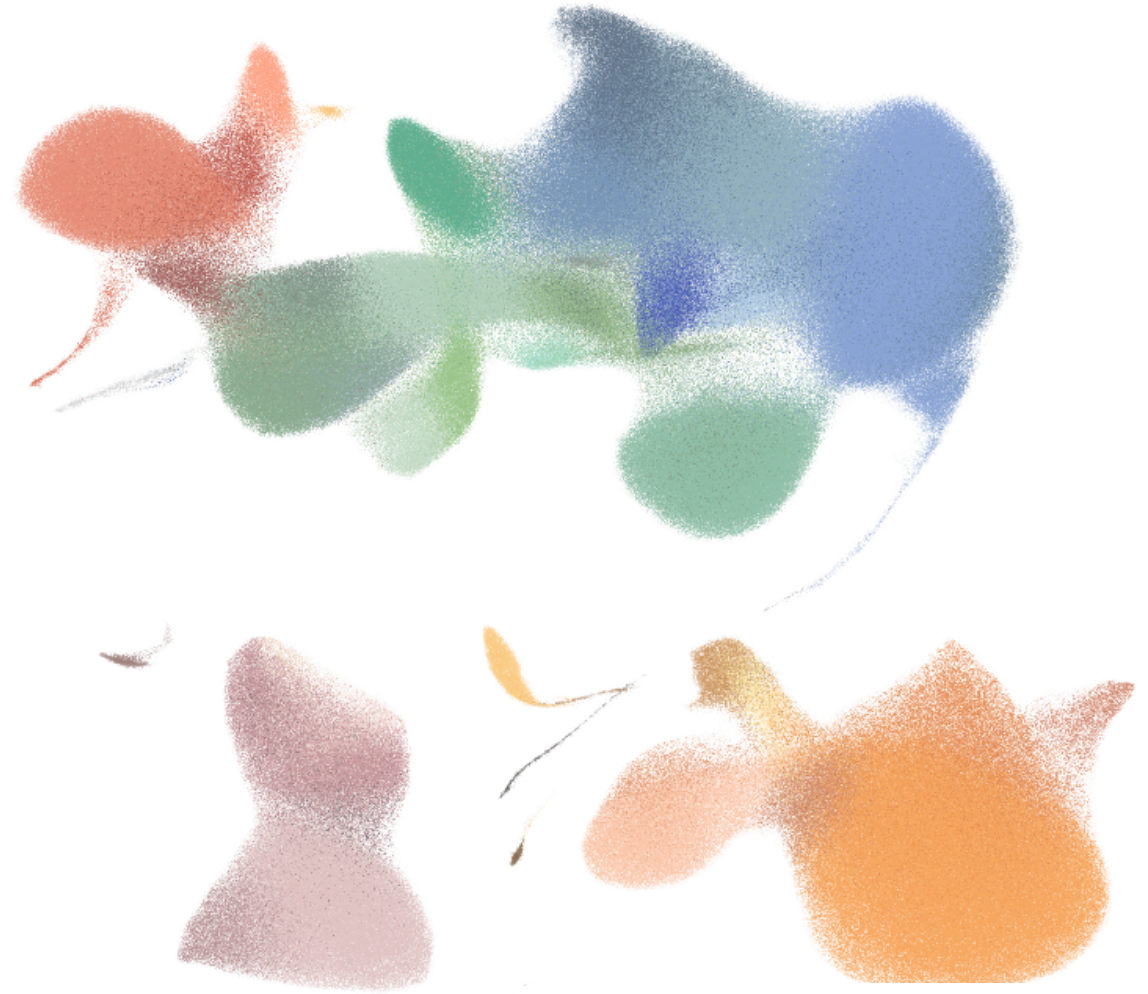


# Clustering

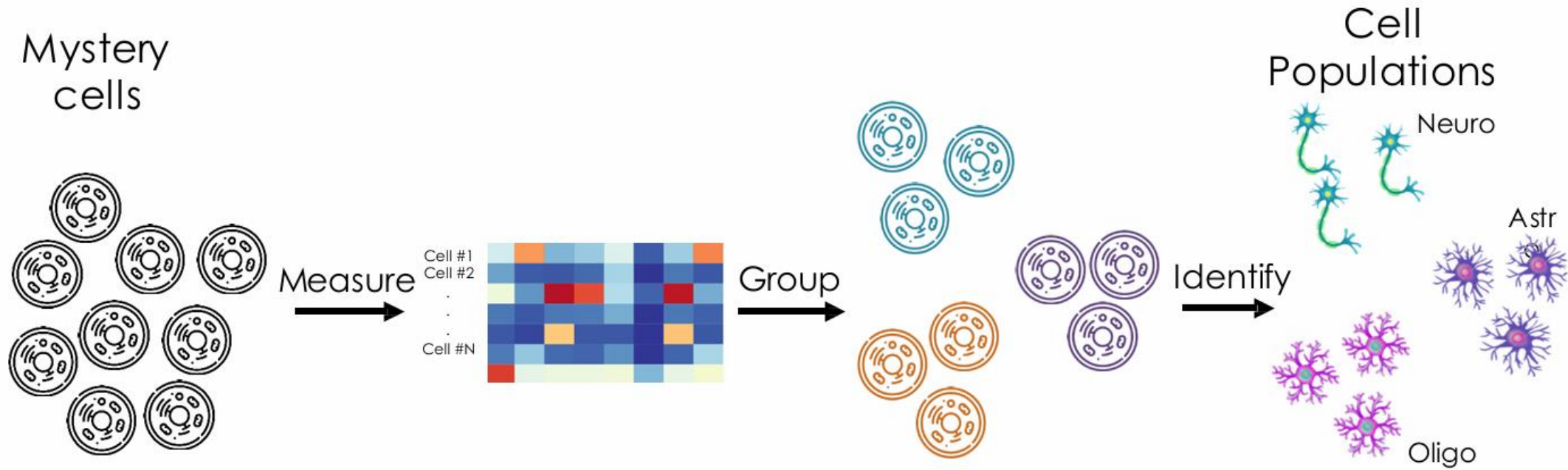
*Yusuf Caglar Odabasi*

*December 1.-3. 2025*

