

A

1

Begin a task from the navigation menu

2

Run a tool with the ability to customize parameters

3

Visualize results in a plot

4

Customize plot options

5

Suggested next steps

Single Cell Toolkit v2.8.1

Data

QC & Filtering

Normalization & Batch Correction

Feature Selection & Dimensionality Reduction

Clustering

Differential Expression & Cell Type Labeling

Enrichment & Pathway Analysis

Trajectory Analysis

Sample Size Calculator

Curated Workflows

Viewers

Clustering

(help)

Select Algorithm

louvain

Select Input Matrix:

decontX_UMAP

K value:

8

Number of Components:

10

Edge Weight Type:

rank

Name of Clustering Result:

scran_snn_cluster

Run

A scatter plot of the selected low-dimensionality representation of the dataset will be generated, with the selected cluster labeling colored on each dot (cell).
If you are using an expression matrix or subset for calculation, please click on the cog icon on the left to specify the dimensions to plot.

seurat_snn_cluster

1

2

3

4

5

6

7

seuratUMAP_2

10

0

-5

0

5

10

seuratUMAP_1

Next Steps

Marker Selection

Compute and visualize marker genes for each cluster using one of the many integrated statistical frameworks for differential expression:

Go to Find Marker

Pathway Analysis

Explore biological activity or functions with pathway analysis using 'VAM' or 'GSVA' statistical frameworks, or perform GSEA with 'enrichR':

Go to Pathway Analysis

Go to EnrichR

B

1

Select a curated workflow

2

Run workflow pipeline step by step

3

Run a step with the ability to customize parameters

4

Interactively filter and select genes

5

Visualize marker genes

Single Cell Toolkit v2.8.1

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Seurat

(help)

Normalize Data

Highly Variable Genes

Dimensionality Reduction

tSNE/UMAP

Clustering

Find Markers

Options

Compute marker genes that are either differentially expressed or conserved between selected groups and visualize them from the selected plots on right panel.

Select type of markers to identify:

markers between all groups

markers differentially expressed between two selected groups

markers conserved between two selected groups

Select biological phenotype:

Seurat_louvain_Resolution0.8

Select test:

wilcox

Only return positive markers?

Find Markers

Marker Genes

You can view the marker genes in the table below and apply custom filters to filter the table accordingly. A joint heatmap for all the marker genes available in the table is plotted underneath the table. Additional visualizations are plotted for select genes which can be selected by clicking on the rows of the table.

Active Filters

avg_log2FC extremes 60,30

p_val_adj <= 1e-59

Set # of Rows

Add Filter

Remove Filter

Show 6 entries

Showing 55 to 60 of 323 entries

	gene_id	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	cluster1	cluster2
11	CD79A	0	63.8042509222262	0.912	0.042	0	2	all
90	CDBA	1.07451189456944e-95	2.42894356691498	0.495	0.075	3.51773704044142e-91	3	all
275	CDA	3.3190476030206e-67	-54.756767175658	0.598	0.116	1.08658980427689e-62	7	all
98	CDKN1C	1.83943658078755e-225	2.12239749486095	0.509	0.008	6.02194747818228e-221	7	all
40	CEBPB	2.51906335235866e-76	16.1548851753175	0.798	0.273	8.24690960295177e-72	4	all
189	CEBPB	4.8609472846503e-96	-9.11829394454056	0.893	0.286	1.59137692204882e-91	7	all

Export

Previous

1

...

9

10

11

...

54

Next

Heatmap Plot

Marker Gene Plots

Click on the rows of the table above to plot the selected marker genes below!

Ridge Plot

Violin Plot

Feature Plot

Dot Plot

Heatmap Plot

Feature Plot

CD3E

CD79A

UMAP_2

10

0

-10

UMAP_1