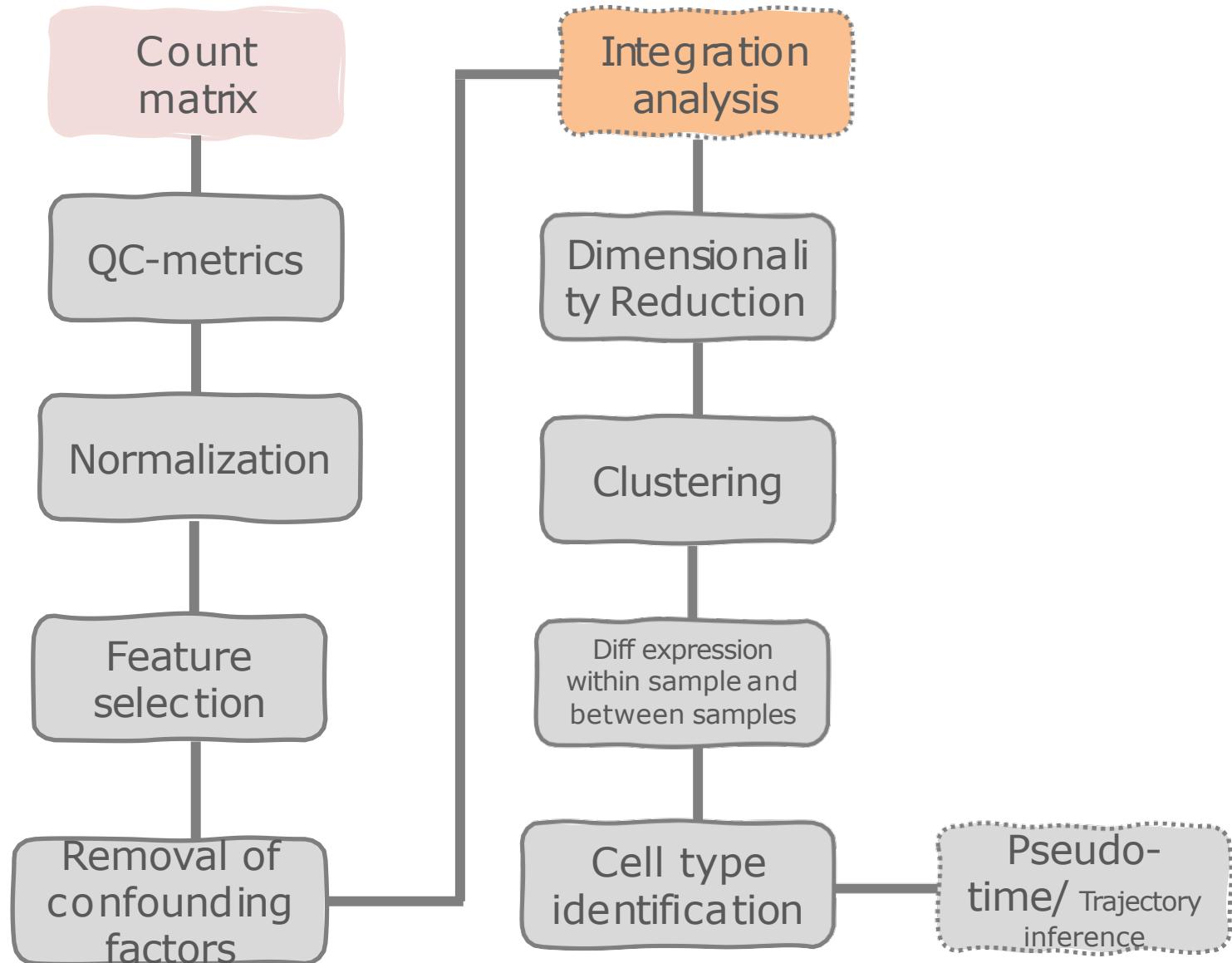


SIB
Swiss Institute of
Bioinformatics

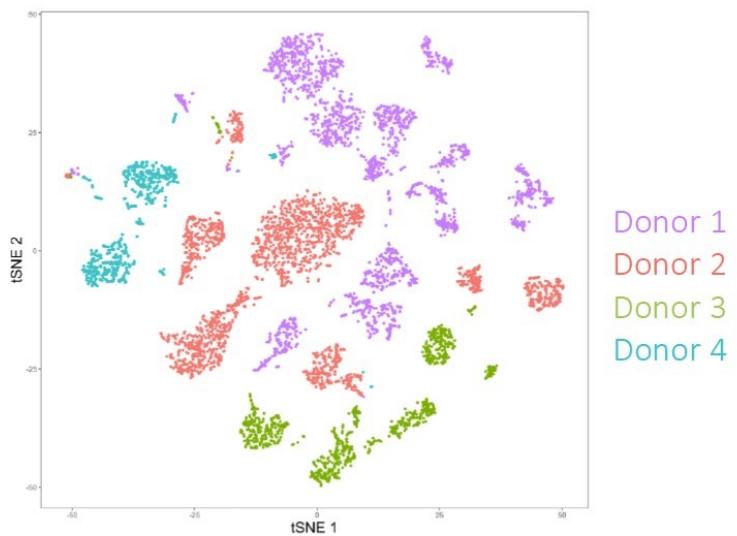
Day 2: Single cell RNA sequencing: The bioinformatic downstream analysis

Geert van Geest, Rachel Marcone, Tania Wyss

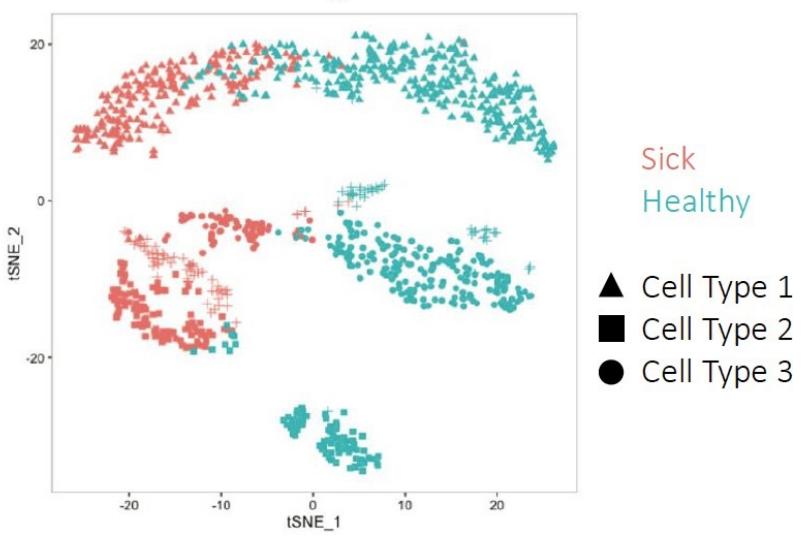


Integration analysis

- Why do we integrate?



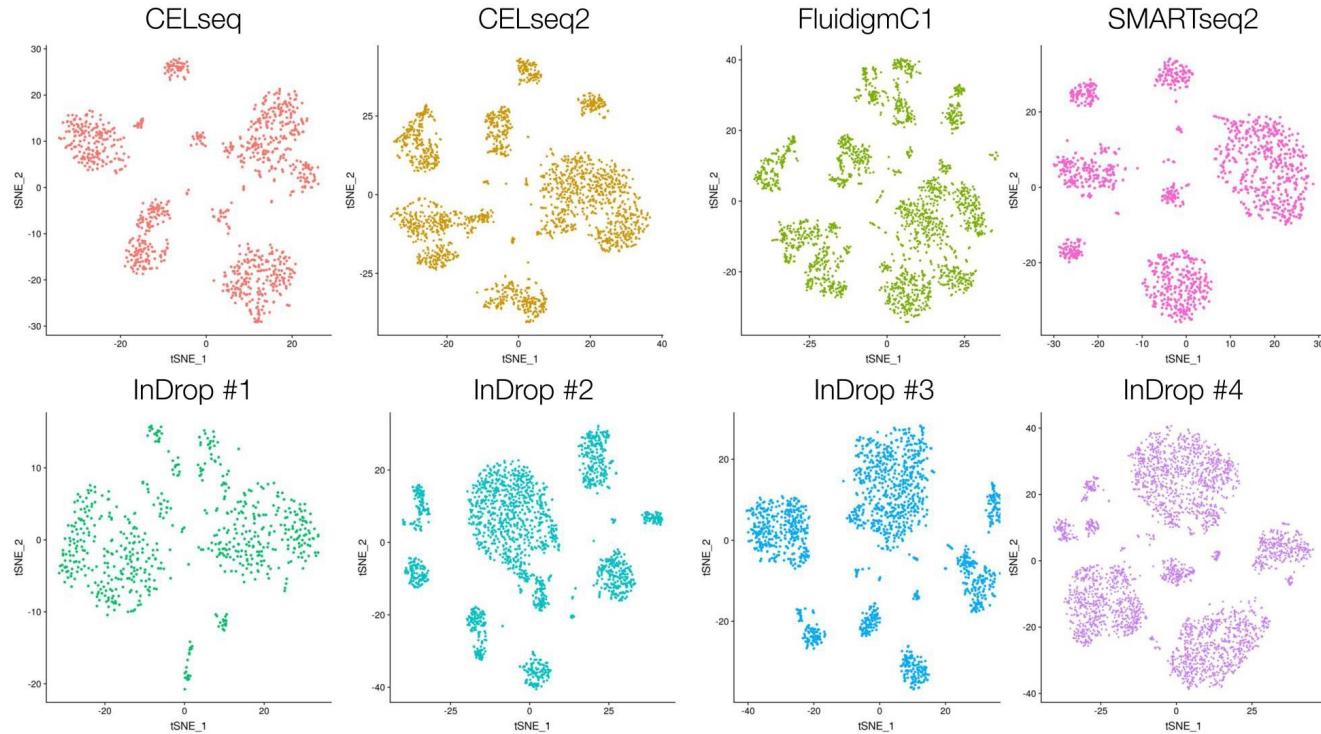
Same tissue from different donors



Cross condition comparisons

Integration analysis

- 8 maps from the human pancreas (Seurat tutorial)



Baron et al. 2016, *Cell Syst.*

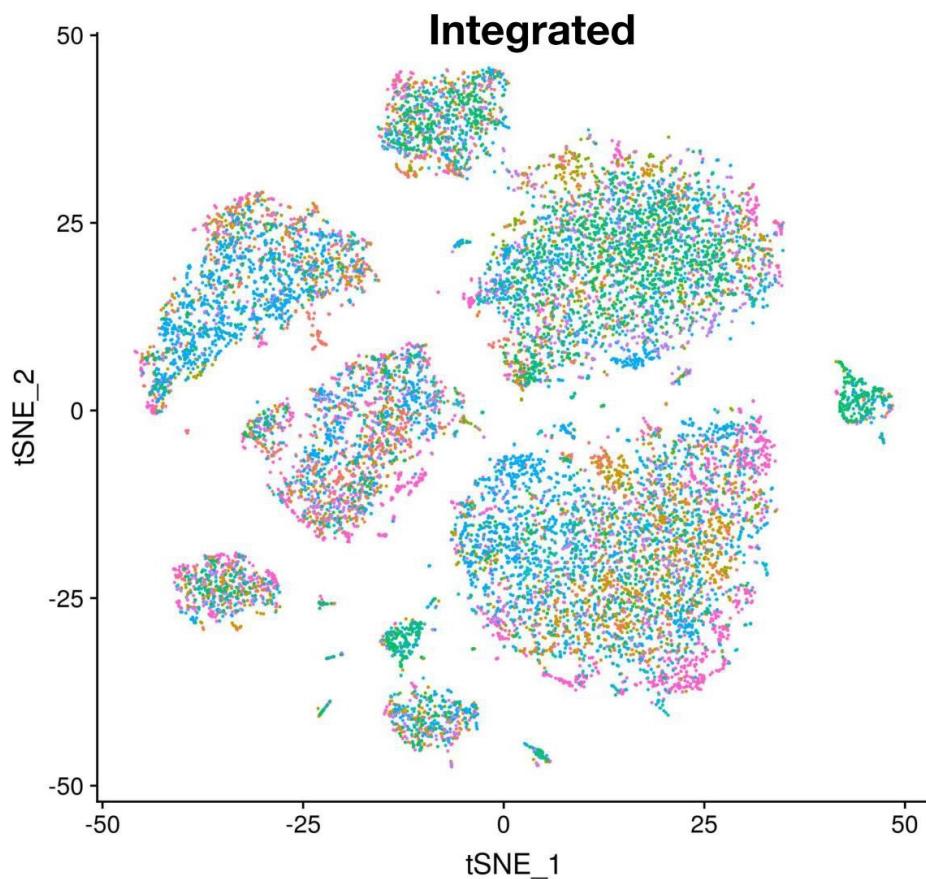
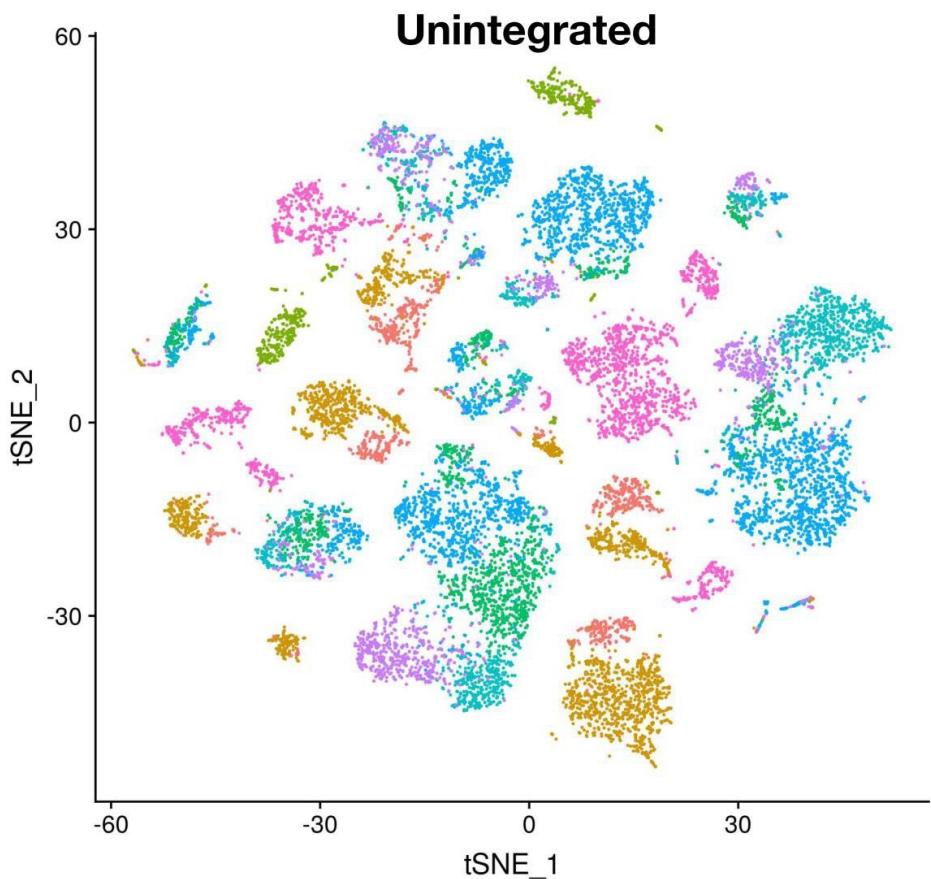
Lawlor et al. 2017, *Genome Res.*

Grun et al. 2016, *Cell Stem Cell*

Muraro et al. 2016, *Cell Syst.*

Integration analysis

- 8 maps from the human pancreas
(Seurat tutorial)



Integration analysis: Confounders and batch effect

1. Technical variability

- Changes in sample quality/processing
- Library prep or sequencing technology

Technical 'batch effects' confound downstream analysis

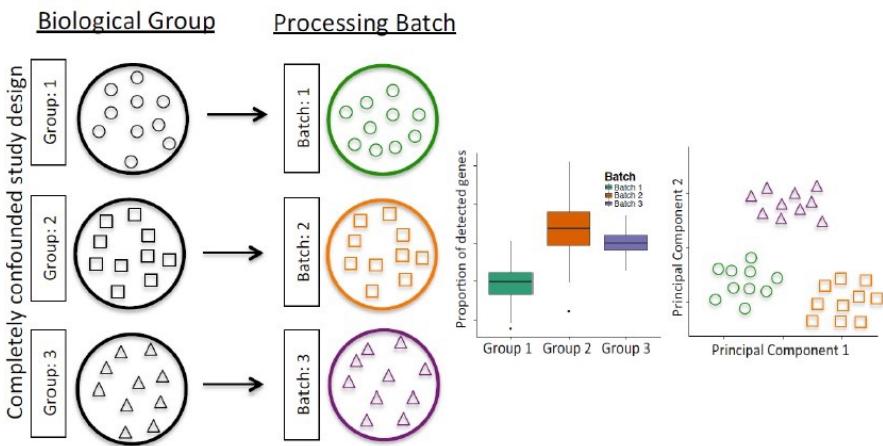
2. Biological variability

- Patient differences
- Evolution! (cross-species analysis)

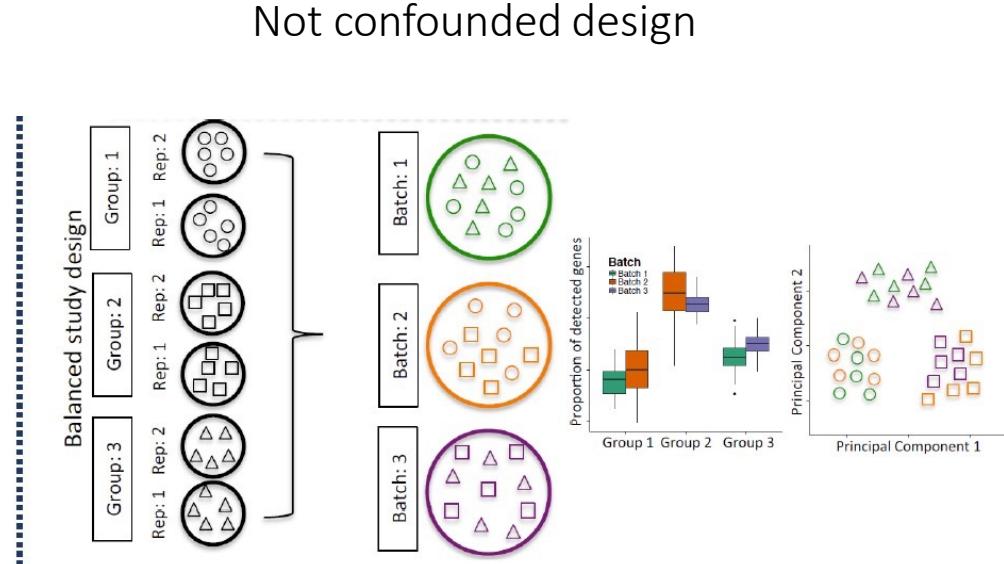
Biological 'batch effects' confound comparisons of scRNA-seq data

Integration analysis: Confounders and batch effect

Confounded design



Not confounded design



Good experimental design *does not remove batch effects*, it prevents them from biasing your results.

