



Seminar/Talk

After the Resolution Revolution Quo Vadis, Cryo-EM?

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In the past five years, single-particle electron cryo-microscopy (cryo-EM) has evolved into a routine technique in structural biology that delivers high-resolution images of molecules and their assemblies, on par with X-ray crystallography. Unlike crystallography, single-particle cryo-EM can also visualize many different conformational states present in a single sample, providing snapshots of the functional cycle of the imaged molecules and assemblies. I will provide examples of what can be done today and discuss challenges for the future. Most molecules and assemblies function within the larger context of a cell, which can be visualized by electron tomography (ET). Despite groundbreaking development of sample preparation and image processing techniques, cryo-ET is still limited to about 2 nm resolution unless averaging techniques can be applied. At this resolution, it is difficult to infer the chemical interactions between the molecules that underlie cellular mechanisms. I will describe a cryo-EM approach that allows the precise placement of molecules of known structure into the context of cellular environments, thereby addressing one of the current limitations of tomography.

Monday, March 19, 2018 10:00am - 11:00am

Big Seminar room Ground floor / Office Bldg West (I21.EG.101)



This invitation is valid as a ticket for the ISTA Shuttle from and to Heiligenstadt Station.

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