

國立臺北大學商學院統計學系

專題演講

講 題：Exploring Heterogeneity and Complex Association in Massive
Multi-omics Data

主講人：何昊 博士 (中央研究院統計科學研究所)

時 間：108 年 6 月 12 日 (星期三，13：10~15：00)

地 點：三峽校區商學院 7F01 教室

Abstract

With the development of sequencing techniques, increased number of multi-omics data from large cohorts are made available, for example, The Cancer Genome Atlas (TCGA) and Roadmap Epigenomics Project. Huge case-to-case heterogeneity is one major challenge for statistical analysis using these databases. Some associations between molecular and clinical features to be consistent only in a subgroup of cases due to the heterogeneity are expected. To explore and interpret the complex association, we developed a web application allowing users to perform exploratory data analysis, statistical analysis, and visualization interactively. In this talk, I will introduction the primary statistical method, liquid association, we adopt in our web application and its application in the massive datasets.

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108.06.11