

中央研究院統計科學研究所

博士後演講

講題：Statistical applications for high dimensional biomedical data

演講人：Dr. Shih-Kai Chu (朱是鍔 博士後研究學者)

Institute of Statistical Sciences, Academia Sinica, Taipei, Taiwan (中央研究院統計科學研究所)

時間：2022年1月19日(星期三) 下午 14:00-15:00

地點：中央研究院統計科學研究所 B1F 演講廳

※茶會：下午 15:00 開始

※實體與線上直播同步進行

Abstract

Data in various forms is now created and accumulated faster than ever before, but the noise or heterogeneity of it poses challenges to mine for useful information. In this talk, by taking human genetic data as an example, I will discuss methods for data quality control and detecting rare variation in high dimensional data analysis. In data quality control, batch correction is an important procedure to remove technical noise in the data, such as linear-model based methods for tackling known covariates, or nearest-neighbor based methods for tackling observed but unidentified covariates. I will introduce the methods and provide a guideline for selecting suitable methods. In detecting rare variation, recent studies show that rare epigenetic variations are associated with a number of human diseases, such as cancer or congenital anomalies, and I will present a statistical test to identify differentially outlying methylation pattern between two groups of individuals.

中央研究院
統計科學研究所