Load data downloaded from SPRING to Partek

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Overview of steps

1. Download data of interest from the SPRING[1,2] interactive data explorer online (or run locally).

2. Run spring_to_partek.py in Terminal using downloaded data as input.

3. Upload data to Partek[3]

[1] Weinreb C, Wolock S, Klein AM. SPRING: a kinetic interface for visualizing high dimensional single-cell expression data. Bioinformatics. 2018 Apr 1;34(7):1246–8.
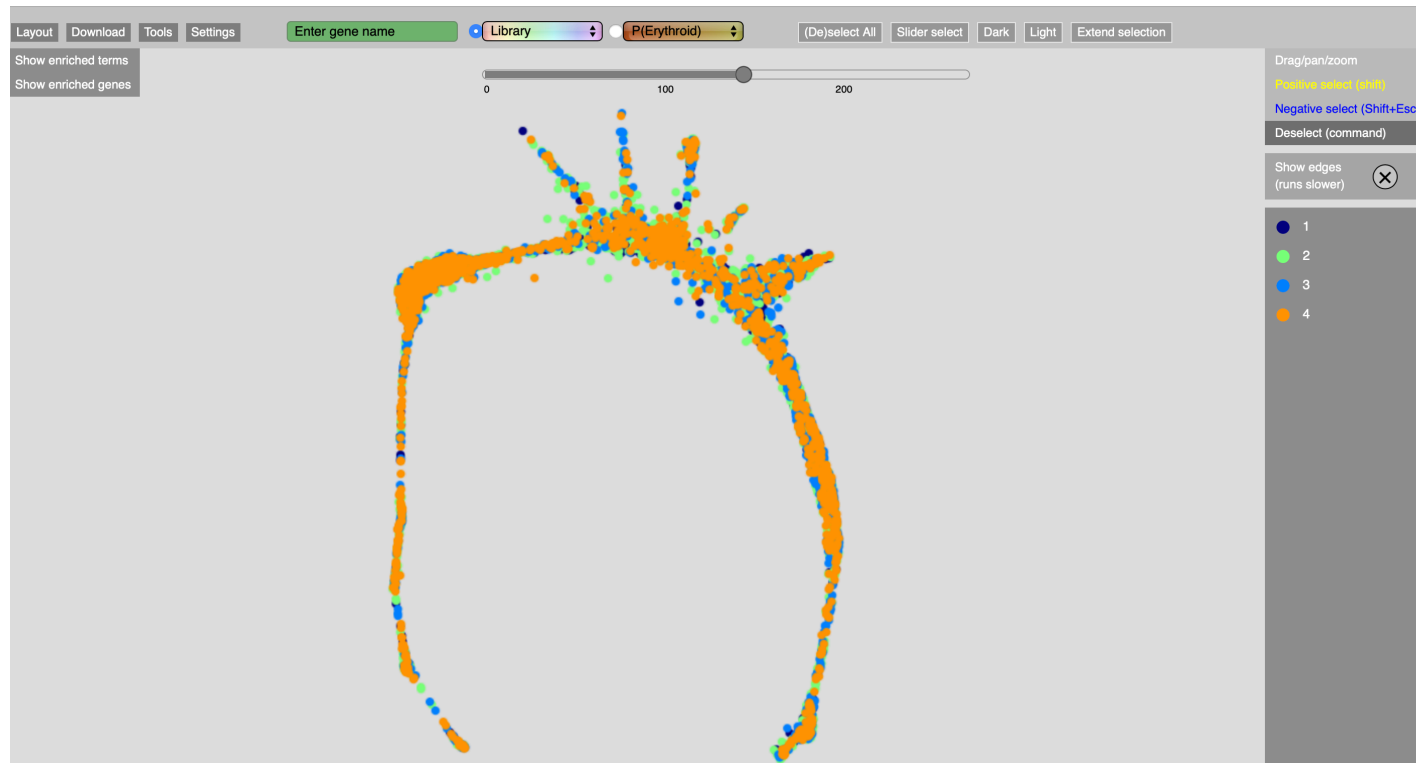[2] https://kleintools.hms.harvard.edu/tools/spring.html
[3] http://www.partek.com

