

THE HONG KONG UNIVERSITY OF SCIENCE & TECHNOLOGY

Department of Mathematics

SEMINAR ON STATISTICS

SifiNet: A robust and accurate method to identify feature gene sets and annotate cells

By

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<u>Abstract</u>

SifiNet is a robust and accurate computational pipeline for identifying distinct gene sets, extracting and annotating cellular subpopulations, and elucidating intrinsic relationships among these subpopulations. Uniquely, SifiNet bypasses the cell clustering stage, commonly integrated into other cellular annotation pipelines, thereby circumventing potential inaccuracies in clustering that may compromise subsequent analyses. Consequently, SifiNet has demonstrated superior performance in multiple experimental datasets compared with other state-of-the-art methods. SifiNet can analyze both single-cell RNA and ATAC sequencing data, thereby rendering comprehensive multi- omic cellular profiles. It is conveniently available as an open-source R package.

Date : 2 August 2023 (Wednesday) Time : 10:30am Venue : Room 2463 (Lifts 25/26)

All are Welcome!