

High-End Biological Imaging Generates Very Large 3D+ and Dynamic Datasets

Paul Matsudaira
Biological Sciences Department
National University of Singapore
dbshead@nus.edu.sg

ABSTRACT

Biological imaging collects data over time and length scales that range from atoms and molecules to cells and tissues with a frequent goal of molecular detection in live tissues and organs. There are two generic approaches employed in microscopy to study the structure and function of molecules, cells, and organisms. Both collect large numbers of images and generate TB-size datasets but for different purposes. In high-content screening applications drugs are applied to live cells grown in wells and imaged in automated microscopes. A thorough study will examine the effects of a pharmacological agent at several dilutions by collecting images of cells at different time-points and generate TB datasets from millions of cells. After image processing and analysis, critical concentrations of drug activity are identified and mechanism of action is extracted from downstream information. The experiment is convoluted by marking various structures or molecules with a signature color, thus allowing for specific objects to be localized in space and tracked in time. The second approach has the goal of a 3D structure. Datasets consist of either serial slices or projections through the object, a cell, tissue, or organism and are acquired by light or electron microscopy. These methods are also linked in a time series to generate the dynamics of the structure from which mechanical and kinetic parameters are extracted. A significant problem is that these approaches can easily generate TBs of image data in minutes to hour periods. Thus, in biological imaging it is easy to generate data but the pressing problems are how to manage and organize image datasets, relate image datasets obtained by different microscopy methods, extract information from images, and to generate dynamic and 3D models of biological structures. These downstream steps contribute to the total dataset for the experiment.

BIOGRAPHY

Paul Matsudaira studied undergraduate biology and chemistry at the University of Washington (Seattle, WA) and received in 1981 a PhD in Biological Sciences from Dartmouth College (Hanover, NH) where he studied the structure of microvilli that line the intestine surface. In 1985, after postdoctoral studies in Germany (Max Planck for Biophysical Chemistry) and England (MRC Laboratory of Molecular Biology) he joined the faculty of the Biology Department at the Massachusetts Institute of Technology and the Whitehead Institute. After 23 years at MIT where he was Professor of Biology and Bioengineering, he moved in 2009 to the National University of Singapore as Professor and Head of the Department of Biological Sciences and founding Director of the NUS Centre for BioImaging Sciences. His lab studies the mechanics of cell movements and the structure of the cellular machinery that powers cell motility.