

PHYSICAL MATHEMATICS SEMINAR

Shape Shifting: Protein Statistical Physics as a Linear Programming Problem

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ABSTRACT:

Since a protein's shape typically provides the basis for its function, the conformational rearrangements of proteins in response to ligand binding, mutation, and covalent modification very often underlie biologically important molecular events, whether in the normal course of transducing a signal or through deleterious misfolding. A new analytical model of how structure depends on sequence enables us to use linear programming to examine many of these phenomena from the standpoint of statistical mechanics, so that we may begin to predict and explain specific changes in protein structure ranging from allosteric motion to the onset of aggregation disease.

TUESDAY, NOVEMBER 15, 2011

2:30 PM

Building 2, Room 105

*Reception at 3:30 PM in Building 2, Room 290
(Math Dept. Common Room)*

<http://math.mit.edu/pms>



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