**Course on scRNA-seq Data Analysis**



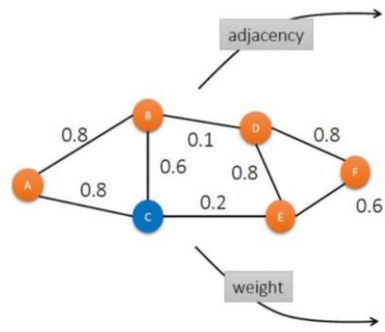
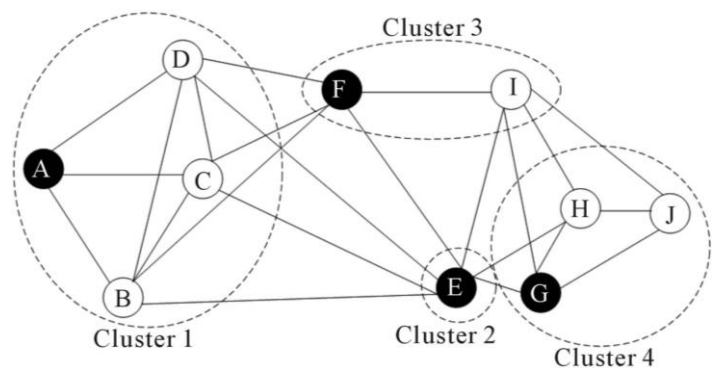
## Clustering



