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Advanced machine-learning algorithms for improving high-performance cryo-EM data analysis

Machine learning technology represents an intriguing avenue in the methodology development for cryo-EM structure determination. In this presentation, we explore two aspects of machine learning development that help advance cryo-EM structure determination. Recently we introduce a statistical manifold learning approach for unsupervised single-particle deep classification. When optimized for Intel High-Performance Computing (HPC) processors, our approach implemented in ROME software package, can generate thousands of reference-free class averages within several hours from hundreds of thousands of single-particle cryo-EM images. Deep classification thus assists in computational purification of single-particle datasets for high-resolution reconstruction. Second, particle extraction represents a major practical bottleneck in the structure determination of biological macromolecular complexes by single-particle cryo-EM micrographs, enabling automated algorithmic framework, DeepEM, for single-particle recognition from noisy cryo-EM micrographs, enabling automated particle picking, selection and verification in an integrated fashion. Our approach exhibits improved performance and high accuracy when tested on the standard KLH dataset as well as several challenging experimental cryo-EM datasets.

Biography

Youdong Mao has obtained his PhD in Physics from Peking University in 2005 and completed his Postdoctoral training in Biophysics at Harvard Medical School in 2012. He has then worked at the Faculty of Dana-Farber Cancer Institute, Harvard Medical School. In 2015, he has joined the Faculty at the School of Physics and Center for Quantitative Biology at Peking University. His research interest lies in developing multidisciplinary approaches across the areas of structural biology, electron microscopy and high-performance machine learning.

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