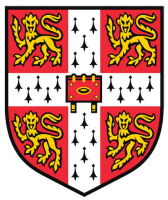

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Clustering

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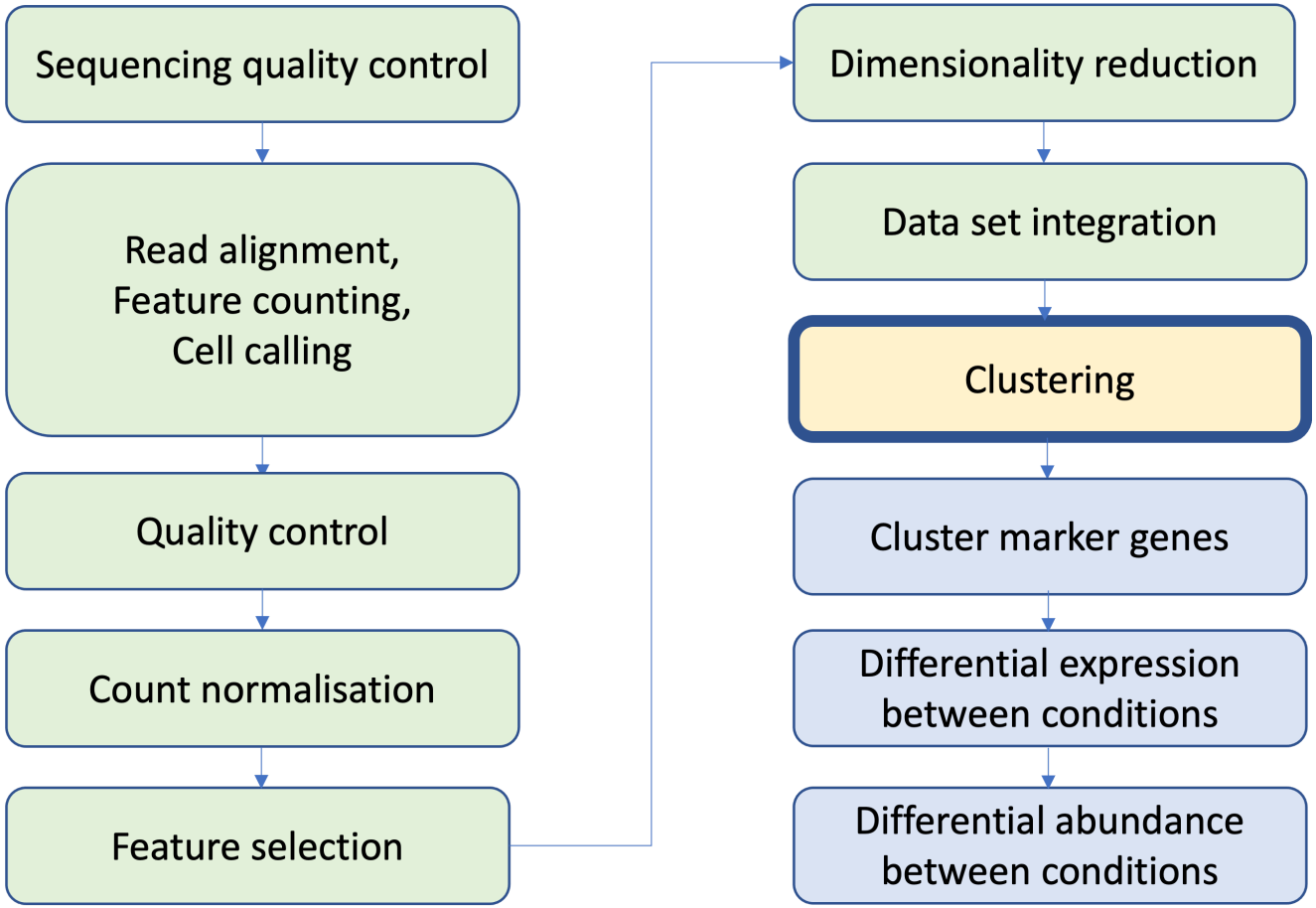
January 2023

Single Cell RNAseq Analysis Workflow



Motivation

The data has been QC'd, normalized, and batch corrected.

We can now start to understand the dataset by identifying cell types. This involves two steps:

- unsupervised clustering: identification of groups of cells based on the similarities of the transcriptomes without any prior knowledge of the labels usually using the PCA output
- annotation of cell-types based on transcription profiles

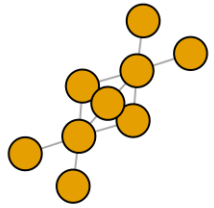
Graph-based clustering

Pros

- fast and memory efficient (no distance matrix for all pairs of cells) compared to hierachical clustering
- no assumptions on the shape of the clusters or the distribution of cells within each cluster compared to e.g. k-means or gaussian mixture models
- no need to specify a number of clusters to identify

Cons

- loss of information beyond neighboring cells, which can affect community detection in regions with many cells.



