

MILRD Virtual Training Projects

Undergraduates · High School Students

VTP OVERVIEW

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

Who should enroll

Undergraduates and high school students who are interested to:

Learn about how single-cell transcriptomics is being used by practitioners in academia, industry, and government. VTPs can help inform: undergraduate/graduate study & program selection, applications for internships and first jobs.

Work alongside professionals and trainees from academia, industry and government. Each participant is assigned their own dataset and works in a small group with other participants. Our personalized platform mixes professionals, trainees, & graduate students with college & high school students to enable peer-learning and networking opportunities—without leaving beginners behind or holding back folks with more expertise.

Develop mentorship and leadership skills. Participants who complete a VTP can apply to serve as an assistant mentor to future cohorts of the project.

Domains

Data science, Neurobiology, Cellular/Molecular Biology, Genomics, Bioinformatics, Single-cell Transcriptomics

Aim

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

Learning Goals

<i>Discussion Topics</i>	<i>Bioinformatics Tasks + Methods</i>
<ul style="list-style-type: none">● Applications of scRNA-seq analysis in research and biotech sectors● Genomics and Next Generation Sequencing● Principles and Methods of scRNA-seq● Cell type characterization in the mammalian brain● Programming languages and data science methods used in bioinformatics analysis	<ul style="list-style-type: none">● Utilize R programming language for statistical analysis and visualization● 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 (optional)

Summary

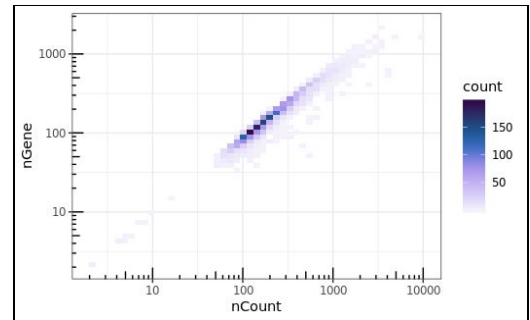
Single-cell RNA-sequencing analysis enables researchers to profile the transcriptome in thousands of individual cells at once. It is a new and powerful genomics technique with profound implications for discovering fundamental questions about biology and disease. It is also a highly in-demand bioinformatics

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skill-set in academia and industry.

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 part of the brain associated with multiple cognitive functions. 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.

Source Data

Wallace et al. *Anatomical and single-cell transcriptional profiling of the murine habenular complex*. [eLife 2020](#).

Schedule

Weeklong VTP Structure



Total Effort: ~15-20 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.