

中央研究院統計科學研究所

學術演講

講題：Unveiling ground truths from data containing vague truths: the story of cryo-electron microscopy

演講人：Prof. Wei-Hau Chang (章為皓 副研究員)

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時間：2019年12月2日 (星期一) 上午10:00-11:00

地點：中央研究院統計科學研究所6005會議室(環境變遷研究大樓A棟)

※茶會：上午09:40開始

Abstract

Detailed interactions between biological molecules are the fundamental to life, of which the compromise may cause diseases. These interactions can be exemplified by famous antibody-antigen interactions and many others. Direct visualization of such interactions at atomic resolution or at the level of chemical bonds have been made possible by protein X-ray crystallography depends on many technical advances in particular, synchrotron radiation and crystallization screen. Recent advance in low temperature electron microscopy (cryo-EM) has fulfilled a long-awaited promise that protein structure can be revealed to near atomic resolution in the absence of crystal. This means a structure of a protein in its working conditions is now accessible. However, it has been a mis-concept that these detailed structures are directly available in the raw data that getting a powerful microscope is sufficient. In this talk, I will first brief X-ray crystallography and the ground truths of protein structure established by it. Then I will use a few detailed structures obtained here to illustrate the process of getting ground truths out from the very noisy cryo-EM data through correct “data averaging” through computation. As it is evident, the challenges of data reduction from very noisy data have presented great opportunities for statisticians.

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