The goal of clustering is to group cells with similar gene expression profiles

# Concept of clustering

Graph-based  
clustering

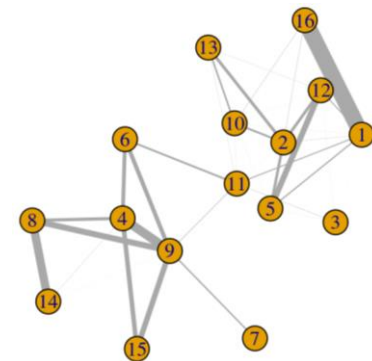


A =

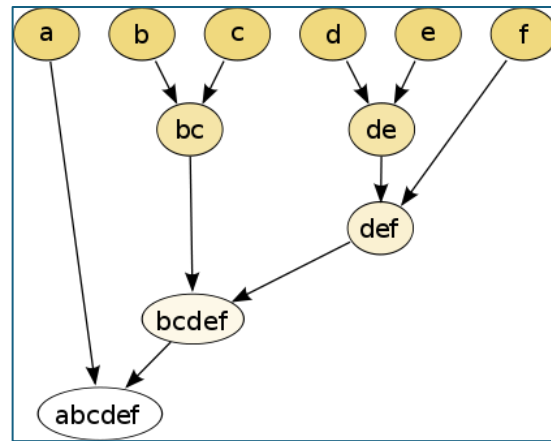
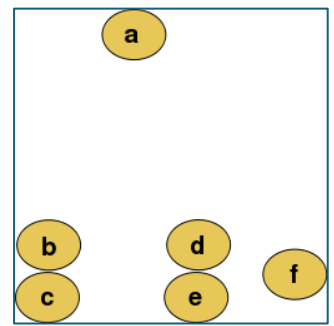
	A	B	C	D	E	F
A	0	1	1	0	0	0
B	1	0	1	1	0	0
C	1	1	0	0	1	0
D	0	1	0	0	1	1
E	0	0	1	1	0	1
F	0	0	0	1	1	0

W = A

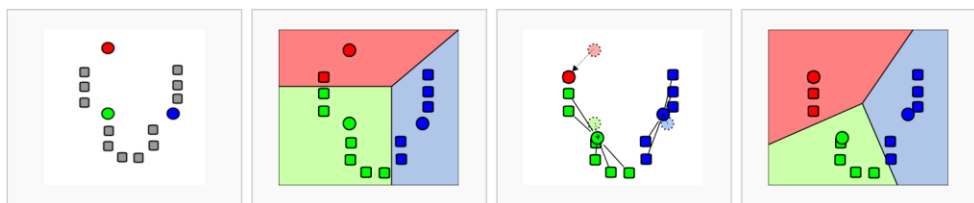
	A	B	C	D	E	F
A	0	0.8	0.8	0	0	0
B	0.8	0	0.6	0.1	0	0
C	0.8	0.6	0	0	0.2	0
D	0	0.1	0	0	0.8	0.8
E	0	0	0.2	0.8	0	0.6
F	0	0	0	0.8	0.6	0



Hierarchical  
clustering



K-means  
clustering



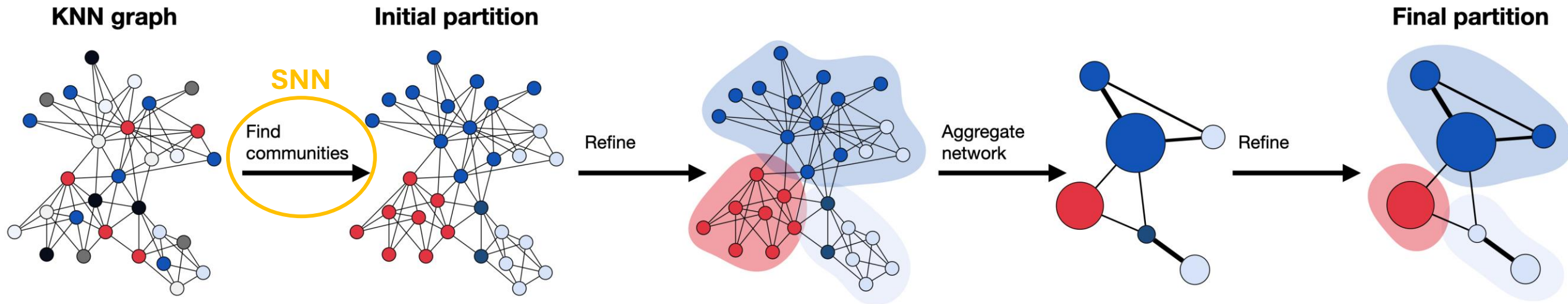
## Graph-based clustering

- K-nearest neighbour (KNN) graph based on the euclidean distance in PCA space.

