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**SOView\_doc**

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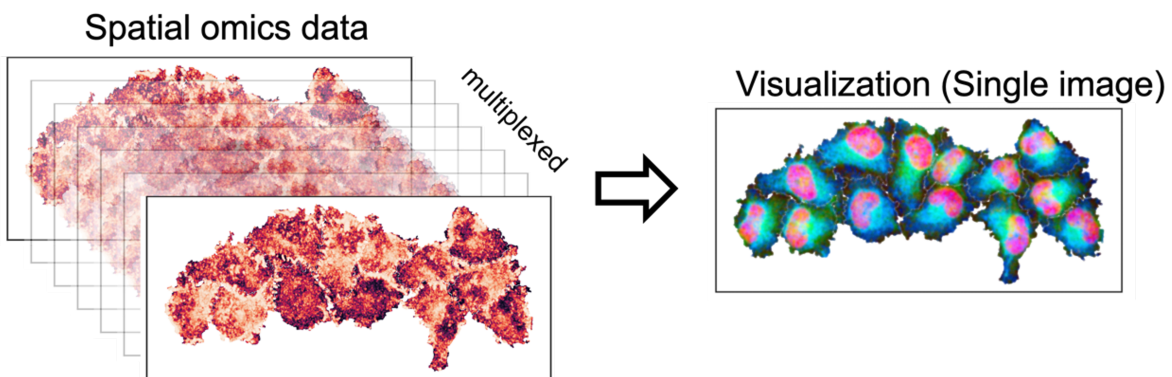
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## INTRODUCTION

SOView is designed for tissue visualization for general spatial omics data, the data input is in Anndata format.



### 1.1 Installation

1. Create a conda environment and activate it.

```
conda create --name SOView python=3.9 -y
conda activate SOView
```

2. Clone the source code.

```
git clone https://github.com/yuanzhiyuan/SOView
```

3. Install SOView as a dependency or third-party package with pip:

```
cd SOView
pip install .
```

4. Also install pysodb to load the data: <https://pysodb.readthedocs.io/en/latest/>

## 1.2 Examples

```
[1]: import warnings
warnings.filterwarnings("ignore")
```

### 1.2.1 load Visium data using pysodb

```
[2]: import pysodb
sodb = pysodb.SODB()
```

```
[3]: dataset_name = '10x'
experiment_name = 'V1_Mouse_Brain_Sagittal_Posterior_filtered_feature_bc_matrix'
adata = sodb.load_experiment(dataset_name, experiment_name)
```

```
load experiment: V1_Mouse_Brain_Sagittal_Posterior_filtered_feature_bc_matrix in dataset:
↪ 10x
```

