

cryo-EM 3D Reconstruction

The Cryo-electron microscopy (cryo-EM) three-dimensional (3D) reconstruction problem can be simplified as finding the 3D structure of a particle given its low-resolution and noisy two-dimensional (2D) projection samples at unknown random directions.

A traditional way to figure out the orientation is called Common-Line method. It finds the pairwise common lines of particle images in the Fourier space. With Central Slice Theorem, one can find the global orientation of each image from pairwise orientations to reconstruct the 3D structure.

However, for the traditional method, we still have quite a number of questions that we cannot answer yet. Due to the low Signal-Noise-Ratio (SNR) of particle images, the distribution function of estimated pairwise orientation is highly non-convex with the global optimal shifted from the groundtruth. So, what is the range of inaccuracy we can tolerate in order to guarantee the convergence of global orientation? With a certain range of inaccuracy, what is the error bound (both statistical error and optimisation error) can we expect from the existing algorithms? Can we improve these algorithms from an information theoretical point of view? If yes, how?

Therefore, in this project, we would like to analyze the global convergence of the algorithms for the 3D reconstruction problem, find their error bounds, analyse from theoretical point of view to see if these bounds can be improved, and if yes, how can I improve the algorithms.