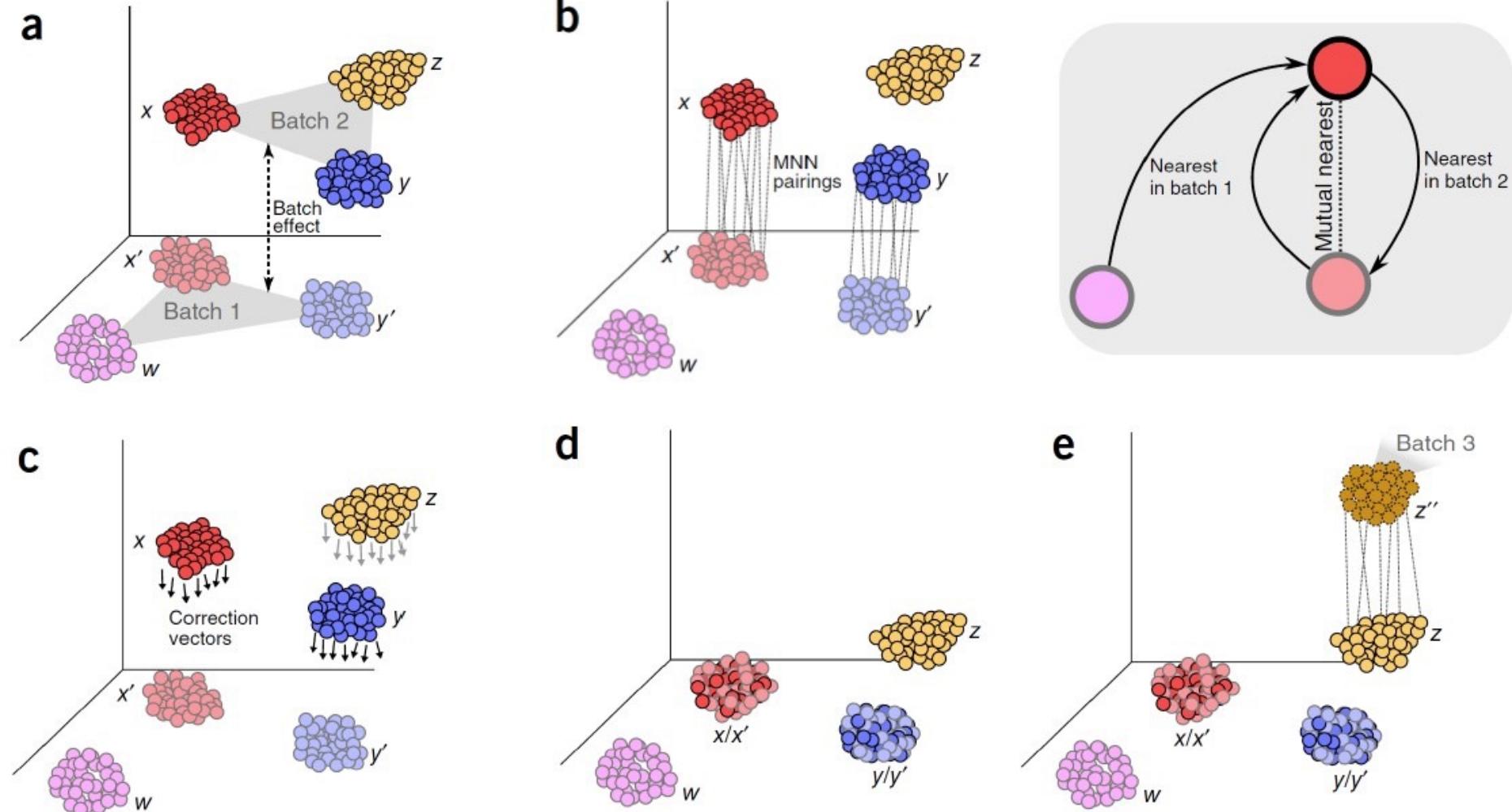
Integration analysis: Batch correction method

- MNNcorrect (<https://doi.org/10.1038/nbt.4091>)
- CCA +anchors (Seurat v3) (<https://doi.org/10.1101/460147>)
- CCA +dynamic time warping (Seurat v2)
(<https://doi.org/10.1038/nbt.4096>)
- LIGER (<https://doi.org/10.1101/459891>)
- Harmony (<https://doi.org/10.1101/461954>)
- Conos (<https://doi.org/10.1101/460246>)
- Scanorama (<https://doi.org/10.1101/371179>)
- scMerge (<https://doi.org/10.1073/pnas.1820006116>)

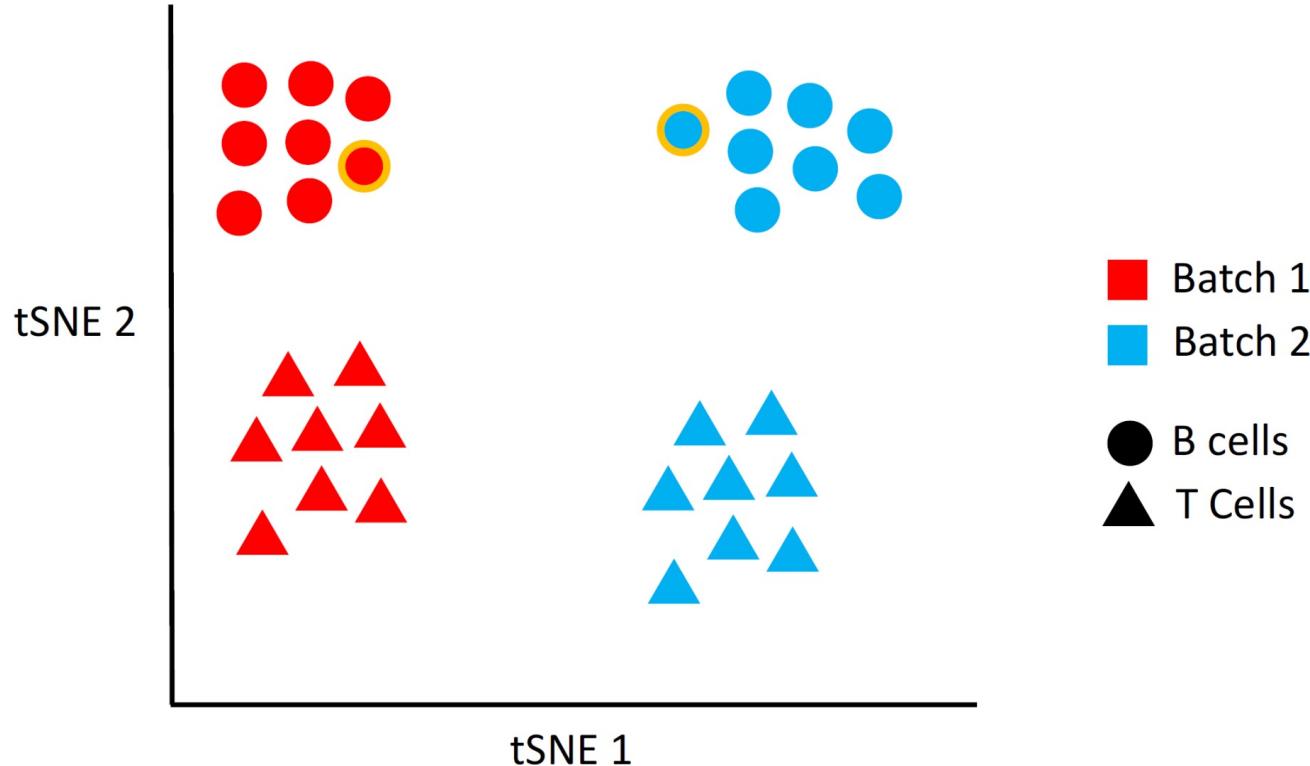
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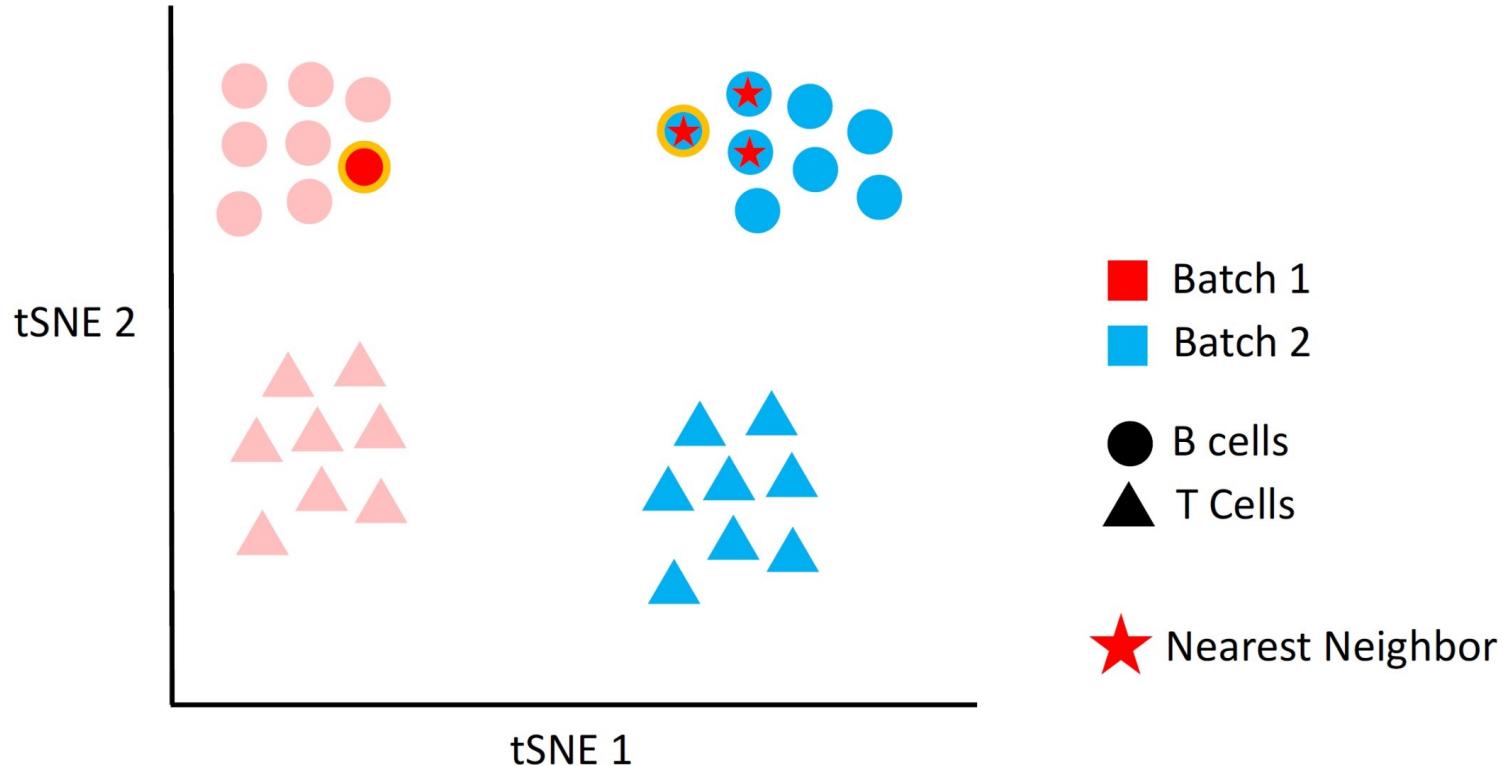
Integration analysis: Mutual Nearest Neighbors (MNN)



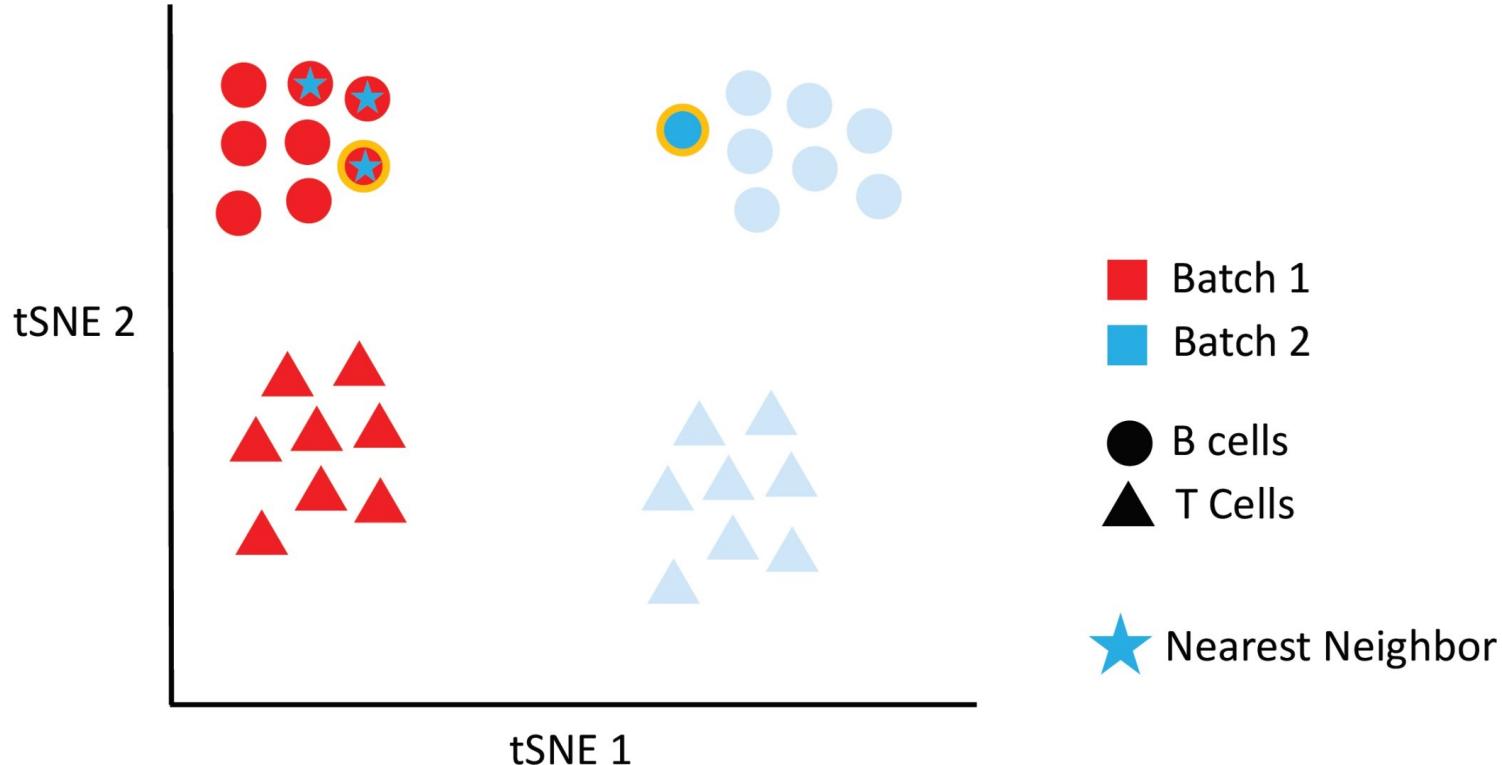
Integration analysis: Mutual Nearest Neighbors (MNN)



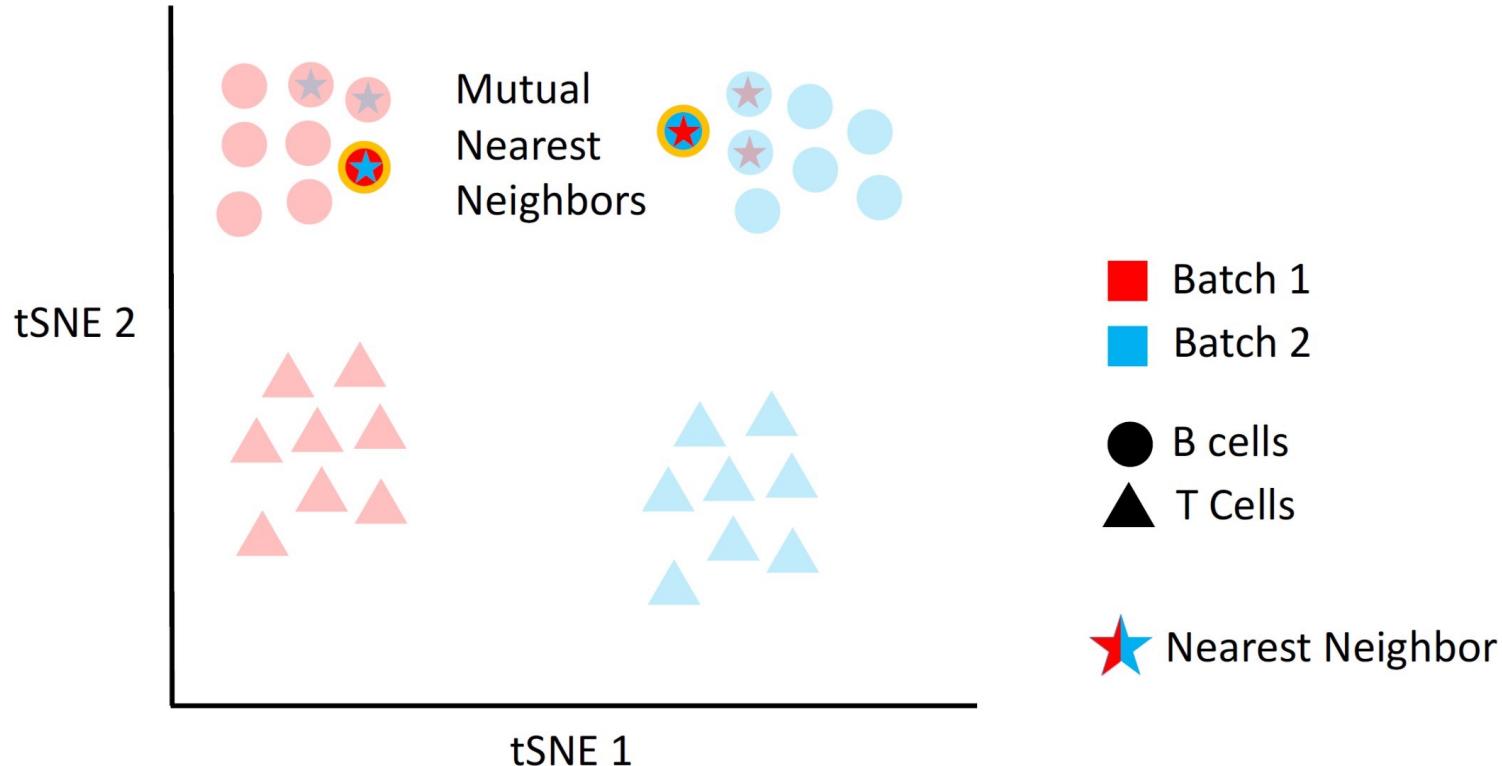
Integration analysis: Mutual Nearest Neighbors (MNN)



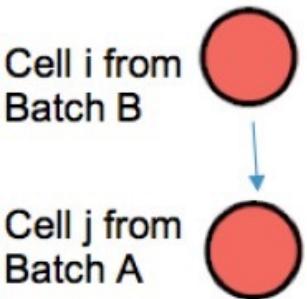
Integration analysis: Mutual Nearest Neighbors (MNN)



Integration analysis: Mutual Nearest Neighbors (MNN)



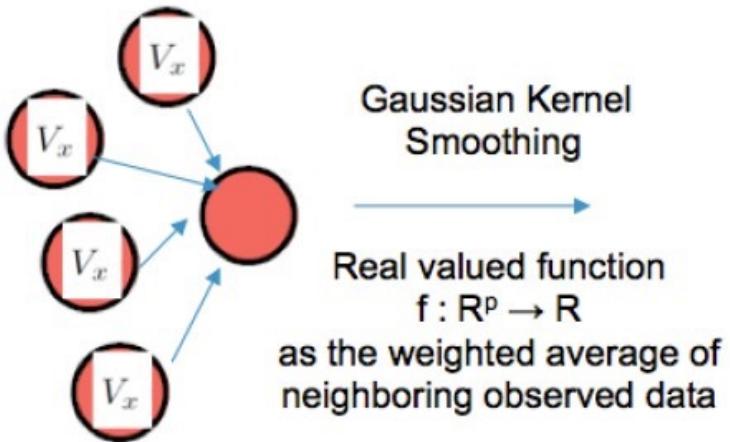
Integration analysis: Mutual Nearest Neighbors (MNN)



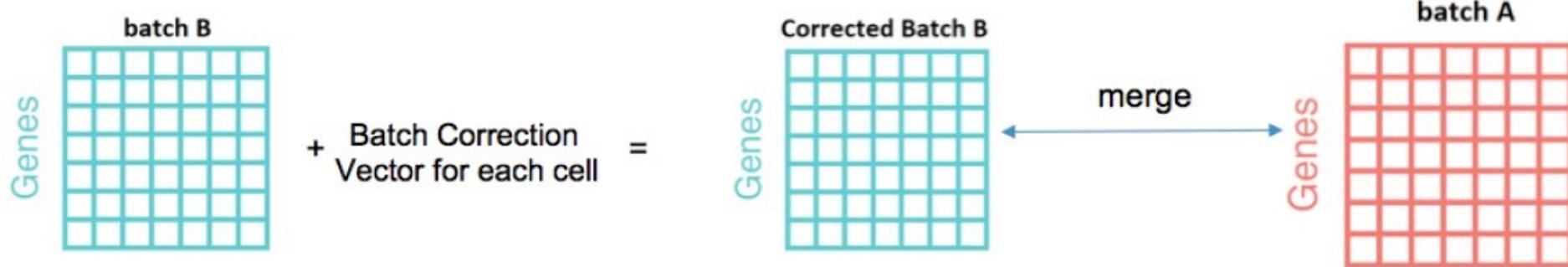
1) For each MNN pair, a pair-specific batch-correction vector is computed as the vector difference between the expression profiles of the paired cells.

$$V_x = \begin{pmatrix} gene1_a - gene1_b \\ gene2_a - gene2_b \\ gene3_a - gene3_b \\ \dots \\ geneN_a - geneN_b \end{pmatrix}$$

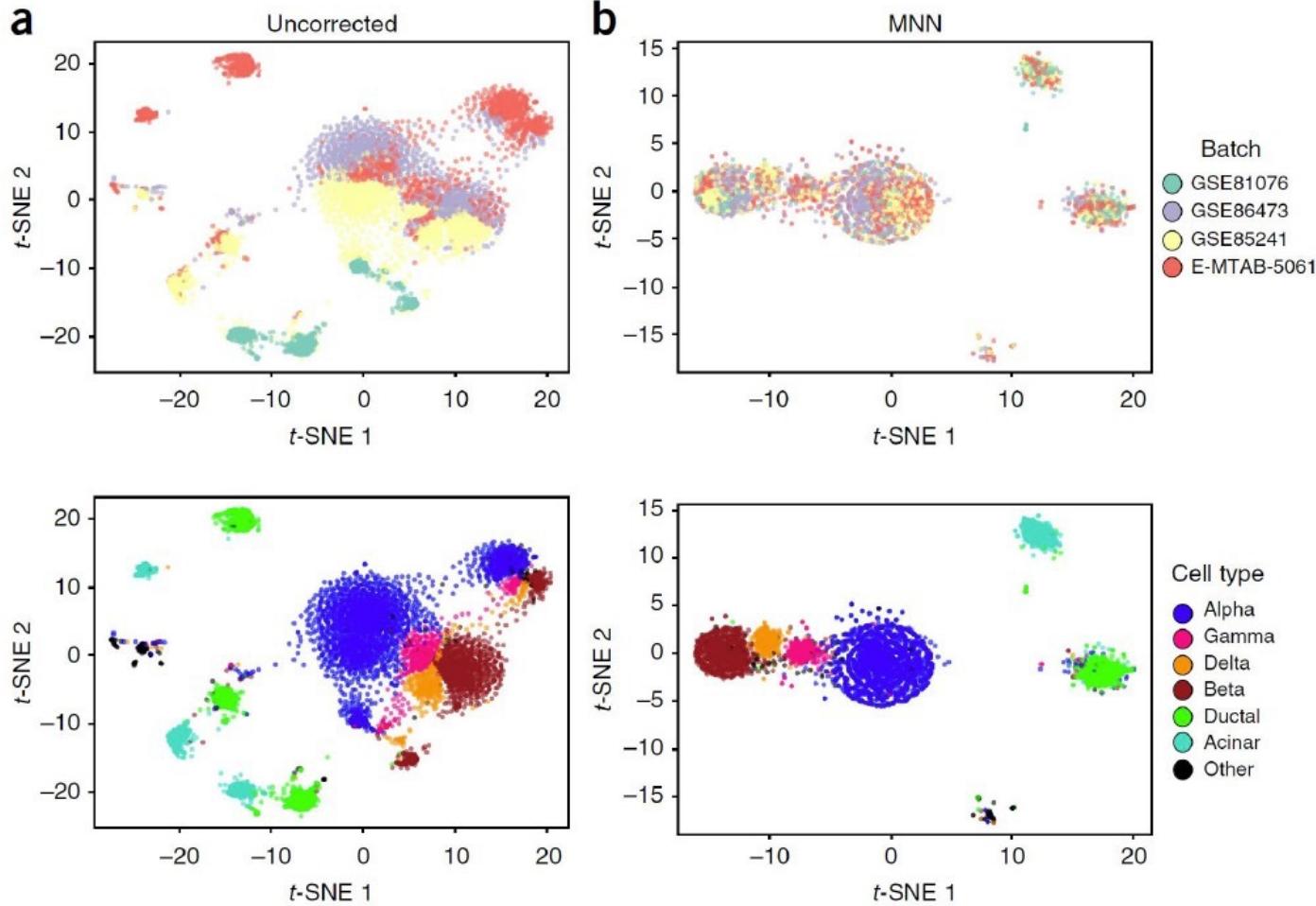
2) A cell-specific batch-correction vector is then calculated as a weighted average of these pair-specific vectors, as computed with a Gaussian kernel.