### 1.2.2 plot SOView for Visium data

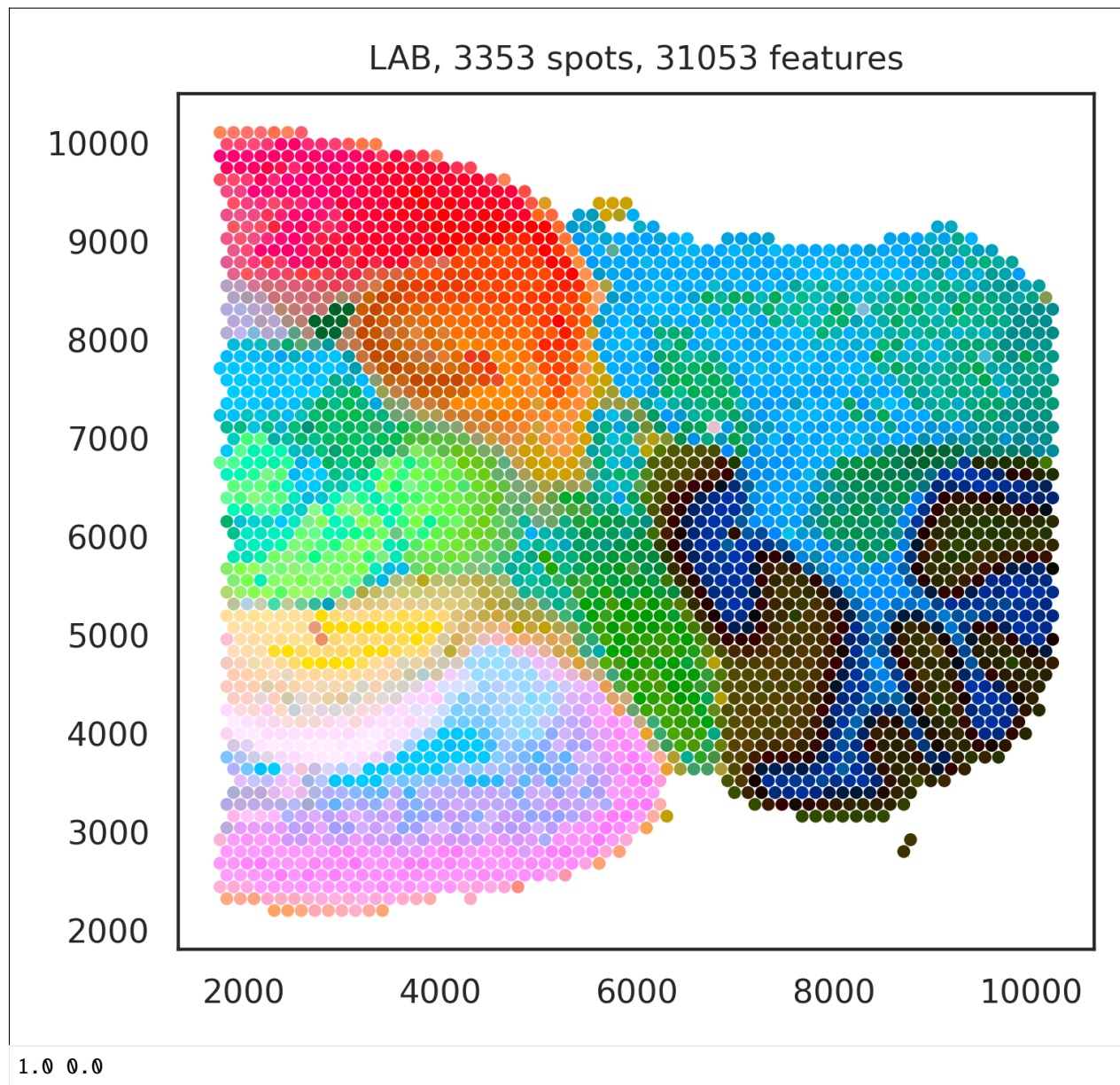
```
[4]: import SOView

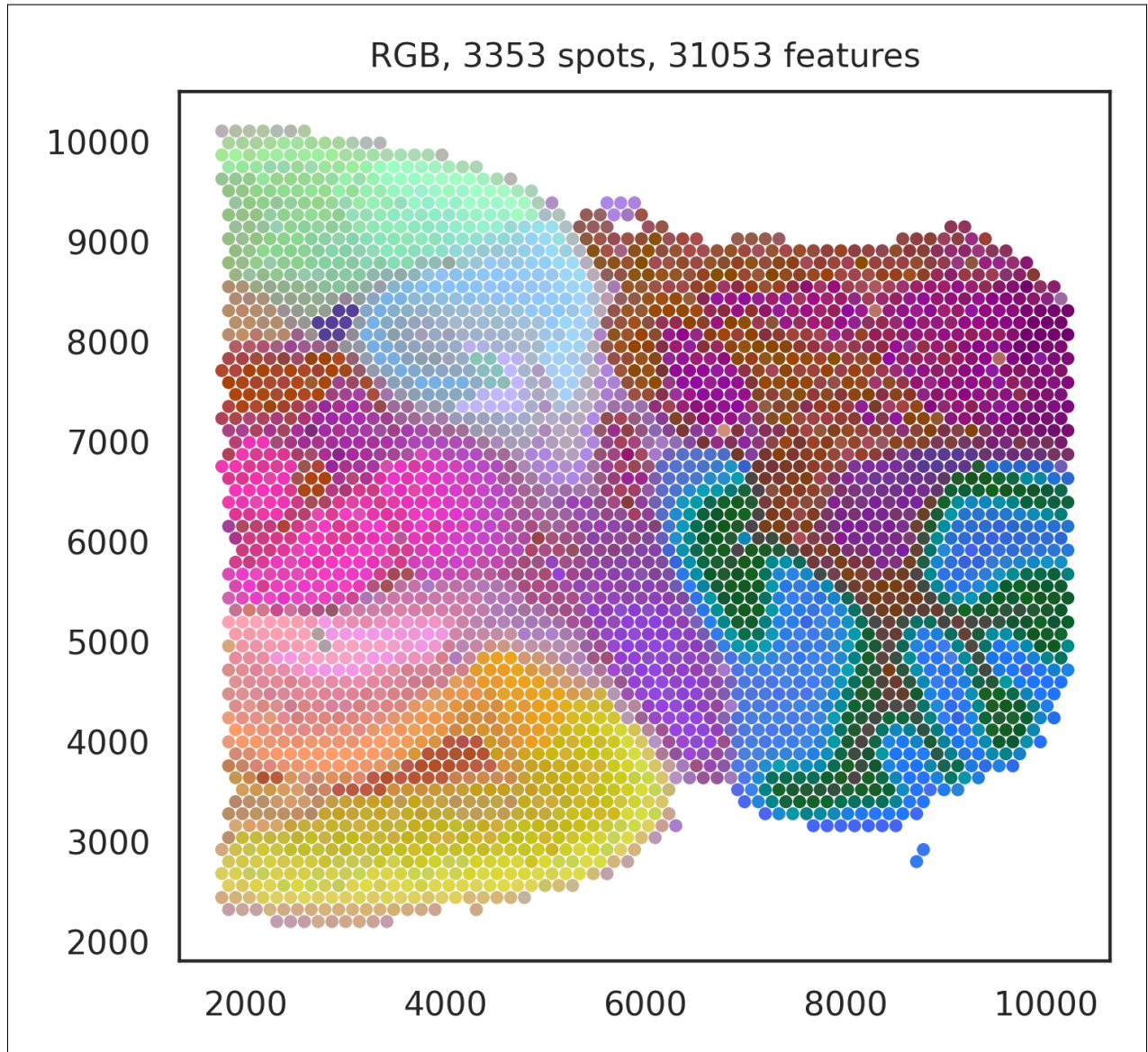
scanpy==1.9.1 anndata==0.8.0 umap==0.5.2 numpy==1.22.4 scipy==1.7.3 pandas==1.5.2 scikit-
↪ learn==1.0.2 statsmodels==0.13.5 python-igraph==0.10.2 pynndescent==0.5.8
squidpy==1.1.2
```

```
[5]: SOView.SOViewer_plot(
    adata = adata, # the data to plot
    save = None, # save the result to specified path or don't save (None)
    embedding_use='X_umap', # which embedding to be used for plot
    dot_size=10, # the marker size of the plot
    marker = 'o' # marker style

)

# SOView function gets results of both CIELAB and RGB color coding
generating color coding...
1.0 0.0
```

