single-cell Panoramic View clustering (PanoView)

Manual

Contents

1. Introduction

2. Installation

PanoView is a python module that uses other common python libraries such as *numpy, scipy, pandas, scikit-learn*, etc. Prior installing *PanoView* from Github repository, please make sure that *Git* is probably installed or go to https://git-scm.com/ for the installation of *Git*.

To install *PanoView* at your local computer, open your command prompt and type the following

```
pip install git+https://github.com/mhu10/scPanoView.git#egg=scPanoView
```

It will install all the required python libraries for executing *PanoView*. To test the PanoView, open the python interpreter or your preferred IDE (Spyder, PyCharm, Jupyter, etc.) and type the following

```
from PanoramicView import scPanoView
```

There should not be any error message popping out.

3. Tutorial

3.1 Pollen data

3.1.1 Initialization and Input expression matrix

The format of the expression matrix should be comma-separated values (csv). The rows are the genes and the columns are the cells. For demonstration, we use expression data (i.e. "PollenRaw.csv") from [Pollen, etc, Nature Biotechnology 2014] as the input matrix. Please make sure that "PollenRaw.csv" is in your python working directory.

First, import PanoView module by `from PanoramicView import scPanoView`. Second, chose a job name ("Pollen" in this tutorial) and initialize PanoView by inputting the filename of the expression matrix, "PollenRaw". (Note: you need to do the initialization whenever starting a new job)

```
from PanoramicView import scPanoView
[1] Pollen = scPanoView.PanoView( "PollenRaw" )
```

You may check the raw expression values of the first three genes/cells from the input matrix. The raw expression value is stored at `Pollen.raw_exp`

```
[2] Pollen.raw_exp.iloc[:3,:3]
```

Gene_Symbol	Hi_2338_1	Hi_2338_2	Hi_2338_3
A1BG	9.08	0.00	0.00
A1BG-AS1	0.00	0.00	3.47
A1CF	0.00	0.05	0.00

3.1.2 Generate clusters

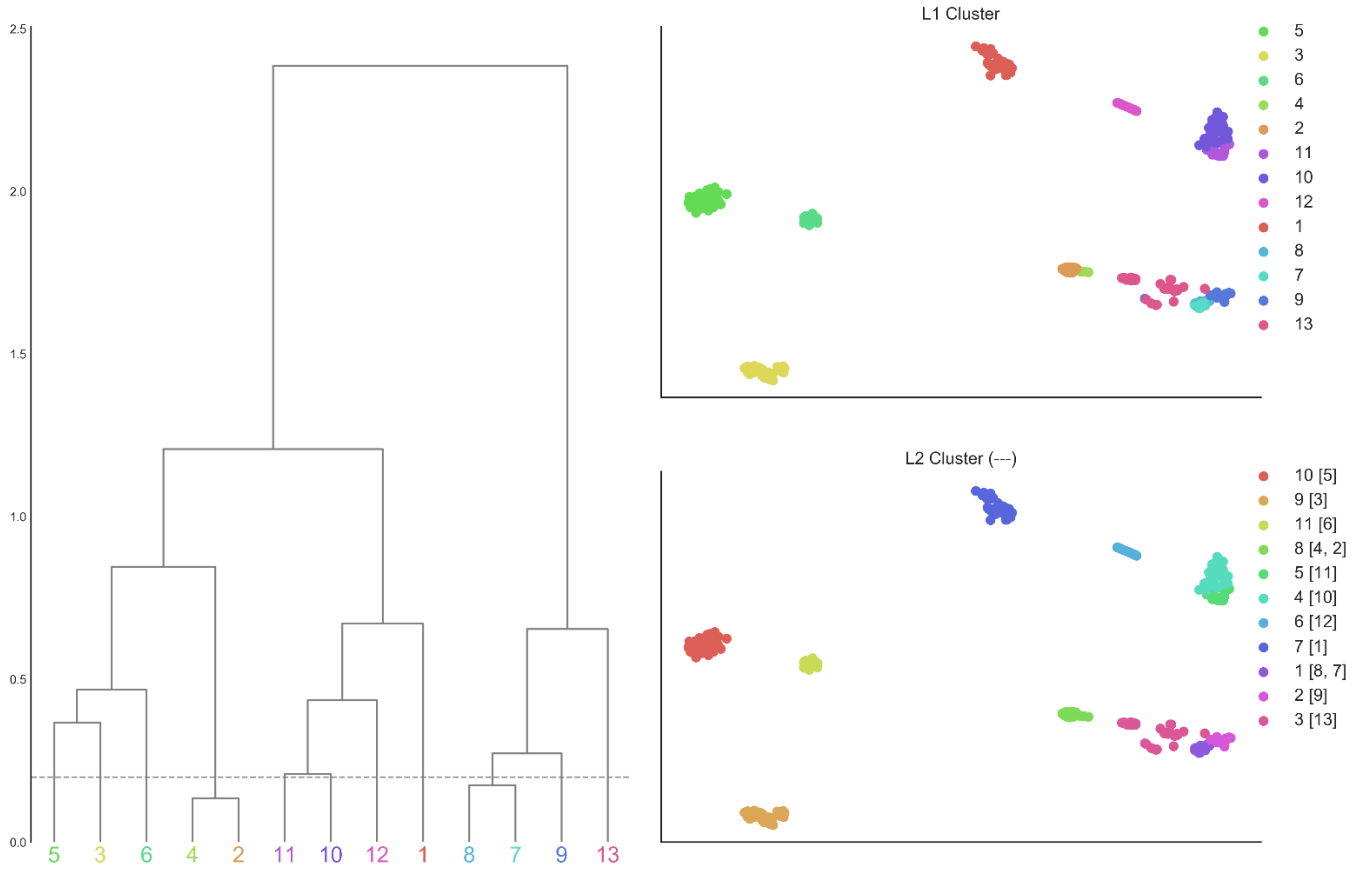
Use `Pollen.RunPanoView( )` to identify single-cell clusters. It will show the progress of algorithm in percentage and display "RunPanoViw-Done" once the searching is finished.

```
[3] Pollen.RunPanoView( )
14%
20%
33%
  :
74%
86%
RunPanoView-Done
```

