

FMf12023 Program

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Title	Computational Mathematics for Cryo-Electron Microscopy
Abstract	<p>Single-particle cryo electron microscopy (cryo-EM) is an increasingly popular technique for elucidating the three-dimensional structure of proteins and other biologically significant complexes at near-atomic resolution. It is an imaging method that does not require crystallization and can capture molecules in their native states. In single-particle cryo-EM, the three-dimensional molecular structure needs to be determined from many noisy two-dimensional tomographic projections of individual molecules, whose orientations and positions are unknown. The high level of noise and the unknown pose parameters are two key elements that make reconstruction a challenging computational problem. Even more challenging is the inference of structural variability and flexible motions when the individual molecules being imaged are in different conformational states. The talk will overview the underlying mathematical theory, computational methods, and notable challenges for structure determination by single-particle cryo-EM.</p>