

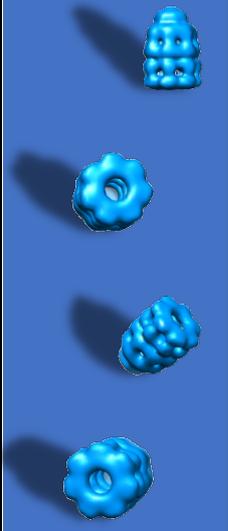
Cryo Electron Microscopy and 3D Image Processing of Macromolecular Assemblies and Cellular Tomography (CEM3DIP)

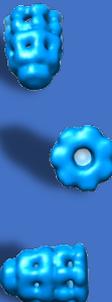
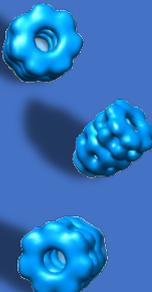
Under MHRD Scheme on Global Initiative on Academic Network (GIAN)

Overview

Proteins are the macromolecular machines that carry out functions of LIFE. Visualising and understanding the structure will help us in better knowledge of structure-function relationship. Structural Biology using Single Particle Cryo Electron Microscopy (SP CryoEM) and cellular tomography has become a major tool for studying macromolecular assemblies and visualizing details of cellular components, respectively. Solving in-situ proteins structure is fast approaching feasibility with advancement in CryoEM methods. However these cutting edge CryoEM methods for structural biology are only a couple of years old in India, This course will deal with Single Particle Cryo Electron Microscopy of biological macromolecular assemblies and Cryo Electron Tomography of Cellular structures.

This is a special course which will be taught probably for the first time in India. This course will be of interest to molecular biologists, cell biologists, microbiologists, structural biologists (crystallographers), theoretical/computational biologists and in general many other area biologists and non-biologists including computational scientists who are working in the field of image processing, and will be very useful at both teachers and students level.

Modules, Dates and Participants 	<ul style="list-style-type: none">• 3D Electron Microscopy: History and Basic Principles• Biological sample and specimen preparation methods for TEM• TEM- principles, image formation , particle detection, Fourier Transform, Convolution, CTF, PSF, Resolution and FSC• Image processing, Point group symmetries, Classification, Orientation and Heterogeneity of particles• Getting the first model using Conical Tilt and Projection Matching• Single particle CryoEM and 3D reconstruction• Challenges of in-situ structural biology• Principles and applications of Cryo Tomography. Cellular Tomography and Subtomogram averaging.• Refinement of atomic models against CryoEM maps, Flexible fitting, Validation, Assessment and Data deposition.• Hybrid methods: Protein Crystallography, Computational methods and CryoEM• Practical software sessions on using EMAN, Relion, IMAGIC, IMOD, refile, prosmart, MODELLER and Chimera <p>Duration: 2nd July 2016 to 13th July 2016 No. of participants for the course will be approximately fifty.</p>
No. of Credits	Two

<p>Who can attend the course?</p> 	<ul style="list-style-type: none"> • PhD-students and postdoctoral fellows who have some experience in EM and want to use CryoEM / Tomography and /or learn advanced imaging techniques can be given preference. Students without experience will also be considered provided they show that these techniques will be useful in their current research project. • Faculties and researchers from reputed academic/technical institutions and manufacturing, service and private/government organisations including R&D laboratories who want to use this technique in their research/lab. • Protein crystallographers who wanted to know and use this technique as hybrid technique in their research, but could not do it so far. 																	
<p>Registration Fee</p> 	<table border="1"> <thead> <tr> <th rowspan="2">Category</th> <th colspan="2">Participants from</th> </tr> <tr> <th>Abroad (US \$)</th> <th>India (INR)</th> </tr> </thead> <tbody> <tr> <td>Industry/Private Research Organization</td> <td>500</td> <td>20,000</td> </tr> <tr> <td>Academic/Non-profit Institutions:</td> <td></td> <td></td> </tr> <tr> <td style="text-align: right;">Students</td> <td>200</td> <td>2,000 (1,000 for SC/ST students)</td> </tr> <tr> <td style="text-align: right;">Non-Students (eg. Postdoctoral fellows, faculties/teachers etc.)</td> <td>300</td> <td>10,000</td> </tr> </tbody> </table> <p>Registration fees include all instructional materials, computer use for tutorials and registration only. Bursaries are available for subset of selected participants.</p>	Category	Participants from		Abroad (US \$)	India (INR)	Industry/Private Research Organization	500	20,000	Academic/Non-profit Institutions:			Students	200	2,000 (1,000 for SC/ST students)	Non-Students (eg. Postdoctoral fellows, faculties/teachers etc.)	300	10,000
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The Faculty



Professor Wah Chiu is an elected Member of United States National Academy of Sciences, the director of the National Center for Macromolecular Imaging, BCM a distinguished service professor and Alvin Romansky professor in Department of Biochemistry and Molecular biology. Few of his research areas include Cryo-Electron Microscopy and Tomography, Biophysics and Computational Biology and Molecular Basis of Human Disease and Behaviour.



