

Seminar

Realising the full potential of electron cryomicroscopy

Vinothkumar Kutti Rangunath

NCBS, Bangalore

There has been enormous progress during the last few years in the determination of three-dimensional (3D) biological structures by single particle electron cryomicroscopy (cryoEM), allowing maps to be obtained to higher resolution and from fewer images than required previously. This is principally due to the introduction of the direct electron detectors that has 2- to 3-fold higher detective quantum efficiency (DQE) and to the improvement of the computational algorithms for image processing. In spite of the great strides that have been made, quantitative analysis shows that there are still significant gains to be made with detectors with higher DQE and faster frame rate and that the problems associated with image degradation can be solved, possibly by minimising beam-induced specimen movement and charge build up during imaging. If this can be achieved, it should be possible to obtain near atomic resolution structures of smaller single particles, using fewer images and resolving more conformational states than at present, thus realising the full potential of the method. I will illustrate using select biological macromolecules how recent advances help in elucidating the atomic resolution structures and distinct states and how the technique is applicable to study macromolecules within the cell.

Tuesday, Jun 18th 2019

4:00 PM (Tea/Coffee at 3:30 PM)

Seminar Hall, TIFR-H