**DATA MANAGEMENT AND SHARING PLAN**

An example from an application proposing to collect single cell genomic data from mice and humans.

**Data Type**

As detailed in the Research Strategy Section, we propose the generation of a spatially-mapped single-cell atlas of the developing mouse brain and include specific deliverables. Our primary deliverable for each modality will be a matrix of cells × (counts in peaks for ATAC, UMIs in genes for RNA, or methylation status for DNAm) along with a dense metadata table with information for each cell.

This includes the animal sex, developmental time point, punch of origin with x,y,z coordinates, assigned cluster and inferred cell type, assigned subcluster and inferred cell type, as well as a number of QC metrics (total reads, passing reads, reads in peaks, TSS enrichment, cell barcode combination, date of preparation for each stage, sequencing platform, likelihood of being a doublet, and any other relevant metrics that arise during the project).

**Related Tools, Software, or Code**

All code and software that will be written for this work will be deposited on GitHub (<https://github.com/labname>) for public access and be provided as Supplementary files for any publications. Code will be available no later than when a publication has been submitted.

In addition to a detailed methods section for any publications associated with this work, we will provide a detailed step-by-step protocol as a Supplementary Protocol document and maintain active protocols.io protocols for each technology and workflow.

We will additionally release protocol links as metadata to be associated with single-cell data deposited to the Neuroscience Multi-omic Archive (NeMO).

In addition to providing detailed protocols, our laboratory has hosted visiting scientists to train on the data analysis pipelines developed and deployed by the lab. We welcome the opportunity to continue these training efforts.

**Standards**

We will use the standards that are adopted or defined by NeMO.

**Data Preservation, Access, and Associated Timelines**

Single-cell datasets: All single-cell epigenomics and transcriptomics data will made available through the BRAIN Initiative Cell Data Center (BCDC) and NeMO after initial data processing. In addition to the deposition of data through the BCDC or NeMO portal, we will also make all data available through the NCBI Gene Expression Omnibus (GEO) and Sequence Read Archive (SRA), for the mouse data sets.

Human single cell data will be deposited to NeMO only.

Upon publication we will host processed data matrixes and associated metadata as compressed downloadable archives either at the BCDC or NeMO and when appropriate as supplementary information in journal publication.

We will release datasets associated with the technological advances proposed in the application once protocols are established and initial analysis performed, at which point data will be released along with a preprint prior to manuscript submission.

**Access, Distribution, or Reuse Considerations**

There are no special considerations related to accessing or distributing the data to be generated in this award.

**Oversight of Data Management and Sharing**

The Office of Sponsored Programs at University X that will be administering this award has created a data management and sharing plan compliance system as part of their process for submitting the annual NIH progress report. That Office will be monitoring submission of data to BCDC and NEMO.

**Validation Schedule**

Data will be validated using the existing pipelines at the BCDC or NeMO. We will submit each dataset once we reach a specific data freeze milestone. Upon each data freeze we will perform an initial phase of analysis that will culminate in the production of the cell × property matrix and associated metadata, at which point the dataset will be released.

These milestones and target timelines include:

* End of 1st quarter of year 2: A full spatial single-cell ATAC-seq map of an entire mouse brain at P14.
* End of 4th quarter of year 2: An accompanying spatially-mapped single-cell RNA-seq dataset for a full mouse brain at P14, integrated with the ATAC dataset.
* End of 2nd quarter of year 3: A full spatial single-cell ATAC-seq map of each time point.
* End of 2nd quarter of year 3: A full spatial single-cell DNA methylation map for P14, integrated with RNA and ATAC datasets.
* End of 4th quarter of year 3: The complete spatial single-cell RNA-seq dataset for all time points, integrated with the ATAC data.
* End of 4th quarter of year 3: A full spatial single-cell map for all modalities, ATAC, RNA, and DNA methylation, integrated across modalities.