

single-cell Panoramic View clustering (PanoView)

Manual

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1. Introduction

2. Installation

PanoView is a python module that uses other common python libraries such as *numpy*, *pandas*, *scikit-learn*, etc. For installing *PanoView* at your local computer, open your command prompt and type the following line

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

It will install all the required python libraries for executing *PanoView*. Please make sure that *Git* is probably installed or go to <https://git-scm.com/> for the installation.

To test the *PanoView*, open the python interpreter or your preferred IDE 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 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.

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

3.1.2 Generate clusters

3.1.3 Output results

3.2 Synthetic data

4. **Functions**

4.1 RunPanoView

Arguments
<pre>RunPanoView(self, Normal=True, Log2=True, GeneLow='default', Zscore='default')</pre>

4.2 OutputPanoView

Arguments

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

4.3 VisCluster

Arguments

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

4.4 VisClusterAnno

Arguments

```
VisClusterAnno(self, annotation)
```

4.5 VisGeneExp

Arguments

```
VisGeneExp(self, genes)
```

4.6 RunVGs

Arguments

```
RunVGs(self, clevel)
```

4.7 HeatMapVGs

Arguments

```
HeatMapVGs(self, pval, number, fd, clevel,  
            genelist=None)
```

4.8 HeatMapGenes

Arguments

HeatMapGenes(self, clevel, genelist)

5. Others