

## **Job Summary:**

The Allen Institute for Brain Science, located in Seattle, Washington, is comprised of a multidisciplinary staff committed to understanding how the brain works and helping to unlock the mysteries of neurological diseases and disorders affecting millions worldwide. Serving the scientific community is at the center of our mission to accelerate progress toward understanding the brain and neurological systems. The Institute is embarked on a 10-year mission to discover underlying principles of cortical organization, circuitry and function. A key part of that mission is to advance our understanding of detailed cortical circuitry by characterizing and classifying the cell type components that comprise the building blocks of these circuits in both mouse and human cortex.

This candidate will work in collaboration with internal scientists, providing data analysis support for transcriptomic and epigenetic efforts to classify and characterize human cortical cell types. Projects involve the use and development of computational tools for analyzing high-throughput single cell/nucleus transcriptomics data sets, and for analysis of ATAC-Seq and other epigenetic data to support the development of cell-type specific reporter tools for mouse and humans. Candidate backgrounds can span bioinformatics, physics, neurobiology, or computer science, ideally with a multidisciplinary computational and biological focus.

## **Job Responsibilities:**

- Develop existing single nucleus/cell RNA-Seq workflows into user friendly software (e.g., R libraries)
- Analyze regulatory motifs in ATAC-Seq data sets to identify cis-regulatory elements
- Alternative splicing / isoform-specific gene expression analysis across cell types
- Improve annotations of the transcriptome
- Implement alternative statistical methods defining differentially expressed genes for marker gene analysis
- Maintain clear and accurate communication with supervisor and team members

## **Basic Qualifications:**

- Bachelors or masters degree in life sciences, physics, math, engineering, or computer science.
- Experience with computational analysis of biological data sets
- Programming experience in R
- Strong written and verbal communication skills.

## **Desired Qualifications:**

- Familiarity with additional programming languages (e.g., python, perl, C/C++).
- Specific experience in analysis of RNA-Seq and ATAC-Seq data sets.
- Expertise with the Linux systems
- Familiarity with basic neuroscience
- Ability to work independently and collaboratively