Two vertices  $p$  and  $q$  are connected by an edge, if the distance between  $p$  and  $q$  is among the  $k$ -th smallest distances from  $p$  to other nodes.

- Shared-nearest neighbour (SNN) graph

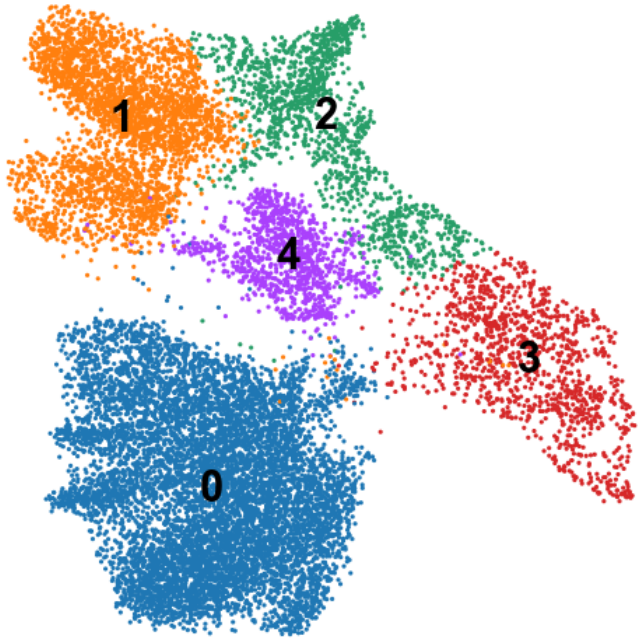
For each pair of cells (nodes), the number of shared neighbours is counted (according to the KNN graph). An edge is created between two cells if they share a sufficient number of nearest neighbours (above a certain threshold).



