**Real data**

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

1. sc\_count (12,801 cells x 18,560 genes): Matrix of raw scRNA-seq count data, each row represents a cell and each column represents a gene.
2. Sc\_meta (12,801 cells x 4 variables): Matrix with four variables “sample”, “cellType”, “sampleInfo”, and “nUMI”.
3. cellType: Unique cell types.
4. K: Number of cell types.
5. st\_count (282 spots x 16,034 genes): Matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
6. loc (282 spots x 2 variables): Matrix with two columns representing the x and y coordinates of the spatial location.
7. st\_meta (282 spots x 5 variables): Variables including x and y coordinates of the spatial location, “Layer”, “Domain” (manual annotation), and “ID”.
8. doaminType: Unique spatial domain label.
9. D: Number of spatial domains.

“PDAC-B.RData” consists of following data:

1. sc\_count (1,733 cells x 19,736 genes): Matrix of raw scRNA-seq count data, each row represents a cell and each column represents a gene.
2. Sc\_meta (1,733 cells x 4 variables): Matrix with four variables “ID”, “cellType”, “cellType\_row”, “cellType\_minor”.
3. cellType: Unique cell types.
4. K: Number of cell types.
5. st\_count (224 spots x 19,736 genes): Matrix of raw SRT count data, each row represents a spatial location and each column represents a gene.
6. loc (224 spots x 2 variables): Matrix with two columns representing the x and y coordinates of the spatial location.
7. st\_meta (224 spots x 5 variables): Variables including x and y coordinates of the spatial location, “Domain” (manual annotation), “annotation”, “Domain\_major”
8. doaminType: Unique spatial domain label.
9. D: Number of spatial domains.

**Simulated data**

“mob\_pattern\_zero\_i\_sparsity\_j\_replicate\_k.RData” consists of following data:

*Note: i = c(5, 10, 30), j = c(10, 30, 50), k = 1,…,30 n = 260, p = 1,000 genes*

Simulated data contain the required input: sc\_count, sc\_meta, st\_count, loc, st\_meta, and others simulated parameters to generate count matrix.

**Demo data:** contains: sc\_count, sc\_meta, st\_count, loc, st\_meta, cellType, K, domainType, and D