Professor Wolfgang Baumeister is a Scientific Member and Director of Max Planck Institut (MPI) für Biochemie, Martinsried, Germany. He is an EMBO member, foreign associate member of US National Academy of Sciences. He pioneered the development of cryo-electron tomography. His contributions to science were recognized by numerous awards including the Otto Warburg Medal, the Schleiden Medal, the Louis-Jeantet Prize for Medicine, the Stein and Moore Award, the Ernst Schering Prize and many more.



Prof. Steven J Ludtke is a professor of Biochemistry at Baylor College of Medicine. He was awarded Burton Medal from Microscopy Society of America. His work primarily focuses on electron cryo microscopy and its application to important problems in structural biology. His major contribution to the field includes the development of EMAN, a software suite for processing images of individual molecules and producing 3D structures at subnanometer resolution.



Dr. Kutti Raghunath Vinothkumar joined as a Marie-Curie postdoctoral fellow in the group of Professor Richard Henderson at MRC Laboratory of Molecular Biology, Cambridge, UK and in his current position he is working as a Group Member in the same lab. In recent years, his research interest has been to visualise membrane proteins as single particles in particular those that have been difficult to crystallise and is also trying to obtain high-resolution structures of macromolecules with less number of particles.



Dr. Lu Gan is an Assistant Professor at NUS, Singapore. He uses state-of-the-art electron tomography to generate “tomograms” to map out how key protein complexes are organized in their native context inside a cell. His research interests include applications of electron tomography to cell biology, Electron cryotomographic analysis of picoplankton and other single-celled eukaryotes



Prof. Elena Orlova works in Birkbeck College & ISMB, UK. She is a Fellow of the Royal Society of Biology and Senior member of the Royal Society of Medicine. She has been elected to be a chair of Commission on Electron Crystallography (IUCr) in 2014. She organises biannual International EMBO courses on Image processing for CryoEM at Birkbeck. Her research interests are Cryo-Electron Microscopy, structural analysis of bio complexes using single particle analysis and tomography.



Dr. Garib N Murshodov, is a leader of Computational Crystallography group in MRC, LMB, Cambridge, UK. His group is developing mathematical and computational methods. He is the principal author of the program reMac and his main focus is in development and implementation of advanced statistical tools to derive as accurate as possible atomic models from crystallographic diffraction data and single particle cryoEM reconstruction maps.



Dr. Ardan Patwardhan is an EM project leader in EMBL-EBI, Cambridge, UK. His work focuses on issues concerned with the collective results of the 3DEM community. He is particularly interested in providing “added-value” services that can be uniquely provided from the vantage point of an organization like the PDB. As a first step, he has developed a statistical service that mines the EMD database and presents the results as interactive charts (pde.org/emstats).



Dr. Manidipa Banerjee is an Assistant Professor in Kusuma School of Biological Sciences, IIT, Delhi. Her research in the fields of virus-host interaction, virus capsid disassembly and membrane penetration and virus-based drug design by utilizing molecular virology and biophysical techniques, electron microscopy and cryo-electron microscopy and molecular dynamics simulation studies. She was instrumental in setting up one of the two first cryoEM facilities within India for high-resolution structural analysis of macromolecular assemblies.



Dr. Jayati Sengupta is a Principal Scientist, IICB Kolkata, India. Her research combines structural biology with functional studies of higher order complexes to understand their roles in health and disease. She did postdoctoral training on structural elucidation of ribosomal complexes by using cryo-electron microscopy (cryo-EM) in conjunction with single particle 3D reconstruction techniques. She was instrumental in setting up one of the two first cryoEM facilities within India for high-resolution structural analysis of macromolecular assemblies.



Dr. Ramanathan Natesh is a DBT Ramalingaswami Fellow and Assistant Professor in the School of Biology at IISER Thiruvananthapuram. As a Wellcome Trust postdoctoral fellow at University of Bath he solved the first crystal structure of human Angiotensin Converting Enzyme, subsequently published in *Nature*, Jan 2003. He worked as a Wellcome Trust Academic Fellow at Birkbeck College, London with Professor Helen Sabil FRS FMedSci., where he obtained the first structure of various states of a non-native protein in complex with GroEL/GroES, by using single particle cryo electron microscopy.

Course Coordinator:

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