This file contains seventeen folders as follows:

- All_h5ad: Contains all the pre-processed H5ad files for Neuronal and Timepoint anndata

- Allen_Layer_Hits: Contains the images for genes associated with the greatest visual expression in a particular layer

- Cluster Distinction: Contains the True/Relative/Non distinct Unique Genes, Clusters, their dotplots and Umaps

- Correlated_Unique_Genes: Contains the correlated unique genes between clusters through time, given as a text file and dotplots

- Dictionary_Files: Holds all the dictionaries associated with running the data. This helps speed up runtime with saved results being loaded instead of produced each time

- Dotplot_Triangles: Internal timepoint Excitatory/Inhibitory gene/cluster/relationships

- Harmony_Integration: Contains the correlated clusters through time as indicated through harmony analysis, also contains the h5ad file for harmony, and umaps

- Inhibitory_Excitatory_Mix: Contains the inhibitory/excitatory/mix umaps for each timepoint

- Layer_Expression_Correlation: Has the bar graph displays for each of the timepoints and the genes corresponding with the layer expression for said timepoint

- Negatively_Correlated_Genes: All genes not expressed between clusters through time

- Neuronal_Dotplots: All the dotplots corresponding to extracting the neuronal clusters

- Neuronal_Umaps: Umap of Neuronal clusters

- Ontology_Files: The ontologies for the unique and correlated unique genes

- Rank_Diff_Genes: The differentially expressed genes ranked, top 20

- RNA-Seq_h5ad: All the original non-pre-processed h5ad files

- Schizophrenia_Autism_Gene_Dotplots

- Timepoint Umps: Umaps for each timepoint including all cell types