Analysis Tutorial Prospectus

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1. Title

Compare single cell RNA transcriptomics in different cell types using Shiny app

2. Research question(s)

How can we organize and interpret a single cell RNA dataset more efficiently? How to identify different stages of spermatogenesis and better visualize their differences in gene expression?

3. Objective(s)

i. Create an interactive app using Shiny that can both import a single cell RNA dataset and sort the samples to different cell types using selected biomarkers, which will facilitate the manipulation of the app to generate and compare gene expression profiles in different cell types.

4. Approach

A selected single cell RNA dataset of mouse testis that is made as Seruat object (Satija Lab, n.d.) will be accessed and re-organized using different biomarkers to distinguish the cell type (Lukassen et al., 2018). A Shiny app (Posit, n.d.) will then be created to open this organized dataset and display gene expression profiles based on cell type, allowing us to compare different cell stages of spermatogenesis and identify potentially novel gene markers. A previously created human infertility single-cell atlas, or HISTA, will serve as reference for what type of gene profiles can be presented through this Shiny app (Mahyari et al., 2024).

5. Selected References

Lukassen, S., Bosch, E., Ekici, A. B., & Winterpacht, A. (2018). Single-cell RNA sequencing of adult mouse testes. *Scientific data*, 5, 180192. https://doi.org/10.1038/sdata.2018.192

Mahyari, E., Vigh-Conrad, K. A., Daube, C., Lima, A. C., Guo, J., Carrell, D. T., Hotaling, J. M., Aston, K. I., & Conrad, D. F. (2024). The human infertility single-cell testis atlas (HISTA): an interactive molecular scRNA-Seq reference of the human testis. *Andrology*, 10.1111/andr.13637. Advance online publication. https://doi.org/10.1111/andr.13637

Posit. (n.d.). Shiny. Retrieved March 23, 2025, from https://shiny.posit.co/

Satija Lab. (n.d.). Seurat. Retrieved March 18, 2025, from https://satijalab.org/seurat/