MILRD Virtual Training Projects

Research Staff · Postdoc · Graduate Student Track

VTP OVERVIEW **Single-cell Transcriptomics + Visual System Characterization**

Aim

Transcriptomically profile the *Drosophila* optic lobe using single-cell RNA-sequencing (scRNA-seq) analysis

Learning Goals

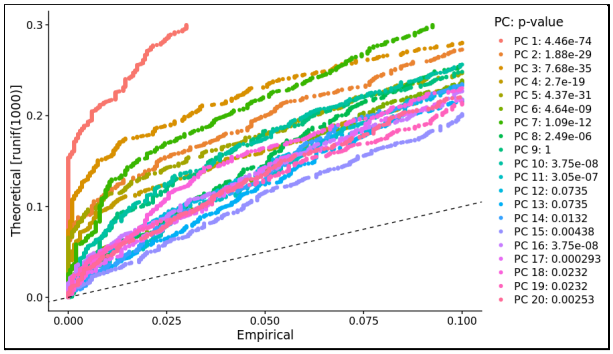
Discussion Topics	*Bioinformatics Tasks + Methods*
• Next Generation Sequencing and RNA-seq • Principles and Methods of scRNA-seq • Discussion of cell size and RNA output in *drosophila* and its implications in scRNAseq analysis • 2D projection mapping (e.g. *t*-SNE vs UMAP) • Principles and methods of scRNA-seq alignment, count generation, and file outputs • Multiple Dataset Integration and Label Transfer	• Downloading data from public repositories • Reference indexing, alignment, counting in Linux terminal • Analysis with Seurat in R • Seurat Object Structure • Library QC • Normalization • Data filtering/clustering/PCA/*t*-SNE • Cell-type Assignment • Gene Expression • (Optional) Merged Analysis and Differential Gene Expression Analysis between developmental stages • (Optional) Comparison of clusters/markers to those from Davis et al. (http://www.opticlobe.com).

Suggested Preparation Linux/Unix command-line & R fundamentals

Summary

Single-cell RNA sequencing enables researchers to profile the transcriptome in thousands of individual cells at once. It is a new and powerful genomics technique with profound implications for elucidating fundamental questions about biology and disease.

This VTP utilizes *Drosophila* scRNA-seq data published by Özel, M.N., Simon, F. et al., who profiled the transcriptomes of 275,000 single cells at adult and at five pupal stages, and built a machine-learning framework to assign them to almost 200 cell types at all time points during development.



As a participant, you'll analyze a dataset from this paper working with your mentor, independently, and by collaborating with your cohort, which can include PhD students, postdocs, and staff researchers from industry.

Throughout the week, you'll profile the single-cell transcriptome of dissociated cells from a single optic lobe sample. In the Linux terminal, on your own

high-performance compute instance which we provide, you'll perform genome alignment, transcript quantification, and in R, you'll conduct library QC, data filtering, clustering, principal component analysis, UMAP dimensionality reduction, marker classification, gene expression analysis, and additional optional analyses.

Source Data

Mehmet Neset Özel, Félix Simon et al. *Neuronal diversity and convergence in a visual system developmental atlas*. Nature 2021.

1-week Extension Options

Analyze *Drosophila* optic lobe bulk RNA-seq from *Davis et al.* and compare them to your scRNA-seq results.

Source Data: Davis, F.P. et al. *A genetic, genomic, and computational resource for exploring neural circuit function*. eLife 2020.

Schedule

Total Effort: ~10 hours

MILRD Provides

- Unlimited support from expert mentors
- Access to all required high-performance cloud-compute resources (AWS), analysis tools and software
- Access to all source data required to complete your project
- Optional Pre-VTP Preparation

Participants Provide

- A computer running Windows or MacOS
- Google Chrome, Safari, Firefox, or Edge
- A stable Internet connection

Sign Up

Review VTP dates and enrollment instructions on our Enrollment & Contact page.