



統計科學研究所
INSTITUTE OF
STATISTICAL SCIENCE



統計所學術演講



中研院統計所

升等演講

講題：An integrated analysis of the cancer genome atlas data discovers a hierarchical association structure across thirty three cancer types

講者：Dr. Chen-Hsiang Yeang (楊振翔 博士)
(中央研究院統計科學研究所)

時間：2023年5月1日(星期一)，10:30-12:00

地點：統計所B1演講廳

Abstract

Cancer cells harbor molecular alterations at all levels of information processing. Genomic/epigenomic and transcriptomic alterations are inter-related between genes, within and across cancer types and may affect clinical phenotypes. Despite the abundant prior studies of integrating cancer multi-omics data, none of them organizes these associations in a hierarchical structure and validates the discoveries in extensive external data. We infer this Integrated Hierarchical Association Structure (IHAS) from the complete data of The Cancer Genome Atlas (TCGA) and compile a compendium of cancer multi-omics associations. Intriguingly, diverse alterations on genomes/epigenomes from multiple cancer types impact transcriptions of 18 Gene Groups. Half of them are further reduced to three Meta Gene Groups enriched with (1) immune and inflammatory responses, (2) embryonic development and neurogenesis, (3) cell cycle process and DNA repair. Over 80% of the clinical/molecular phenotypes reported in TCGA are aligned with the combinatorial expressions of Meta Gene Groups, Gene Groups, and other IHAS subunits. Furthermore, IHAS derived from TCGA is validated in more than 300 external datasets including multi-omics measurements and cellular responses upon drug treatments and gene perturbations in tumors, cancer cell lines, and normal tissues. To sum up, IHAS stratifies patients in terms of molecular signatures of its subunits, selects targeted genes or drugs for precision cancer therapy, and demonstrates that associations between survival times and transcriptional biomarkers may vary with cancer types. These rich information is critical for diagnosis and treatments of cancers.

※ 實體與線上視訊同步進行。

※ 茶會：10：10開始。