

# single-cell Panoramic View clustering (PanoView)

## Manual

### Contents

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- 1. Introduction
- 2. Installation
- 3. Tutorial
  - 3.1 Input data
  - 3.2 Generate clusters
  - 3.3 Output results
- 4. Functions
  - 4.1 RunPanoView
  - 4.2 OutputPanoView
  - 4.3 VisCluster
  - 4.4 VisClusterAnno
  - 4.5 VisGeneExp
  - 4.6 RunVGs
  - 4.7 HeatMapVGs
  - 4.8 HeatMapGenes

### 1. Introduction

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### 2. Installation

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*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**

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3.1 Input data

3.2 Generate clusters

3.3 Output results

### 4. **Functions**

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#### 4.1 RunPanoView

##### Arguments

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

#### 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
<code>VisGeneExp(self, genes)</code>

#### 4.6 RunVGs

Arguments
<code>RunVGs(self, clevel)</code>

#### 4.7 HeatMapVGs

Arguments
<code>HeatMapVGs(self, pval, number, fd, clevel, genelist=None)</code>

#### 4.8 HeatMapGenes

Arguments
<code>HeatMapGenes(self, clevel, genelist)</code>

#### 5. Others