Mouse Neurovascular scRNAseq Workflow:

1. Mouse\_Neurovascular\_scRNAseq\_QC\_Integration
   1. Using Seurat pipeline with QC, normalization, SCTransform, and integration steps.
2. Mouse\_Neurovascular\_scRNAseq\_Clustering
   1. Use signature gene identifiers from literature + exported cluster signature gene excel spreadsheets + Mouse\_Neurovascular\_scRNAseq\_Cluster\_Interrogation
3. Mouse\_Neurovascular\_scRNAseq\_CSDvsHC\_Differential\_Expression
   1. Creates DE gene lists for all clusters identified
4. Mouse\_Neurovascular\_scRNAseq\_DE\_Gene\_Pathway\_Enrichment\_Analysis
   1. Condenses pathway analyses run (i.e., Reactome, GO: Biological Processes) using DE genes into a heatmap figure
5. Mouse\_Neurovascular\_scRNAseq\_Cluster\_Interrogation
   1. Used to examine clusters by gene expression, create feature plots, and make heatmaps
6. Mouse\_Neurovascular\_scRNAseq\_CellChat\_Analysis
   1. CellChat analysis of cell-cell communication and ligand-receptor interactions

Other Important Scripts:

1. R\_Package\_and\_Version\_Extraction\_Code
   1. Creates a list of all packages used during the workflow along with the package versions