The steps of involved:

1. Identify edges between nodes (cells) to generate a graph
2. Weight the edges with a similarity score
3. Identify clusters/communities in the weighted graph

Making a graph

Nearest-Neighbour (NN) graph:

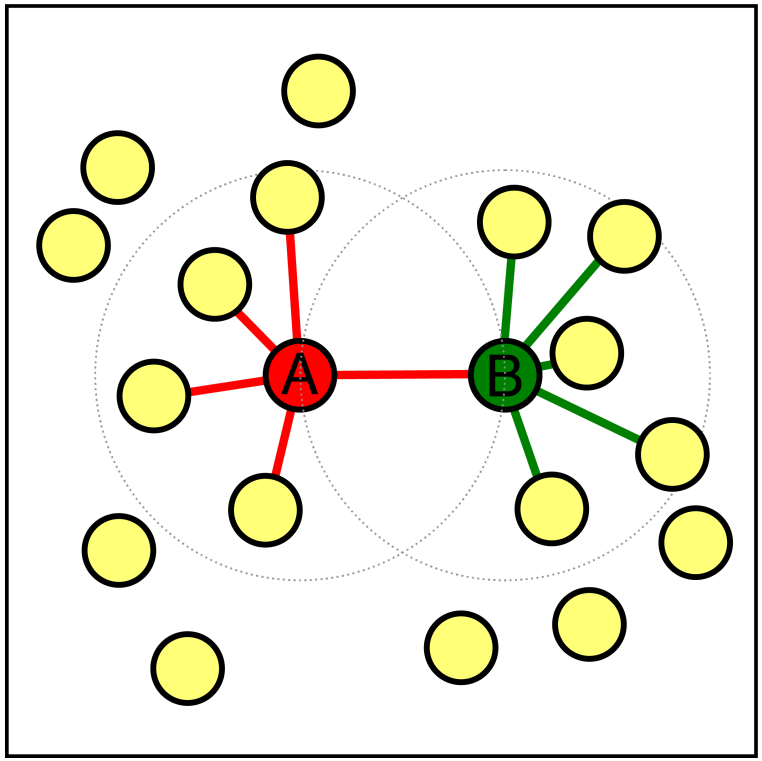
- cells as nodes
- their similarity as edges

In a NN graph two nodes (cells), say A and B, are connected by an edge if:

- the distance between them (in e.g. principal component space) is amongst the **k** smallest distances (here k = 5) from A to other cells, (**K**NN)

or

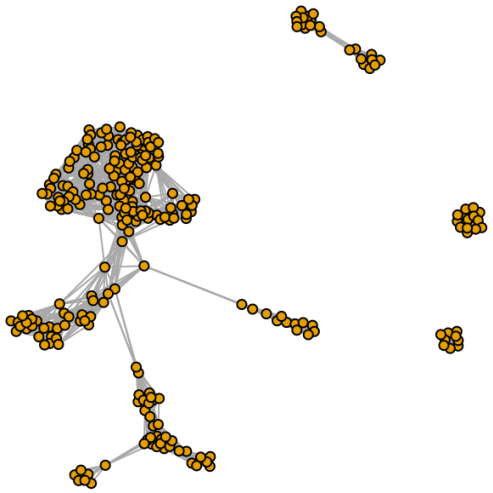
- In a **shared**-NN graph (**S**NN) two cells are connected by an edge if any of their nearest neighbors are shared (n.b. in Seurat this is different)



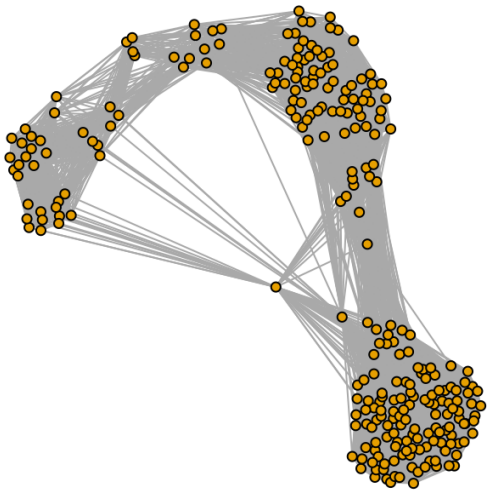
Once edges have been defined, they can be weighted. By default the weights are calculated using the 'rank' method which relates to the highest ranking of their shared neighbours.

