

Computational Methods for Three-Dimensional Microscopy Reconstruction

A course to be given at the Graduate Center of CUNY in the Fall, 2013

Instructor:

Gabor T. Herman, Distinguished Professor of Computer Science

Outline:

Biological structure, on the level of molecule or cell, is imaged by electrons or soft X-rays in conditions that preserve native structure as much as possible. Approaches to the computerized recovery of three-dimensional information on a biological object, which are oftentimes formulated or implemented initially in an intuitive way, will be discussed based on physical models of the object and the image formation process. Both three-dimensional electron microscopy and X-ray tomography can be captured in the same mathematical framework, leading to closely related computational approaches, but the methodologies differ in detail and hence pose different challenges.

Administrative:

The course will meet once a week for two hours. Each of these meetings will comprise a two-hour presentation by one of the participants, beginning with presentations by the instructor. The presentations will be based on chapters in a forthcoming book, whose details are given below. The level of presentations should be suitable for understanding by graduate students in computer science or in biology or in physics; assuming no mathematical knowledge beyond what can be expected to be possessed by such students. There will be no homeworks or exams. The grade will be determined based on the quality of the presentations. For a good grade, the student will be expected to attend all the meetings from beginning to end.

Text for the course:

Computational Methods for Three-dimensional Microscopy Reconstruction; edited by Gabor T. Herman (City University of New York) and Joachim Frank (Columbia University); to be published by Springer's imprint Birkhäuser Boston.

1. Introduction
2. Trypanosoma brucei ribosome at 4.9 Å resolution – a case study
3. Classification using manifold embedding
4. Quantitative analysis in iterative classification schemes for cryo-EM applications
5. Interchanging geometry conventions in 3DEM: Mathematical context for the development of standards
6. X-ray tomography imaging
7. Reconstruction from microscopic projections with defocus-gradient and attenuation effects
8. Electron tomography of influenza virus by algebraic reconstruction (ART) with optimized blobs
9. Using component trees to explore relationships between biological structures

Student learning outcomes:

After completing this course students will be able to:

1. Carefully state and present applications of computers in 3D microscopy of biological structures
2. Understand the nature of computational approaches for solving problems of structural biology
3. Apply computer concepts (such as classification, reconstruction, tree algorithms) to practical problems