**Real data**

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

1. count (282 spots x 16034 genes): 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): 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” (manual annotation), and “ID”.

“human\_breast\_cancer\_ffpe.RData” consists of following data:

1. count (2518 spots x 17943 genes): Matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
2. loc (2518 spots x 2 variables): Matrix with two columns representing the x and y coordinates of the spatial location.
3. metadata (2518 spots x 3 variables): Variables including x and y coordinates of the spatial location, “Layer” (manual annotation).

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

1. count (1207 cells x 1020 genes): 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): 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” (manual annotation), and “Cell”.

**Simulated data**

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

*Note: pattern = c(bc\_pattern, mob\_pattern), zero = c(5, 10, 30), i = 1, …, 30, n = 250 spots for bc\_pattern, n = 260 spots for mob\_pattern, p = 1,000 genes*

1. count (n spots x p genes): 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): Matrix with two columns representing the x and y coordinates of the spatial location.
3. label: Vector of cluster ground truth.

Others are the simulated parameters to generate count matrix.

**Demo data**

“demo.RData” consists of following data:

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