



統計科學研

INSTITUTE C

STATISTICAL SC



S.E.M.I.N.A S.T.A.T.A

## Seminar

Title : Tukey計畫報告

Speaker : Dr. Hsuan-Yu Chen, Dr. Shin-Sheng Yuan, Dr.  
Chen-Hsiang Yeang, and Dr. Shwu-Rong Grace Shieh  
( 陳璿宇博士、袁新盛博士、楊振翔博士與  
謝叔蓉博士 )  
( Institute of Statistical Science, Academia Sinica )

Time : 11:00 ~ 11:30, Monday, December 4, 2023

Place : Auditorium, B1F, Institute of Statistical Science

### Abstract

In this talk, we will report our progress. It will focus on the three topics as following:

1. In sub-project 1, the convolution neural network (CNN) was used to identify the risk fingerprint from the gene expression data (total 443 patients) and the accuracies were 100% and 0.3-0.76% for training and testing datasets, respectively.
2. In sub-project 2 and 4, for targeted therapy Erlotinib, LogitDA achieved prediction AUC 0.94-1.00 for two sets of patients. For response of 81 NSCLC patients (phase I trial) to PD-L1 blockade (atezolizumab), our predictor achieved AUC 0.69.
3. In the sub-project 3, we have completed integrative analysis of The Cancer Genome Atlas omics data, identified thousands of associations between molecular alterations on DNA and transcriptional variations within and across cancer types, and organized them in an Integrated Hierarchical Association Structure (IHAS). We also verified IHAS in about 300 external datasets of cancers and normal tissues. We have also developed an algorithm to assess heterogeneity of specimen by integrating bulk-level and single-cell RNAseq data. Unlike existing approaches, we deconvolve bulk-level RNAseq data by several methods and compared their likelihood scores on single-cell RNAseq data.

※ The seminar is exclusively in-person.