MILRD Virtual Training Projects

Research Staff · Postdocs · Graduate Students

VTP OVERVIEW

Single-cell Transcriptomics + Habenula Neuron Characterization (collaboration with Dr. Michael Wallace, Sabatini Lab at Harvard Medical Scho

Aim

Transcriptomically profile cells in the murine habenula using single-cell RNA-sequencing (scRNA-seq).

Learning Goals

Discussion Topics	*Bioinformatics Tasks + Methods*
• Next Generation Sequencing and RNA-seq • Principles and Methods of scRNA-seq • scRNAseq Platform Comparison: inDrop, Drop-Seq, 10X Genomics • 2D projection mapping (e.g. TSNE vs UMAP) • Multiple Dataset Integration and Label Transfer • Neural cell types	• Analysis with Seurat • Seurat Object Structure • Library QC • Normalization • Data filtering/clustering/PCA/*t*-SNE • Cell-type Assignment • Gene Expression • Merged Analysis and Differential Gene Expression Analysis

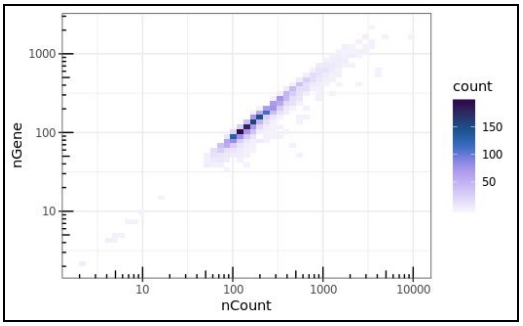
Suggested Preparation

Linux/Unix command-line & R fundamentals

Summary

Single-cell RNA-sequencing analysis 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. It is also a highly in-demand bioinformatics skill-set.

This VTP utilizes mouse scRNA-seq data published by Wallace *et al*., whose work involved generating single-cell suspensions from the mouse habenular complex, a subcortical structure associated with the pineal gland. You'll analyze one of these scRNA-seq datasets 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 disaggregated cells from a single mouse habenula sample. In R, you'll conduct library QC, data filtering, clustering, principal component analysis, *t*-SNE dimensionality reduction, gene expression analysis, and merged analysis. To conclude, you'll cluster genes representative of neuronal cells to identify and discuss *in vivo* validation of Wallace *et al*. results.

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Source Data

Wallace et al. *Anatomical and single-cell transcriptional profiling of the murine habenular complex.* eLife 2020.

Schedule

Total Effort: ~10 hours

MILRD Provides

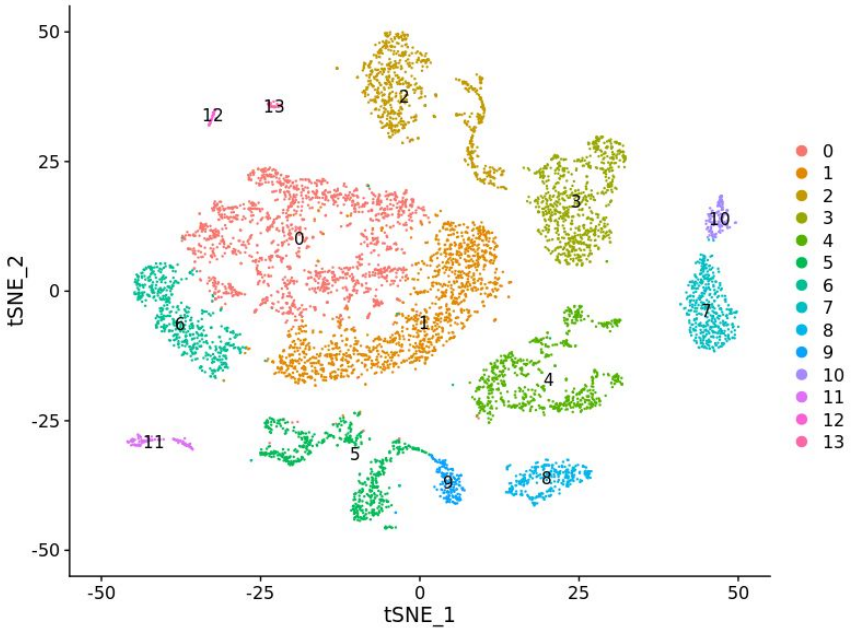
- Unlimited support from expert mentors
- Access to all required high-performance cloud-compute resources (AWS), analysis tools and software
- Access to all source data required to complete your project
- Optional Pre-VTP Preparation

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.



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