統計科學研
INSTITUTE (

統計所學術演 中研院統計

學 術 演 講

講　題：Tukey計畫報告

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時　間：2023年12月4日(星期一)，11:00-11:30

地　點：統計所B1演講廳

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.

※ 實體演講，不開放線上視訊。