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# Pantheon

*Release 0.0.2*

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## **INTRODUCTION**

Pantheon is an application that provides interactive functions for single cell data analysis. For **researchers**, Pantheon allows users to quickly preprocess and easily analyzing single cell data. For **developers**, Pantheon allows extensions of the interface for further analysis with certain tools written in python.



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CHAPTER  
TWO

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**DOWNLOAD**



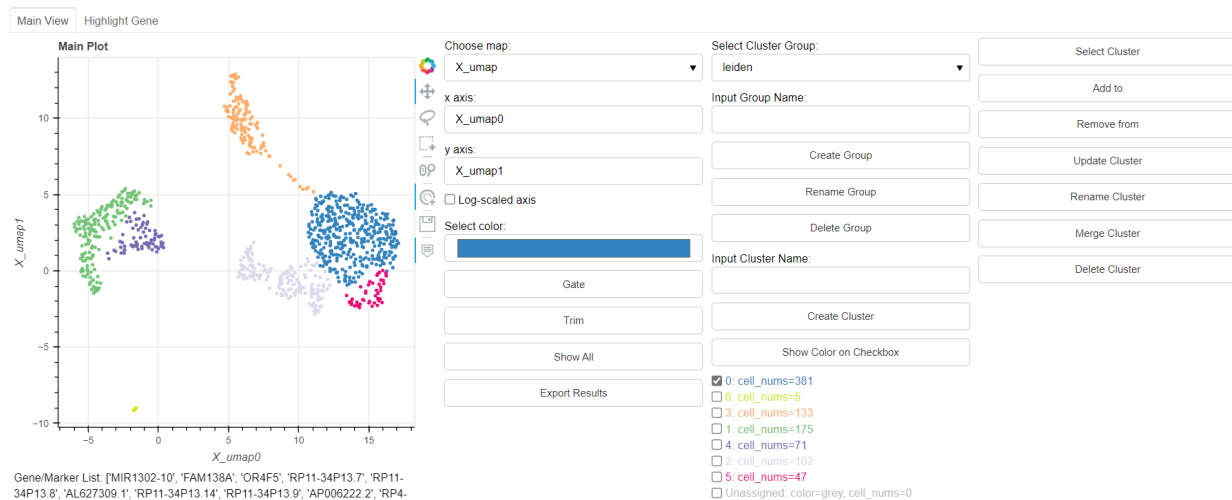


## TUTORIALS

### 3.1 Navigation

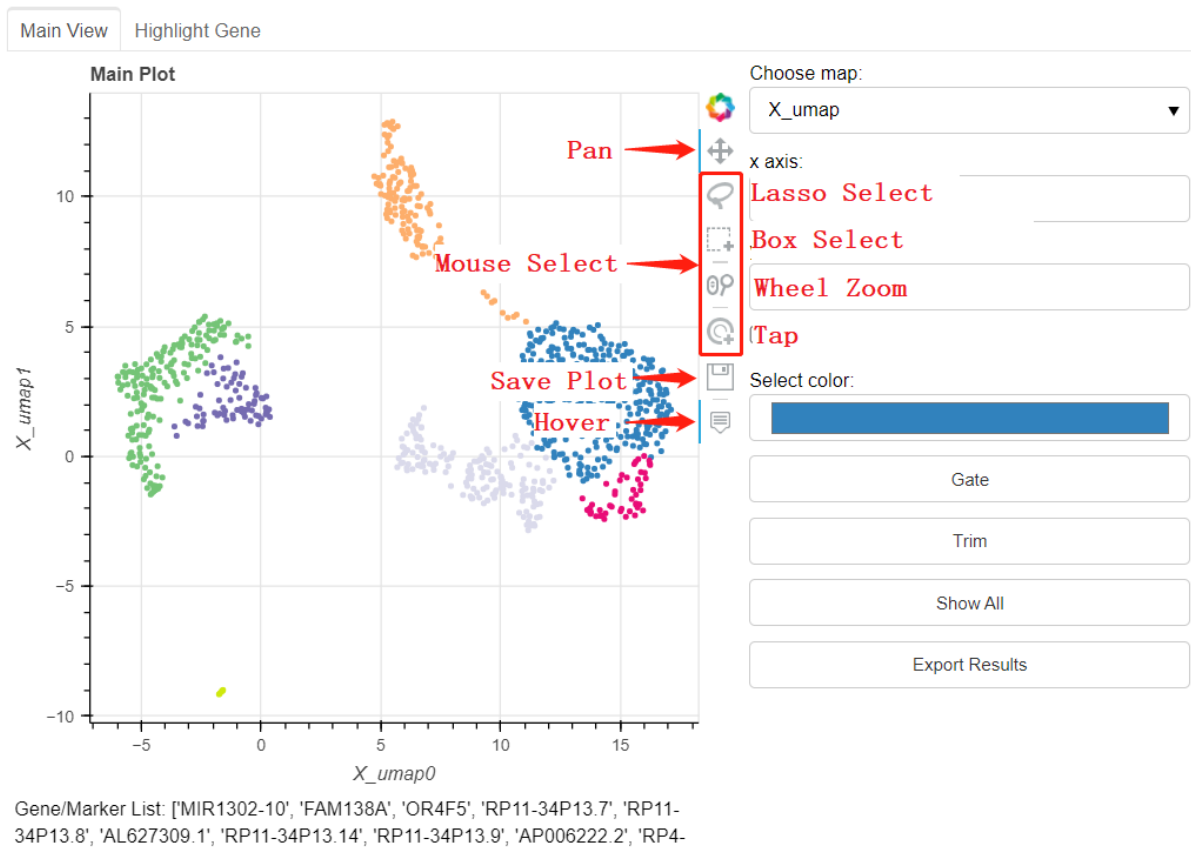
#### 3.1.1 Overview

This is an example of PBMC\_3k scRNA-seq data labeled by leiden and showed with umap.



### 3.1.2 Toolbox

The Toolbox is just on the right of main plot.



### 3.1.3 Map Editor

Click to choose the map.

Choose map:

The screenshot shows a dropdown menu for selecting a map. The menu is titled 'Choose map:' and has a search bar. The dropdown list is open, showing three options: 'X\_pca', 'X\_umap', and 'generic\_columns'. The 'X\_umap' option is currently selected and highlighted in a dark grey bar. The search bar contains the text 'X\_umap'.

The option of map is decided by the existed view. If there is not existed view of data, the plot map will be constructed by the feature, which is named by **generic\_columns**.

Then input the x and y axis.

x axis:

X\_umap0

y axis:

