Reproducibility in the Real Application mouse

This file contains instructions for reproducing the results and figures contained in the real application to the dataset MERFISH mouse hypothalamus data. We assume the working directory has been appropriately set.

**Step 1: "Step1\_Preprocessing.R"**

Preprocess raw data. The output of this step is given by "ID35\_preprocessed.RData".

In the "ID35\_preprocessed.RData":

* X: The gene expression matrix.
* cell.info: Cell information matrix with n (number of cells) rows and 3 columns, the first column of which is the cell type of cells, the last two columns corresponds to X coordinates and Y coordinates of cells.

**Step 2: "Step2\_Network.R"**

Apply two-step algorithm and WGCNA to the preprocessed data. The output of this step is stored in "Sparse\_est\_70\_0.1.RData" and "WGCNA\_result.RData".

In the "Sparse\_est\_70\_0.1.RData":

* Sparse.Corr: Estimated sparsed gene correlation matrix of each cell by two-step algorithm, the dimension of which is (G,G,n), where n is the number of cells.

In the "WGCNA\_result.RData":

* wgcna.Corr: Estimated sparsed gene correlation matrix of each cell by WGCNA, the dimension of which is (G,G,n), where n is the number of cells.

**Step 3: "Step3\_Figures.R"**

Draw Figure 4—Figure 7 in the manuscript using the output of step 2.