Batch Correction vector for each cell



Integration analysis: Mutual Nearest Neighbors (MNN)

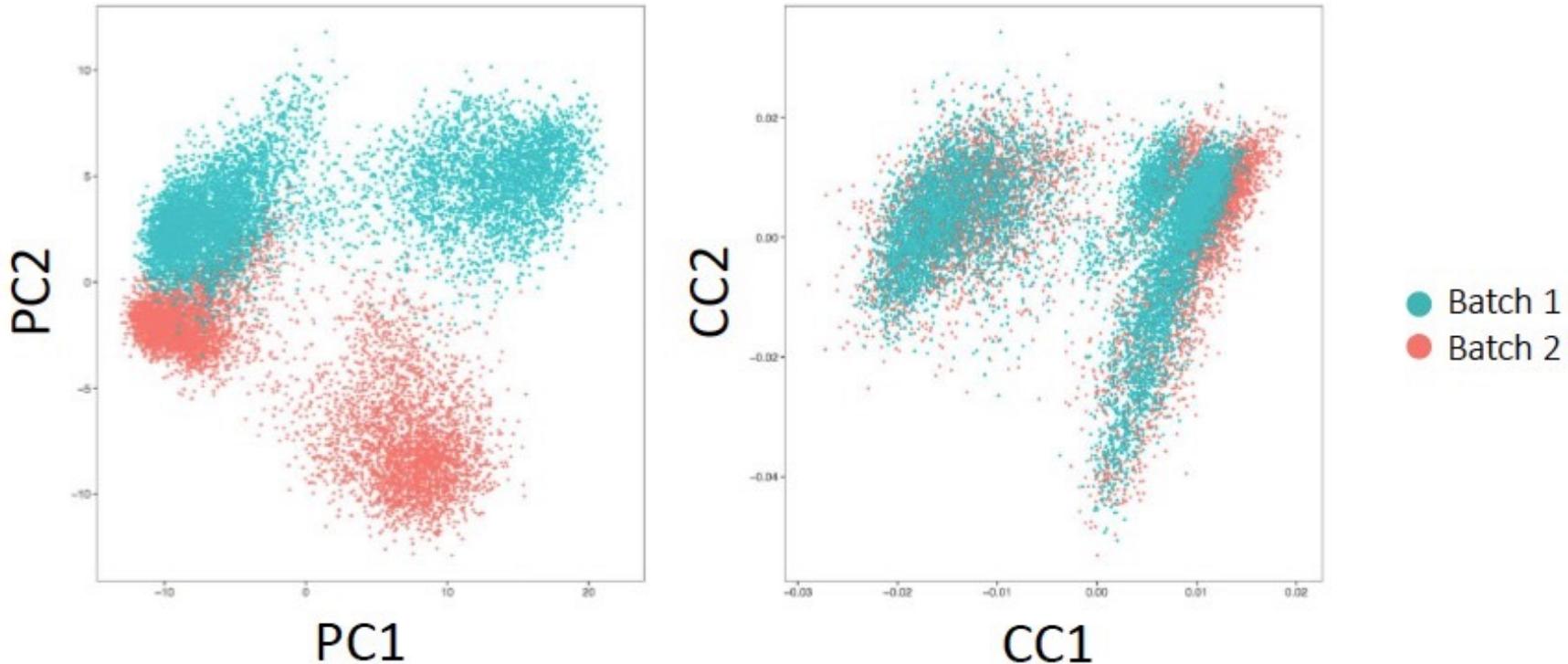


Integration analysis: CCA +anchors (Seurat v3)

1. Find corresponding cells across datasets
2. Compute a data adjustment based on correspondences between cells
3. Apply the adjustment

Integration analysis: CCA + anchors (Seurat v3)

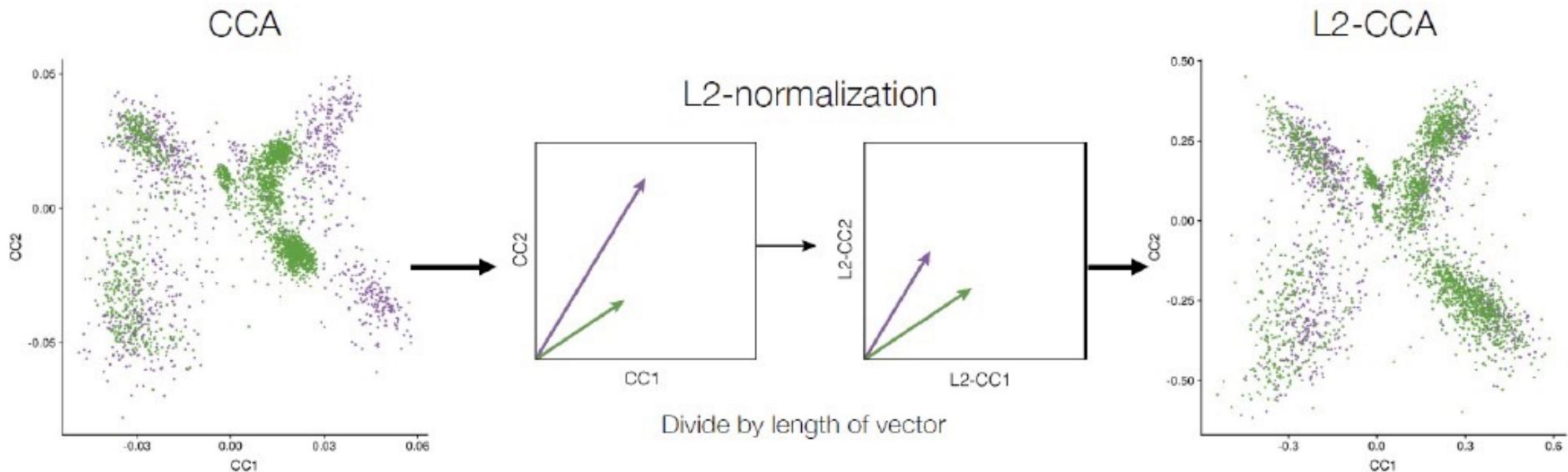
1. Find corresponding cells across datasets



CCA captures correlated sources of variation between two datasets

Integration analysis: CCA + anchors (Seurat v3)

1. Find corresponding cells across datasets

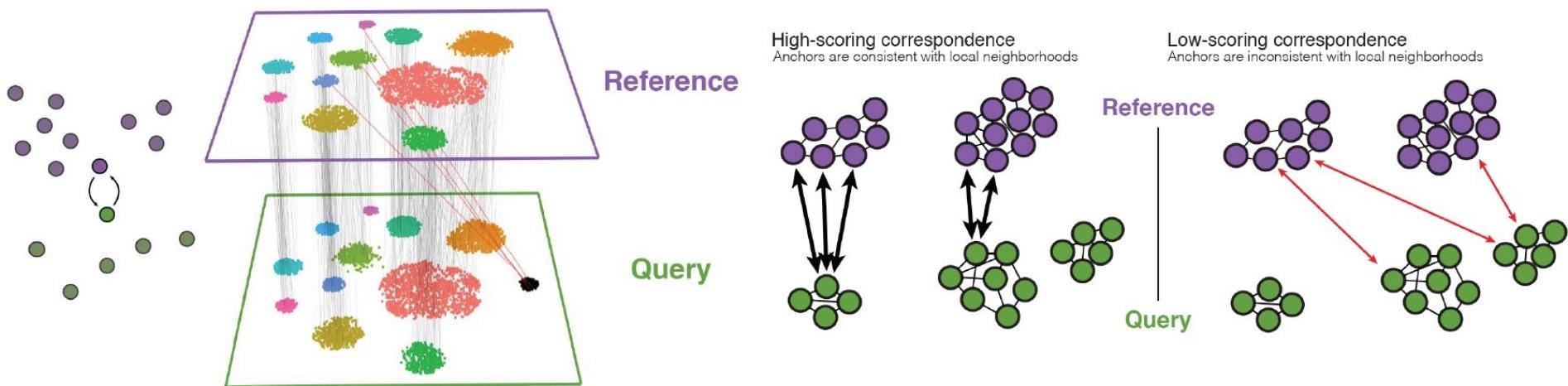


L2-normalization corrects for differences in scale

Integration analysis: CCA +anchors (Seurat v3)

1. Find corresponding cells across datasets

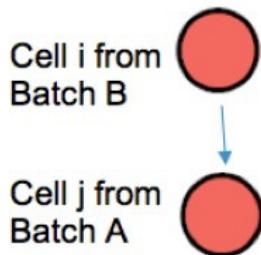
Anchors: Mutual nearest neighbors



Seurat(v3)::FindIntegrationAnchors()

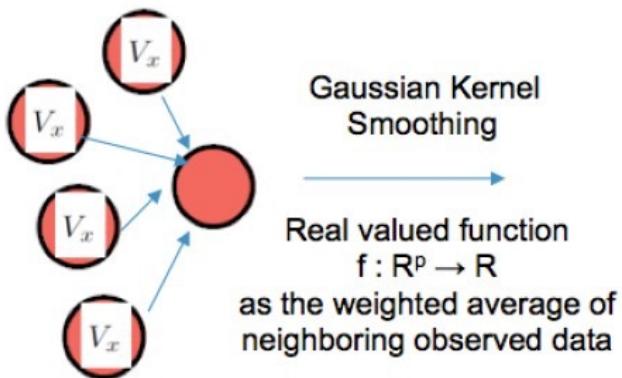
Integration analysis: CCA + anchors (Seurat v3)

2. Data integration



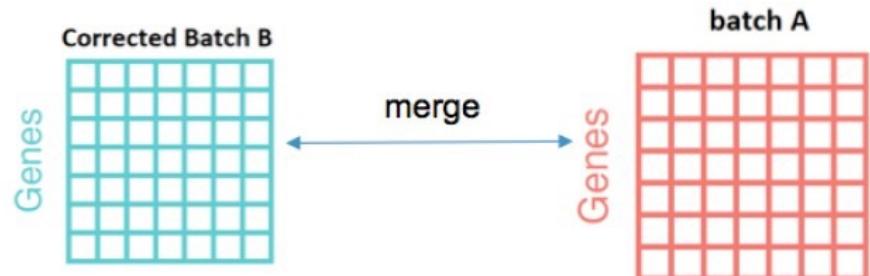
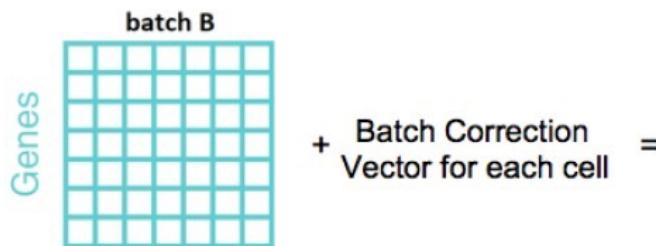
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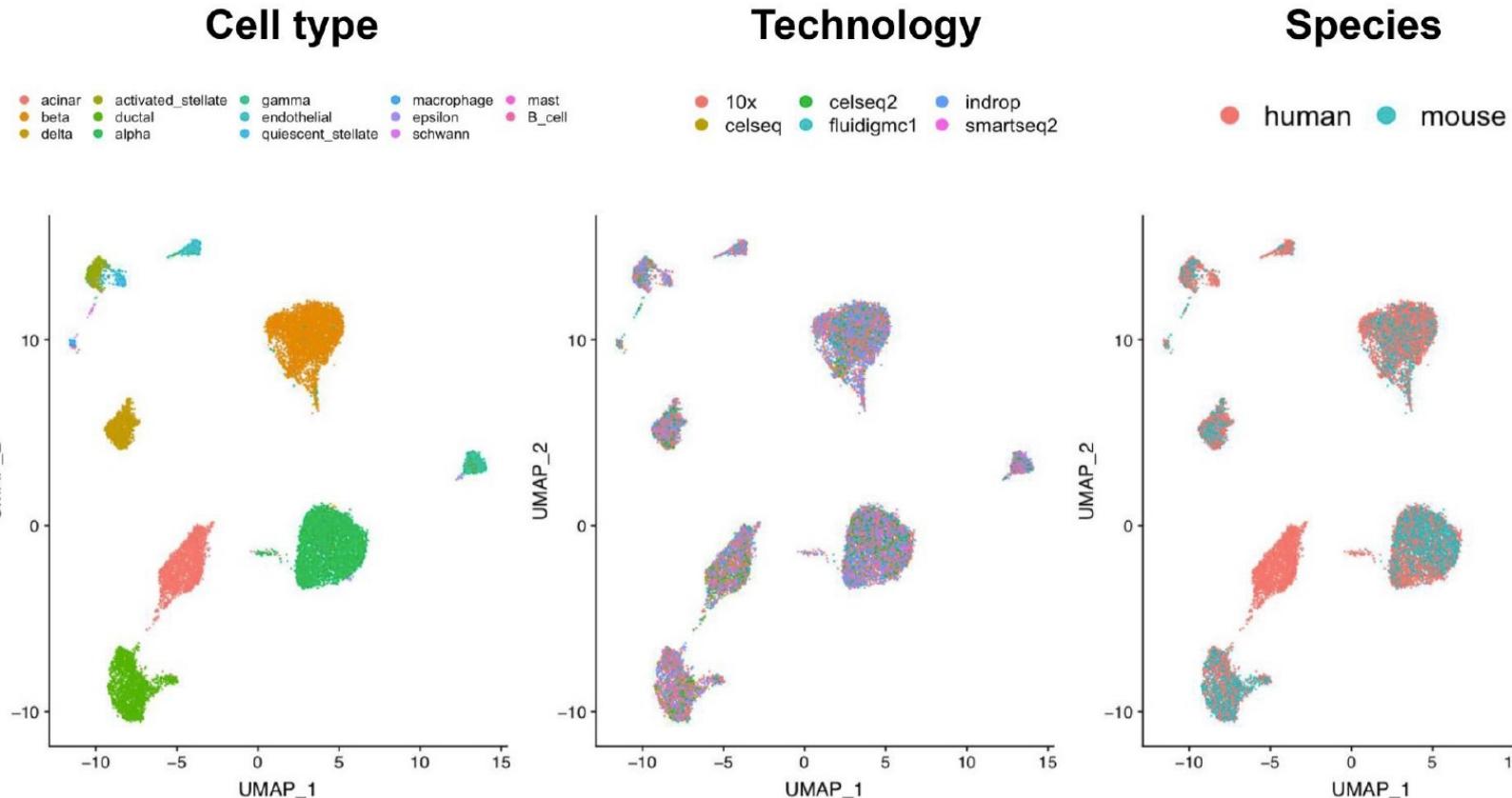
$$V_x = \begin{pmatrix} gene1_a - gene1_b \\ gene2_a - gene2_b \\ gene3_a - gene3_b \\ \dots \\ geneN_a - geneN_b \end{pmatrix}$$

Batch Correction vector
for each cell



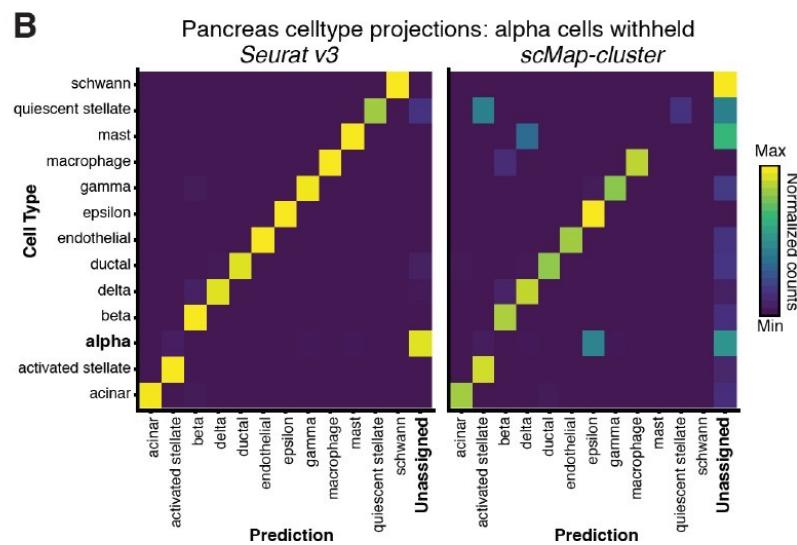
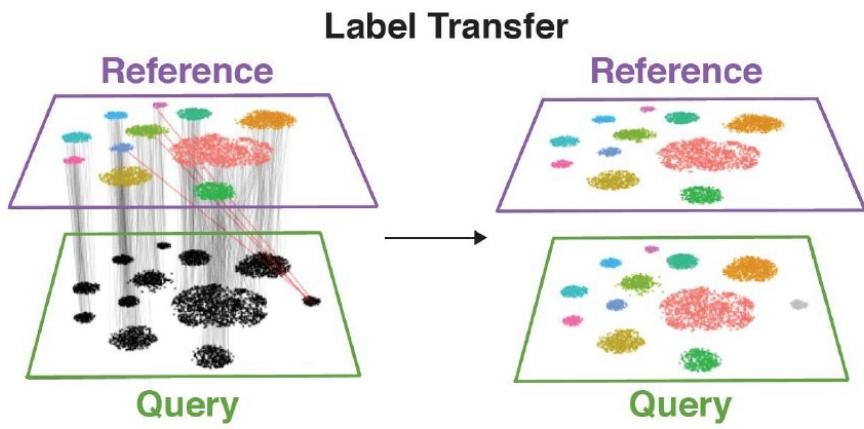
Seurat(v3)::IntegrateData()

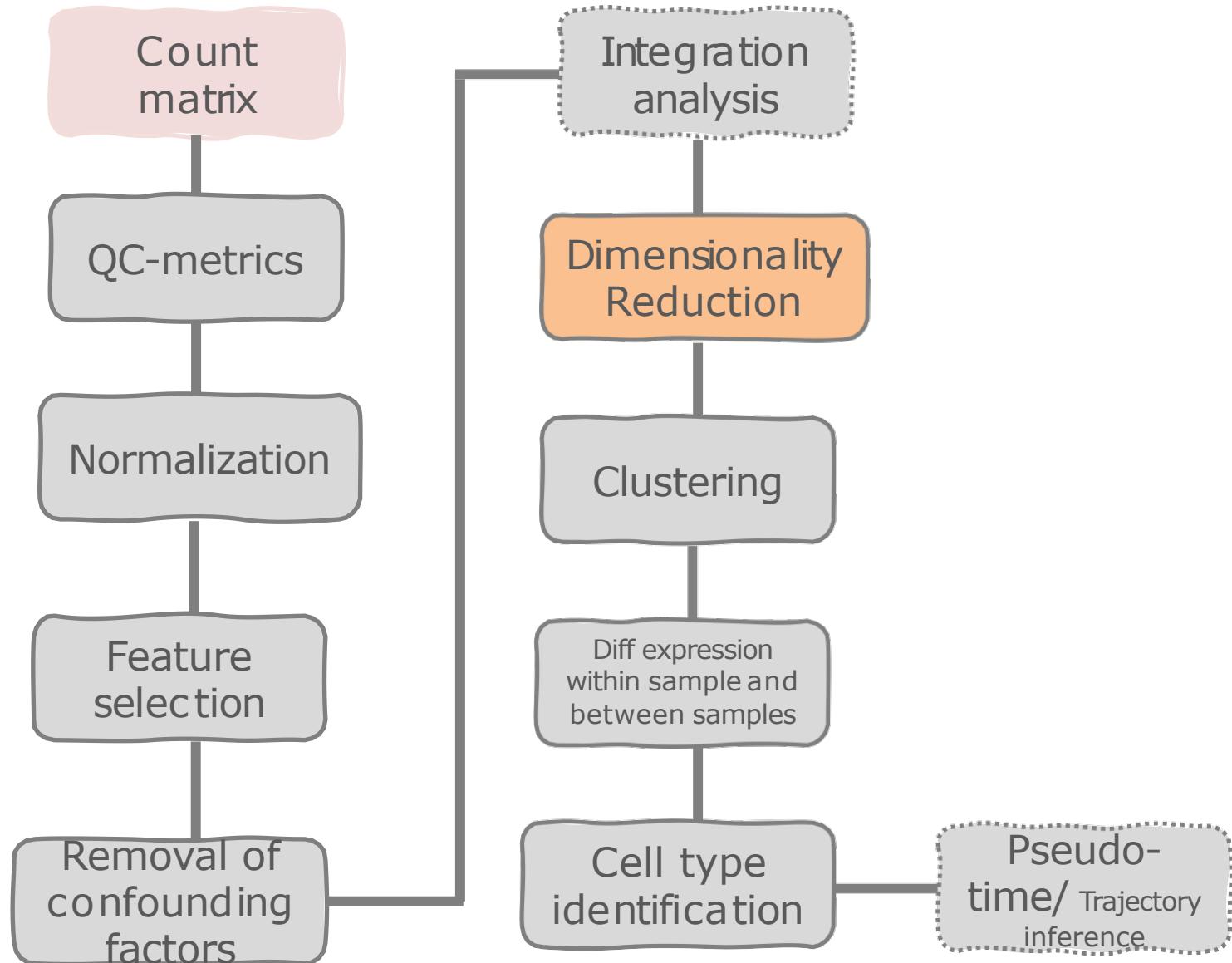
Integration analysis: CCA + anchors (Seurat v3)