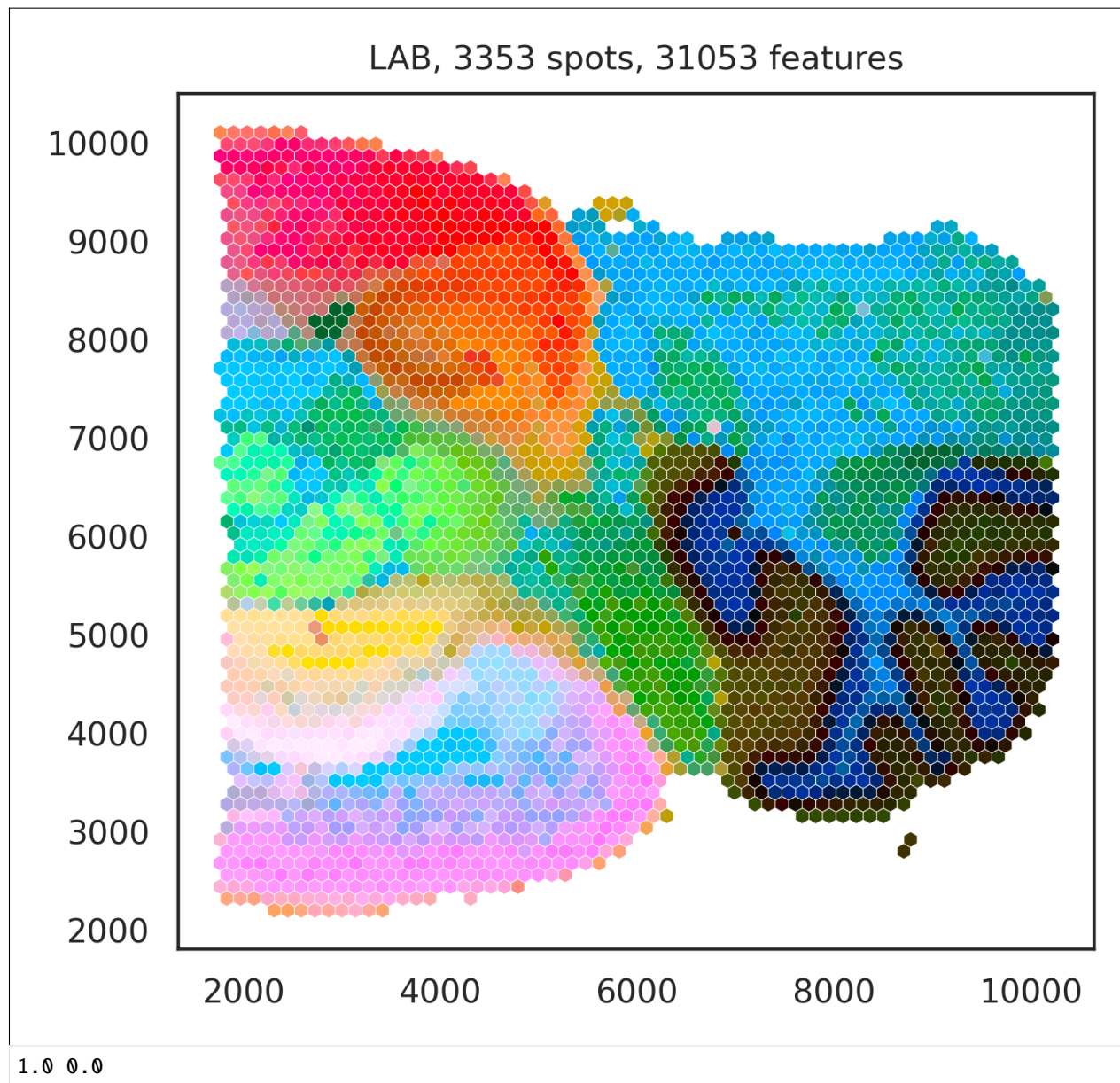


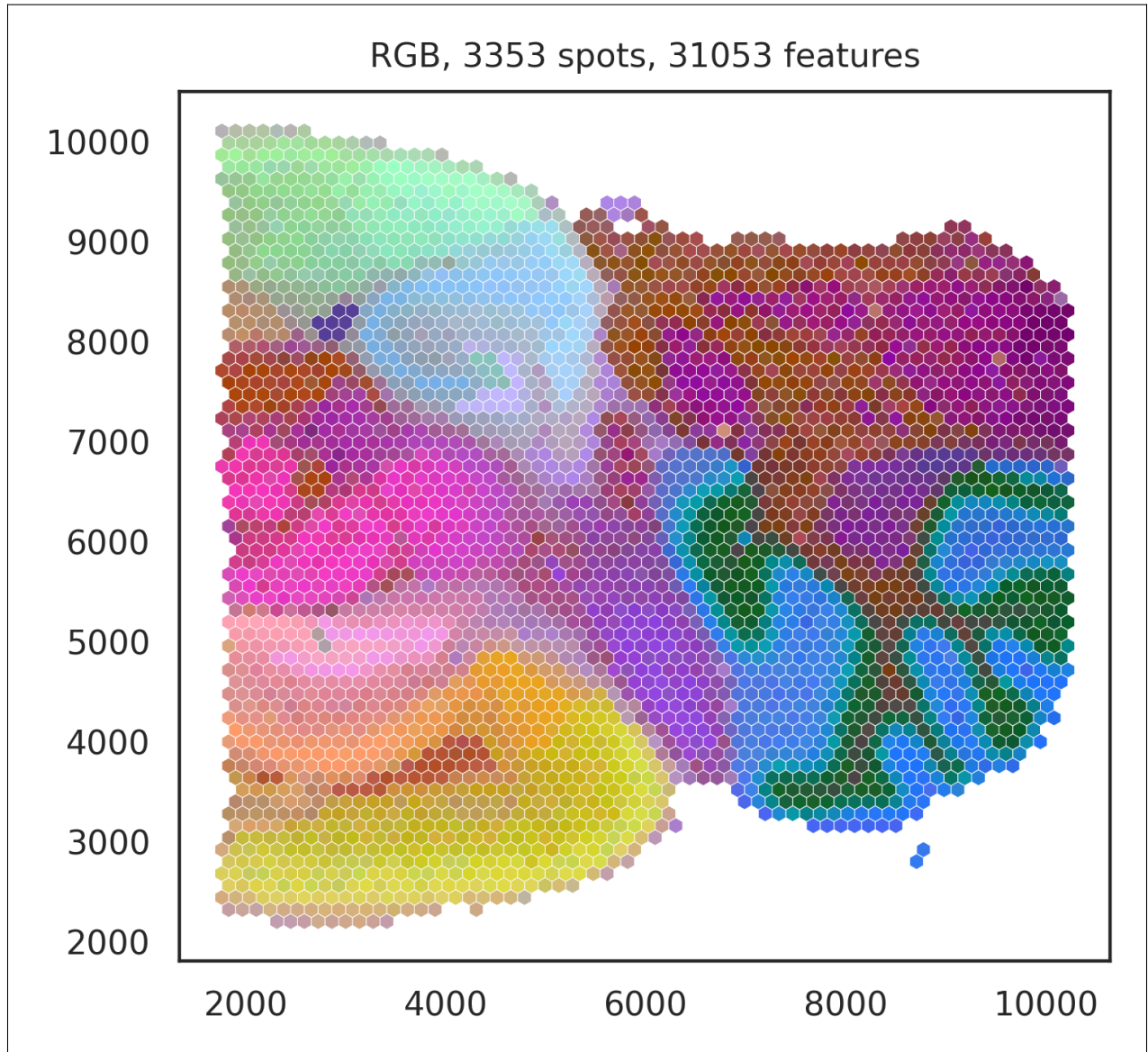


```
[9]: # change the marker style to hexagon to fit for 10X Visium
SOView.SOViewer_plot(
    adata = adata, # the data to plot
    save = None, # save the result to specified path or don't save (None)
    embedding_use='X_umap', # which embedding to be used for plot
    dot_size=13, # the marker size of the plot
    marker = 'h' # marker style

)
```

```
generating color coding...
1.0 0.0
```





```
[ ]:
```

```
[1]: import warnings
      warnings.filterwarnings("ignore")
```



### 1.2.3 load stereo-seq data using pysodb

```
[2]: import pysodb
      sodb = pysodb.SODB()
```

```
[7]: dataset_name = 'chen2022spatiotemporal'
      experiment_name = 'E14.5_E1S1.MOSTA'
      adata = sodb.load_experiment(dataset_name, experiment_name)
```

```
load experiment: E14.5_E1S1.MOSTA in dataset: chen2022spatiotemporal
```

