



**L.H. BAKER CENTER FOR BIOINFORMATICS AND
BIOLOGICAL STATISTICS AND IGERT
SEMINAR SERIES**

SAMUEL KOU, Ph.D.

**Department of Statistics,
Harvard University**

Statistical Computation in Protein Folding

Predicting the native structure of a protein from its amino acid sequence is a long standing problem. A significant bottleneck of computational prediction is the lack of efficient sampling algorithms to explore of the configuration space of a protein. In this talk we will introduce a sequential Monte Carlo method to address this challenge: fragment regrowth via energy-guided sequential sampling (FRESS). The FRESS algorithm combines statistical learning (namely, learning from the protein data bank) with sequential sampling to guide the computation, resulting in a fast and effective exploration of the configurations. We will illustrate the FRESS algorithm with both lattice protein model and real proteins.

Date: Wednesday, April 25

Time: 4:00-5:00 PM

Room: 1414 Molecular Biology