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Simultaneous determination of protein structure and dynamics using cryo-electron microscopy

Cryo-electron microscopy is rapidly emerging as a powerful technique to determine the structures of complex macromolecular systems elusive to other techniques. Since many of these systems are highly dynamical, characterising also their movements is a crucial step to unravel their biological functions. In this talk, I will present an integrative modelling approach to simultaneously determine structure and dynamics from cryo-electron microscopy density maps. By quantifying the level of noise in the data and dealing with their ensemble-averaged nature, this approach enables the integration of multiple sources of information to model ensembles of structures and infer their populations. I will illustrate the method with two examples: the characterization of structure and dynamics of the ClpP protease by a combined cryo-EM and NMR approach and the study of the effect of acetylation on microtubule structure and stability.

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