Seminar

Title：Statistical applications in single-cell RNA-seq data analysis

Speaker：Prof. Chih-Yuan Hsu

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Time：10:30 ~ 12:00, Wednesday, December 27, 2023

Place：Auditorium, B1F, Institute of Statistical Science

Abstract

Single-cell RNA sequencing (scRNAseq) has been widely used to characterize cellular heterogeneity in complex tissues. This talk will introduce our proposed methods that can be applied in single-cell RNA-seq data analysis. These methods include 1) a new normalization method to correct unwanted biases caused by sequencing depth, capture efficiency, dropout, and other technical factors 2) a new power and sample size calculation for scRNAseq experiments, and 3) a new method to detect dysregulated ligand-receptor interactions from single cell transcriptomics.

※ **Tea reception starts at 10：10.**

※ **Online live streaming through Cisco Webex will be available.**