Retinal bipolar datasets: 51K cells, 6 technologies, 2 Species

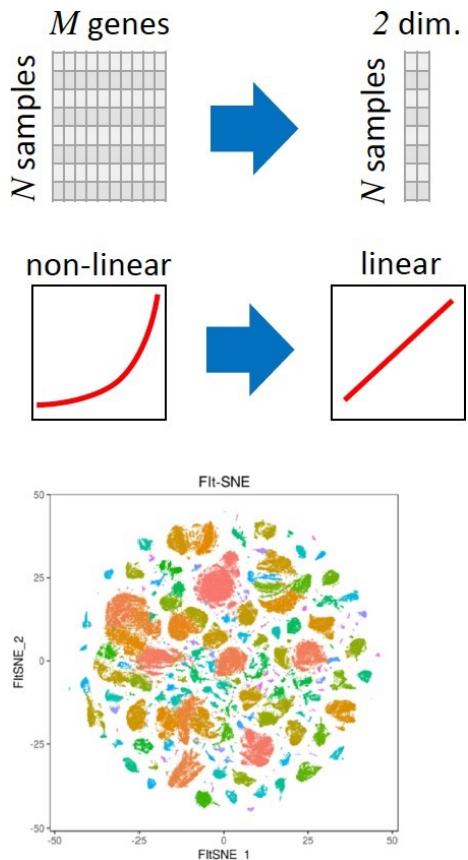
Label transfer: CCA +anchors (Seurat v3)



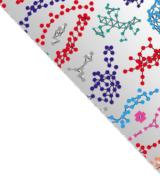


Dimensionality Reduction

- **Simplify complexity**, so it becomes easier to work with.
 - Reduce number of features (genes)
 - In some: Transform non-linear relationships to linear
- “Remove” **redundancies** in the data
- Identify the **most relevant** information (find and filter noise)
- Reduce **computational time** for downstream procedures
- **Facilitate clustering**, since some algorithms struggle with too many dimensions
- Data **visualization**



Dimentionality reduction: Algorithms



PCA	linear	Matrix Factorization			
ICA	linear	Matrix Factorization			
MDS	non-linear	Matrix Factorization			
Sparce NNMF	non-linear	Matrix Factorization	2010	https://pdfs.semanticscholar.org/664d/40258f12ad28ed0b7d4c272935ad72a150db.pdf	
cPCA	non-linear	Matrix Factorization	2018	https://doi.org/10.1038/s41467-018-04608-8	
ZIFA	non-linear	Matrix Factorization	2015	https://doi.org/10.1186/s13059-015-0805-z	
ZINB-WaVE	non-linear	Matrix Factorization	2018	https://doi.org/10.1038/s41467-017-02554-5	



Diffusion maps	non-linear	graph-based	2005	https://doi.org/10.1073/pnas.0500334102	
Isomap	non-linear	graph-based	2000	10.1126/science.290.5500.2319	
t-SNE	non-linear	graph-based	2008	https://lvdmaaten.github.io/publications/papers/JMLR_2008.pdf	
- BH t-SNE	non-linear	graph-based	2014	https://lvdmaaten.github.io/publications/papers/JMLR_2014.pdf	
- Flt-SNE	non-linear	graph-based	2017	arXiv:1712.09005	
LargeVis	non-linear	graph-based	2018	arXiv:1602.00370	
UMAP	non-linear	graph-based	2018	arXiv:1802.03426	
PHATE	non-linear	graph-based	2017	https://www.biorxiv.org/content/biorxiv/early/2018/06/28/120378.full.pdf	



scvis	non-linear	Autoencoder (MF)	2018	https://doi.org/10.1038/s41467-018-04368-5	
VASC	non-linear	Autoencoder (MF)	2018	https://doi.org/10.1016/j.gpb.2018.08.003	

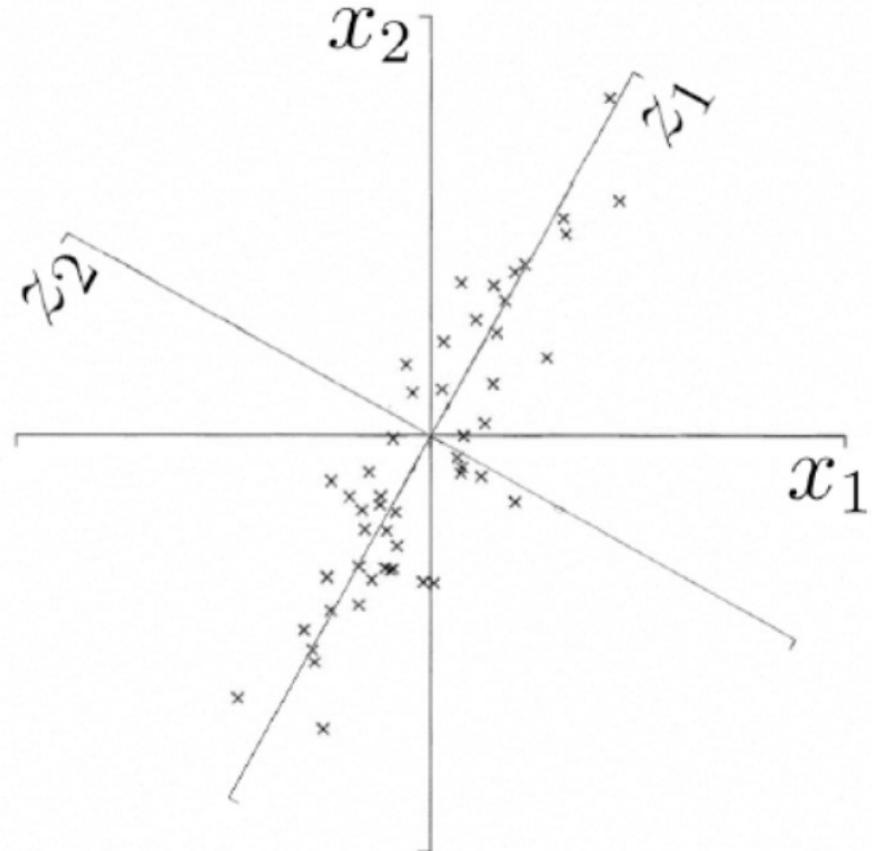
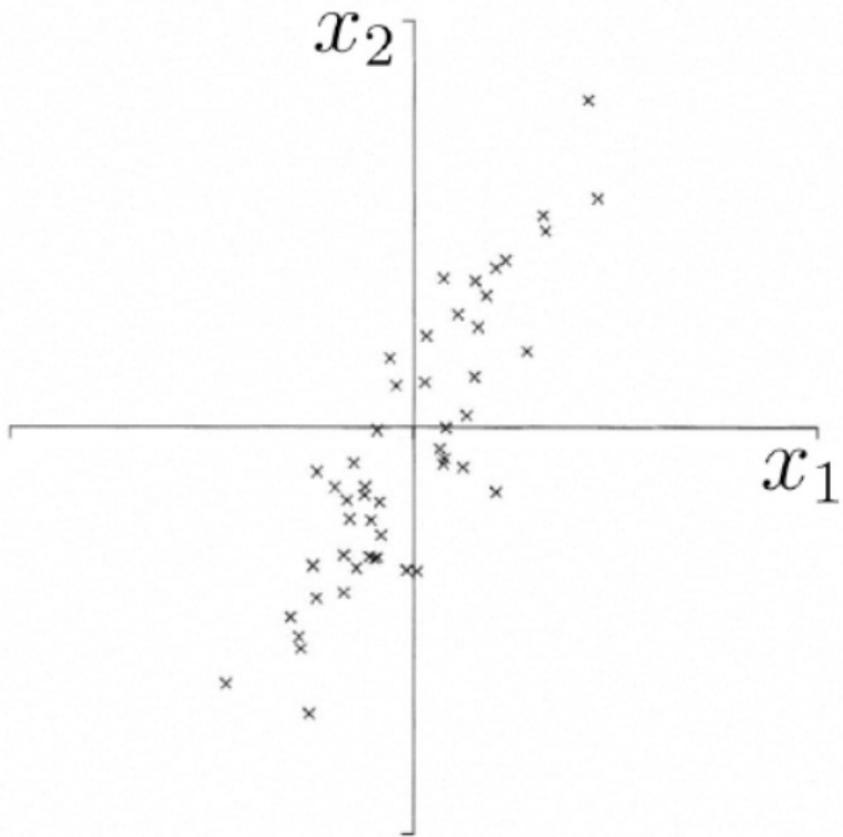
PCA- Principal component analysis

- PCA is based on variance
- PCA is the best angle to see and evaluate the data

PCA- Principal component analysis

Which and how ?

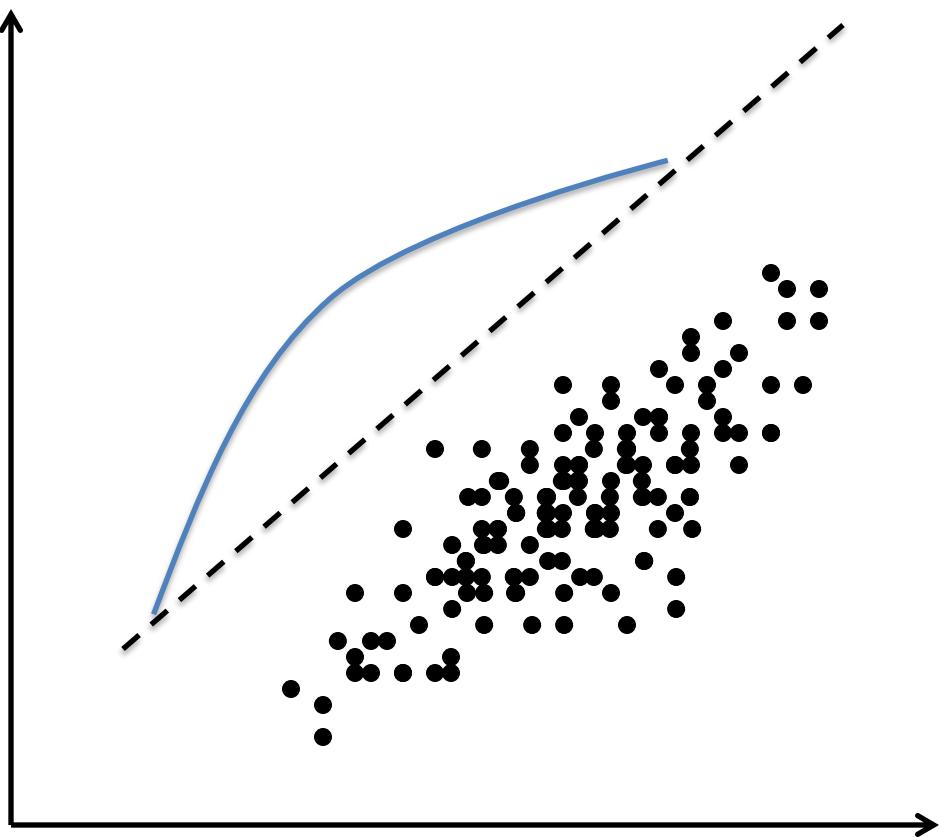
PCA- Principal component analysis



PCA- Principal component analysis

1. Largest variance first

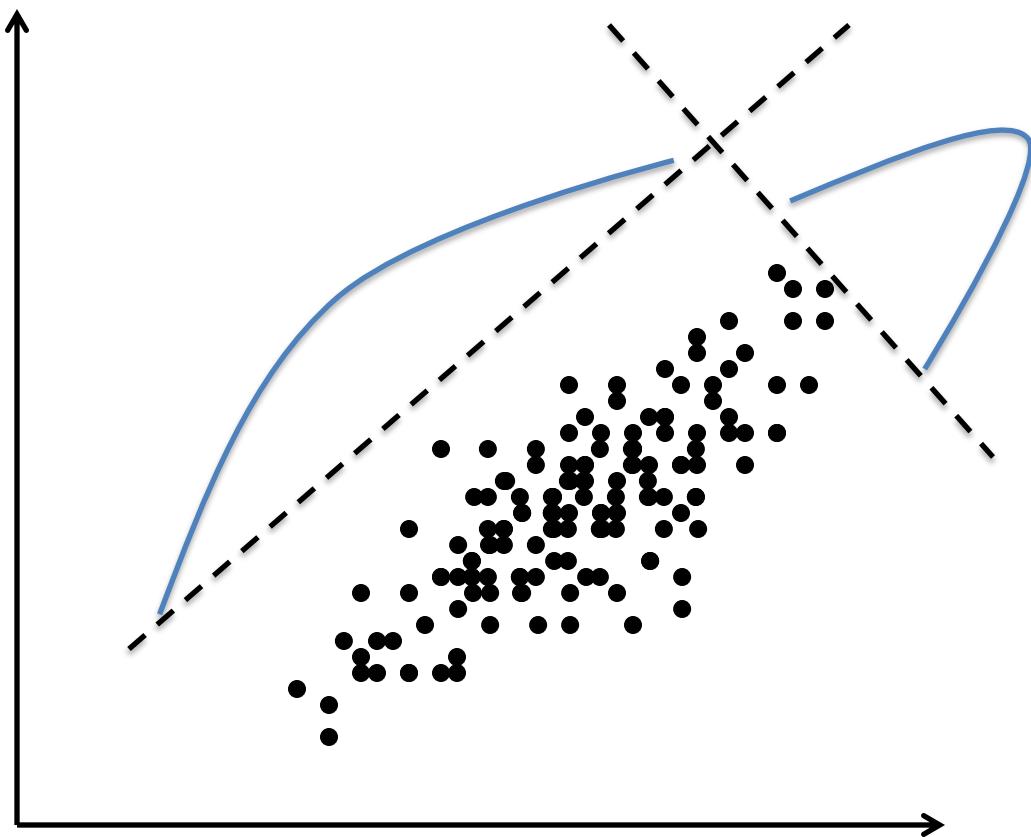
PCA- Principal component analysis



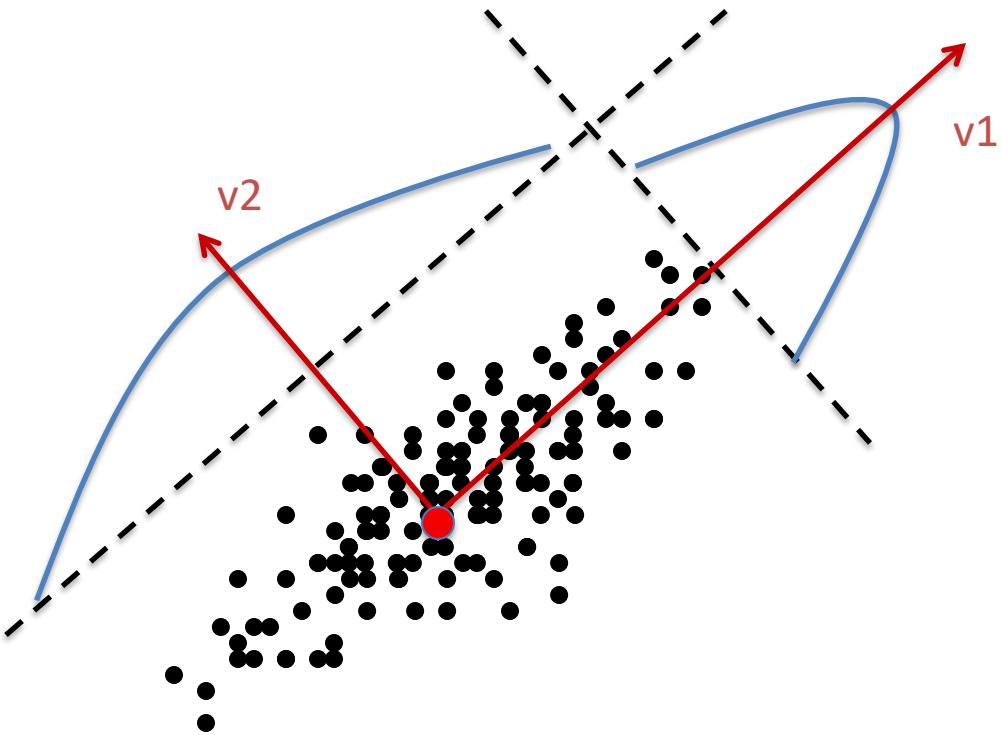
PCA- Principal Component Analysis

2. Select uncorrelated principal axis
(orthogonal)

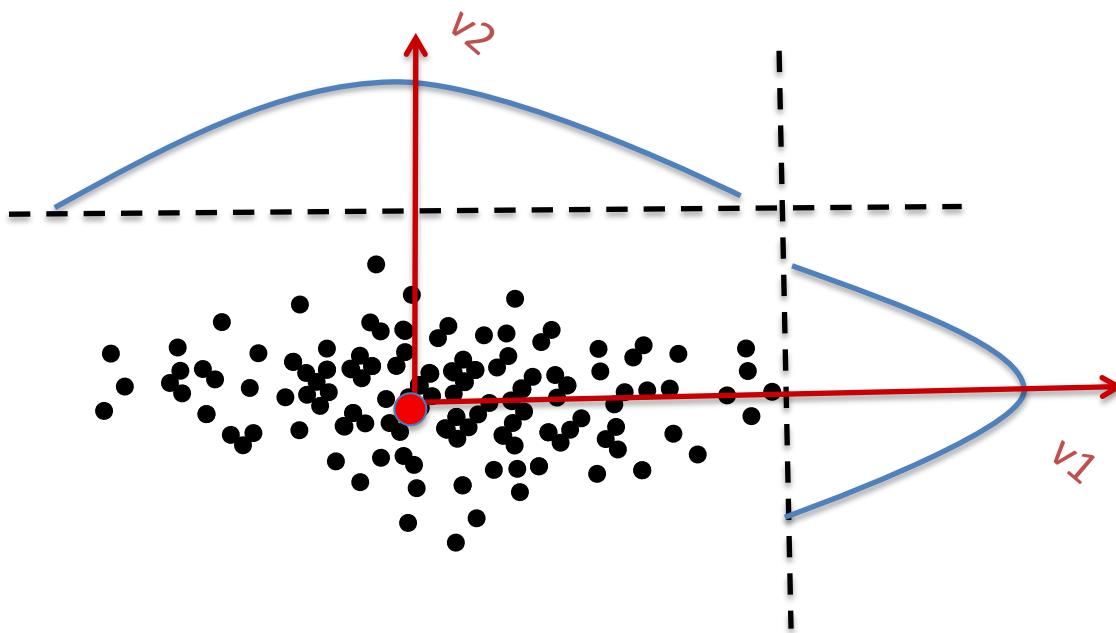
PCA- Principal Component Analysis



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PCA- Principal Component Analysis

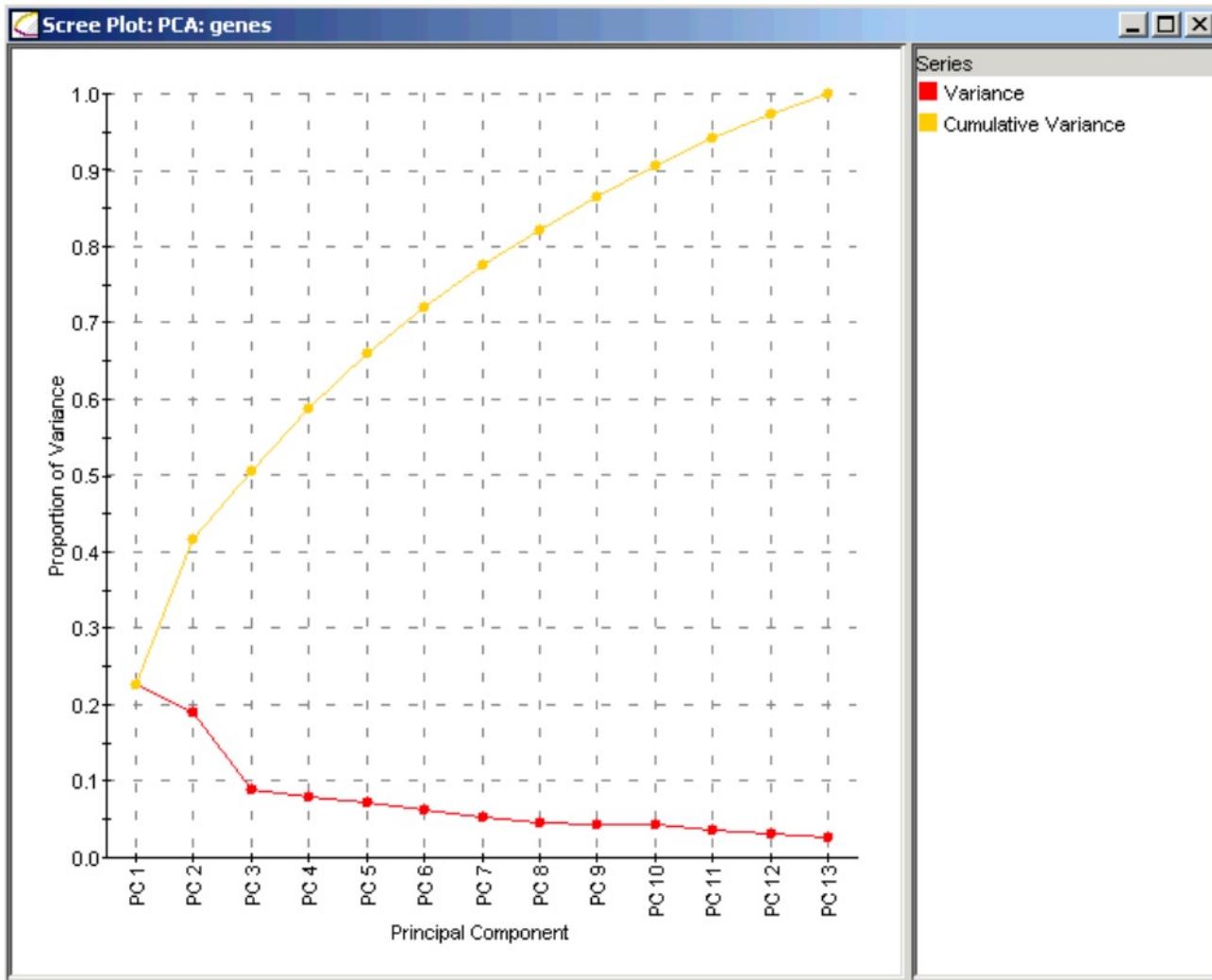


Mathematically

Calculate the eigenvectors of the **Covariance matrix** are *the directions of the axes where there is the most variance (this is something you can prove mathematically!)*

eigenvalues are the coefficients attached to eigenvectors, which give the *amount of variance carried in each Principal Component.*

After having the principal components, to compute the percentage of variance (information) accounted for by each component, we divide the eigenvalue of each component by the sum of eigenvalues.



