



統計科學研究所

INSTITUTE OF  
STATISTICAL SCIENCE



統計所學術演講



中研院統計所

## 學 術 演 講

講 題：Statistical applications in single-cell RNA-seq data analysis

講 者：Prof. Chih-Yuan Hsu

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時 間：2023年12月27日(星期三)，10:30-12:00

地 點：統計所B1演講廳

### 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.

※ 茶 會：10：10開始。

※ 實體與線上視訊同步進行。