Reproducibility in the Real Application human

This file contains instructions for reproducing the results and figures contained in the real application to the dataset MERFISH U-2 OS cell line datasets. 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 "data.RData".

In the "Idata.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\_0.3.RData".

In the "Sparse\_est\_70\_0.3.RData":

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

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

Draw Figure 8—Figure 9 in the manuscript using the output of step 2.