

Graph-based Clustering

What is Graph-based clustering?

Graph-based clustering is a method for identifying groups of similar cells or samples. It makes no prior assumptions about the clusters in the data. This means the number, size, density, and shape of clusters does not need to be known or assumed prior to clustering. Consequently, graph-based clustering is useful for identifying clustering in complex data sets such as scRNA-seq.

Running Graph-based clustering

We recommend normalizing your data prior to running Graph-based clustering, but the task will run on any counts data node.

- Click the counts data node
- Click the **Exploratory analysis** section of the toolbox
- Click **Graph-based clustering**
- Configure the parameters
- Click **Finish** to run

Graph-based clustering produces a *Clustering result* data node. The task report lists the cluster results and cluster statistics (Figure 1). If clustering was run with *Split cells by sample* enabled on a single cell counts data node, the cluster results table displays the number of clusters found for each sample and clicking the sample name opens the sample-level report.

Cluster results		
Maximum modularity: 0.863005		
Cluster statistics		
Total number of clusters 9		
Cluster ↑⇅	Size ↑↓	Size % ↑↓
1	1816	23.76%
2	965	12.63%
3	891	11.66%

4	836	10.94%
5	824	10.78%
6	800	10.47%
7	727	9.51%
8	478	6.25%
9	306	4.00%

[Task details](#)

Figure 1. Graph-based clustering task report

Cluster results

The *Maximum modularity* is a measure of the quality of the clustering result. Modularity measures how much cells within a cluster are similar to each other and less similar to cells in other clusters. Higher modularity indicates a better result. Optimal modularity is 1, but may not be attainable for the input data.

Cluster statistics

The total number of clusters is listed along with the number and percentage of cells in each cluster.

The *Clustering result* data node includes the input values for each gene and adds cluster assignment as a new attribute, *Graph-based*, for each observation. If the *Clustering result* data node is visualized by *Scatter plot*, *PCA*, *t-SNE*, or *UMAP*, the plot will be colored by the *Graph-based* attribute (Figure 2).



Figure 2. Visualizing Graph-based clustering results

Basic Graph-based clustering parameters

Clustering algorithm

Choose which version of the Louvain clustering algorithm to use. Options are *Louvain* [1], *Louvain with refinement* [2], and *SLM* [3]. The most recent version is Smart Local Moving (SLM). The default is *Louvain*.

Compute biomarkers will compute features that are highly expressed when comparing each cluster.

Split cells by sample

Chose whether to run Graph-based clustering on all samples together or on each sample individually.

Checking the box will run Graph-based clustering on each sample individually.

Include features where "Feature type" is

This option appears when there are multiple feature types in the input data node (e.g., CITE-Seq data).

Select *Any* to run on all features or pick a feature type.

Advanced Graph-based clustering parameters

Resolution

To increase the number of clusters, increase the resolution (Figure 3). To decrease the number of clusters, decrease the resolution. Default is 1.

A larger number may be more appropriate for larger numbers of cells.

