A Dimension Reduction Method For Cryo-EM Image Processing

Szu-Chi Chung

Academia Sinica

Abstract

With the recent breakthrough in the camera together with microscopy automation, advancement of algorithms and GPU-accelerated computations, cryo-EM has become a mainstream technique to solve structures of macromolecules at near atomic resolution. As a result, single particle cryo-EM has been highlighted as the method of 2015 by Nature Method and then awarded Nobel Prize in chemistry in 2017. However, further extending to atomic resolution has been hindered by the noisy nature of the images, caused by very low doses of electrons used for cryo-EM imaging because the biological molecules are extremely vulnerable. Enhancement of the signal-to-noise Ratio (SNR) of these images is thus the key for solving higher resolution 3D structure. In this talk, we propose a dimension reduction method called Two Stage Dimensional Reduction (2SDR) and demonstrate that 2SDR can realize effective de-noising. The proposed method is applied to different stages of the workflow of cryo-EM processing including assessing micrographs, screening particles, and enhancing 2D alignment performance. Furthermore, two cryo-EM benchmark data sets are used to test our method: a 70S Ribosome set and a beta-galactosidase set. By applying 2SDR preprocessing strategy prior to several state-of-the-art cryo-EM 2D clustering method, we can obtain better 2D class average results and achieve faster convergence speed. Finally, we show that by using the improved 2D class averages we can reach higher resolution in the final 3D map.

This is a joint work with Po-Yao Niu, Su-Yun Huang, Wei-Hau Chang and I-Ping Tu.