3.1.3 Output result

Use `Pollen.OutputPanoView()` to output the result of *PanoView* at your working directory. The result includes a table ("Cell_Membership.csv") storing clustering membership of cells and a figure ("PanoView_output.png") that consists of one cluster hierarchy and two TSNE plots.

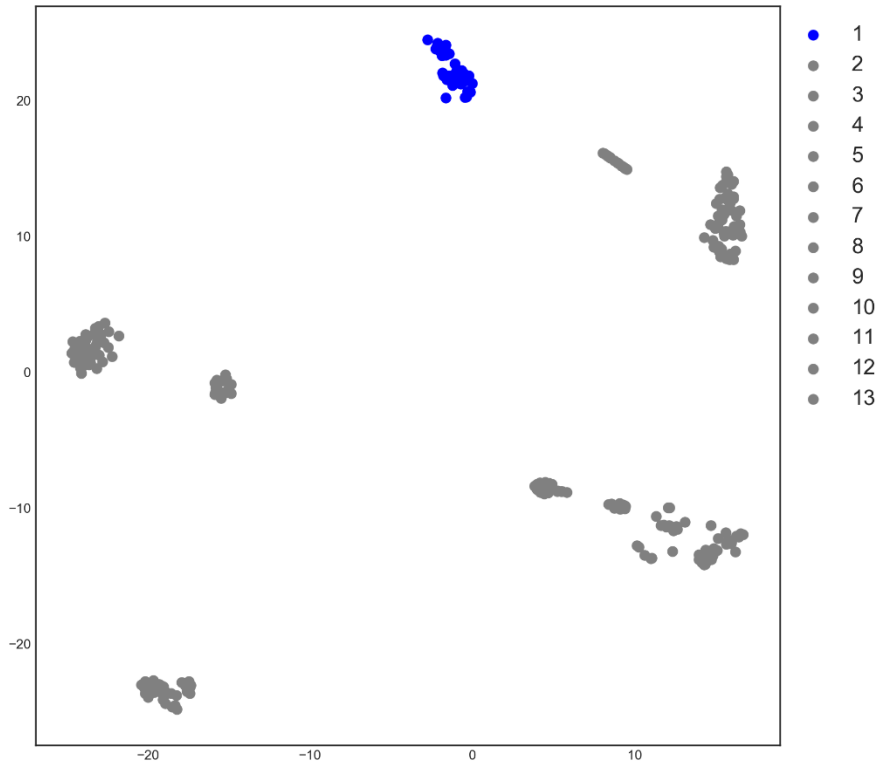
```
[4] Pollen.OutputPanoView()
Cell_Membership.csv
PanoView_output.png
```



