

國立成功大學統計學系

專題演講

時 間：108 年 12 月 26 日 (星期四) 下午 2:00 – 3:00

地 點：統計學系三樓視聽教室 (62331)

演講者：Jung-Ying Tzeng (Professor)

Department of Statistics and Bioinformatics Research Center,
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題 目：Gene-set Integrative Omics Analysis Using Tensor-based
Association Tests

茶 會：下午 3:00 – 3:25 (統計學系二樓教師休息室)

Abstract

Integrative multi-omics analyses integrate complementary level of information from different molecular events and have great potential to detect novel disease genes and elucidate disease mechanisms. One major focus of integrative analysis has been on identifying gene-sets associated with clinical outcomes, and a common strategy is to regress clinical outcomes on all genomic variables in a gene set. However, such joint modeling methods encounter the challenges of high-dimensional inference, especially the sample size is usually moderate either due to research resources or missing data. In this work, we consider a tensor-based framework to enhance model efficiency for variable-wise inference. The tensor framework reduces the number of parameters by accounting for the inherent matrix structure of an individual's multi-omics data and naturally incorporates the relationship among omics variables. We study the variable-specific testing procedure under tensor regression framework, and derive an alternative variance formula of the coefficient estimators that enhances computational efficiency of omics tensor modeling. We evaluate the performance of the tensor-based test using simulations and real data application on the Uterine Corpus Endometrial Carcinoma dataset from the Cancer Genome Atlas (TCGA).

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