Download data from SPRING

Using the following dataset as an example[4]:
https://kleintools.hms.harvard.edu/tools/springViewer_1_6_dev.html?datasets/mouse_HPCs/basal_bone_marrow/full
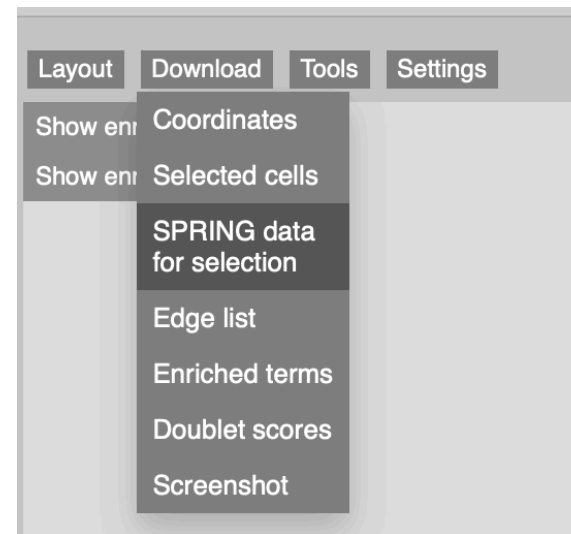
[4] Tusi BK, Wolock SL, Weinreb C, Hwang Y, Hidalgo D, Zilionis R, et al. Population snapshots predict early haematopoietic and erythroid hierarchies. Nature. 2018 Mar 1;555(7694):54–60.

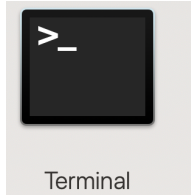# Download data from SPRING

Select cells to download

Download

Untar the downloaded file, place in one directory together with spring_to_partek.py

Run SPRING to partek
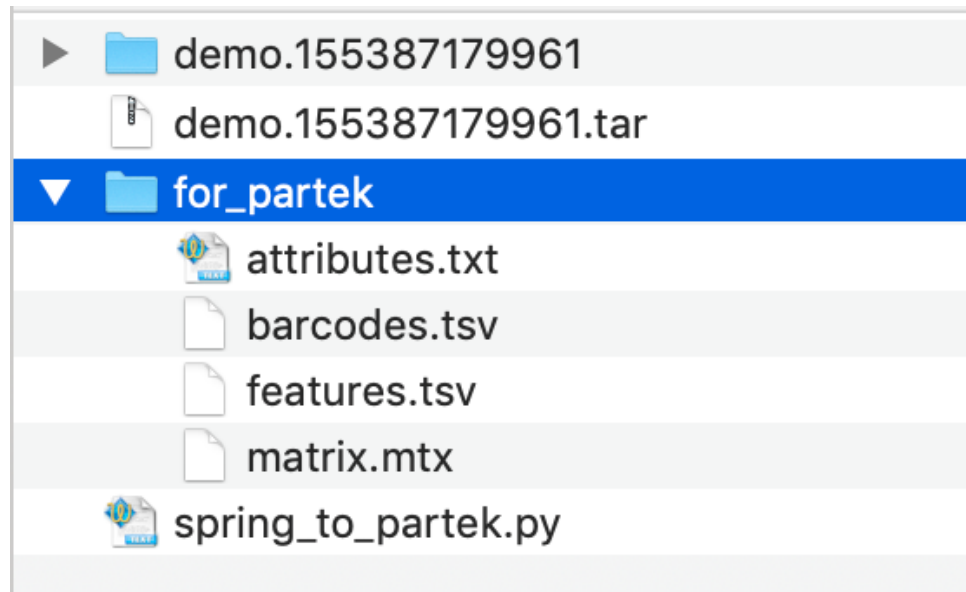
Open Terminal* `>_`

