Cell-Type Deconvolution of A1 Tissue Section with SpaDecon

1 Import Packages

```python
[1]: import SpaDecon as spd
     import scanpy as sc
     import pandas as pd
     import numpy as np
     from skimage import io
```

```
Using TensorFlow backend.
```

2 Read Histology Image

```python
[2]: histology = io.imread('A1/A1 1_RGB.tif')
```

3 Read scRNA-seq and Visium Gene Expression Matrices

```python
[3]: adata_sc = sc.read('1cyc_sc.h5ad')
     adata_st = sc.read_10x_h5('A1/filtered_feature_bc_matrix.h5')
```

4 Read Spatial Locations

```python
[4]: locations = pd.read_csv('A1/spatial/tissue_positions_list.csv', index_col = 0,
       →header = None)
     locations = locations.loc[adata_st.obs.index]
```

5 Perform Cell-Type Deconvolution Using SpaDecon

```python
[5]: np.random.seed(10)
     clf = spd.SpaDecon()
     clf.deconvolution(adata_sc, adata_st, histology, locations)
```

```
...Calculating adjacency matrix using spatial locations and histology image...
   Adjacency matrix calculated
...Finding optimal l for p=0.5...
   l=0.8570000000000001, p=0.49262
the var_names of adata.raw: adata.raw.var_names.is_unique=: True
the var_names of adata.raw: adata.raw.var_names.is_unique=: True
...Initializing source network using stacked autoencoder...
   The number of training cell types is 10
   The numbers of nodes in the SAE encoder layers are [64]
   The pre-processed scRNA-seq data have 1060 cells and 147 genes
   The pre-processed ST data have 1264 spots and 147 genes
   ...Pretraining the 1th layer...
      The 1th layer has been pretrained
   ...Copying layer-wise pretrained weights to deep autoencoders...
   ...Fine-tuning autoencoder end-to-end...
...Optimizing source network through cell clustering...
   Source network optimized
```

[5]:

	A1	A2	A3	A4	A5 \
AAACCGGGTAGGTACC-1	0.364754	0.065695	0.048730	0.035769	0.078514
AAACCGTTCGTCCAGG-1	0.021577	0.083210	0.146379	0.587111	0.052379
AAACCTAAGCAGCCGG-1	0.258752	0.072169	0.054339	0.043160	0.089231
AAACGGTTGCGAACTG-1	0.023040	0.132662	0.266442	0.393866	0.068963
AAACTCGGTTCGCAAT-1	0.319665	0.097713	0.066319	0.057778	0.100225
...	...	...	...	...	...
TTGTGTATGCCACCAA-1	0.016658	0.090247	0.169562	0.583472	0.052054
TTGTGTTTCCCGAAAG-1	0.024579	0.095816	0.150641	0.534823	0.060977
TTGTTTCACATCCAGG-1	0.021615	0.178876	0.443274	0.168513	0.077394
TTGTTTCATTAGTCTA-1	0.058947	0.168667	0.200915	0.128577	0.196190
TTGTTTCCATACAACT-1	0.210829	0.168748	0.104576	0.086951	0.128086

	Endothelial	Fibroblast	Immune	Skeletal Muscle \
AAACCGGGTAGGTACC-1	0.084429	0.093237	0.080743	0.045277
AAACCGTTCGTCCAGG-1	0.025810	0.021238	0.022438	0.017875
AAACCTAAGCAGCCGG-1	0.101426	0.121869	0.101189	0.050959
AAACGGTTGCGAACTG-1	0.026720	0.023748	0.023865	0.017477
AAACTCGGTTCGCAAT-1	0.085722	0.084954	0.074333	0.037813
...	...	...	...	...
TTGTGTATGCCACCAA-1	0.021025	0.017872	0.018111	0.013390
TTGTGTTTCCCGAAAG-1	0.031381	0.025988	0.027685	0.021807
TTGTTTCACATCCAGG-1	0.025625	0.023385	0.022325	0.016058
TTGTTTCATTAGTCTA-1	0.059198	0.053862	0.051217	0.034140
TTGTTTCCATACAACT-1	0.071111	0.065941	0.063409	0.034422

	Smooth Muscle
AAACCGGGTAGGTACC-1	0.102851
AAACCGTTCGTCCAGG-1	0.021981

```
AAACCTAAGCAGCCGG-1        0.106907
AAACGGTTGCGAACTG-1        0.023217
AAACTCGGTTCGCAAT-1        0.075479
...                           ...
TTGTGTATGCCACCAA-1        0.017610
TTGTGTTTCCCGAAAG-1        0.026303
TTGTTTCACATCCAGG-1        0.022934
TTGTTTCATTAGTCTA-1        0.048287
TTGTTTCCATACAACT-1        0.065928

[1264 rows x 10 columns]
```

6   Save Cell-Type Proportions

```python
spadecon_props = clf.props
spadecon_props.to_csv('spadecon_A1_props.csv')
```