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***Predicting Protein Interactions using
the Docking Mesh Evaluator (DoME)***

Abstract:

Protein-protein docking algorithms provide a means for predicting protein interactions. In this seminar, we present the challenges involved with such predictions and the various approaches that address these challenges. In particular, we present the Docking Mesh Evaluator, a software package for protein docking and energy evaluation. This method employs a high-resolution scan for favorable configurations coupled with a global optimization routine for predicting the global minimum of an energy function defined by electrostatic, van der Waals, hydrogen bond, and solvation energy terms. We will present some preliminary results from an ongoing benchmarking test.

**Tuesday, January 18th, 2005
4:00 p.m.**

Genetics/Biotechnology Center Auditorium
425 Henry Mall