### 1.2.4 plot SOView for stereo-seq data

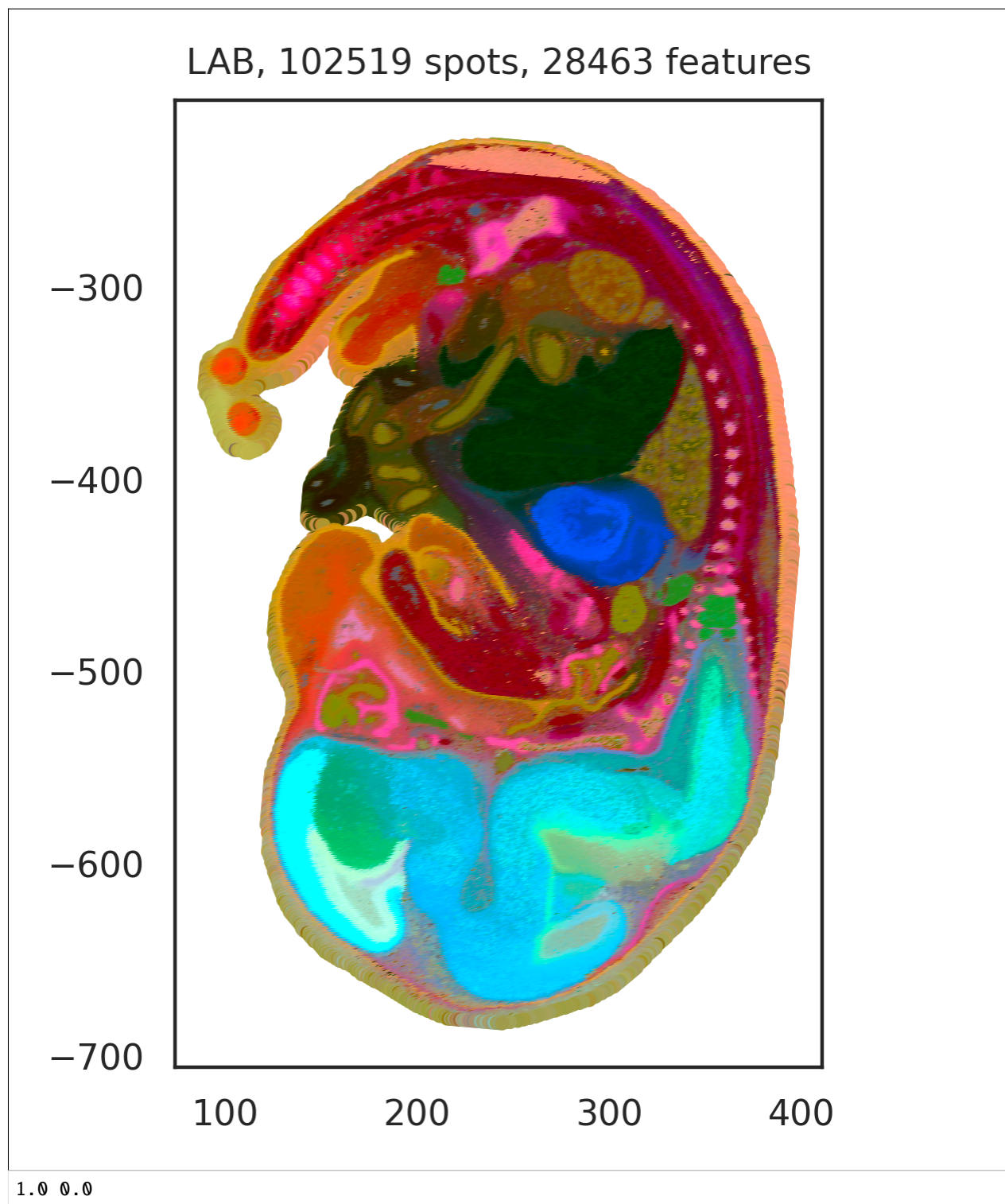
```
[5]: import SOView

scanpy==1.9.1 anndata==0.8.0 umap==0.5.2 numpy==1.22.4 scipy==1.7.3 pandas==1.5.2 scikit-
→learn==1.0.2 statsmodels==0.13.5 python-igraph==0.10.2 pynndescent==0.5.8
squidpy==1.1.2
```