X\_umap1

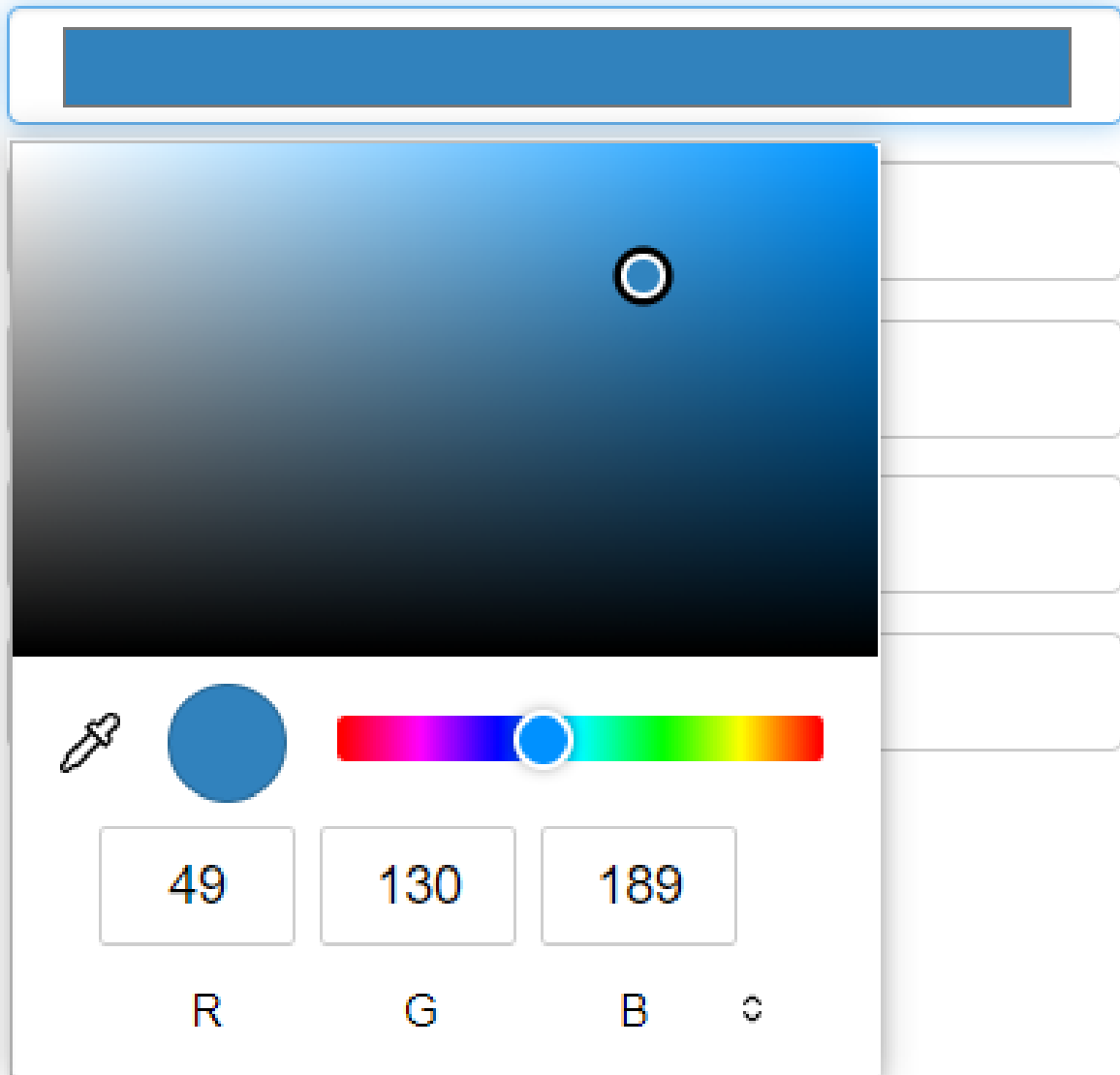
### 3.1.4 Plot Editor

Check **Log-scaled axis** if log scaled feature is expected to show.

☒ **Log-scaled axis**

Select current color with color selection button.

Select color:



**Gate:** click *Gate* button, then only the selected dots will show in the plot. **Trim:** click *Trim* button, then selected dots will be removed in the plot. **Show All:** click *Show All* button, then all the dots will show in the plot.



### 3.1.5 Export Results

The exported results include one anndata file (in form of '.h5ad') and a file to save result of clustering, whose head is name of the cluster group.

### 3.1.6 Cluster Group Editor

Firstly *select the cluster group* in the dropdown list. If there is not existed cluster group, input the group name and click the **Create Group** button to create a new group. (The default group name will be construction of name of x- and y-axis). Users can also edit the selected group by **Rename Group** and **Delete Group** buttons.

Select Cluster Group:

 ▼

Input Group Name:

### 3.1.7 Cluster Options

Select dots, input the name of this cluster, and click **Create Cluster** button. Then the created cluster will be shown in the followed checkbox list.

