MINISYMPOSIUM ON COMPUTATIONAL METHODS IN EM-RELATED THREE DIMENSIONAL RECONSTRUCTION

NOV 30 2009

Columbia University Medical Center, Hammer Health Sciences Building, HSC LL103
168th St. and Fort Washington Ave., New York, NY *

Jointly organized by Joachim Frank, Dept. of Biochemistry & Molecular Biophysics, and Gabor Herman, Dept. of Computer Science, CUNY.

Registration is free; however, if you plan to attend, we ask you to please contact Tornubari Barinee at tb2319@columbia.edu

PROGRAM

9-9:10 am **-- Introduction**, by Joachim Frank, HHMI, Columbia University Dept. of Biochemistry and Molecular Biophysics, and Dept. of Biological Sciences

9:10-10:00 am -- **tmRNA: a Lasso Gone Wild**, by Jie Fu, Columbia University Dept. of Biochemistry and Molecular Biophysics
Successful classification of heterogeneous projection images can provide information about the equilibrium and dynamics of the biological system being studied. Here, using maximum likelihood classification followed by single particle reconstruction, we obtained several structures of the transfer-messenger RNA (tmRNA) bound ribosomes. These structures depict key events of the interaction between tmRNA and ribosome and show dramatic conformational changes of the transfer-messenger RNA.

10:00-10:20 am -- **Break**

10:20-11:10 am -- **We Focus on Distance**, by Joanna Klukowska, City University of New York, Graduate Center, Dept. of Computer of Science
In electron microscopy, and even more so in the newly-developing technology of soft X-ray microscopy, the microscope depth of field (specifically its dependence on distance from the source) is a resolution limiting factor in 3D reconstruction from projections, specially for large objects. New techniques are proposed that can effectively eliminate the depth of field limitation. We present preliminary results produced by our techniques on simulated data.

11:10-noon -- **GPU 101: Parallel Computing for the Masses**, by Ryan Bubinski, Columbia University Dept. of Biological Sciences
An introduction to programming Graphics Processing Unit (GPU) and how the devices are being used to accelerate scientific computing in the biological sciences. GPUs, once restricted to the realm of video games and animations, offer increasingly powerful parallel computing

solutions for a fraction of the cost of traditional CPU clusters. This talk will be an overview of the NVIDIA GPU hardware, the CUDA programming architecture, and how this technology is accelerating supervised 3D projection matching algorithms in the Frank Lab.

noon-1:30 pm -- **Lunch Break**

1:30-2:20 pm -- **Building Atomic Models for Macromolecular Assemblies by Cryo-electron Microscopy, Homology Modeling and Multi-scale Structure-based Refinement**, by Jiang Zhu, NIH/NIAID/Vaccine Research Center
We have developed a simple yet effective method for refining local structures of a protein using its cryoEM map as a constraint. Based on this method, we further developed a multi-scale structure-based refinement strategy that allows building and refining protein structures within their cryoEM maps. This strategy was used to construct the first full-backbone model of an entire grass carp reovirus (GCRV) virion.

2:20-3:10 pm -- **Graph-cutting Magic**, by Gabor Herman, City University of New York, Graduate Center, Dept. of Computer of Science
Some methods that are in use for the classification of heterogeneous electron microscopic projections into homogeneous subsets are computer intensive, but here we present a method based on graph-cutting that does in hours what an alternative method that we have been using required months to do.
The time in our method taken up by the creation of a graph that describes for any pair of images how likely they are to be projections of the same conformation, the classification is done by cutting this graph into optimal parts that determine the classes to which the images belong. The graph-cutting itself takes only minutes, which allows investigation of the consequences of alternative choices (for example, the number of classes) at essentially no extra cost.

3:10-3:40 pm -- **Break**

3:40-4:30 pm -- **Achieving Separation by Re-mixing: a Bootstrap Method for Classifying Noisy Particles**, by Hstau Liao, Columbia University Dept. of Biochemistry and Molecular Biophysics
In single-particle reconstruction methods, noisy projections of macromolecules (particles) at random orientations are collected. Often, several classes of conformations or binding states coexist in a biological sample, which requires classification, so that each conformation can be reconstructed separately. In bootstrapping, the particles are randomly sampled with replacement and a bootstrap volume is reconstructed from each sample; analysis of the bootstrap volumes reveals the class to which a particle belongs.

4:30-5:20 pm -- **A Robustly-Simplifiable Tree Descriptor for 3D Volumes**, by Lucas Oliveira City University of New York, Graduate Center, Dept. of Computer of Science

A Foreground Component Tree Structure (FCTS) is a topological / geometric descriptor of three-dimensional arrays of real numbers (volumes) that shows the relations between connected components in the volume; in particular, they can be helpful in understanding the relations between substructures of reconstructed macromolecules in volumes obtained by 3D electron microscopy.

This is due to the existence of a simplification methodology that reduces the originally large FCTS associated with a volume to a much smaller one, without losing essential information about the structure in the molecule, in a robust fashion (in the sense that essentially the same simplified FCTSs are obtained from volumes that are small perturbations of each other). We demonstrate the potential applicability of our methodology by showing that simplified FCTSs can be used to distinguish between two slightly different versions of an adenovirus and present some possible further applications of FCTSs to structural analysis.

***Directions to Columbia University Medical Center:**
The Center is located at West 168th Street and Broadway, immediately southeast of the George Washington Bridge, in the Heights/Inwood section of northern Manhattan.

By Public Transportation:
By Subway - Take the 1, A, C, trains to the 168th Street station. From midtown Manhattan, the A train provides express service.

By Bus -- A number of city buses serve the Medical Center: M-2, 3, 4, 5, and 100. For additional bus and subway information, call the Transit Authority at 718-330-1234.

By Automobile
The fastest and most convenient way to reach the medical center by automobile is to follow directions to the George Washington Bridge. Then exit onto Riverside Drive. From there, proceed south and turn left onto West 165th Street (the first left), and then right onto Fort Washington Avenue to the medical center parking facility.

From upstate New York and New Jersey: After crossing the George Washington Bridge, follow signs to the Henry Hudson (also called the West Side Highway), and then to Riverside Drive.

From Riverdale and Westchester via the Saw Mill River Parkway : Exit the Henry Hudson Parkway at the Riverside Drive exit, which is immediately past the George Washington Bridge.

From Westchester, Connecticut, or the East Side of Manhattan via the Major Deegan, Cross-Bronx Expressway, or Harlem River Drive: approaching the George Washington Bridge, take the Henry Hudson Parkway, stay to the left and follow signs to Riverside Drive.

From the West Side of Manhattan: Take the Henry Hudson Parkway to exit 15-Riverside Drive South.

Map: http://www.cumc.columbia.edu/about/cumc_map.html