Machine Learning Approaches for Biological Function and Dynamics

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Without any doubt, revolutionary progress has been made with Alphafold2 and RoseTTAfold in predicting static structures. However, biological function involves structural changes, as they occur for example in molecular machines and in the presence of ligands.

Data-analytic algorithms based on Geometric Machine Learning made it possible to retrieve continuous conformations and free-energy landscapes from experimental cryoEM single-particle snapshots in thermal equilibrium. However, to understand biological function and dynamics, we need to include the underlying energetics of pathways away from thermal equilibrium. For such non-equilibrium processes, the functional pathways are time-dependent and regulated by the environmental protocol.

Recent advances with Physics-Informed Neural Networks (PINN) allow to incorporate fundamental laws of Physics and Chemistry and consequently require much less data for Machine Learning. Based on these promises, we propose a conceptional data-algorithmic framework, capable of extracting the dynamics from sparse non-equilibrium time-resolved measurements and to retrieve functional pathways for any choice of environmental protocol.