**Real data**

“mouse\_olfactory\_bulb\_replicate\_12.RData” consists of following data:

1. count (282 spots x 16034 genes): a matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
2. loc (282 spots x 2 variables): a matrix with two columns representing the x and y coordinates of the spatial location.
3. metadata (282 spots x 4 variables): variables including x and y coordinates of the spatial location, “Layer” (ground truth), and “ID”.

“mouse\_visual\_cortex\_STARmap.RData” consists of following data:

1. count (1207 cells x 1020 genes): a matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
2. loc (1207 cells x 2 variables): a matrix with two columns representing the x and y coordinates of the spatial location.
3. metadata (1207 spots x 4 variables): variables including x and y coordinates of the spatial location, “Layer” (ground truth), and “Cell”.

**Demo data**

“demo.RData” consists of following data:

1. count (260 spots x 100 genes): a matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
2. loc (260 spots x 2 variables): a matrix with two columns representing the x and y coordinates of the spatial location.

**Simulated data**

“pattern\_zero\_zero\_replicate\_i.RData” consists of following data:

*Note: pattern = c(bc\_pattern, mob\_ii\_pattern), zero = c(0, 10, 30), i = 1, …, 30; n = 250 for bc\_pattern, n = 260 for mob\_ii\_pattern*

1. count (n spots x 100 genes): a matrix of raw SRT count data, each row represents a spatial location, and each column represents a gene.
2. loc (n spots x 2 variables): a matrix with two columns representing the x and y coordinates of the spatial location.
3. parameters: list of parameters used to generate simulated data.
4. gamma: discriminating genes indicator vector of length 100.

“ground\_truth.RData” consists of the cluster ground truth.