Scree Plot for Genetic Data. ([Source](#).)

<https://towardsdatascience.com/a-one-stop-shop-for-principal-component-analysis-5582fb7e0a9c>

Dimentionality reduction: PCA doesn't fit

- It is a **LINEAR** method of dimensionality reduction
- It is an **interpretable** dimensionality reduction
- Data is usually **SCALED** prior to PCA (Z-score | see ScaleData in the Seurat)
- The **TOP** principal components contain higher variance from the data
- Can be used as **FILTERING**, by selecting only the top significant PCs
 - PCs that explain at least 1% of variance
 - Jackstraw of significant p-values
 - The first 5-10 PCs
 - Scater library describes correlation between PCs and metadata, take PCs until metadata information is covered

Problems:

- The two first PC in SC-RNAseq often account for only few percent of the total variance
- It performs poorly to separate cells in 0-inflated data types (because of its non-linearity nature)
- Cell sizes and sequencing depth are usually captured in the top principal components

In R, Elbow plot

RunPCA – Computes the PCA with default : 50 pcs.

Check Elbow plot to see if 50 pcs are explaining well your data.

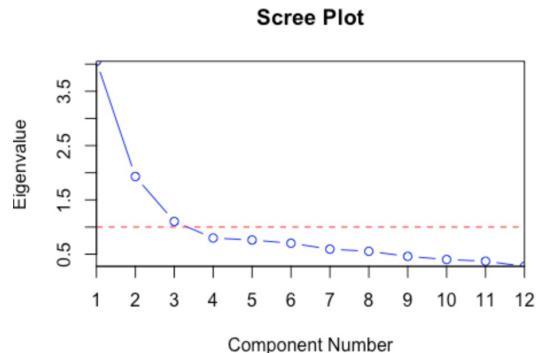
RunPCA will output a message with the genes contributing most to the PC (positif and negatif).

Uses irlba: Fast Truncated Singular Value Decomposition and Principal Components

Analysis for Large Dense and Sparse Matrices (!!Approximation of PCA).

Usually first PCs only account for few percentages of the total variance.

```
obj <- RunPCA( obj )
ElbowPlot(obj,ndims=50)
```



Wikipedia:
https://en.wikipedia.org/wiki/Scree_plot

T-SNE



T-SNE

T-SNE = t-distributed stochastic neighborhood embedding

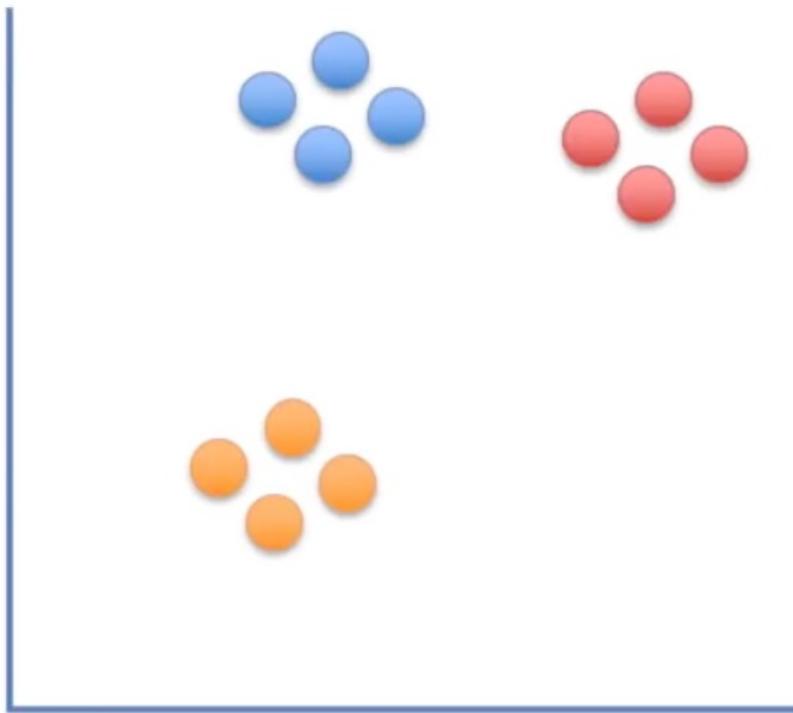
Laurens van der Maaten, Geoffrey Everest Hinton

<http://www.jmlr.org/papers/volume9/vandermaaten08a/vandermaaten08a.pdf>

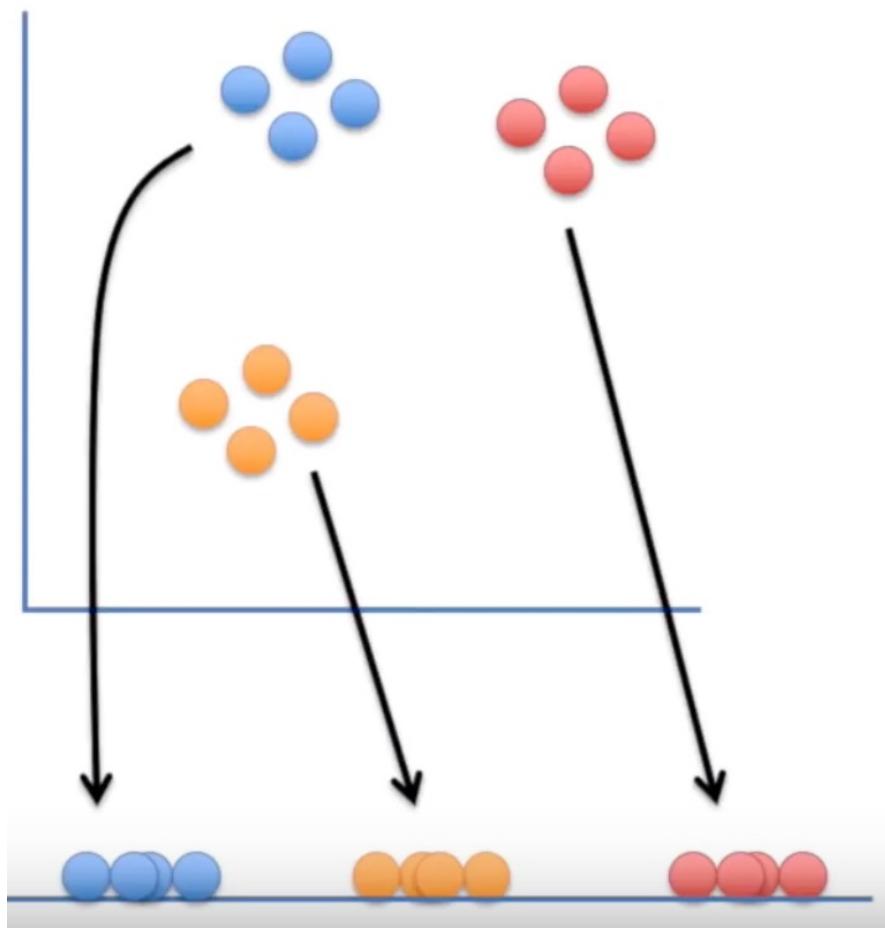
<https://www.youtube.com/watch?v=NEaUSP4YerM>

Many of the following figures are inspired by this youtube link check out his channel !
(StatQuestion with Josh Starmer)

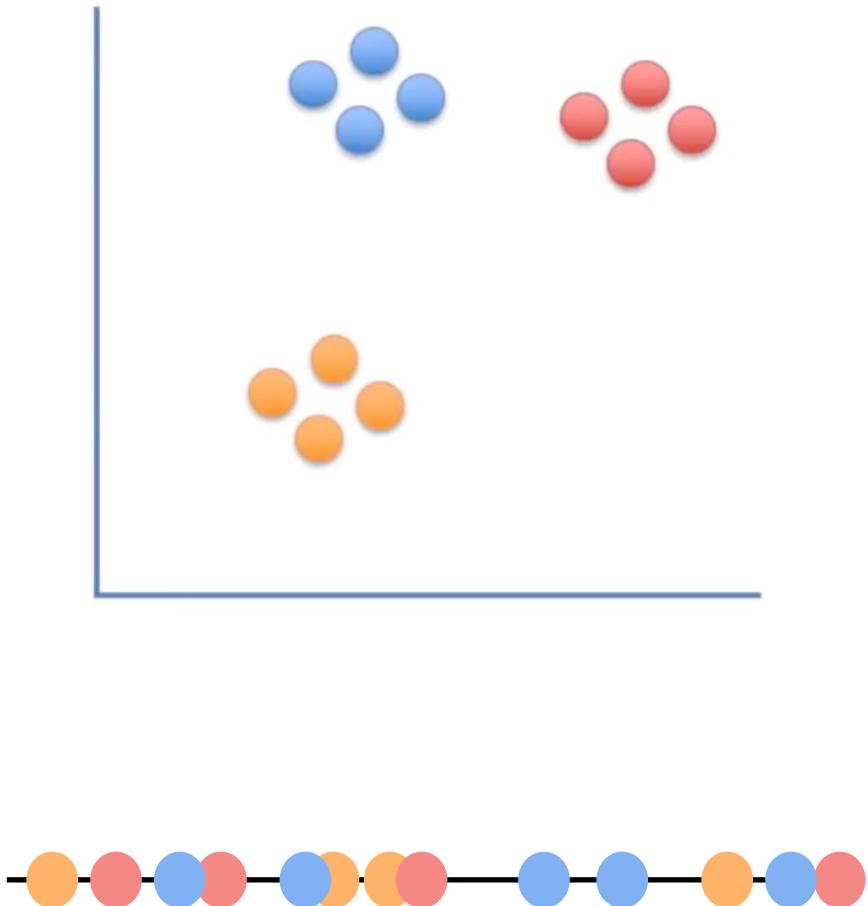
Start with a data-set



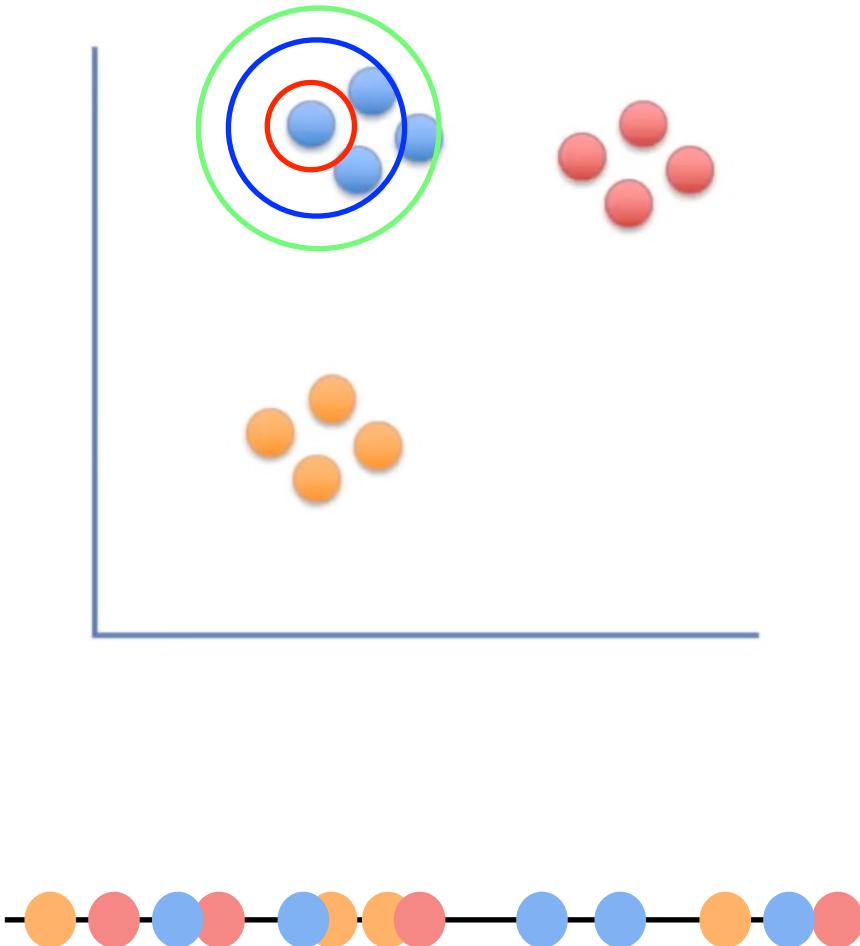
Find a right way to reduce dimension



Basic idea (!! set a seed)



Normal distribution around a point



We calculate

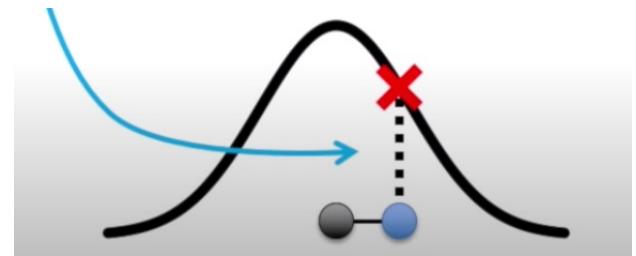
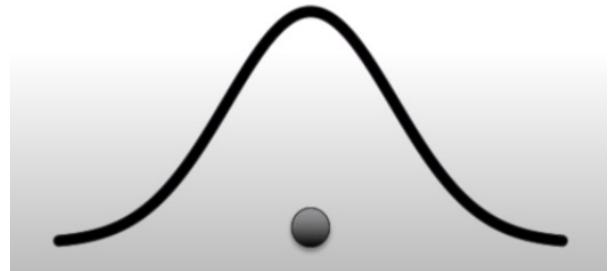
The similarity of datapoint A to datapoint B is the conditional probability, that A would pick B as its neighbor, if neighbors were picked in proportion to their probability density under a Gaussian centered at B, written $p_A|B$.

$$p_A|A = 0$$

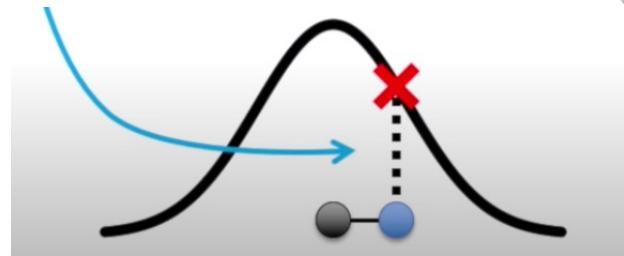
The variance of this normal distribution depends on the density around C (the more cells closer to C the lower the variance of this normal distribution will be).

Steps

1. Take a point A.
2. Take another point B
3. Plot that point on a normal distribution distributed around A.
4. Take another point B and plot it on that distribution, this will be called the unscaled similarity.

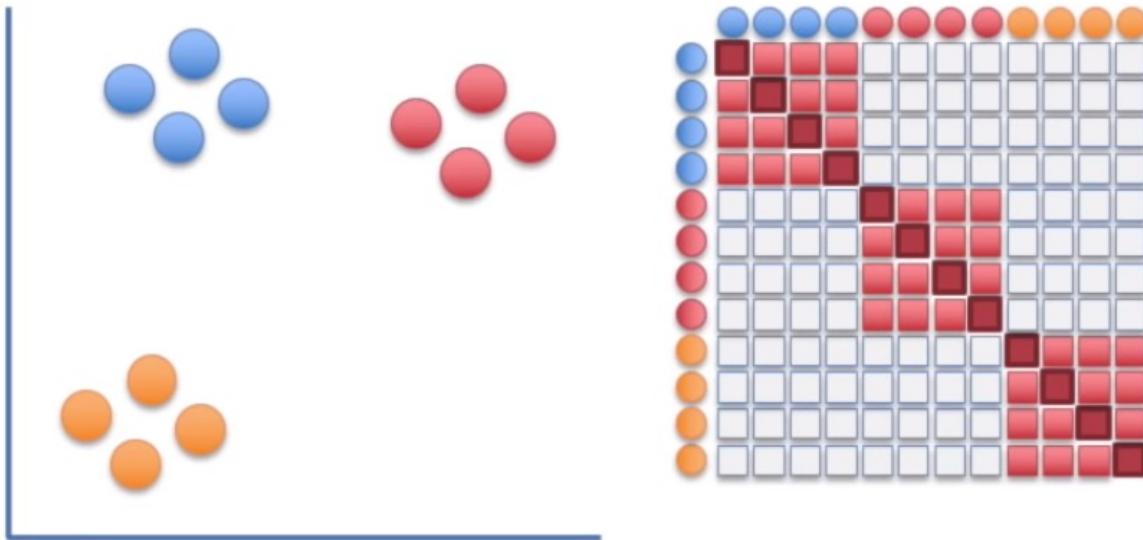


Steps



5. This is done for all the points. Distant points will have a very low similarity, whereas close points a very high similarity.
6. These unscaled similarities are then scaled so that they add up to one.
7. The similarity between A and B might be different than the similarity between B and A, so to correct for that the mean of the two values is taken.

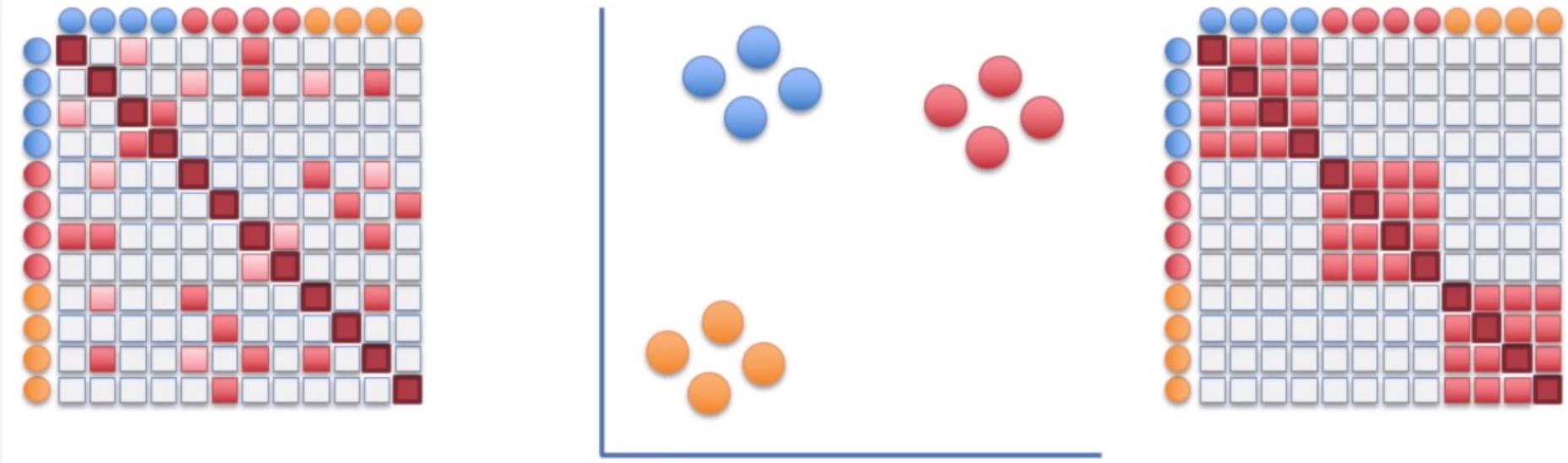
Illustration



On the projection

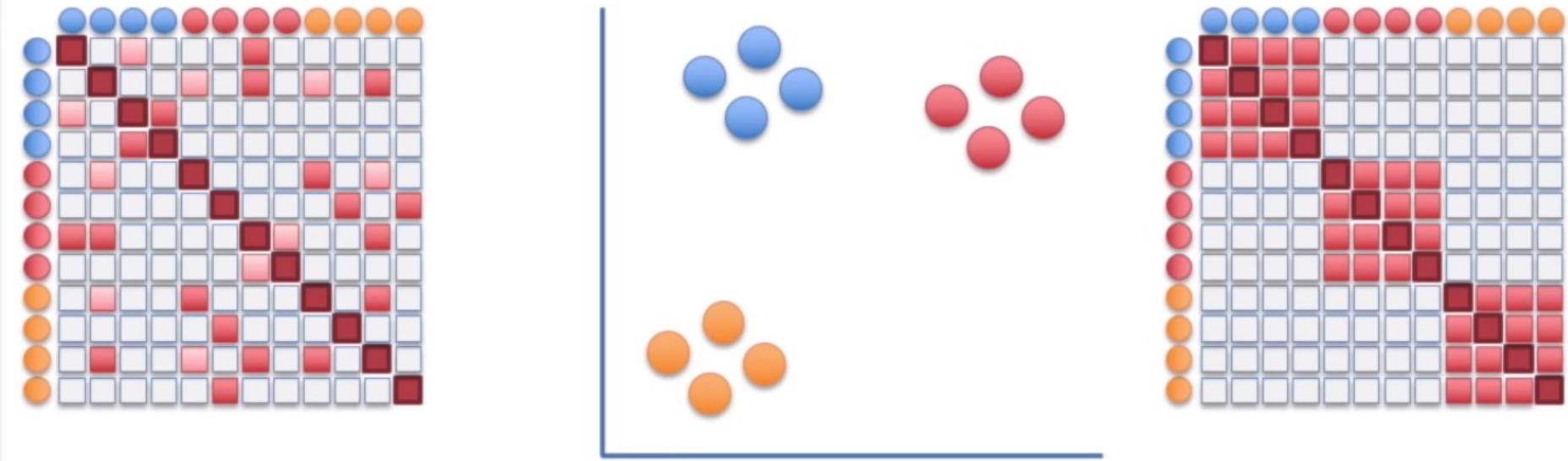
Do the same into the randomly projected points.

