CryoRL: Reinforcement Learning Enables Efficient Cryo-EM Data Collection

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Single-particle cryo-electron microscopy (cryo-EM) has become one of the mainstream structural biology techniques because of its ability to determine high-resolution structures of dynamic bio-molecules. However, cryo-EM data acquisition remains expensive and labor-intensive, requiring substantial expertise. We sought to design and implement an reinforcement learning-based approach to navigate cryo-EM samples to find the best regions in the shortest amount of time. We show that reinforcement learning offers an effective way to plan cryo-EM data collection, successfully navigating heterogenous cryo-EM grids. The approach we developed, cryoRL, successfully navigates cryo-EM grids, collecting images from grid regions that contain high-density areas of good exposures. We benchmarked the performance of cryoRL against cryo-EM experts and showed that cryoRL rivals experts who have 5-10 years of expertise.