Making a graph

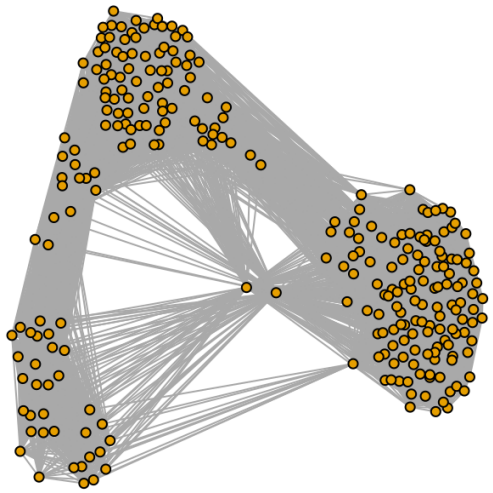
Example with different numbers of neighbours (k):



5-NN



15-NN



25-NN

Identifying communities/clusters

Here we will address three community detection algorithms: **walktrap**, **louvain** and **leiden**.

Modularity

These methods rely on the 'modularity' metric to determine a good clustering.

For a given partition of cells into clusters, modularity measures how separated clusters are from each other. This is based on the difference between the observed and expected (i.e. random) weight of edges within and between clusters. For the whole graph, the closer to 1 the better.

Walktrap

The walktrap method relies on short random walks (a few steps) through the network. These walks tend to be 'trapped' in highly-connected regions of the network. Node similarity is measured based on these walks.

- Nodes are first each assigned their own community.
- Pairwise distances are computed and the two closest communities are grouped.
- These steps are repeated a given number of times to produce a dendrogram.
- Hierarchical clustering to optimise partition based on modularity.

Identifying communities/clusters - Louvain

Nodes are also first assigned their own community.

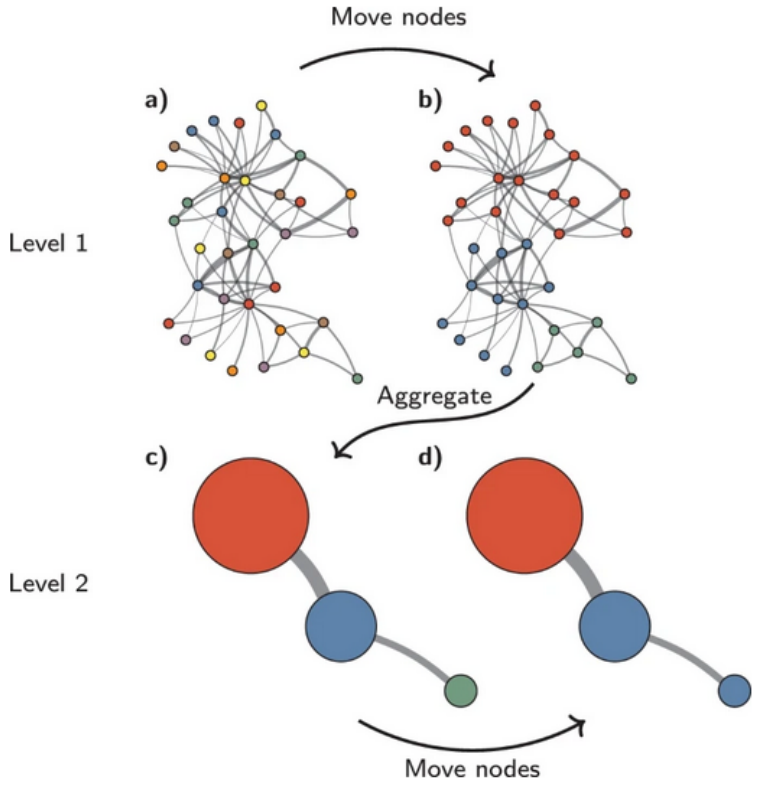
Two-step iterations:

- nodes are re-assigned one at a time to the community for which they increase modularity the most,
- a new, 'aggregate' network is built where nodes are the communities formed in the previous step.

This is repeated until modularity stops increasing.

(Blondel et al, Fast unfolding of communities in large networks)

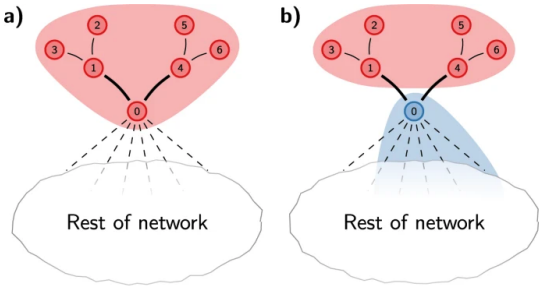
(Traag et al, From Louvain to Leiden: guaranteeing well-connected communities)