Terminal

Navigate to the folder with spring_to_partek.py

```
cd ~/Desktop/demo
```

Run the python** code to prepare data for partek

```
python spring_to_partek.py "demo.155387179961"
```
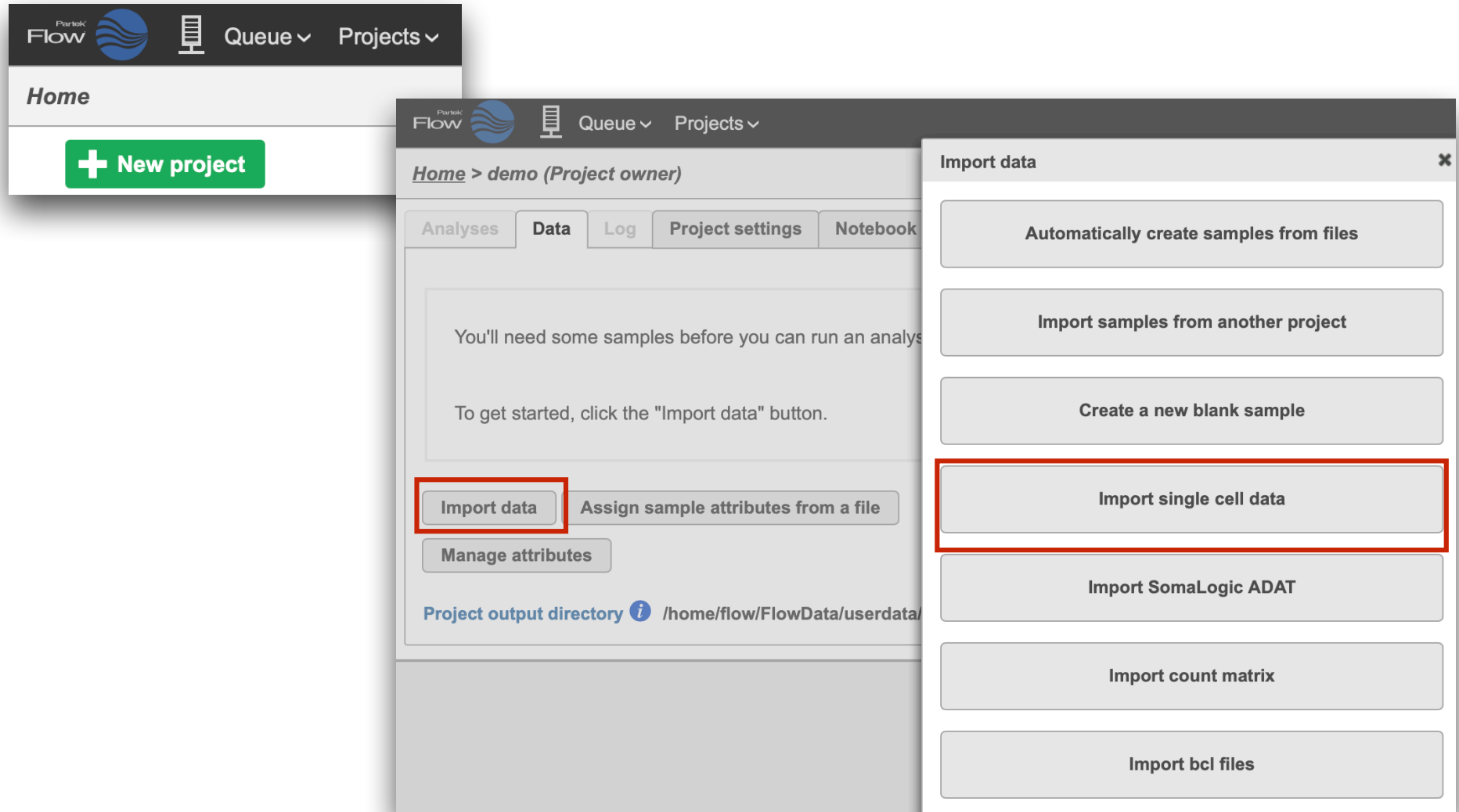
The output is a folder called "for_partek"

```
▶  📁 demo.155387179961
   📄 demo.155387179961.tar
▼  📁 for_partek
      📄 attributes.txt
      📄 barcodes.tsv
      📄 features.tsv
      📄 matrix.mtx
   📄 spring_to_partek.py
```

