MILRD Virtual Training Projects

Research Staff · Postdoc · Graduate Student Track

VTP OVERVIEW **Single-cell Epigenomics + Neurodegenerative Disorder Elucidation**

Aim

Profile the epigenomic state of human brain cells using single-cell Assay for Transposase-Accessible Chromatin sequencing (scATAC-seq) analysis and explore their implications for Alzheimer's and Parkinson's diseases.

Learning Goals

Discussion Topics	*Bioinformatics Tasks + Methods*
• Next Generation Sequencing and chromatin accessibility assays • Principles and Methods of scATAC-seq • 2D projection mapping (e.g. *t*-SNE vs UMAP) • Principles and methods of scATAC-seq alignment, peak calling and file outputs	• Downloading data from public repositories • Alignment and peak calling • Analysis with Seurat in R • Seurat Object Structure • Library QC • Normalization • Data filtering/clustering/PCA/*t*-SNE • Cell-type Assignment • (Optional) Merged Analysis

Suggested Preparation Linux/Unix command-line & R fundamentals

Summary

Single-cell Assay for Transposase-Accessible Chromatin sequencing (scATAC-seq) 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 human adult brain scATAC data published by M. Ryan Corces et al., who created "a multi-omic epigenetic atlas of the adult human brain" and "developed a machine-learning classifier to integrate this multi-omic framework and predict dozens of functional SNPs for Alzheimer's and Parkinson's diseases…".

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 epigenome of dissociated cells from a single brain sample. On your own high-performance compute instance which we provide, you'll perform genome alignment, peak calling, library QC, data filtering, clustering, principal component analysis, UMAP dimensionality reduction, marker classification, cell-type assignement, and additional optional analyses.

Source Data

M. Ryan Corces et al. *Single-cell epigenomic analyses implicate candidate causal variants at inherited risk loci for Alzheimer's and Parkinson's diseases*. Nature Genetics.

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Schedule

Total Effort: ~10 hours

MILRD Provides

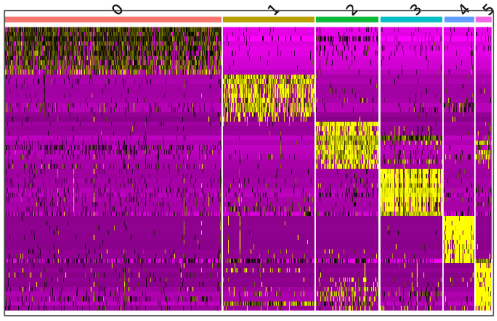
- Unlimited support from expert mentors
- Access to all required high-performance cloud-compute resources (AWS), analysis tools and software
- Access to all source data required to complete your project
- Optional Pre-VTP Preparation

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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