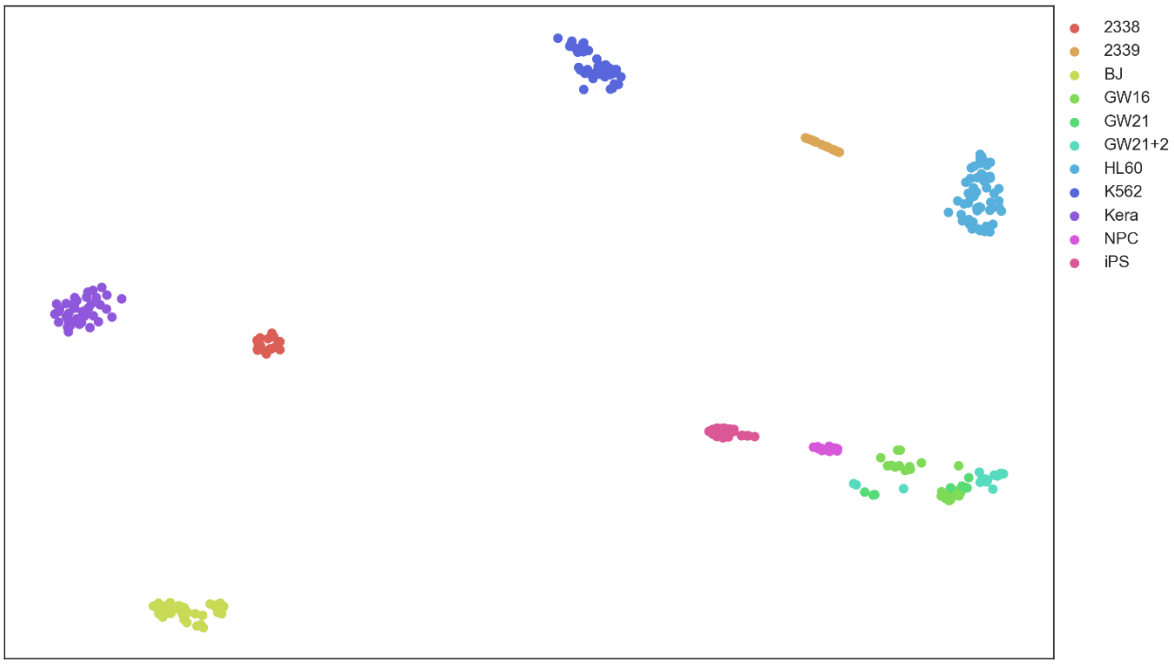
As shown in the figure, *PanoView* identified 13 clusters (Level-1 clusters) and used hierarchical tree to show the similarity of identified clusters. One intuitive parameter in *PanoView* is the height (fclust_dis = 0.2) of the hierarchical tree that would further merge nearby similar clusters. In this tutorial, the default value of 0.2 produced a total of 11 Level-2 clusters that merged cluster#2 and cluster#4 as cluster 8, and cluster#7 and cluster#8 as cluster 1.

