



FALL SEMESTER 2005 Bio/Cheminformatics Course (84.467/84.567)

**Instructor: Prof. Ruxandra Dima, Department of Chemistry, University of Massachusetts,
Lowell**

Tuesday 10:30-12:00, 518 Olney Hall and Thursday 10:30-12:00, 522 Olney Hall

*Course open to graduate and advanced undergraduate students in Chemistry, Biology, Computer Science,
Mathematics, Physics and Engineering*

Scope: This course will introduce students to statistics-based computational methods used to predict the structure and function of proteins and RNA molecules and to probe protein-protein interactions. It will also include an overview of the physical principles behind experimental methods used to study proteins and RNA and their link with theoretical approaches. Ample opportunities will be provided to gain hands-on experience in using databases and packages related to protein families, protein-protein functional interactions, RNA and secondary structure prediction, protein secondary and tertiary structure prediction and visualization of biological macromolecules.

Topics:

- Probability distributions for one or more random variables
- Statistical hypothesis testing
- Sequence alignments, BLAST
- Clustering of data points, DNA microarrays
- Hidden Markov Models, PFAM and PROSITE databases
- Secondary structure in proteins: experiments and theory (PHD)
- Secondary structure in RNA: experiments and theoretical predictions (MFOLD)
- Proteins tertiary structure: prediction (threading) and experiments
- Macromolecular assemblies

Textbooks:

1. W. J. Ewens and G. R. Grant, “Statistical Methods in Bioinformatics”, 2nd edition, Springer Verlag 2004. **2.** T. E. Creighton, “Proteins. Structures and Molecular Properties.”, 2nd edition, W. H. Freeman and Company, NY.

Prerequisites: Calculus. Prospective students should be familiar with the use of computers. Basic knowledge of Biology, Programming and Chemistry is highly desirable.

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