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***Pictorial Structures for Pattern Recognition
in Crystallographic Maps***

A key step in high-throughput protein structure determination is the development of an automated technique for decoding x-ray crystallographic electron density maps. My work investigates the use of pictorial structures in recognizing patterns in these three-dimensional images. A pictorial structure is a way of representing an object as a collection of parts connected by deformable "springs." They have been applied to several problems in pattern recognition, such as face and body recognition. Recent work by Felzenszwalb and Huttenlocher has allowed pictorial structure matching in linear time, by restricting the model somewhat. By generalizing their algorithm to three dimensions, a "screw joint model" can be built which allows a single pictorial structure to match all possible conformations of a molecule. This allows a globally optimal configuration of the molecule to be matched to a region of the electron density map. This could prove an important step in an automated map interpretation.

Tuesday, April 8th
4:00 p.m.

Room 1221
Computer Sciences / Statistics Building
1210 West Dayton Street