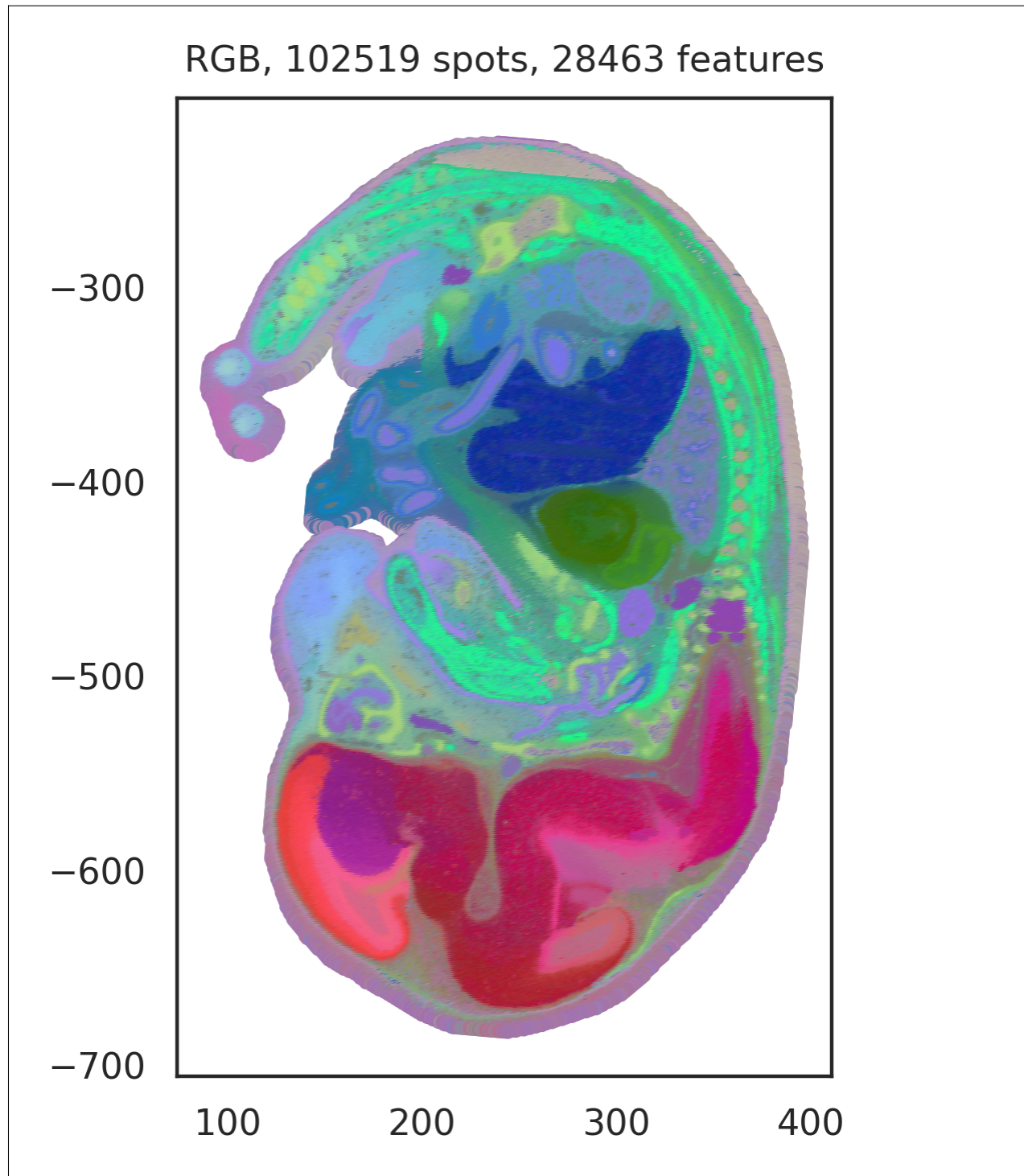
```
[8]: SOView.SOViewer_plot(
      adata = adata, # the data to plot
      save = None, # save the result to specified path or don't save (None)
      embedding_use='X_umap', # which embedding to be used for plot
      dot_size=10, # the marker size of the plot
      marker = 'o' # marker style
```

```
)
```

```
generating color coding...
1.0 0.0
```







```
[ ]:
```

## 1.3 Other

Users can try other data in SODB for other test.

**IF YOU FIND SOVIEW USEFUL IN YOUR RESEARCH, PLEASE  
CONSIDER CITING:**

TBD