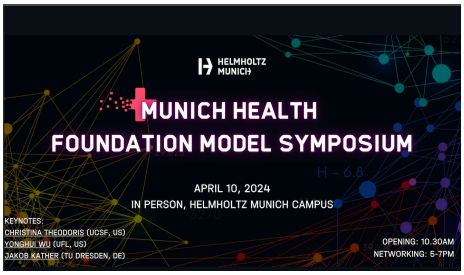

Contribution ID: **7** Type: **Talk**

Joint cell type identification in spatial transcriptomics and single-cell RNA sequencing data

Understanding the intricate composition of tissues in complex living organisms is crucial for unraveling the mechanisms underlying health and disease. This study addresses the challenge of dissecting cell types within tissues by integrating information from two powerful experimental techniques: single-cell RNA-sequencing (scRNA-seq) and spatial transcriptomics (ST). While scRNA-seq offers insights into transcriptional heterogeneity at the cellular level, ST provides spatial information within tissues. Current methods for cell-type annotation in scRNA-seq and mixture decomposition in ST data are often conducted independently, resulting in reduced statistical power and accuracy.

To bridge this gap, we propose ST-Assign [1], a novel hierarchical Bayesian probabilistic model that jointly performs cell-type annotation in scRNA-seq data and cell-type mixture decomposition in ST data. ST-Assign accounts for shared variables such as gene expression profiles and leverages prior knowledge about marker genes, amplifying statistical strength and mitigating experimental noise. The model's excellent performance is demonstrated on simulated and real mouse brain data, showcasing accurate cell-type mixture decomposition and cell-type assignment. In comparison to existing tools, namely Celloscpe [2] and CellAssign [3], ST-Assign demonstrates superior capabilities, particularly in the task of assigning cell types to individual cells.

ST-Assign enables exploring the spatial composition of cell types and holds the potential for enhancing our comprehension of diverse biological systems.

References

[1] Geras, A., Domżał, K., Szczurek, E. Joint cell type identification in spatial transcriptomics and single-cell RNA sequencing data. bioRxiv 2023.05.29.542559. https://doi.org/10.1101/2023.05.29.542559

[2] Geras, A., Darvish Shafighi, S., Domżał, K. et al. Celloscope: a probabilistic model for marker-gene-driven cell type deconvolution in spatial transcriptomics data. Genome Biol 24, 120 (2023). https://doi.org/10.1186/s13059-023-02951-8

[3] Zhang, A.W., O'Flanagan, C., Chavez, E.A. et al. Probabilistic cell-type assignment of single-cell RNA-seq for tumor microenvironment profiling. Nat Methods 16, 1007–1015 (2019). https://doi.org/10.1038/s41592-019-0529-1

Primary authors: GERAS, Agnieszka (Warsaw University of Technology); DOMŻAŁ, Kacper (University of Warsaw); SZCZUREK, Ewa (Helmholtz Munich)

Session Classification: Break + Posters session

Track Classification: Poster