* Instructions for Mac
** Written for python 3, specifically my python version is: Python 3.6.6 :: Anaconda custom (64-bit)

Upload data to Partek
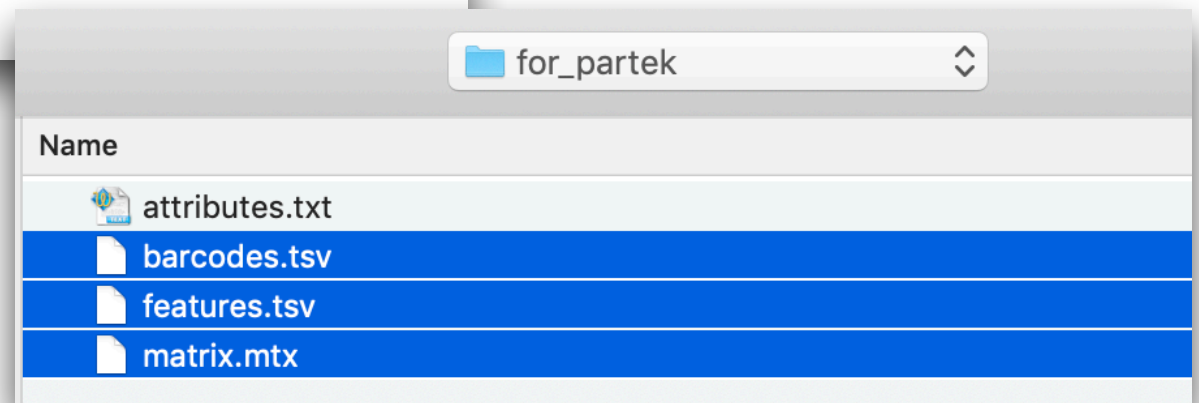
New project > import data > import single cell data

Select 3 files: barcodes.tsv, features.tsv, matrix.mtx
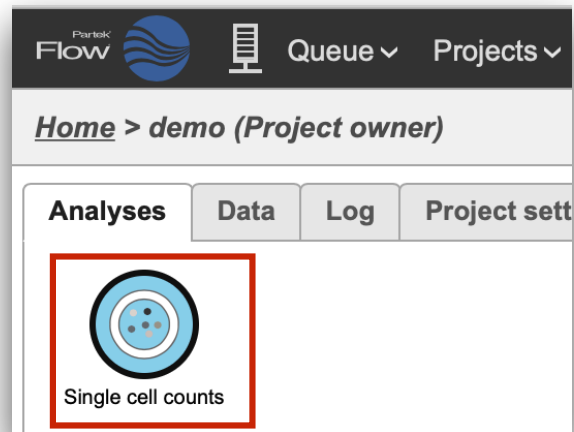**Press "Next"**