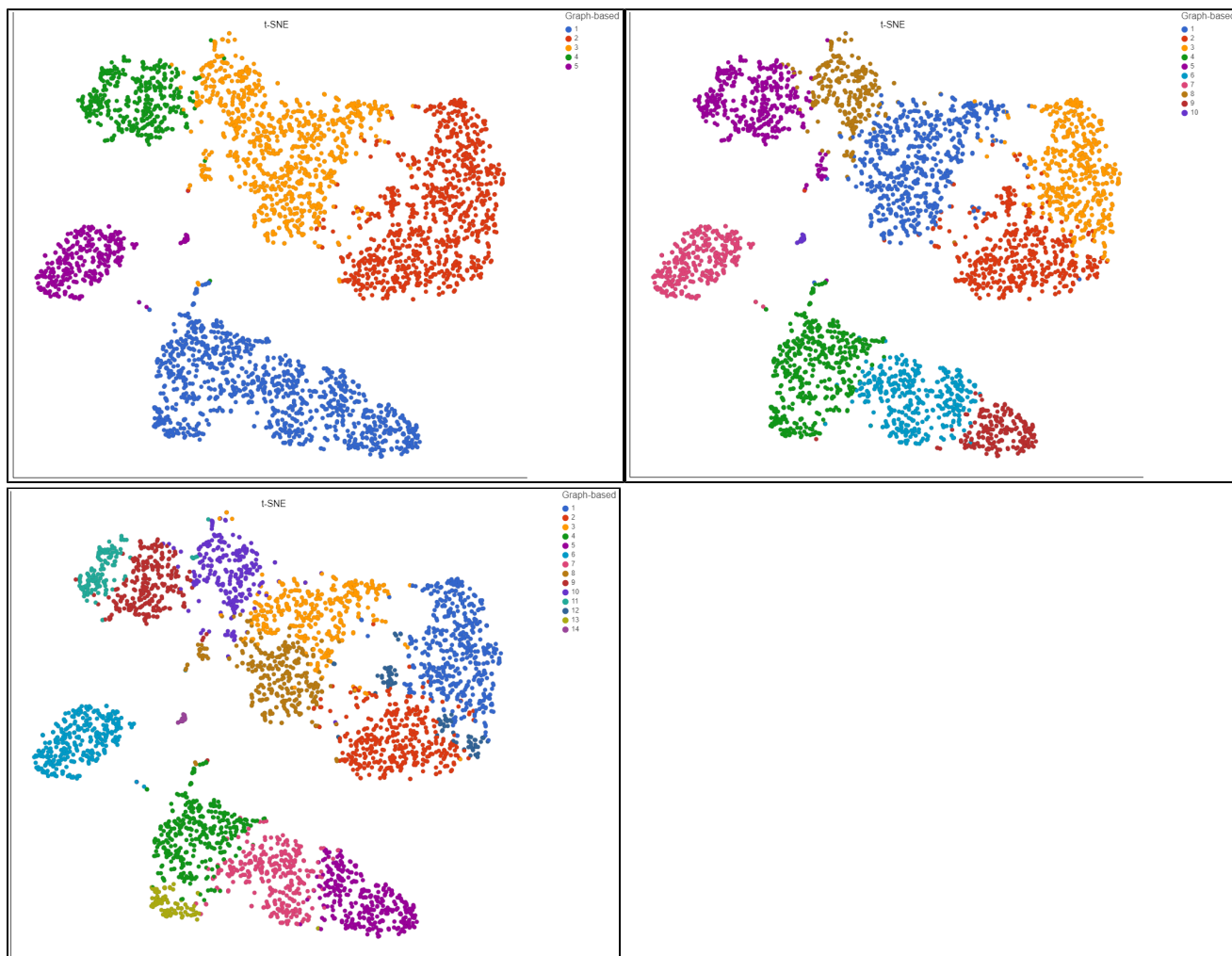


Figure 3. Graph-based clustering results visualized by t-SNE. Colors correspond to clusters. Clustering resolution of 0.3 (left), 1 (center), and 2 (right). Note the number of clusters per resolution

Prune parameter

Removes links between pairs of points if their similarity is below the threshold. Larger values lead to a shorter run time, but can result in many singleton clusters. Default is 0.0.

Number of nearest neighbors

Clustering preserves the local structure of the data by focusing on the distances between each point and its k nearest neighbors. The optimal perplexity depends on the size and density of the data. Generally, a larger and/or more dense data set will benefit from a larger number of nearest neighbors. Increasing the number of nearest neighbors will increase the size of clusters and vice versa (Figure 4). Default is 30. The range of possible values is 3 to 100.

