



The University of Chicago
Department of Statistics

Seminar Series

JINBO XU

Toyota Technical Institute

**Statistical Learning Machines
for Protein Alignment and Folding**

MONDAY, March 14, 2011, at 4:00 PM

133 Eckhart Hall, 5734 S. University Avenue

Refreshments following the seminar in Eckhart 110.

ABSTRACT

If we know the primary sequence of a protein, can we predict its 3D structure by computational methods? This is one of the most important and difficult problems in computational molecular biology and has tremendous implications for protein functional study and drug discovery. Depending on whether or not there is one solved structure similar to the protein sequence under consideration, computational methods for protein folding can be classified into two categories: template-based and template-free modeling. The former uses similar solved structures as templates to predict the structure of a protein while the latter does not.

This talk will demonstrate how statistical learning methods can be applied to both template-based and free protein folding by leveraging the large number of protein sequences and structures. In particular, this talk will present two probabilistic methods for template-based modeling: regression-tree-based Conditional Random Fields (CRFs) and probabilistic-consistency transformation. Combined together, these two methods can accurately align a single protein sequence to one or multiple templates, from which a 3D structure model can be built for the sequence. This talk will also briefly present a statistical learning method Conditional Neural Fields (CNFs) to fold a protein sequence when no similar templates are available (i.e., template-free modeling).

Short Bio: Dr. Jinbo Xu currently is an assistant professor at the Toyota Technological Institute at Chicago. He is also a visiting scientist at the CSAIL of the Massachusetts Institute of Technology. Dr. Xu received his PhD in Computer Science from the University of Waterloo and then spent one year as a Postdoctoral Fellow in the Department of Mathematics, MIT. Dr. Xu's primary research interest is computational biology and bioinformatics including analysis and modeling of biological sequences, structures and networks. His RaptorX/RAPTOR programs have been ranked very top in several CASP (Critical Assessment of Structure Prediction) events, the most well-known competitions in the field of protein structure prediction. Dr. Xu was also invited several times to speak at the CASP meetings and publish papers in the CASP special issues.

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