Walkthrough on simulation datasets (take dataset 1 and 8 as examples)

Dataset 1

```
addpath('./Data')
load('dataset1.mat')
```

Run scAl

```
K = 3;
alpha = 1; lambda = 10000; gamma = 1; s = 0.25;
result = run_scAI(X1,X2,K,alpha,lambda,gamma,s);
result

result = 1×10 cell array
{1×1 struct} {1×1 struct} {1×1 struct} {1×1 struct} {1×1 struct} {1×1 struct}
```

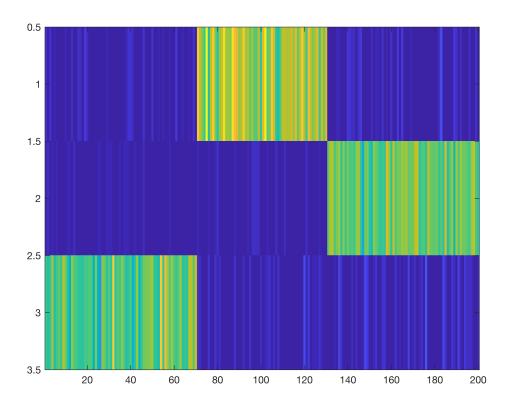
Select the best solution of scAl

```
best_one = choose_best_performance(result);
The best seed is 1
```

Downstream analyses

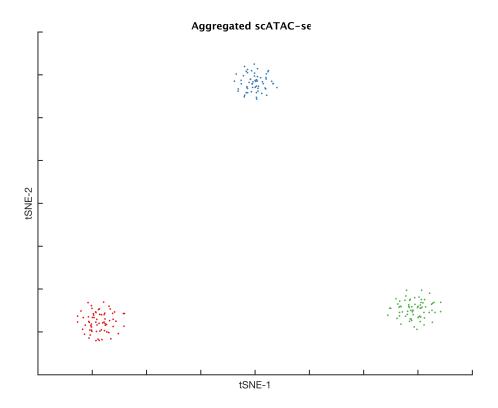
1. Heatmap of cell loading matrix H

```
figure; imagesc(best_one.H)
```



2. Visualize the cells by performing t-SNE (UMAP) on the aggregated epigenomic data obtained by scAl

```
X2a = generate_aggregated_matrix(X2,best_one);
Cells = []; method = 'tSNE';
cell_coords = reducedDims(X2a,Cells,method);
title_name = 'Aggregated scATAC-seq';
clust = []; term = true_label; colors = [];
cellVisualizaiton(cell_coords,clust,term,colors,title_name,method);
```



Dataset 8

```
addpath('./Data')
load('dataset8.mat')
```

Run scAl

```
K = 5;
alpha = 1; lambda = 10000; gamma = 1; s = 0.25;
result = run_scAI(X1, X2, K, alpha, lambda, gamma, s);
result

result = 1×10 cell array
{1×1 struct} {1×1 struct} {1×1 struct} {1×1 struct} {1×1 struct}
```

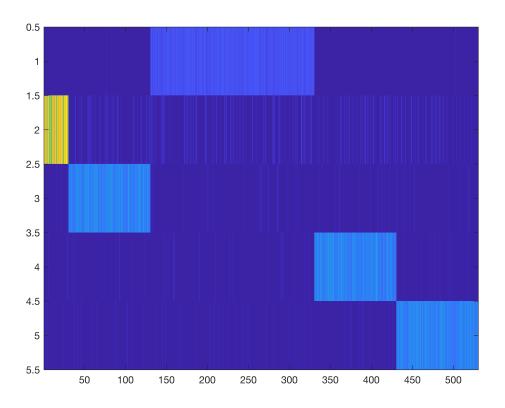
Select the best solution of scAl

```
best_one = choose_best_performance(result);
```

Downstream analyses

1. Heatmap of cell loading matrix H

```
figure; imagesc(best_one.H)
```



2. Visualize the cells by performing t-SNE (UMAP) on the aggregated epigenomic data obtained by scAl

```
X2a = generate_aggregated_matrix(X2,best_one);
Cells = []; method = 'tSNE';
cell_coords = reducedDims(X2a,Cells,method);
title_name = 'Aggregated scATAC-seq';
clust = []; term = true_label2; colors = [];
cellVisualizaiton(cell_coords,clust,term,colors,title_name,method);
```

