ISTA

Seminar/Talk

Finding needles in haystacks A new approach to template matching

Nikolaus Grigorieff

Janelia Research Campus, Howard Hughes Medical Institute

Host:

The development of electron cryo-microscopy (cryo-EM) to visualize macromolecules and their assemblies has been significantly accelerated in the last five years by the introduction of direct detectors. It is now almost routine to obtain near-atomic resolution structures of non-crystalline samples (single particles) of purified material, often leading to atomic models of the molecules. More irregular biological structures, such as cellular compartments and organelles, can also be reconstructed, using electron tomography, but the resolution is limited to about 2 nm unless averaging techniques can be applied. It is therefore difficult to build reliable atomic models of these larger structures using tomography data. I will describe a new cryo-EM approach that allows the precise placement of molecules of known atomic structure into the context of more crowded environments. This approach, therefore, has the potential to yield atomic models of more complex biological assemblies of unique and irregular structure.

Thursday, October 19, 2017 11:00am - 12:00pm

Mondi Seminar Room 2, Central Building

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