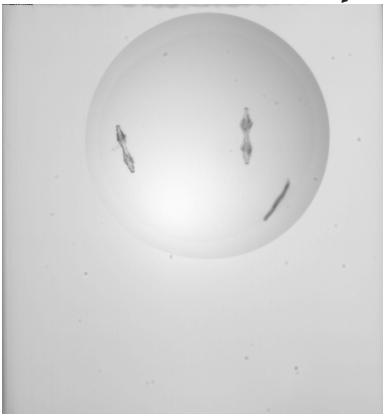
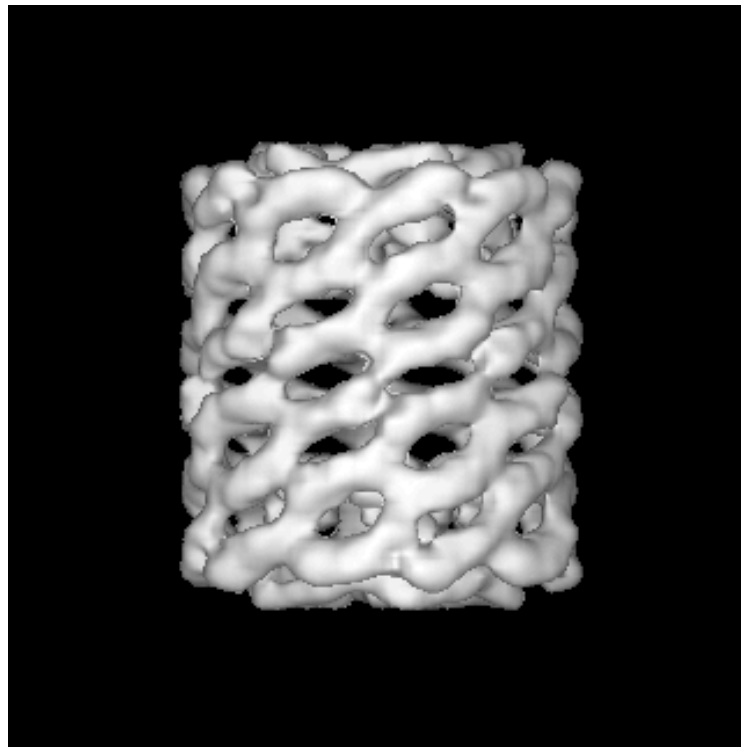


Caltech  
Department of  
Computer  
Science

Information Science Seminar Series

Wednesday,  
November 13th,  
4 - 5pm  
Moore 070



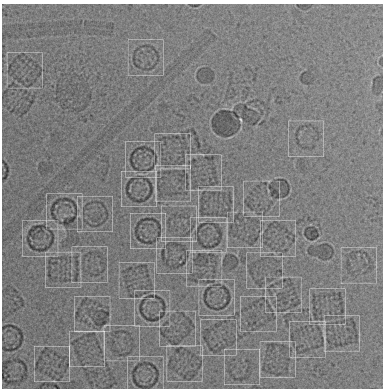
## Two Computer Vision Problems in Structural Biology

**Marshall Bern**  
**Palo Alto Research Center (PARC)**

I will talk about two computer vision / image processing problems, both arising in efforts to determine the structures of biological molecules.

The first problem is automatic classification of drop images from a high-throughput protein crystallization system. A robot prepares 100,000 crystallization experiments a day, and takes photographs of experiments in progress. Now someone or something has to decide whether a crystal (or a precipitate or nothing) has formed inside each drop of solution.

The second problem is to pick out the locations of individual molecules in very noisy, low-contrast electron microscope (cryo-EM) micrographs. Using something like computed tomography, the picked images can be combined to give a 3D reconstruction of the molecule. Resolution depends upon the number of molecule images: 10 Angstrom resolution has been achieved with 50,000 hand-picked images, but atomic resolution (3 Angstrom) will require millions of images.



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