SEMINAR

DEPARTMENT OF STATISTICS
THE CHINESE UNIVERSITY OF HONG KONG

Atlas-scale single-cell multi-sample multi-condition data integration to uncover disease signatures

INVITED SPEAKER

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TIME

December 3, 2024 (Tue) · 10:00 am - 11:00 am

Zoom meeting

Zoom ID: 995 0808 3317 · Password: cuhkstat · Zoom link

ABSTRACT

The recent emergence of multi-sample multi-condition single-cell multi cohort studies allows researchers to investigate different cell states. The effective integration of multiple large-cohort studies promises biological insights into cells under different conditions that individual studies cannot provide. Here, we present scMerge2, a scalable algorithm that allows data integration of atlas-scale multi-sample multi-condition single-cell studies. We have generalized scMerge2 to enable the merging of millions of cells from single-cell studies generated by various single-cell technologies. Using a large data collection with over five million cells from 1000+ individuals, we demonstrate that the integration of multi-sample multi-condition scRNAseq from multiple cohorts reveals signatures derived from cell-type expression that are more accurate in discriminating disease progression.