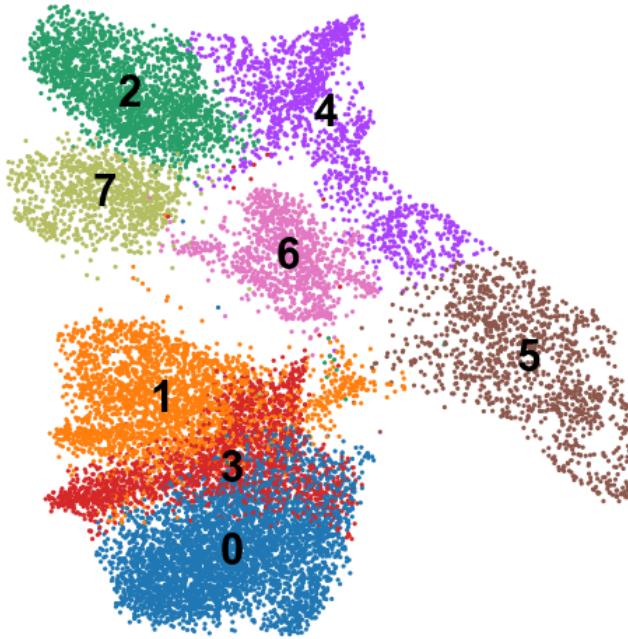
Leiden and Louvain



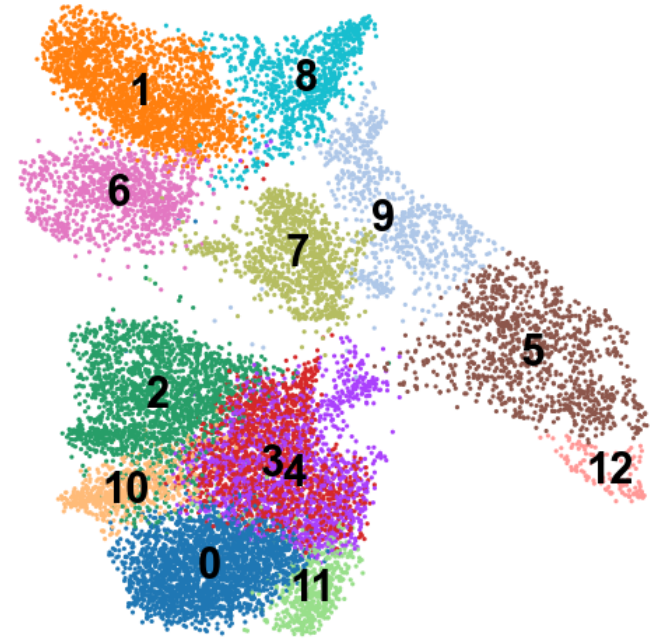
leiden\_res0\_25



leiden\_res0\_5



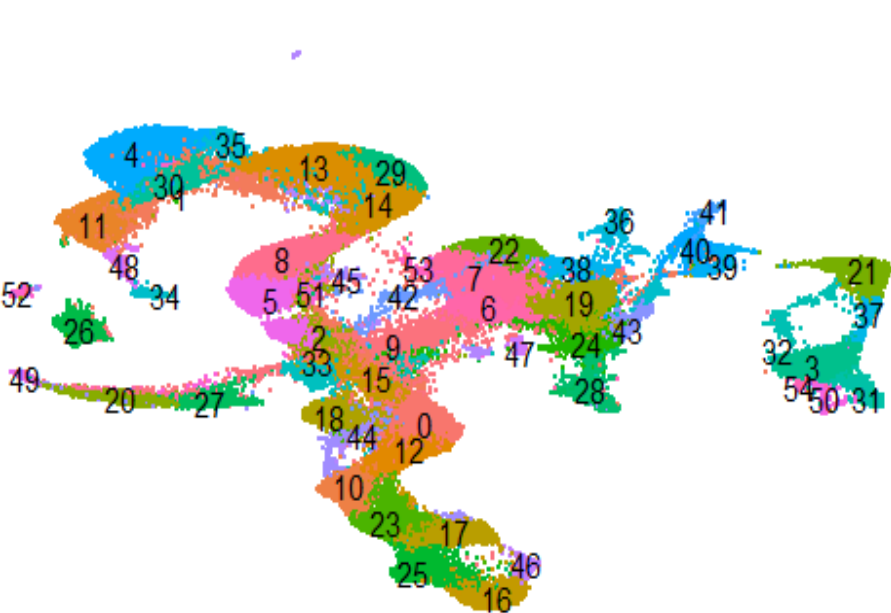
leiden\_res1



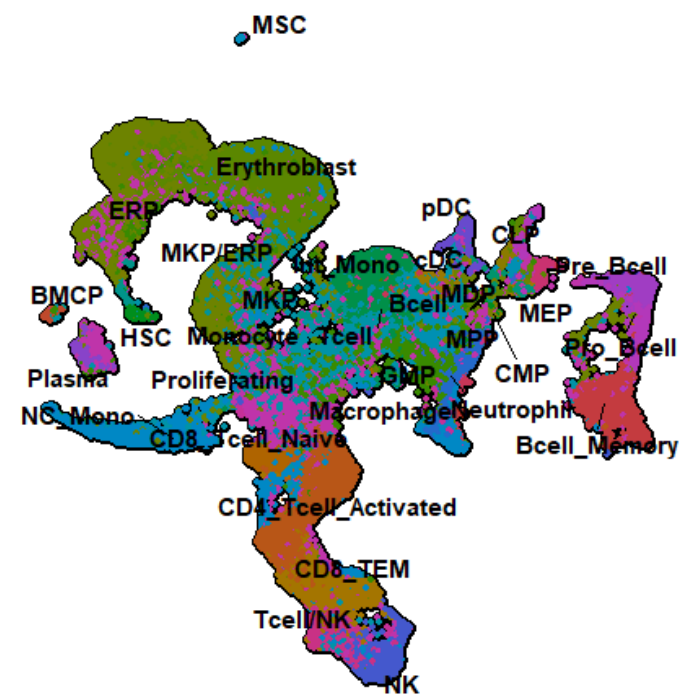
There is not a correct number of clusters, it will depend on the context and biological question



