

Schedule and location

CMS 5th floor conference room (Rm 5112). Mon & Wed 10:30 am – 12:00 pm.

Syllabus

Followed by a short introduction, the course is divided into three blocks according to the principle methods discussed and biological/functional issues addressed:

Course overview, introduction and objectives. Bioinformatics profiling.

- (i) *Low to medium resolution methods.* Optical, spectroscopic and scattering methods
Optical methods and sophisticated imaging techniques using high-end light and electron microscopy, laser microsurgery for structural and functional studies of cells, organelles and other large assemblies associated with malignant tumours.

Circular dichroism and fluorescence spectroscopy to determine overall fold and structural integrity of disease-related proteins.

Small angle X-ray scattering, analytical ultracentrifugation and dynamic light scattering to study the oligomeric state and the polydispersity of biological macromolecules and assemblies from human pathogens or aberrant forms found in prion diseases.

Electron spray mass spectrometry combined with nanoscale reverse phase high pressure liquid chromatography for general protein characterization, molecular weight determination of fragments and analysis of post-translational modifications.

- (ii) *Medium to high resolution methods*
Conventional electron microscopy and advanced tomography/imaging techniques at cryogenic temperatures

Principles and applications of conventional transmission and scanning electron microscopy (SEM demo).

Single-particle, electron-crystallographic, tomographic and serial-section image processing and systems methods for three-dimensional reconstructions of molecular machines and viruses.

- (iii) *Atomic resolution methods*
Single crystal X-ray diffraction, crystallization theory and practice, cryogenic crystal handling, lattice symmetry, classical/std. and anomalous phasing methods, difference Fourier and Patterson methods, computing and structure evaluation.

Nuclear magnetic resonance, principles and applications or ¹H NMR, 2D methods and multi-dimensional approaches to determine biological structure, chemical exchange, dynamics and study flexibility.

Computational methods and 3D modeling using molecular dynamics simulations, normal mode analyses, molecular and quantum mechanics applications.

Instructors

The teaching faculty listed below will be available for student questions either by appointment or during regular office hours (each instructor will announce appropriate office hours during their first lecture). If you are experiencing any problems in understanding a lecture or a topic, you are encouraged to meet individually with the instructor or one of the Course Directors.

Joachim Jaeger (Director), jj@wadsworth.org	CMS 2009	408-2225
Daniele Fabris, fabris@albany.edu	SUNY, LS 1109	437-4464
Tanvir Shaikh, tapu@wadsworth.org	ESP C279	474-6516
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Hongmin Li, lih@wadsworth.org	CMS 1155	486-9154
David LeMaster, lemaster@wadsworth.org	ESP C294A	474-6396
and Nilesh Banavali, banavali@wadsworth.org	CMS 2008	474-0569

Textbooks and Course Materials

Cantor and Schimmel - Biophysical Chemistry: Parts I II & III (1980)

Methods in Molecular Biophysics: Structure, Dynamics, Function (Hardcover)
by Igor N. Serdyuk, Nathan R. Zaccai, Joseph Zaccai (2007)

Relevant Chapters from Methods in Enzymology (Vols. 276, 277, 394, 405) and

various additional reviews and monographs.

Online materials and hardware

EBI website (www.ebi.ac.uk), NCBI website (www.ncbi.nlm.nih.gov), PDB website (www.rcsb.org), Expasy (expasy.org),

Freeware versions of: PyMol0.99rc6 (www.pymol.org), WebMol (www.cmpharm.ucsf.edu/cgi-bin/webmol.pl) SwissPdbViewer (spdbv.vital-it.ch)

If possible: personal laptop (if not available various computers with WinXP, Mac OS X, or IRIX platforms are available at CMS in Rooms 2009 & 2011).

Prerequisites

None