Upload data to Partek

Continue with default setting, except for the Raw counts box, counts from spring are not raw, they are normalized.
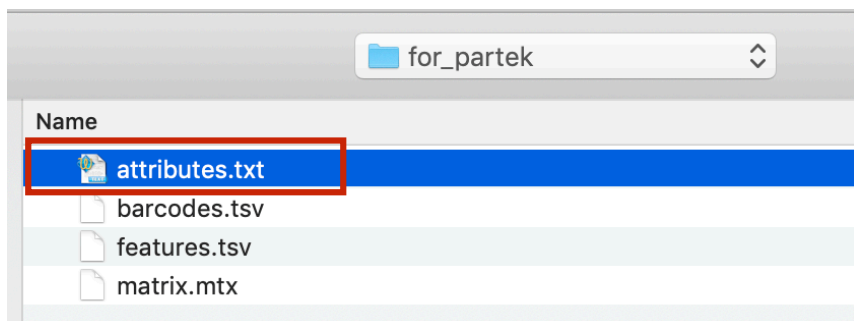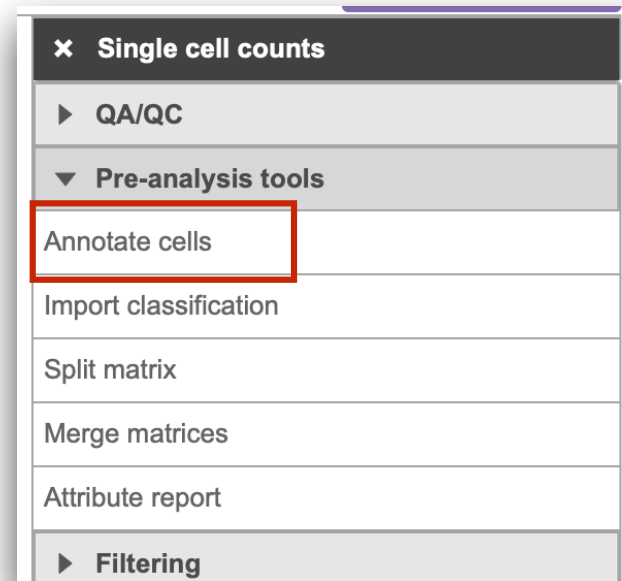Press "Finish".
Wait, check "Queue" for progress.

Upload data to Partek: Attributes from SPRING

Click on node (red rectangle)

Partek Flow

Queue ∨   Projects ∨

Home > demo (Project owner)

Analyses	Data	Log	Project sett

Single cell counts

Under pre-analysis tools, click on Annotate cells

✕ **Single cell counts**

▶ **QA/QC**

▼ **Pre-analysis tools**

Annotate cells

Import classification

Split matrix

Merge matrices

Attribute report

▶ **Filtering**

for_partek

Name

attributes.txt

barcodes.tsv

features.tsv

matrix.mtx

Browse > My computer > choose file > select attributes.txt

Upload data to Partek: Attributes from SPRING

From here, further instructions by Partek:
https://documentation.partek.com/display/FLOWDOC/Annotate+cells

Attribute name	Terms	Import	Attribute type
Cell name	cell_1056, cell_1082, cell_1108,...	☐	Categorical
numeric_P(Erythroid)	0.0, 0.00020563, 0.00024764, 0...	☑	Numeric ⇕
numeric_P(Granulocyte)	0.00012293, 0.0015918, 0.0026...	☑	Numeric ⇕
numeric_P(Lymphoid)	0.0, 0.00021641, 0.0003168, 0....	☑	Numeric ⇕
numeric_P(Dendritic cell)	0.0, 0.0001238, 0.00013700000...	☑	Numeric ⇕
numeric_P(Megakaryocyte)	0.0, 0.00010067, 0.00011106, 0....	☑	Numeric ⇕
numeric_P(Monocyte)	0.0, 0.0001695, 0.01003499999...	☑	Numeric ⇕
numeric_P(Basophil/Mast cell)	0.0, 0.00013663, 0.00014897, 0...	☑	Numeric ⇕
numeric_Total counts	1005.0, 1017.0, 1031.0, 1035.0,...	☑	Numeric ⇕
numeric_Uniform	0.0	☑	Numeric ⇕
Louvain cluster	10, 11, 2, 3, 6, 8	☑	Categorical ⇕
Library	1, 2, 3, 4	☑	Categorical ⇕
Prep Batch	1, 4	☑	Categorical ⇕

The code spring_to_partek.py prepends the prefix "numeric_" to colotracks that were numeric in SPRING. All other colotracks are categorical.