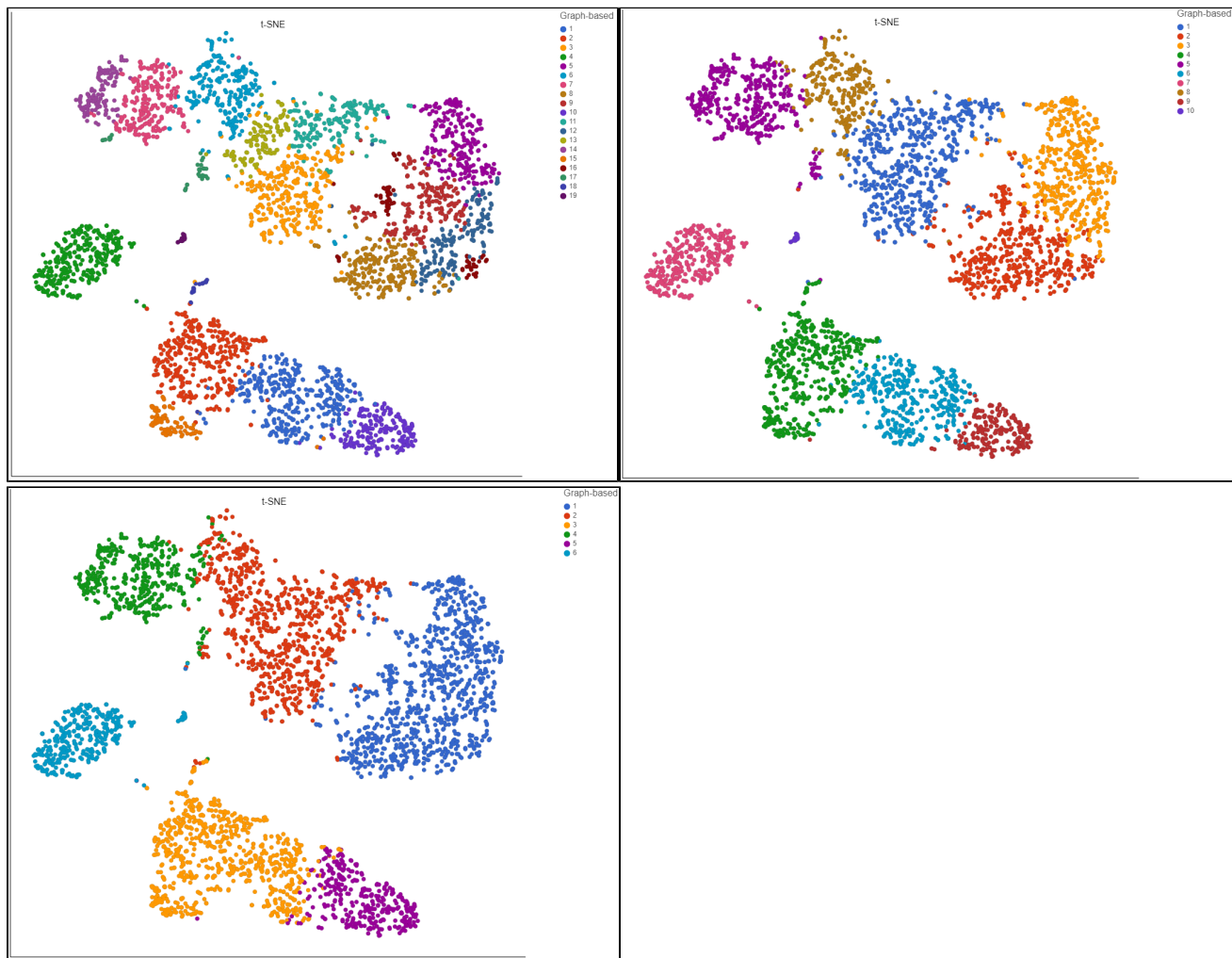


Figure 4. Graph-based clustering results visualized by t-SNE. Colors correspond to clusters. Number of nearest neighbors set to 5 (left), 30 (center), 100 (right).

Scale

This parameter can be used to speed up clustering at the expense of accuracy. Larger scale implies greater accuracy and helps avoid singletons, but takes more time to run. To maximize accuracy, the total count of observations being clustered should be below the product of nearest neighbors and scale. Default is 100,000. The range of possible values is 1 to 100,000.

Modularity function

The modularity function measures the overall quality of clustering. Graph-based clustering amounts to finding a local maximum of the modularity function. Possibilities are *Standard* [4] and *Alternative* [5]. Default is *Standard*.

Number of random starts

The clustering result depends on the order observations are considered. Each random start corresponds to a different order and result. A larger number of random starts can deliver a better result because the result with the highest quality (modularity) out of all of the random starts is chosen. Increasing the number of random starts will increase the run time. The range of possible values is 3 to 1,000. The default is 100.

Random seed

The random seed is used in the random starts portion of the algorithm. Using a different seed might give a better result. Use the same random seed to reproduce results. Default is 0.

Number of iterations per random start

To maximize modularity, clustering proceeds iteratively by moving individual points, clusters, or subsets of points within clusters. A larger number of iterations can give better results, but will take longer to run. Default is 10.

Minimal cluster size

Clusters smaller than the minimal cluster size value will be merged with a nearby cluster unless they are completely isolated. To avoid isolation, set the prune parameter to zero (default) and the scale parameter to the maximum (default). Default is 1.

Sequential random starts

Enable this option to use the slower sequential ordering of random starts. Default is disabled.

Nearest Neighbor Type

Different methods for determining nearest neighbors. The K nearest neighbors (K-NN) algorithm is the standard. The NN-Descent algorithm is used by UMAP and is an alternative. Default is *K-NN*.

Distance metric

If NN-Descent is chosen for Nearest Neighbor Type, the metric to use when determining distance between data points in high dimensional space can be set. Options are *Euclidean*, *Manhattan*, *Chebyshev*, *Canberra*, *Bray Curtis*, and *Cosine*. Default is *Euclidean*.

PCA: Number of principal components

Graph-based clustering uses principal components as its input. The number of principal components to use is set here.

We recommend using the PCA task to determine the optimal number of principal components for your data. Default is 100.

PCA: Features contribute

Options are *equally* or *by variance*. Feature values can be standardized prior to PCA so that the contribution of each feature does not depend on its variance. To standardize, choose *equally*. To take variance into account and focus on the most variable features, choose *by variance*. Default is *by variance*.

Normalization: Log transform data

You can choose to log transform the data prior to running PCA as part of Graph-based clustering. Default is disabled.

Normalization: Log base

If you are normalizing the data, choose a log base. Default is 2 when *Log transform data* is enabled.

Normalization: Log offset

If you are normalizing the data, choose an offset. Default is 1 when *Log transform data* is enabled.

References

- [1] Blondel, V. D., Guillaume, J. L., Lambiotte, R., & Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of statistical mechanics: theory and experiment*, 2008(10), P10008.
- [2] Rotta, R., & Noack, A. (2011). Multilevel local search algorithms for modularity clustering. *Journal of Experimental Algorithmics (JEA)*, 16, 2-3.
- [3] Waltman, L., & Van Eck, N. J. (2013). A smart local moving algorithm for large-scale modularity-based community detection. *The European Physical Journal B*, 86(11), 471.
- [4] Newman, M. E., & Girvan, M. (2004). Finding and evaluating community structure in networks. *Physical review E*, 69(2), 026113.
- [5] Traag, V. A., Van Dooren, P., & Nesterov, Y. (2011). Narrow scope for resolution-limit-free community detection. *Physical Review E*, 84(1), 016114.



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