

iNEXT workshop on Integrated methodologies and approaches for structural biology

Name of Speaker: **Florian Schur**

University / Research Institute / Department: **Institute of Science and Technology Austria**

Title of Lecture: **Cryo-electron tomography and subtomogram averaging: structural biology in complex environments**

Abstract:

Cryo-electron tomography (cryo-ET) provides unprecedented molecular insights into complex biological environments. In combination with subtomogram averaging, detailed 3D structures of biological molecules can be then obtained in *in situ* environments or in large and irregular reconstituted assemblies. This allows linking structural contextual information that can be derived by cryo-ET and subtomogram averaging with available functional data. Despite the tremendous potential of cryo-ET and subtomogram averaging, the resolutions that usually can be obtained via these techniques have been restricted by methodological limitations. Exciting progress over the last years managed to mitigate several of these resolution limiting factors, such as the aggravated defocus estimation and imprecise contrast transfer function (CTF) in the low-dose micrographs of tilt series. This allows now reaching unprecedented resolutions using cryo-ET and subtomogram averaging, ranging in optimal cases beyond the nanometer barrier. *In vitro* reconstituted assemblies or purified pleomorphic viruses have been optimal models to optimize cryo-ET and subtomogram workflows and allowed even to reach near-atomic resolutions.

In addition to discussing the principles of cryo-ET and subtomogram averaging, current frontiers and future challenges will be addressed that remain to be overcome to routinely determine high-resolution structures using these methods. In specific, retrovirus particles and reconstituted assemblies will be used as examples to discuss approaches that have been used to reach near-atomic resolution using cryo-ET and subtomogram averaging.

Research Profile:

2016 PhD at the European Molecular Biology Laboratory (EMBL) Heidelberg in the lab of John Briggs working on high-resolution cryo-electron tomography and subtomogram averaging of retroviral assemblies

since 2017 Assistant Professor at the Institute of Science and Technology (IST) Austria. The research of the Schur group focuses on the structural biology of cell migration and viral infection (schurlab.pages.ist.ac.at). The group also develops new workflows in cryo-ET sample preparation, data acquisition and image processing.

Three selected publications:

1. Turonova B, Schur FKM, Wan W, Briggs JAG, (2017) Efficient 3D-CTF correction for cryo-electron tomography using NovaCTF improves subtomogram averaging resolution to 3.4 Å, *Journal of Structural Biology*. 199(3); 187-105. doi:10.1016/j.jsb.2017.07.007
2. Schur FKM, Obr M, Hagen WJH, Wan W, Jakobi AJ, Kirkpatrick JM, Sachse C, Kräusslich H-G, Briggs JAG, (2016), An atomic model of HIV-1 capsid-SP1 reveals structures regulating assembly and maturation, *Science*, 353(6298):506-508
3. Schur FKM, Hagen WJ, de Marco A, Briggs JA. (2013) Determination of protein structure at 8.5Å resolution using cryo-electron tomography and sub-tomogram averaging. *Journal of Structural Biology*. 184(3):394-400.