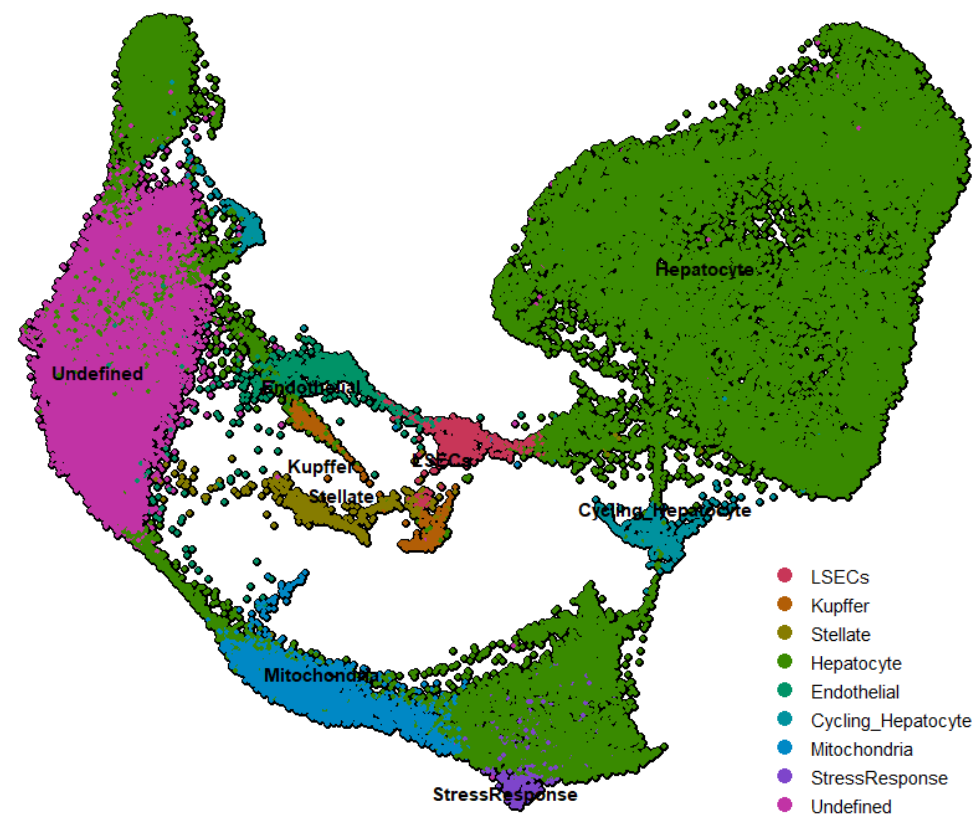
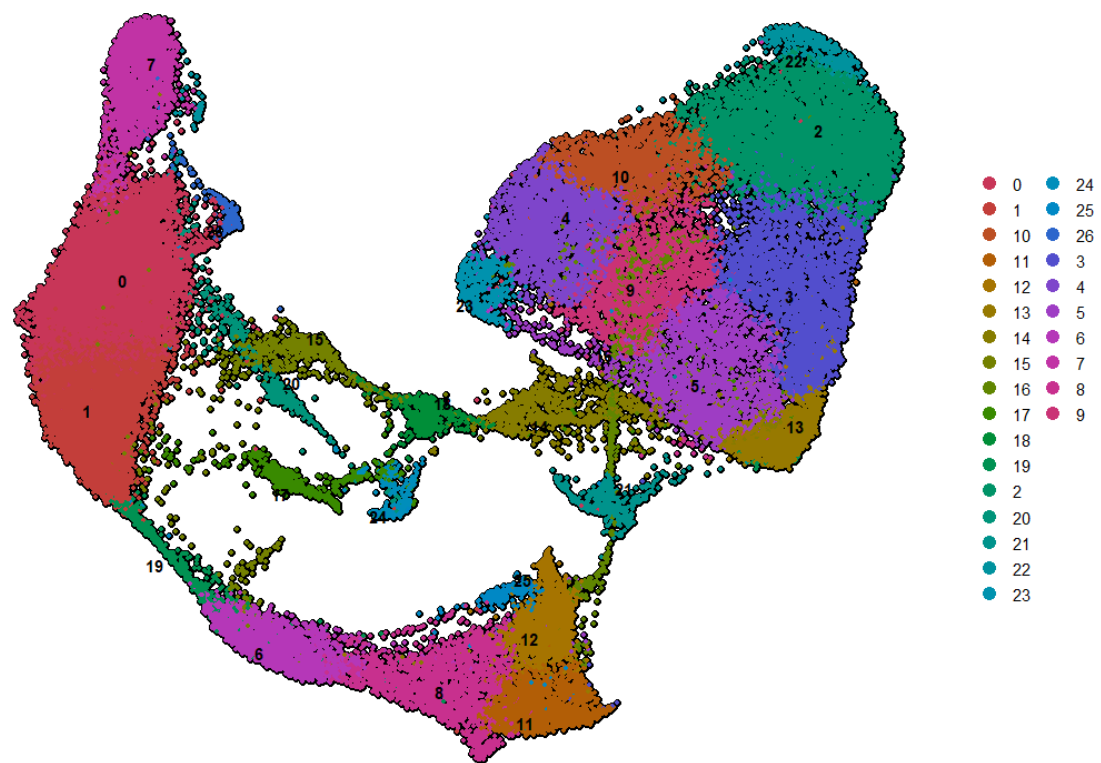
- BOD17-1
- BOD17-3
- BOD18KV
- BOD19-1
- BOD20-3
- BOD21-3
- BOD22-1
- OBE-DIA 1-1
- OBE-DIA 2-1