Using a t-distribution instead of a normal distribution.



On the projection

Move points little by little and redo calculation until you are « as close as possible » to the original similarity matrix or you reach a certain number of iteration (chosen by the user).



« As close as possible »

To measure the minimization of the sum of difference of conditional probability t-SNE minimizes the sum of Kullback-Leibler divergence of overall data points using a *gradient descent method*.

In other words : tSNE minimizes the divergence between two distributions: a distribution that measures pairwise similarities of the input objects and a distribution that measures pairwise similarities of the corresponding *low-dimensional* points in the embedding

To measure the minimization of the sum of difference of conditional probability t-SNE minimizes the sum of Kullback-Leibler divergence of overall data points using a gradient descent method.

$$C = \sum_i KL(P_i || Q_i) = \sum_i \sum_j p_{j|i} \log \frac{p_{j|i}}{q_{j|i}},$$

Parameters for T-sne

perplexity = $30L \Rightarrow$ linked to parameter σ_i

momentum = 0.5, \Rightarrow linked to optimisation

final_momentum = 0.8, \Rightarrow linked to
optimisation

A cool webpage:

<https://distill.pub/2016/misread-tsne/>

(used to generate the figures in the next slides)

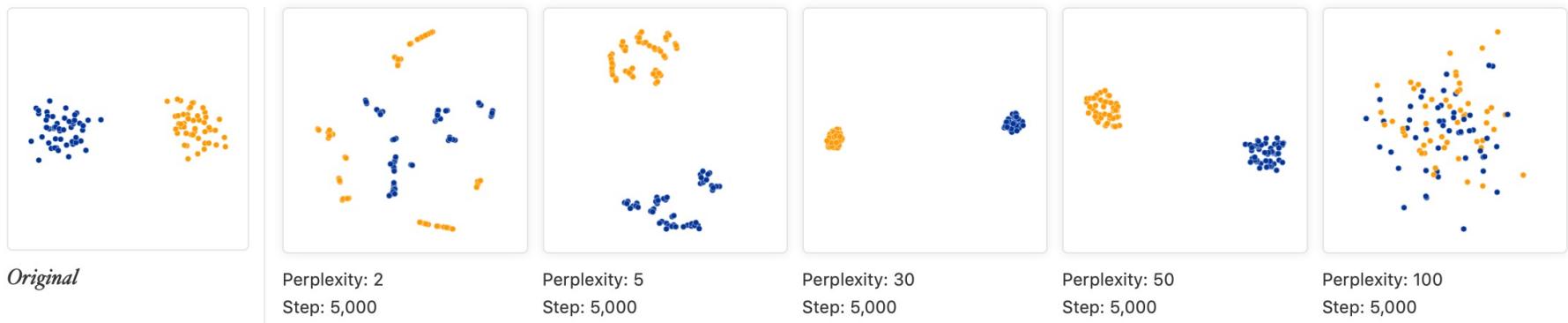
Getting the most from t-SNE may mean analyzing multiple plots with different perplexities.

The perplexity can be interpreted as a smooth measure of the effective number of neighbors

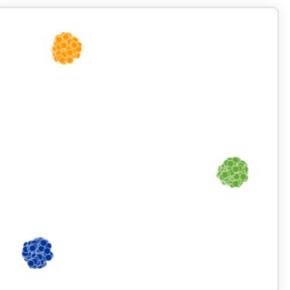
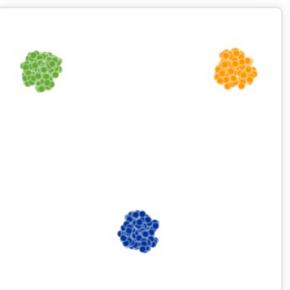
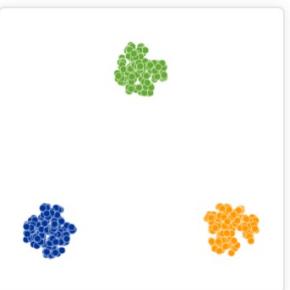
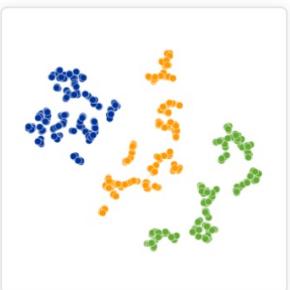
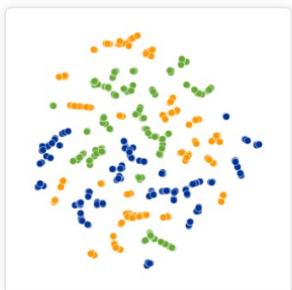
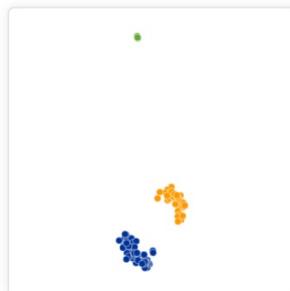
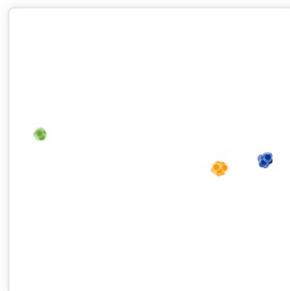
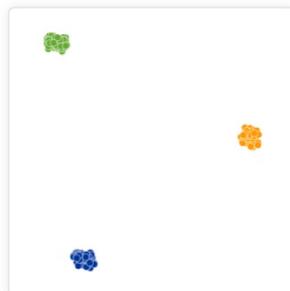
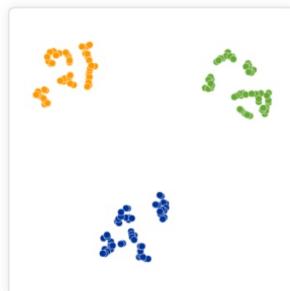
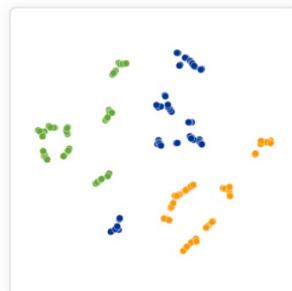
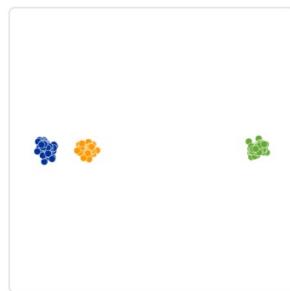
$$Perp(P_i) = 2^{H(P_i)},$$

where $H(P_i)$ is the Shannon entropy of P_i measured in bits

$$H(P_i) = - \sum_j p_{j|i} \log_2 p_{j|i}.$$



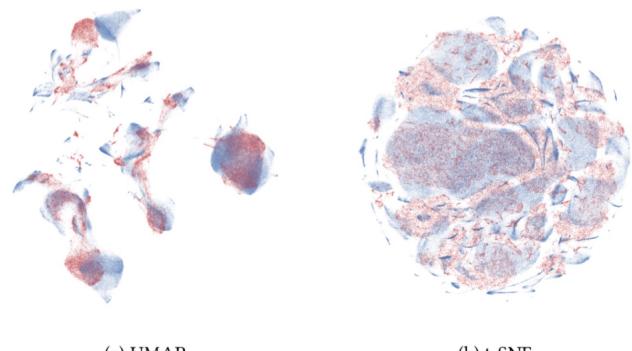
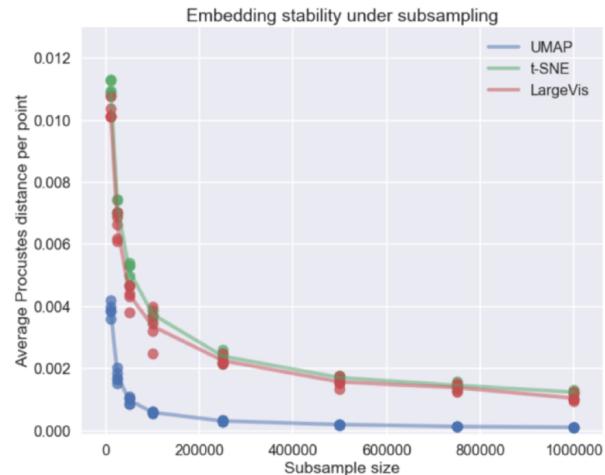
Between cluster distances do not matter !



Dimentionality reduction: UMAP

UMAP: **U**niform **M**anifold **A**pproximation and **P**rojection

- It is a **NON-LINEAR** graph-based method of dimensionality reduction
- UMAP assumes that there is a manifold in the dataset, it could also tend to cluster noise.
- **Very efficient** - $O(n)$
- Can be run from the top PCs (e.g.: PC1 to PC10)
- Can use any distance metrics!
- Can integrate between different data types (text, numbers, classes)
- It is **no longer completely stochastic** as t-SNE
- Defines both **LOCAL** and **GLOBAL** distances
- Can be applied to **new data points**



(a) UMAP

(b) t-SNE

UMAP

UMAP: Uniform Manifold Approximation and Projection for Dimension Reduction

Leland McInnes (Mathematician), John Healy (Computing theorist), James Melville (Computing in R)

<https://arxiv.org/abs/1802.03426>

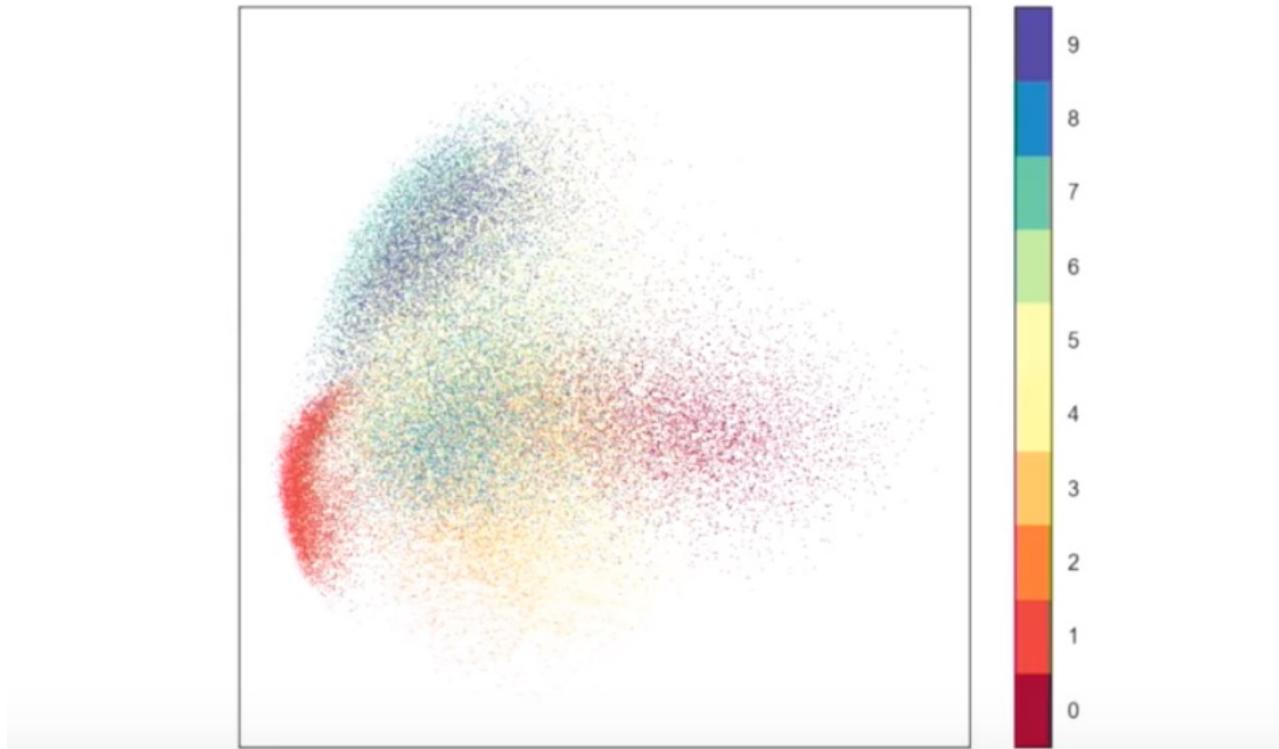
<https://www.youtube.com/watch?v=nq6iPZVUxZU>

<https://umap.scikit-tda.org/parameters.html>

PCA is good, but one can do better!



PCA on MNIST digits

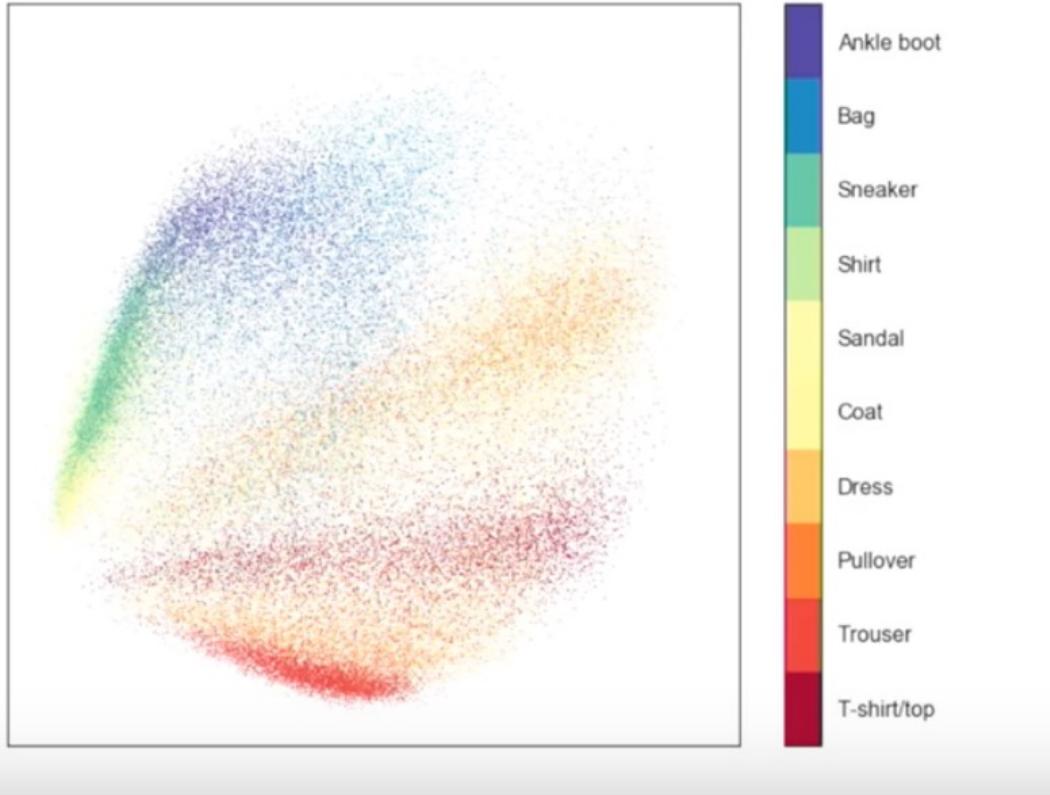


From L.McInnes, SciPy 2018

PCA is good, but one can do better!