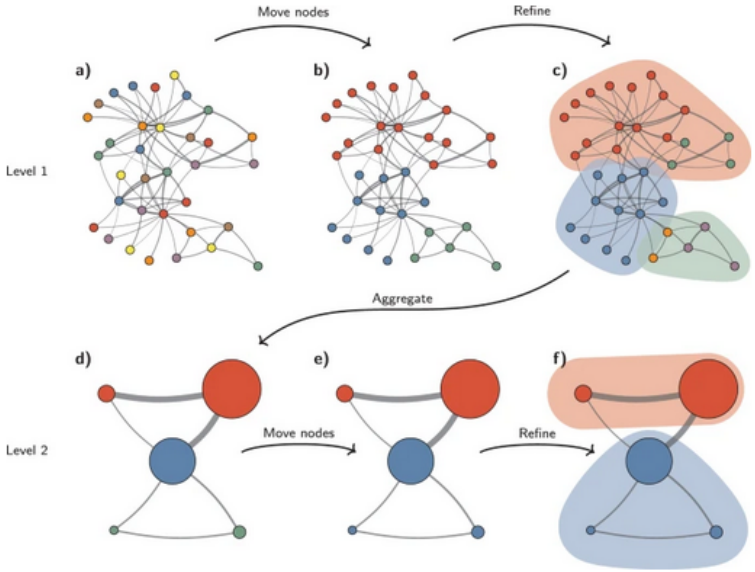
Identifying communities/clusters - Leiden

There is an issue with the Louvain method - some communities may become disconnected.

The Leiden method improves on the Louvain method by guaranteeing that at each iteration clusters are connected and well-separated. The partitioning is refined (step2) before the aggregate network is made.



Disconnected community. Consider the partition shown in (**a**). When node 0 is moved to a different community, the red community becomes internally disconnected, as shown in (**b**). However, nodes 1–6 are still locally optimally assigned, and therefore these nodes will stay in the red community.

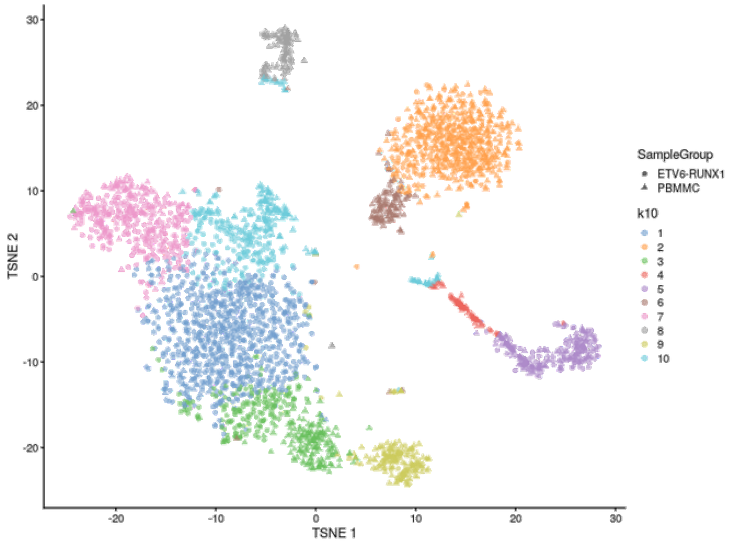


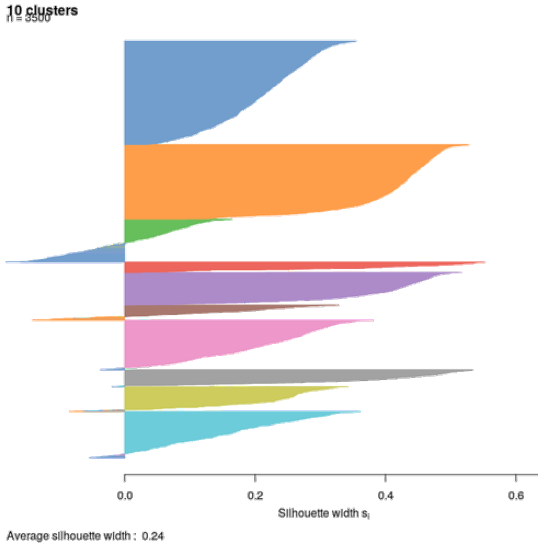
Separatedness - silhouette width

Silhouette width is an alternative to modularity for determining how well clustered the cells are.

```
((mean distance to cells in next closest cluster) - (mean distance to other cells in same cluster))
/ biggest of those means
```

Cells with a large positive width are close to cells in their cluster, while cells with a negative silhouette width are closer to cells of another cluster.





Is there a "correct" clustering?

Clustering, like a microscope, is a tool to explore the data.

We can zoom in and out by changing the resolution of the clustering parameters, and experiment with different clustering algorithms to obtain alternative perspectives on the data.

Asking for an unqualified "best" clustering is akin to asking for the best magnification on a microscope.

A more relevant question is "how well do the clusters approximate the cell types or states of interest?". Do you want:

- resolution of the major cell types?
- Resolution of subtypes?
- Resolution of different states (e.g., metabolic activity, stress) within those subtypes?

Explore the data, use your biological knowledge!

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