:30-3:00	Discussion/Student Paper presentation	

Prerequisites

This course is intended for students who have had some previous exposure to topics in computational biology. Thus we require 1 year of calculus, 1 course in statistics or the equivalent training in mathematics or physics, 1 course in molecular biology, facility with at least one computer programming language (e.g. Perl, C/C++, or Java), as well as prior exposure to the material covered in Biology W4037 or Engineering E3060/E4060.

Course objectives.

This course is designed to fill an important, unmet need for graduate-level courses in computational biology and bioinformatics. This course constitutes the second half of a two-course series that will be considered fundamental to the curriculum of graduate students pursuing a PhD with a concentration in computational biology (e.g., through the Integrative Program's computational biology track; or for Biomedical Informatics students with a computational biology emphasis). This course is designed to complement and build upon other courses taught in the College and in the Medical School.

Course Description.

The CompBio2 course is designed to introduce students to modern methods and active research areas of computational biology. The course will have two main units: Structural/Functional Proteomics and Cellular Network Biology.

The proteomics unit will cover prediction of protein structure and protein function from sequences, structure, and evolutionary information. We will describe methods based on neural networks, support-vector machines, tree-algorithms and Bayesian classifiers. Application of the methods to annotation of entire proteomes will be discussed.

The cellular networks unit of the course will present computational approaches of reconstruction, analysis, and simulation of cellular networks. Metabolic, signaling, and protein-interaction networks will be covered. The

networks will be discussed at several levels of structural organization: overall network, functional and structural modules, network motifs. We will emphasize how specific biophysical and biochemical properties of different networks lead to conceptual simplifications for analysis and simulation. Network evolution and similarities between cellular and non-biological networks will be discussed.

Course structure.

The course will consist of lectures (once a week) and important paper presentations by students (once a week). At the end of the course students will work on small scientific projects (by teams of 2-3 people).

Grade: 50% Class participation/paper presentations, 50% final project.