Understanding the structural dynamics of biomolecules through experimental data and mathematical modeling

Speaker: Dr. Dmitry Kondrashov
Date: Friday, March 12, 2010
Time: 3:30-4:30pm, Room COB 265

Abstract: Biological molecules like proteins require flexibility in order to function. The structures of proteins, most commonly determined using X-ray crystallography, are still typically seen as a static arrangement of atoms. Mathematical models can be used to predict the modes of flexibility given the static equilibrium structure. In this talk we will compare these predicted modes from different models, and describe their validation using experimental measures of flexibility. The models can be used to formulate hypotheses about the mechanism of protein function, which will be illustrated by a study of a newly solved SNAP protein structure.