



生物信息学研究中心

Center of Bioinformatics

学术报告

题目： Template-free detection of macromolecular complexes in cryo electron tomograms

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地点： 思源楼 1013 室

摘要： Cryo electron tomography (CryoET) produces 3D density maps of biological specimen in its near native states. Applied to small cells cryoET produces 3D snapshots of the cellular distributions of large complexes. However, retrieving this information is non-trivial due to the low resolution and low signal-to-noise ratio in tomograms. Current pattern recognition methods identify complexes by matching known structures to the cryo electron tomogram. However, so far only a small fraction of all protein complexes have been structurally resolved. It is therefore of great importance to develop template-free methods for the discovery of previously unknown protein complexes in cryo electron tomograms.

Here, we have developed an inference method for the template-free discovery of frequently occurring protein complexes in cryo electron tomograms. We provide a first proof-of-principle of the approach and assess its applicability using realistically simulated tomograms, allowing for the inclusion of noise and distortions due to missing wedge and electron optical factors. Our method is a step towards the template-free discovery of the shapes, abundance and spatial distributions of previously unknown macromolecular complexes in whole cell tomograms.