

A dimension reduction algorithm and its application on Cryo-EM images

I-Ping Tu (杜憶萍)

Institute of Statistical Science, Academia Sinica

Abstract

In the last decade, cryo-electron microscopy (cryo-EM) has been emerging as a powerful tool for obtaining high resolution three-dimension (3-D) structures of biological macro-molecules. A Cryo-EM data set usually contains at least thousands of low signal-to-noise ratio images with random rotations and orientations and each image contains 100×100 pixels. Further clustering analysis is expected to increase the signal-to-noise ratio after taking average over subgroups. The performance of clustering strongly depends on the efficiencies of dimension reduction. In this talk, we will introduce a multilinear PCA which keeps the data's natural tensorial structure and looks for low-dimensional multilinear projection that captures most of the data variation. Our study shows that this algorithm performs much better than the conventional PCA in reducing the high dimensional image data.