3.1.4 Visualization

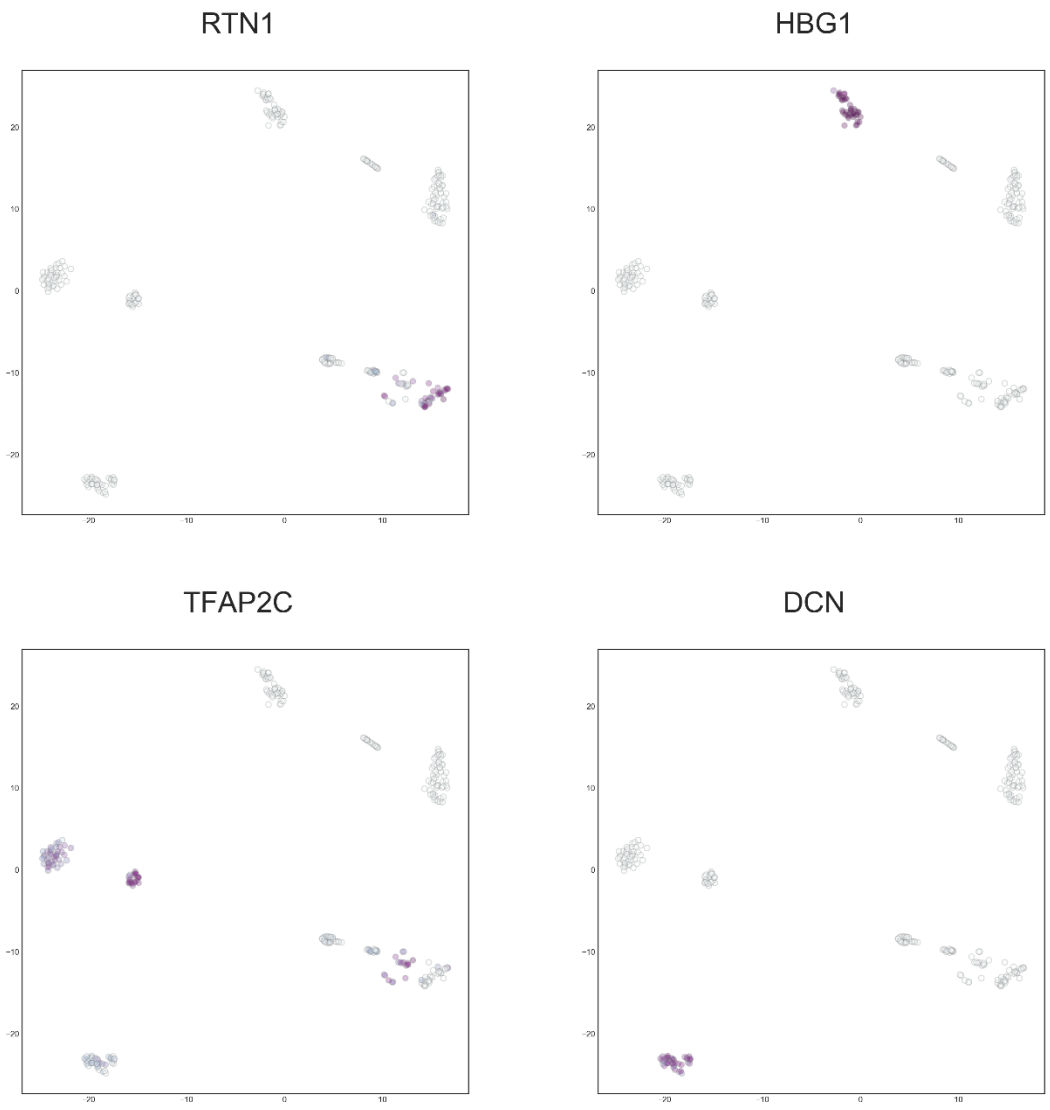
```
[5] Pollen.VisCluster(clevel=1,cnumber=1)
```



[6] Pollen.VisClusterAnno(annotation)