- |      |      |      |
|------|------|------|
| ● 0  | ● 26 | ● 43 |
| ● 1  | ● 27 | ● 44 |
| ● 10 | ● 28 | ● 45 |
| ● 11 | ● 29 | ● 46 |
| ● 12 | ● 3  | ● 47 |
| ● 13 | ● 30 | ● 48 |
| ● 14 | ● 31 | ● 49 |
| ● 15 | ● 32 | ● 5  |
| ● 16 | ● 33 | ● 50 |
| ● 17 | ● 34 | ● 51 |
| ● 18 | ● 35 | ● 52 |
| ● 19 | ● 36 | ● 53 |
| ● 2  | ● 37 | ● 54 |
| ● 20 | ● 38 | ● 6  |
| ● 21 | ● 39 | ● 7  |
| ● 22 | ● 4  | ● 8  |
| ● 23 | ● 40 | ● 9  |
| ● 24 | ● 41 |      |
| ● 25 | ● 42 |      |



- |                       |                      |
|-----------------------|----------------------|
| ● Bcell               | ● MKP                |
| ● Bcell_Memory        | ● MKP/ERP            |
| ● BMCP                | ● Monocyte           |
| ● CD4_Tcell_Activated | ● MPP                |
| ● CD8_Tcell_Naive     | ● MSC                |
| ● CD8_TEM             | ● NC_Mono            |
| ● cDC                 | ● Neutrophil         |
| ● CLP                 | ● NK                 |
| ● CMP                 | ● pDC                |
| ● ERP                 | ● Plasma             |
| ● Erythroblast        | ● Pre_Bcell          |
| ● GMP                 | ● Pro_Bcell          |
| ● HSC                 | ● Proliferating      |
| ● Int_Mono            | ● Tcell              |
| ● Macrophage          | ● Tcell/NK           |
| ● MDP                 | ● Transitional_Bcell |
| ● MEP                 |                      |



- [https://satijalab.org/seurat/articles/integration\\_introduction](https://satijalab.org/seurat/articles/integration_introduction)
- [https://www.sc-best-practices.org/cellular\\_structure/integration.html](https://www.sc-best-practices.org/cellular_structure/integration.html)
- <https://www.singlecellcourse.org/biological-analysis.html#clustering-introduction>
- <https://bioconductor.org/books/3.12/OSCA/clustering.html#k-means-clustering>
- [https://github.com/quadbio/scRNAseq\\_analysis\\_vignette/blob/master/Tutorial.md#step-2-3-data-integration-using-liger](https://github.com/quadbio/scRNAseq_analysis_vignette/blob/master/Tutorial.md#step-2-3-data-integration-using-liger)