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A Hierarchical Linear Model for Cryo-Em Analysis

Wednesday, September 18th, 2024

12:00 PM

110 Frelinghuysen Road, Hill Center, Room 116

Zoom Meeting: Meeting ID: 969 0606 4706

Password: 745339

<https://rutgers.zoom.us/j/96906064706?pwd=ZklvbExpRVBJQ3c5dUhhYTFuR2ZrZz09>

Light refreshments will be served in Hill 452, 11:20am

Abstract: Cryo-electron microscopy (cryo-EM) is essential for determining high-resolution three-dimensional maps of biological macromolecules, which subsequently facilitate atomic model generation. The atomic models and their corresponding cryo-EM maps are archived in the Protein Data Bank (PDB) and the Electron Microscopy Data Bank (EMDB), respectively. In this study, we present a robust hierarchical modeling approach that quantitatively links cryo-EM maps with atomic models. Our model accounts for parameter variations based on atom types and amino acid categories, effectively capturing the nuanced influences of the local electron distribution environment. By applying the minimum power divergence method, we derive robust estimates that minimize the impact of outliers. The effectiveness and robustness of our approach have been validated through applications to both simulated and real datasets.

Bio: I-Ping Tu received her Ph.D. in Statistics from Stanford University in 1997. She has been a member of the Institute of Statistical Science at Academia Sinica since 2003. Over the last decade, her research has primarily focused on developing statistical methods for analyzing cryo-electron microscopy (cryo-EM) image data.