Input Cluster Name:

Create Cluster

Show Color on Checkbox

- ☒ 0: cell\_nums=381
- ☐ 6: cell\_nums=5
- ☐ 3: cell\_nums=133
- ☐ 1: cell\_nums=175
- ☐ 4: cell\_nums=71
- ☐ 2: cell\_nums=162
- ☐ 5: cell\_nums=47
- ☐ Unassigned: color=grey, cell\_nums=0

The **Select Cluster** button will highlight the dots of the checked clusters in the checkbox list.

Click **Add to** button, the selected dots will be added to the checked cluster.

Click **Remove from** button, the selected dots will be removed from the checked cluster.

Click **Update Cluster** button to easily update the checked cluster with the selected dots.

Input the new name of cluster and click **Rename Cluster** to change name of checked cluster.

**Merge Cluster** button merges the checked clusters into one cluster(defaultly merged into the first checked cluster).

Click the **Delete Cluster** will delete the checked cluster.

Select Cluster

Add to

Remove from

Update Cluster

Rename Cluster

Merge Cluster

Delete Cluster

### 3.1.8 Highlight Gene

Choose the **Highlight Gene** panel to show the level of gene expression.

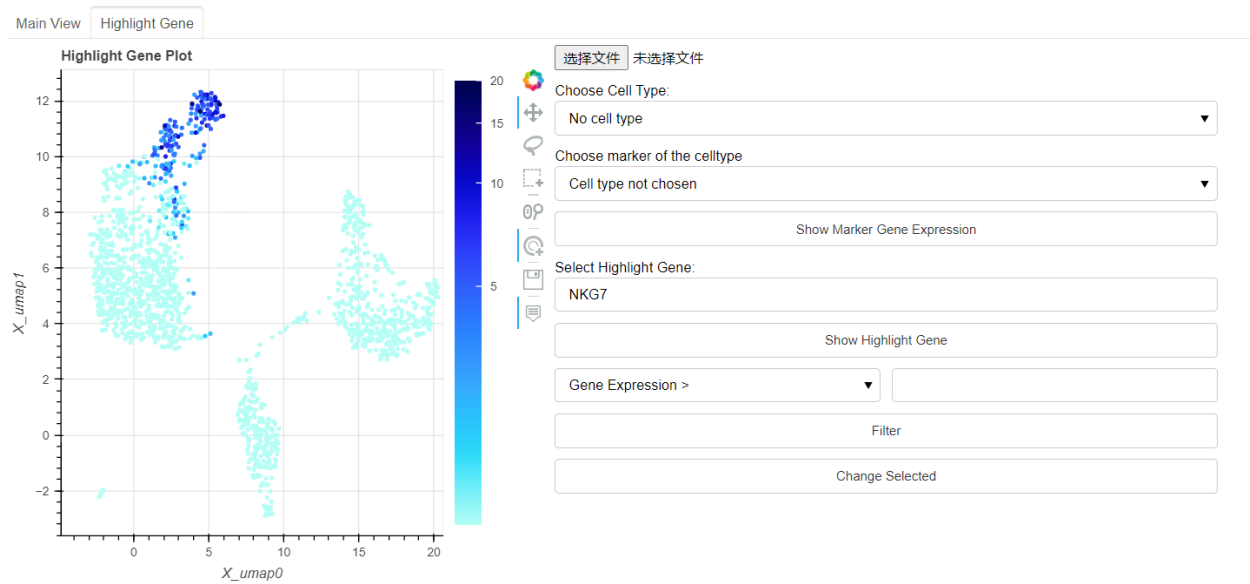
Input the gene to analyse, click the **Show Highlight Gene** button, then the degree of gene expression will show in plot.

Users can also import marker list(in form of .csv file) to define marker gene expression leve of certain celltype.

With the **Filter** button, only the cells meet the conditions of hightlight gene will be highlighted in the plot.

Click the **Change Selected** button, the selected dots in the Highlight Gene panel will Synchronously show in the main panel for further options.





## 3.2 Preprocessing with scanpy

## 3.3 Clustering with sacnpy