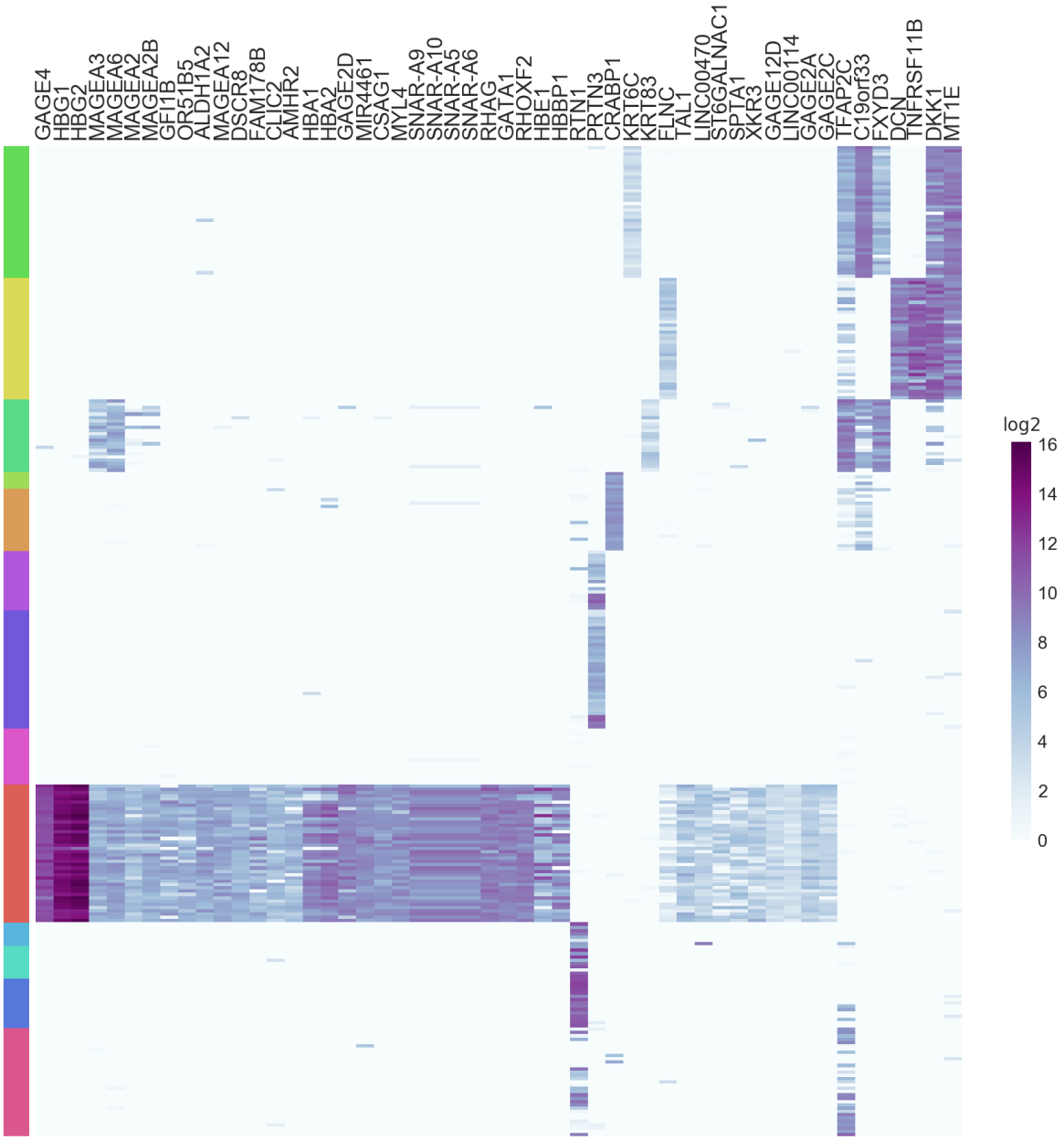


```
[7] Pollen.VisGeneExp(['DCN','RTN1','HBG1','TFAP2C'])
```



3.1.5 Variable Genes

```
[8] Pollen.VisGeneExp(pval=0.05,number=50,fd=2,clevel=1,genelist=['DCN','RTN1','HBG1','TFAP2C'])
```



4. **Functions**

4.1 RunPanoView

```
RunPanoView(GeneLow='default',Zscore='default', Normal=True,Log2=True)
```

4.2 OutputPanoView

```
OutputPanoView(clust_merge = 'default', metric_dis =  'default', fclust_dis = 'default', init = 'default', n_PCs = 'default')
```

4.3 VisCluster

```
VisCluster(clevel,cnumber)
```

4.4 VisClusterAnno

```
VisClusterAnno(annotation)
```

4.5 VisGeneExp

```
VisGeneExp(genes)
```

4.6 RunVGs

```
RunVGs(clevel)
```

4.7 HeatMapVGs

```
HeatMapVGs(pval,number,fd,clevel,genelist='none')
```

5. Others