PCA on Fashion MNIST



See the
global structure
and
Interpretable axis

From L.McInnes, SciPy 2018

T-SNE manages to see the local structure



t-SNE on MNIST digits

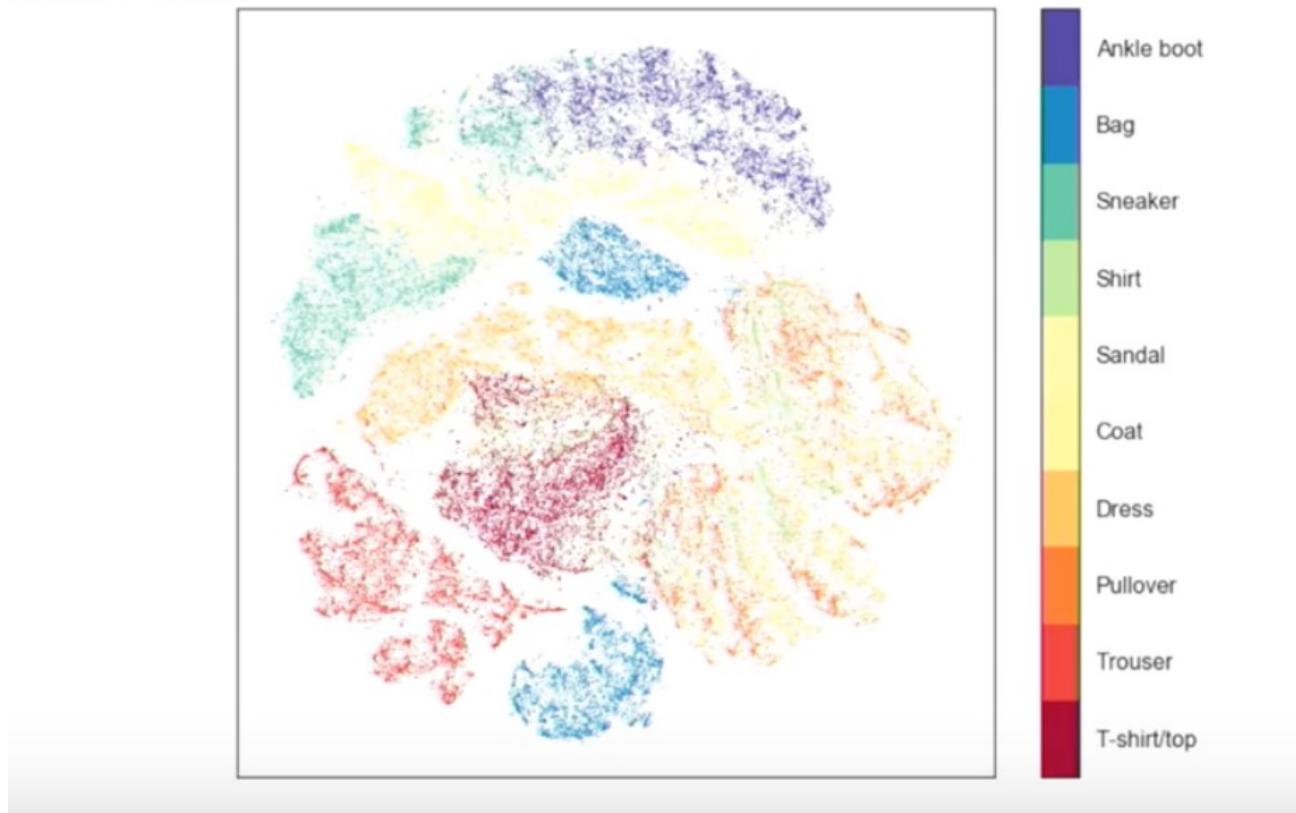


From L.McInnes, SciPy 2018

T-SNE manages to see the local structure



t-SNE on Fashion MNIST



From L.McInnes, SciPy 2018

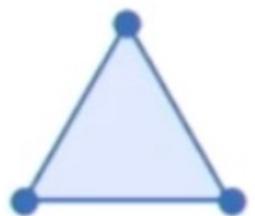
0-simplex



1-simplex



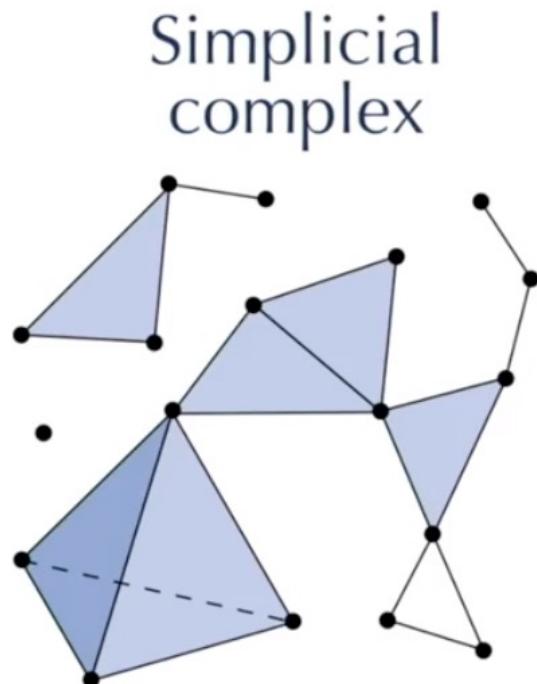
2-simplex



3-simplex



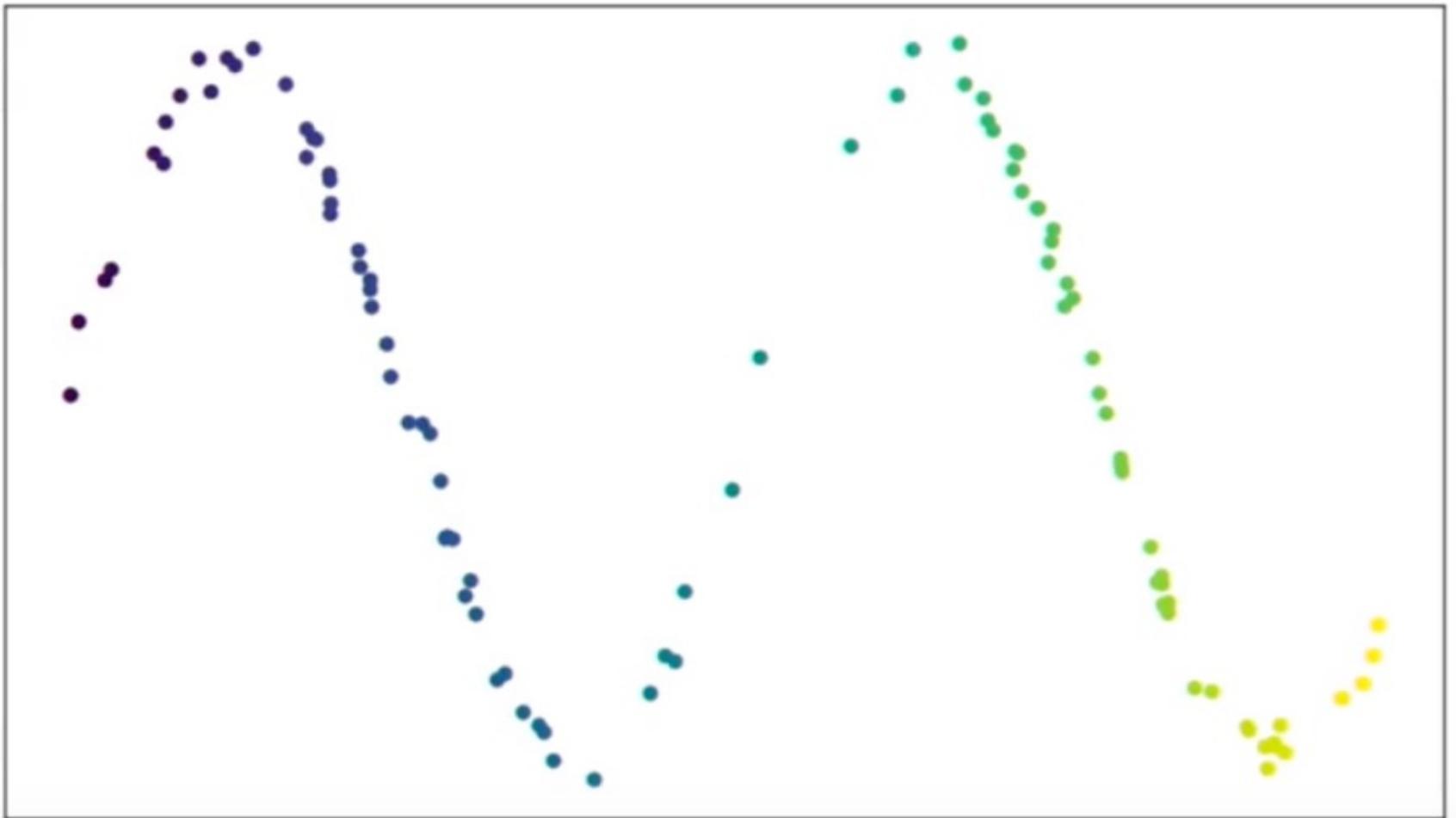
What it enables you to represent



1. Combinatorial
2. Simple to implement
3. Keeps the information of the global structure
4. Nice theorems exist on those (Nerve theorem)

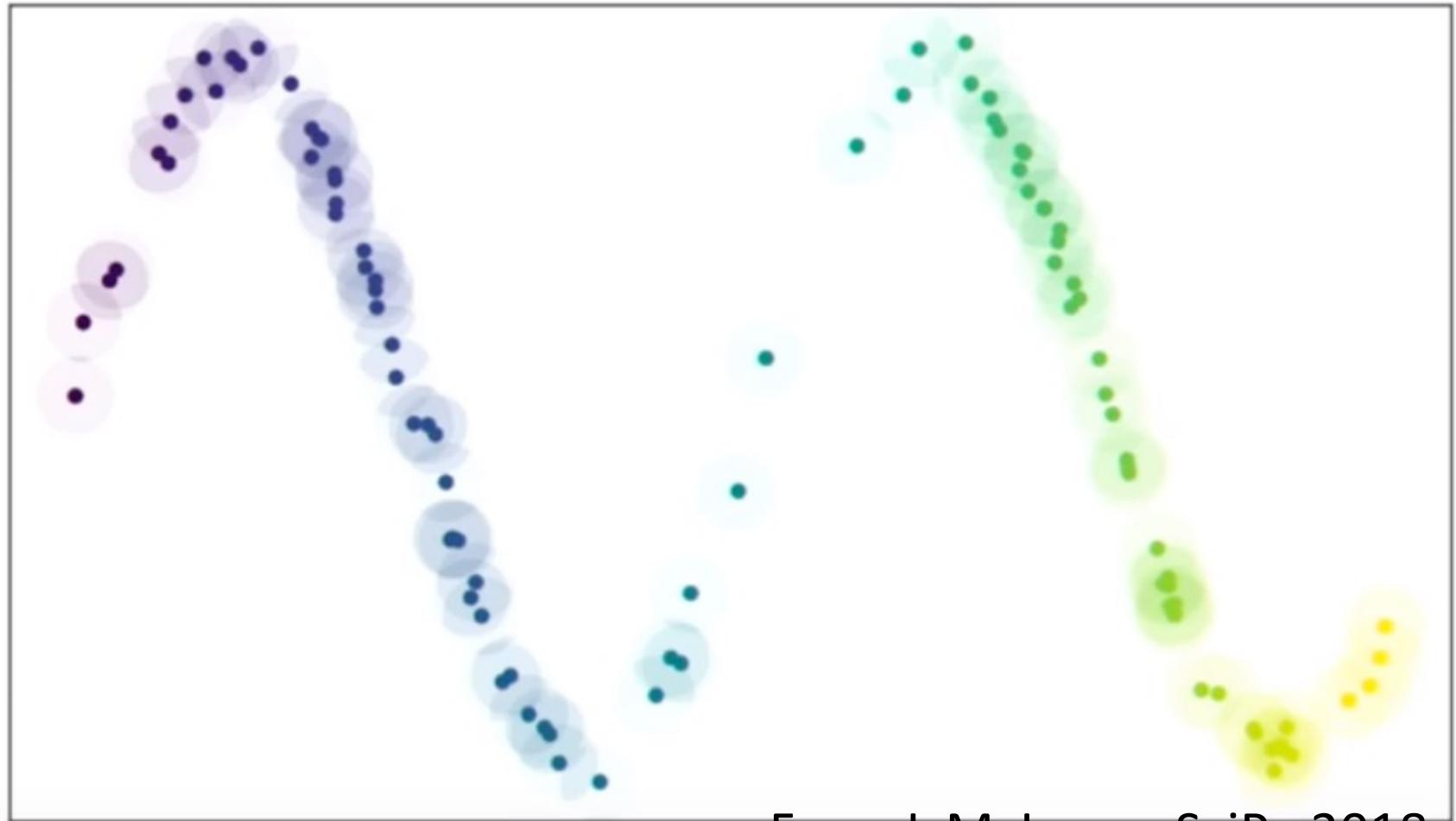


How do we build a
simplicial complex on top
of a data set?



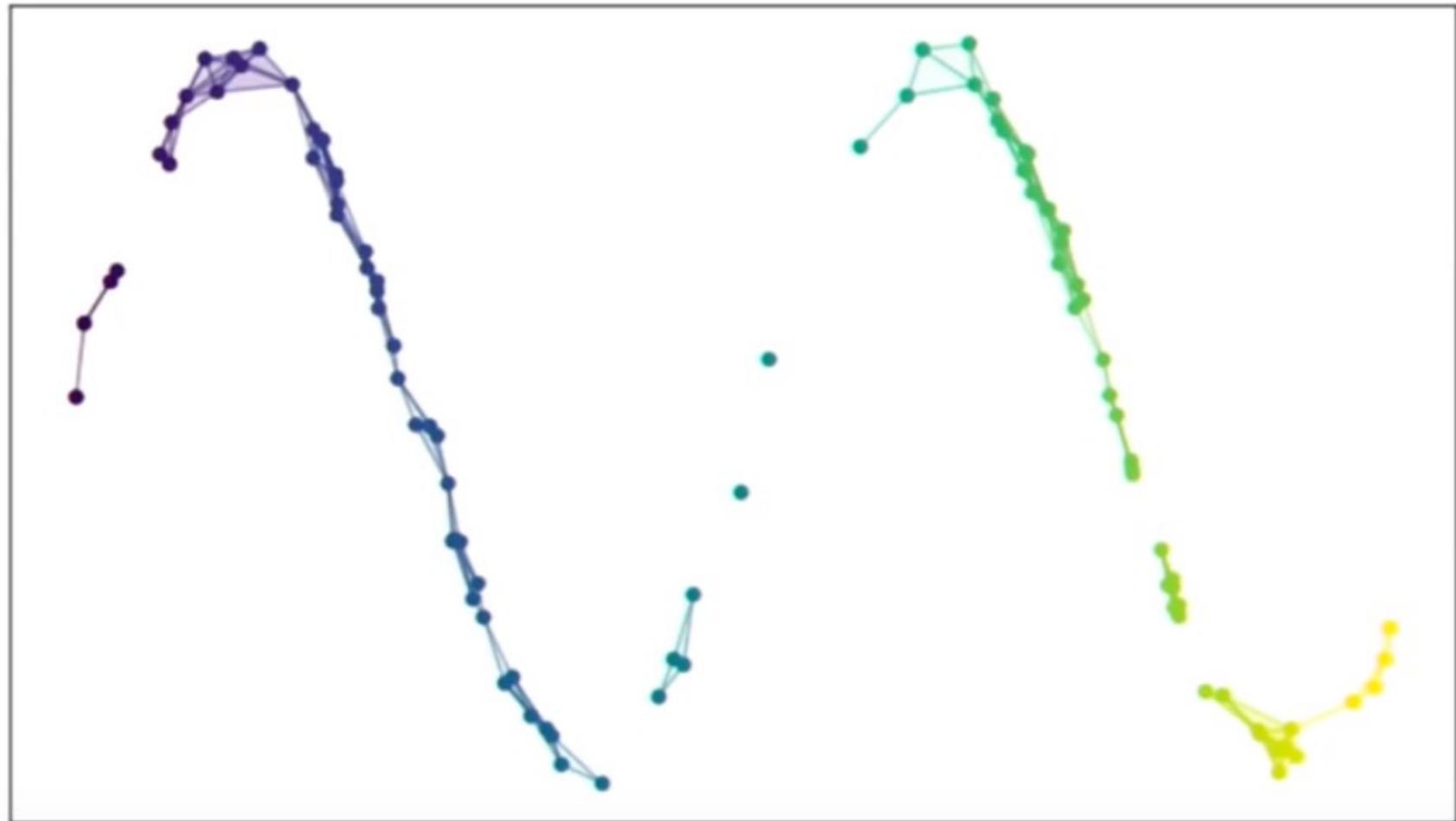
From L.McInnes, SciPy 2018

Step 1: draw unit-balls with a



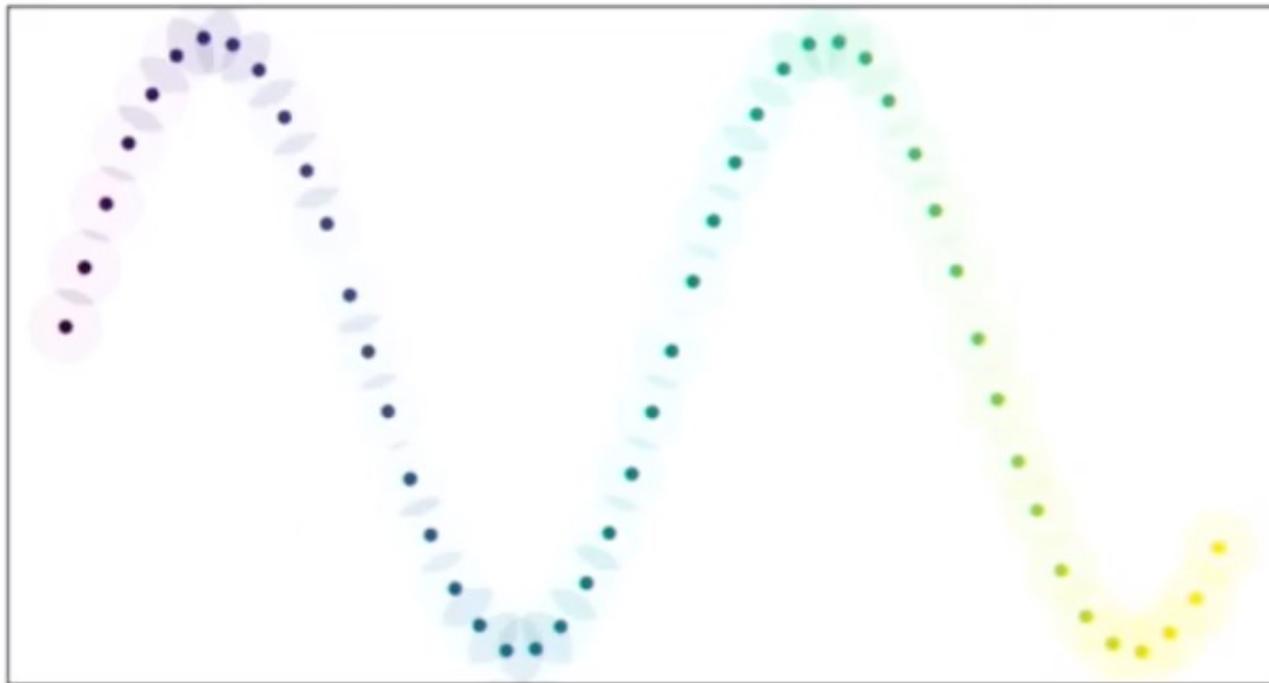
From L.McInnes, SciPy 2018

Step 2: Draw the Nerve of that



From L.McInnes, SciPy 2018

The data is not uniformly distributed on the underlying manifold

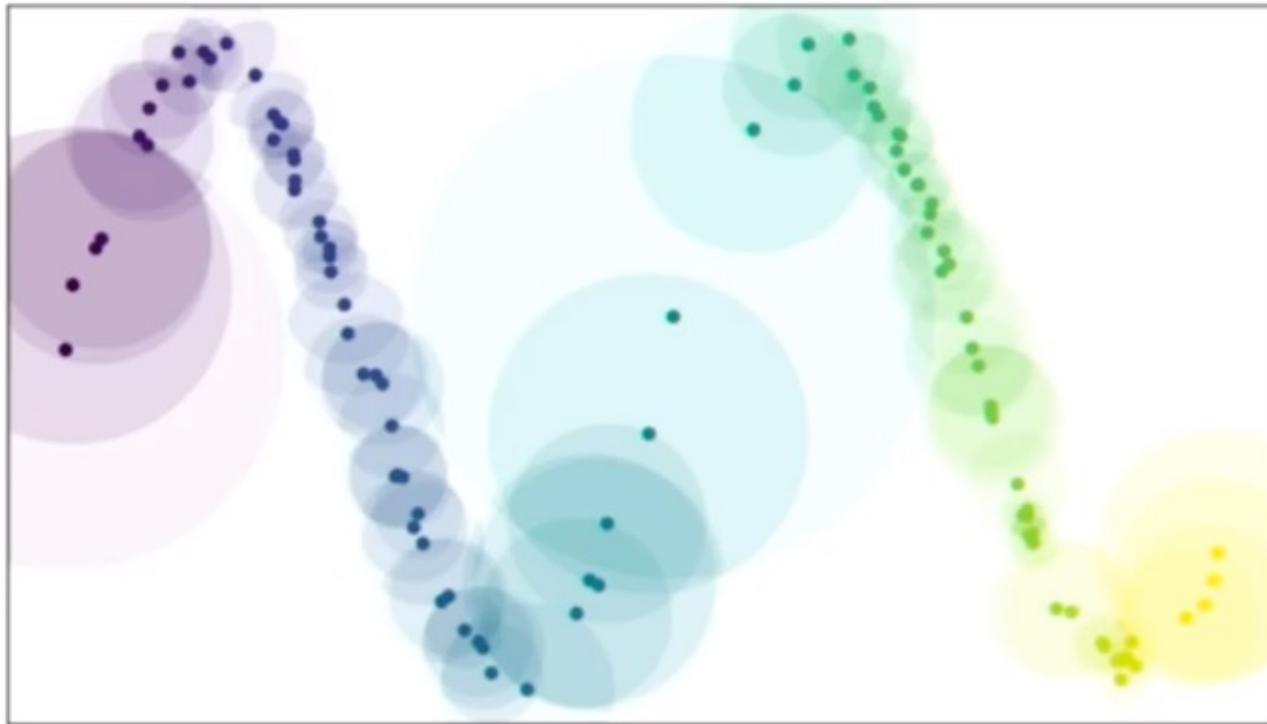


From L.McInnes, SciPy 2018

However... Data is not so nicely distributed

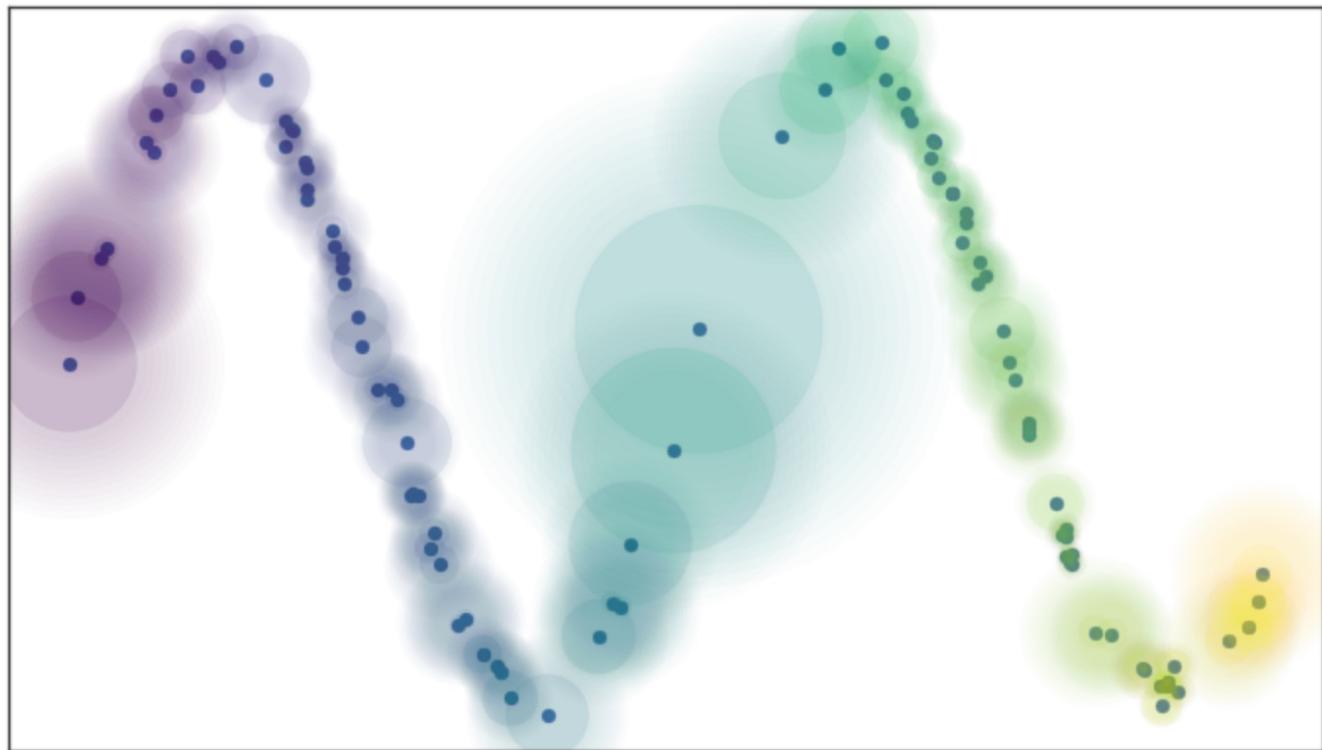
Solution: We vary the notion of metric and effectively the data will be with that metric uniformly distributed on the underlying manifold

How it looks like on the example



The radius of each ball is equal to one.

