Reproducibility in the Simulation

This file contains instructions for reproducing the results and figures in the simulation. We assume the working directory has been appropriately set.

**Step 1: "Step1\_Data\_generation.R"**

Generate the three spatial pattern in the simulation. The outputs of this step are "Sim\_linear.RData"/"Sim\_ gau.RData"/"Sim\_cos.RData".

In the "Sim\_linear.RData"/ "Sim\_ gau.RData"/ "Sim\_cos.RData":

* Y: Simulated bulk ST data (each row represents a gene, and each column corresponds to a spot).
* W: True cell-type proportion matrix (each row stands for a spot and each column represents a cell type.
* spot.coor: The coordinates matrix of bulk ST data (each row represents a spot, the first column corresponds to its row index, the second column corresponds to its column index)
* gamma\_true: A G by K matrix with 0 or 1, when a gene g is an SV gene in cell-type k, the (g,k)-th clement of gamma\_true is 1, otherwise is 0.

**Step 2:**

**"Step2\_SIM\_CTSV.R****"/"Step2\_SIM\_SPARKX.R"/"Step2\_SIM\_SPARK.R"/**

**"Step2\_SIM\_BOOSTGP.R"/"Step2\_SIM\_trendsceek.R"/**

**"Step2\_SIM\_SpatialDE.****ipynb"/"Step2\_SIM\_SOMDE. ipynb "**

Apply CTSV, SPARK-X, SPARK, BOOST-GP, trendsceek, SpatialDE, and SOMDE to the simulated data in Step1. The results are saved as ".csv" files.

**Step 3: "Step3\_SIM\_Figure.R"/ Step 3: "Step3\_SIM\_Table.R"**

Draw the figure 2-4 and obtain table 1-2 based on the results of step 1 and step 2.