

MILRD Virtual Training Projects

Undergraduates · High School Students

VTP OVERVIEW

Single-cell Transcriptomics + Lung Cell Characterization
(collaboration with Dr. Martina Bradic, Memorial Sloan Kettering Cancer Center)

Who should enroll

Undergraduates and high school students who are interested to:

Learn 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, Cellular/Molecular Biology, Genomics, Pulmonology, Bioinformatics, Single-cell Transcriptomics

Aim

Transcriptomically profile the aging lung using single-cell RNA-sequencing (scRNA-seq) analysis

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 lung● Programming languages and data science methods used in bioinformatics analysis	<ul style="list-style-type: none">● Utilize the Linux and R programming languages for statistical analysis and visualization● Downloading raw data from ENA● Reference indexing, alignment, counting in Linux terminal● Analysis with Seurat in R● Seurat Object Structure● Library QC and normalization● Data filtering/clustering/PCA/t-SNE● Cell-type Assignment● Gene Expression● (Optional) Merged Analysis and Differential Gene Expression Analysis

Suggested Preparation

Linux, command-line & R fundamentals (optional)

Summary

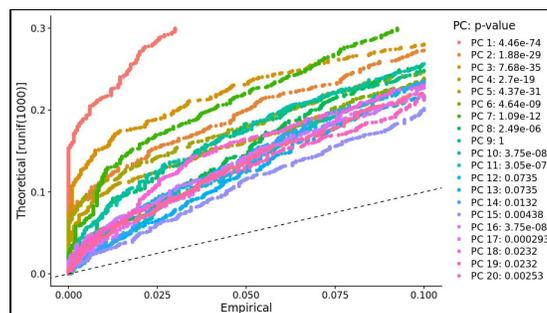
Single-cell RNA-sequencing analysis enables researchers to profile the transcriptome in thousands of individual cells at once. It is a new and powerful

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genomics technique with profound implications for elucidating fundamental questions about biology and disease. It is also a highly in-demand bioinformatics skill-set.

Throughout the week, you'll profile the single-cell transcriptome of disaggregated cells from a single lung tissue sample. In the Linux terminal, on your own high-performance compute instance, 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 and more. To conclude, you'll investigate the expression of *ACE2*—the gene for the receptor the new coronavirus SARS-CoV-2 uses to enter host cells.



Source Data

Angelidis, I., Simon, L.M., Fernandez, I.E. et al. *An atlas of the aging lung mapped by single cell transcriptomics and deep tissue proteomics*. [Nature Communications 2019](#), [Preprint on bioRxiv](#).

Schedule



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.