MILRD Virtual Training Projects

Research Staff · Postdocs · Graduate Students

VTP OVERVIEW

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

Aim

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

Learning Goals

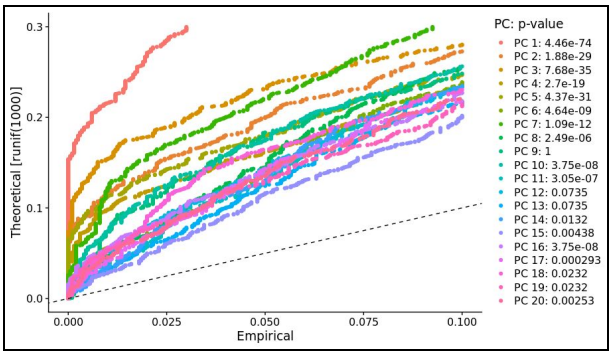
Discussion Topics	*Bioinformatics Tasks + Methods*
• Next Generation Sequencing and RNA-seq • Principles and Methods of scRNA-seq • scRNAseq Platform Comparison: inDrop, Drop-Seq, 10X Genomics • 2D projection mapping (e.g. *t*-SNE vs UMAP) • Principles and methods of scRNA-seq alignment, count generation, and file outputs • Multiple Dataset Integration and Label Transfer • Lung cell types	• 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

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. It is also a highly in-demand bioinformatics skill-set.



This VTP utilizes mouse scRNA-seq data, published by Angelidis *et al.*, whose work involved generating single-cell suspensions from whole-lung tissue for eight 3-month old mice and seven 24-month old mice. 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 lung tissue 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 and more.

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: ~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.