Example: make t-SNE plot with Partek and color by uploaded attributes

Next slides
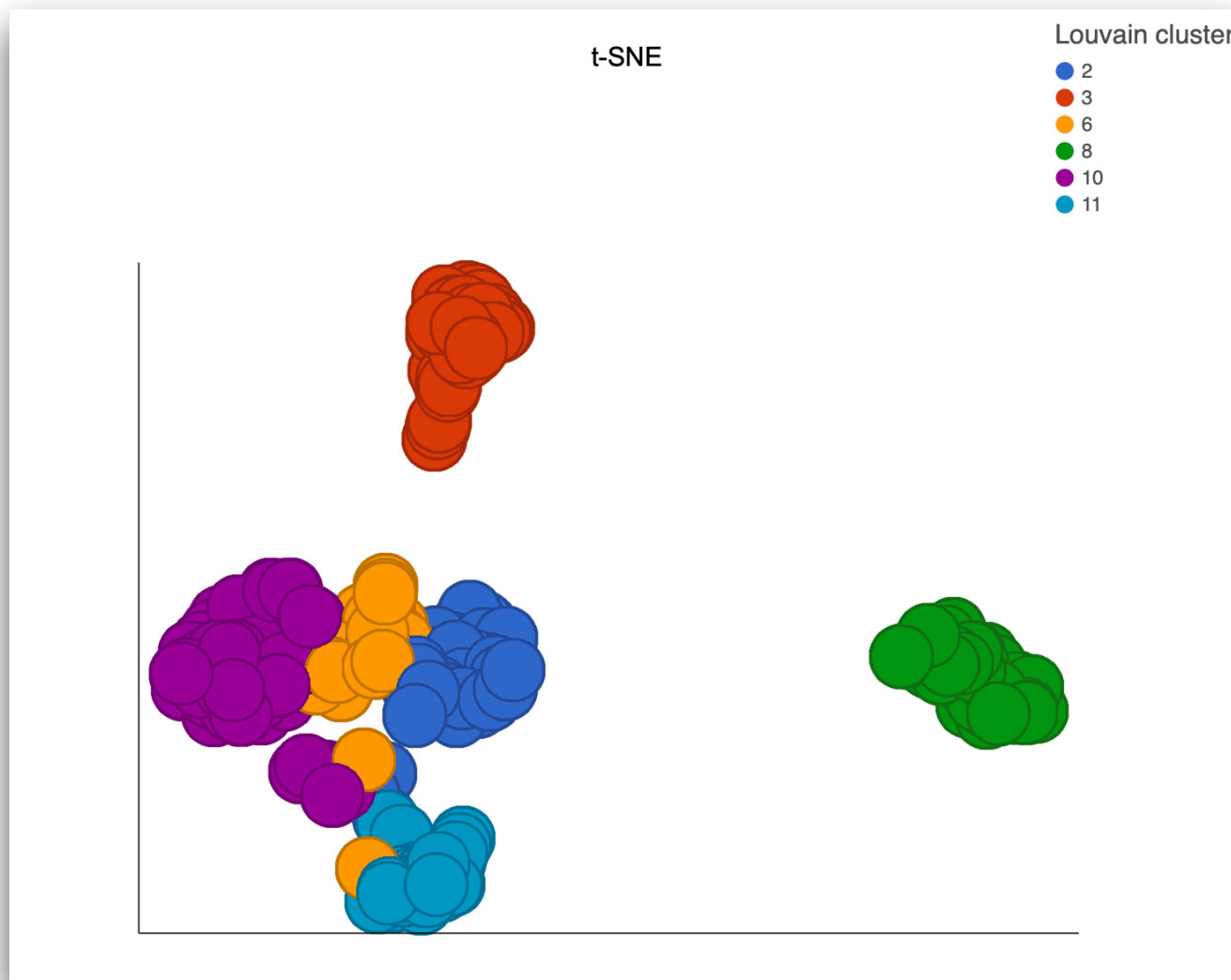
t-SNE by Partek, colotrack "Louvain cluster" from SPRING