MPI-NAT SEMINAR SERIES

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Microsecond Time-Resolved Cryo-EM

Protein structure determination and prediction have made stunning progress. In contrast, it is generally not possible to observe proteins while they perform their tasks, which leaves our understanding of protein function fundamentally incomplete. My group has recently introduced a novel approach to time-resolved cryo-EM that improves its time resolution by about 3 orders of magnitude. This makes it fast enough to observe the microsecond dynamics of proteins that are frequently associated with function. Our method involves melting a cryo sample with a laser beam, which allows dynamics of the embedded particles to occur in liquid when a suitable stimulus is provided. Once the heating laser is switched off, the sample rapidly revitrifies, trapping the particles in their transient configurations, which we subsequently image. I will illustrate how this approach allows us to capture protein dynamics far from equilibrium and to reconstruct the trajectories involved. Laser revitrification leaves the particles intact, so that reconstructions with near-atomic resolution can be obtained. It can even be used to overcome preferred particle orientation, an issue that still causes many cryo-EM projects to fail. Finally, I will show recent developments that significantly expand the utility of our method by extending its temporal observation window. By making a wide range of protein dynamics observable that were previously inaccessible, our method promises to fundamentally advance our understanding of protein function.

Tuesday, 01.04.2024, 11 AM

Host: Helmut Grubmüller & Holger Stark

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