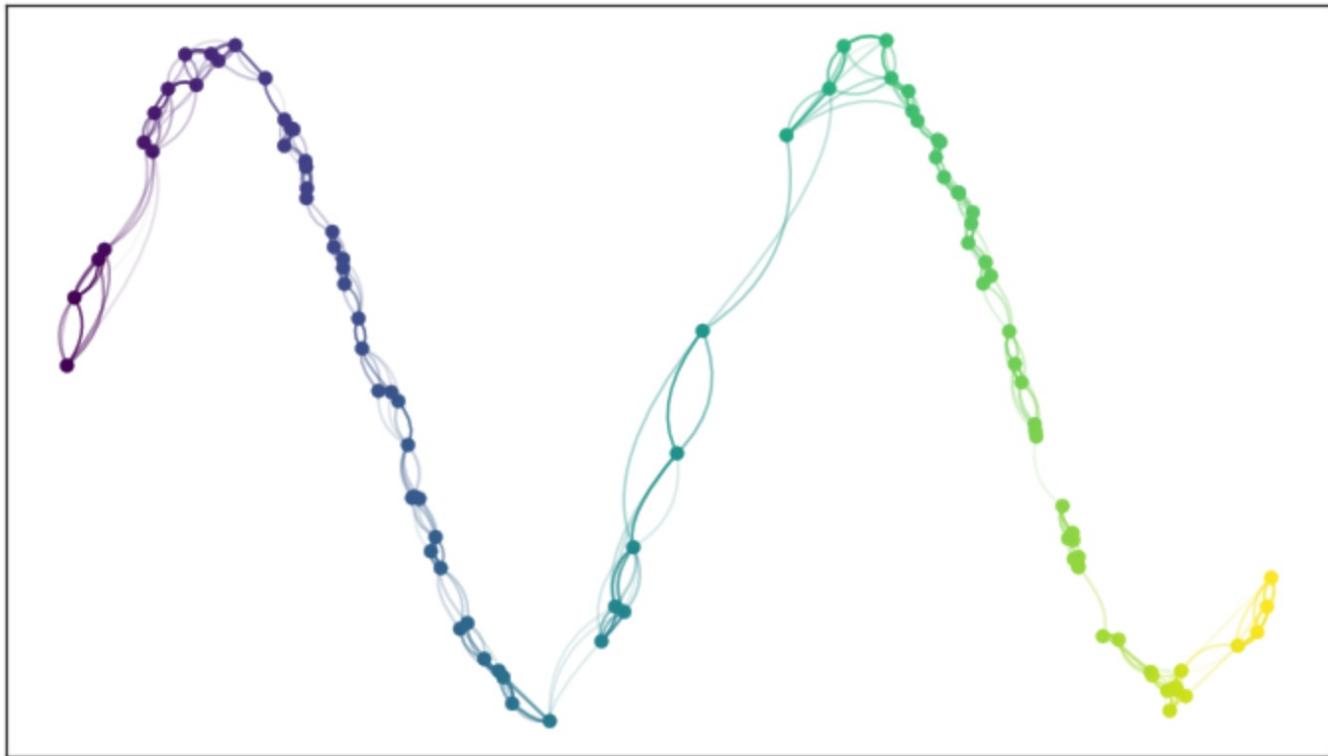
How it looks like on the example



Equivalent to choosing a cover of balls with varying radii. This is what Fuzzy covers try to do.

There are nice theorems again justifying that all of this is valid.

New directed graph



From L.McInnes, SciPy 2018

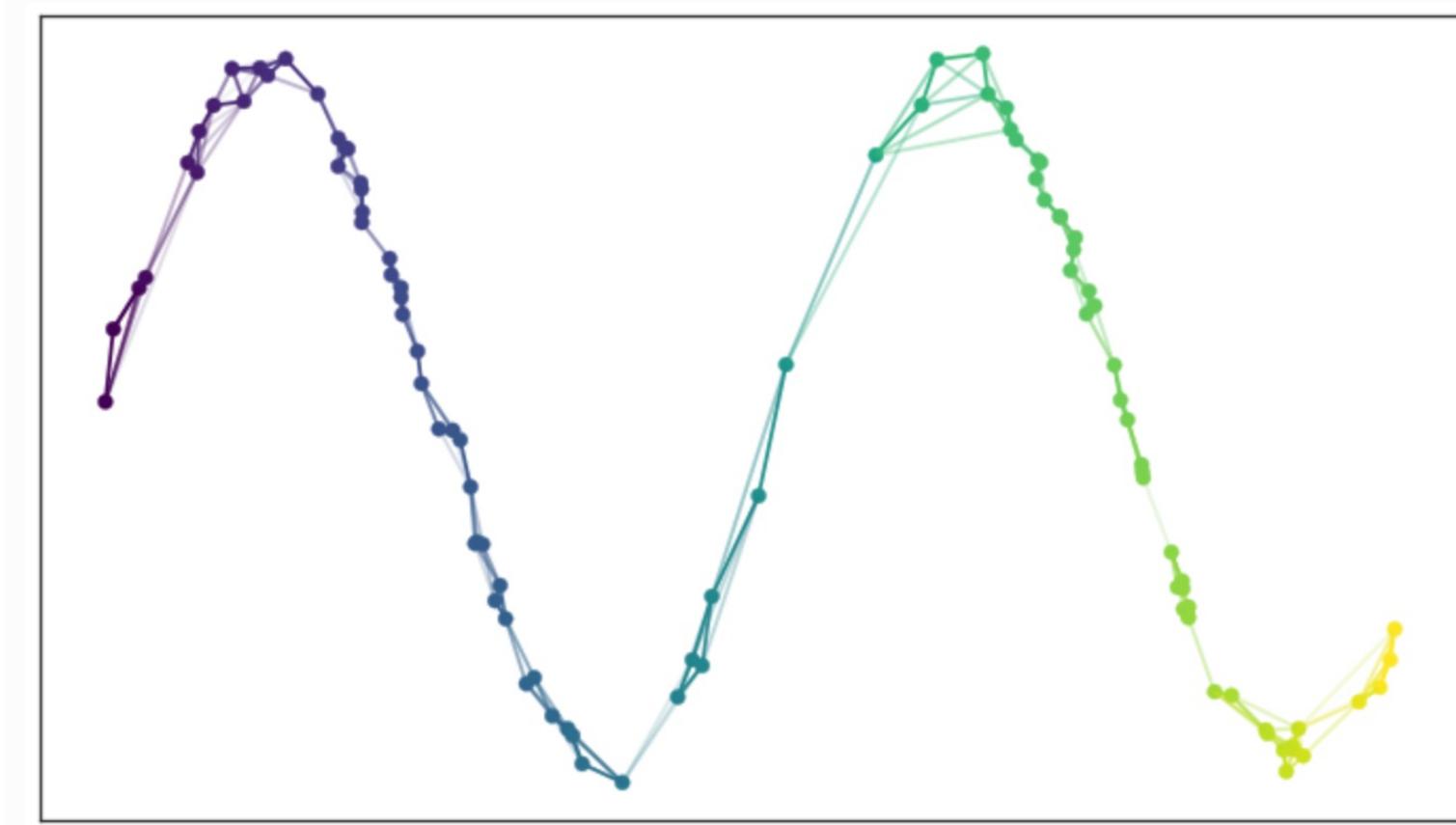


But we needed a
(weighted) simplicial
complex...

$$f(a,b) = a+b - a^*b$$

Solving the problem...

New simplicial complex



From L.McInnes, SciPy 2018

2nd assumption

The second assumption : the manifold is locally connected.

They use that for mathematics to work but has as an implication that in practice you will not find isolated points in your dataset.

Dimension reduction

Now, UMAP is a dimension reduction method. Let us say you would like to project the data onto \mathbb{R}^2

It will therefore take $Y = \{y_1, \dots, y_N\}$ in \mathbb{R}^2

Compute the fuzzy topological considering \mathbb{R}^2 to be the underlying manifold.

Optimizing this dimension reduction

Given fuzzy simplicial set representations : X and Y , a means of comparison is required.

For the purpose of calculations only the 1-skeleton of the fuzzy simplicial sets is considered (the l-skeletons are calculated using the 1-skeleton and can therefore be shown to be negligible)

To compare two fuzzy sets we will make use of fuzzy set ***cross entropy***.

Get the clumps right

$$\sum_{a \in A} \mu(a) \log \left(\frac{\mu(a)}{\nu(a)} \right) + (1 - \mu(a)) \log \left(\frac{1 - \mu(a)}{1 - \nu(a)} \right)$$

Get the gaps right

Summary

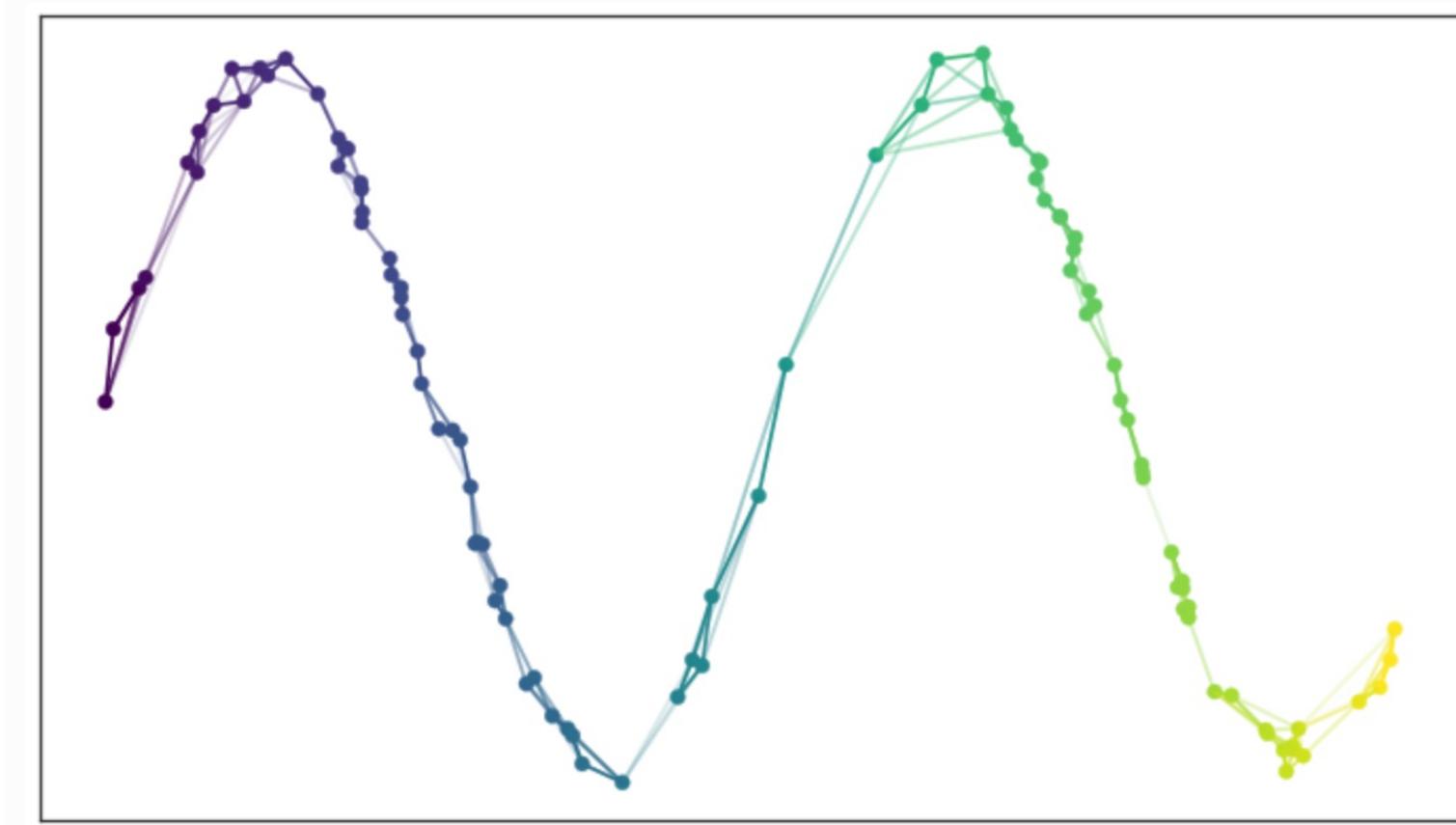
The first phase consists of constructing
a fuzzy topological representation
(edges and weights).

The second phase is optimizing the low
dimensional representation to have as
close as possible a fuzzy topological
representation as measured by cross
entropy.

Two shortcuts are needed for the computations

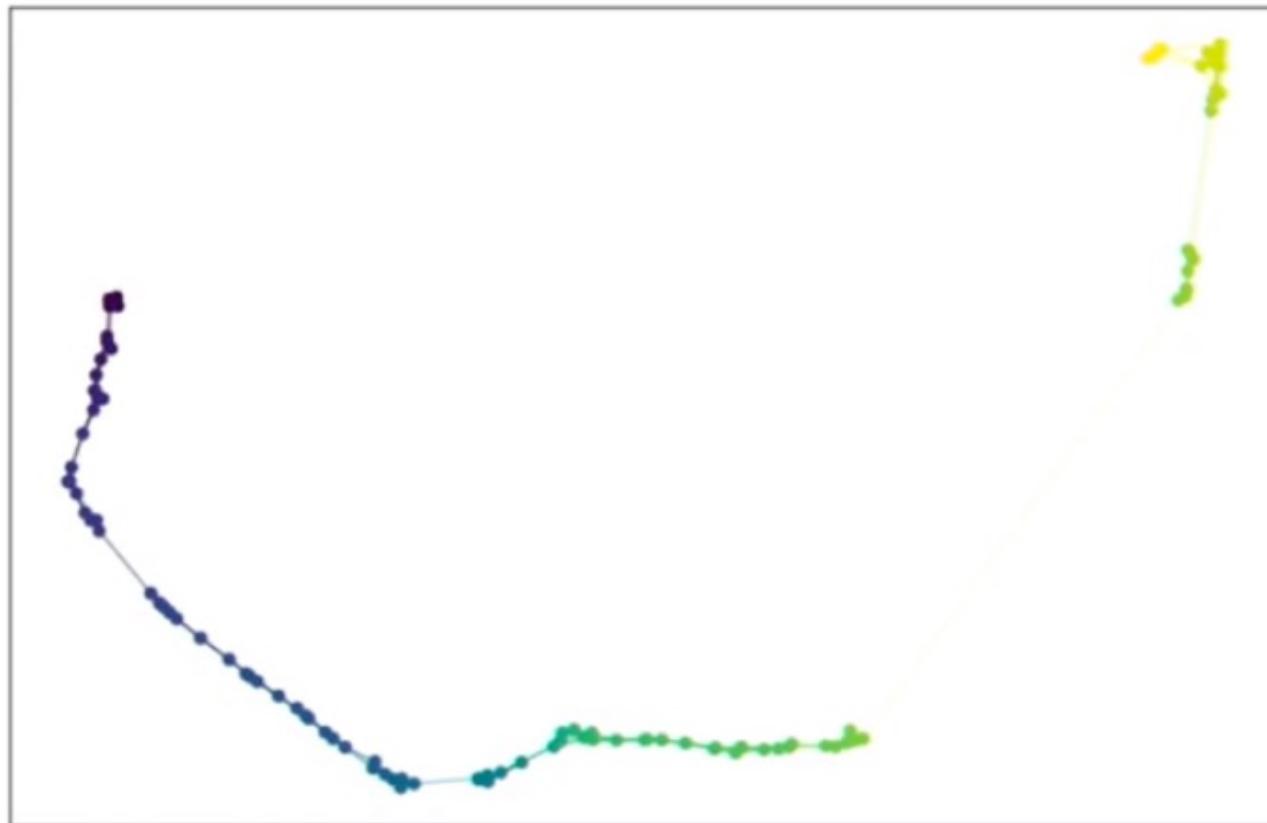
NNdescent: kNN approximation
algorithm
stochastic gradient descent + negative
sampling trick: Algorithms for
optimizing the cross entropy.

New simplicial complex



From L.McInnes, SciPy 2018

How the UMAP embedding looks



From L.McInnes, SciPy 2018

Input parameters

X: the data

n: the neighborhood parameter: number of neighbors to consider when approximating the local metric

d: the target embedding dimension (2 usually)

min-dist: »beauty» parameter for the local embedding in 2D: the desired separation between close points in the embedding space: this determines how closely points can be packed together in the low dimensional representation

n-epochs: optimization parameter for the local embedding in 2D the number of training *epochs (batches)* to use when optimizing the low dimensional representation.

Some parameters in Seurat:

```
n_neighbors = 30L,  
min_dist = 0.3,  
metric = "correlation",  
seed.use = 42,  
n_epochs=None
```

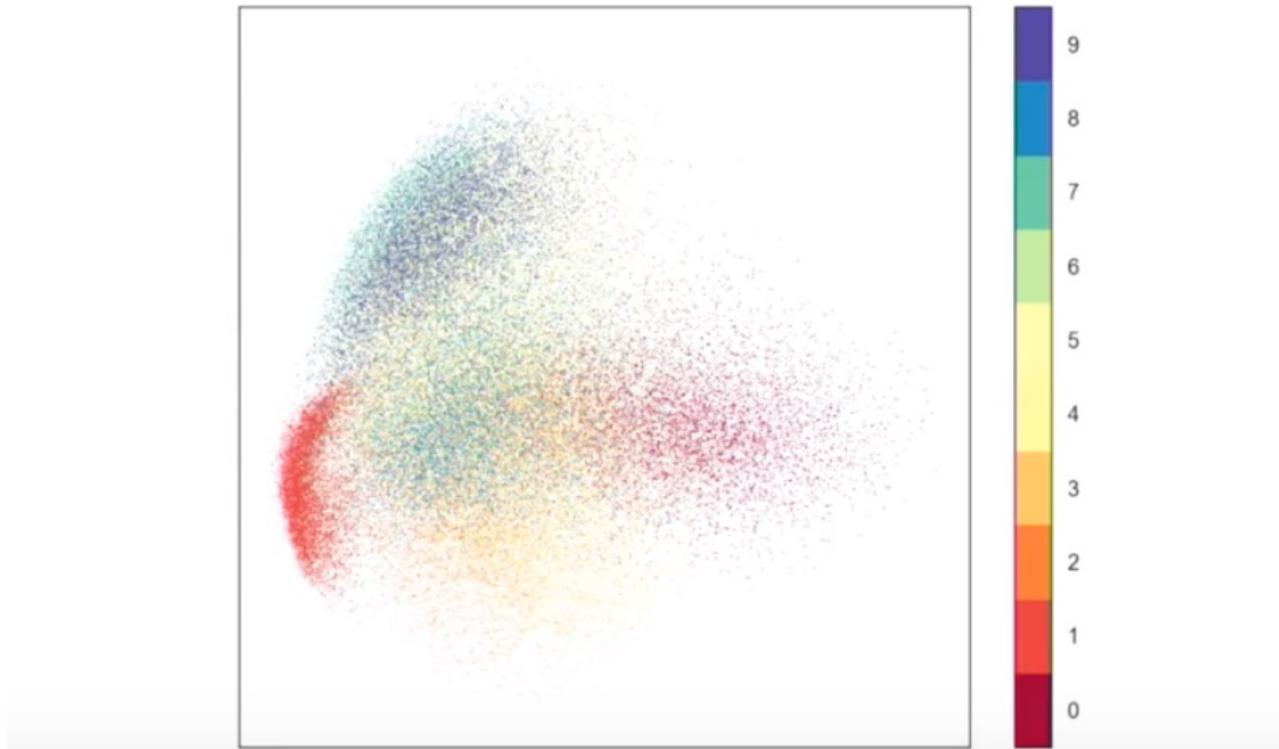
Comparing tSNE and UMAP in terms of computation time

	t-SNE	UMAP
COIL20	20 seconds	7 seconds
MNIST	22 minutes	98 seconds
Fashion MNIST	15 minutes	78 seconds
GoogleNews	4.5 hours	14 minutes

PCA is good, but one can do better!



PCA on MNIST digits



From L.McInnes, SciPy 2018

T-SNE manages to see the local structure



t-SNE on MNIST digits



From L.McInnes, SciPy 2018

UMAP



UMAP on MNIST digits

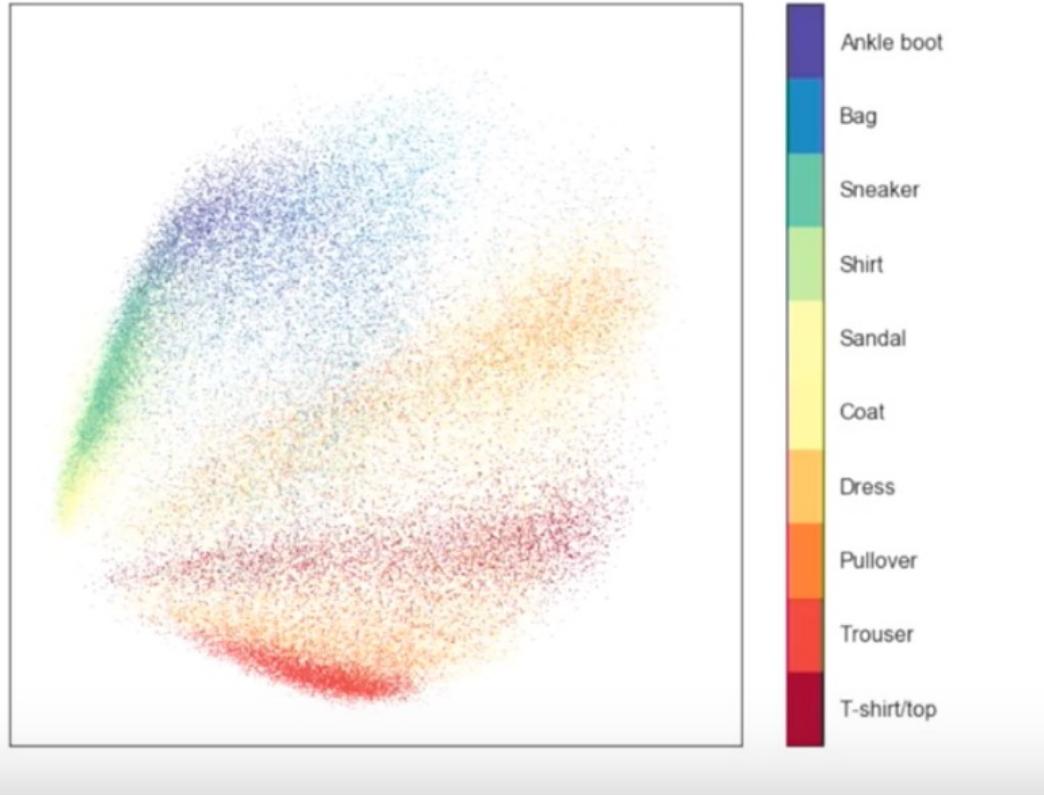


From L.McInnes, SciPy 2018

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PCA on Fashion MNIST



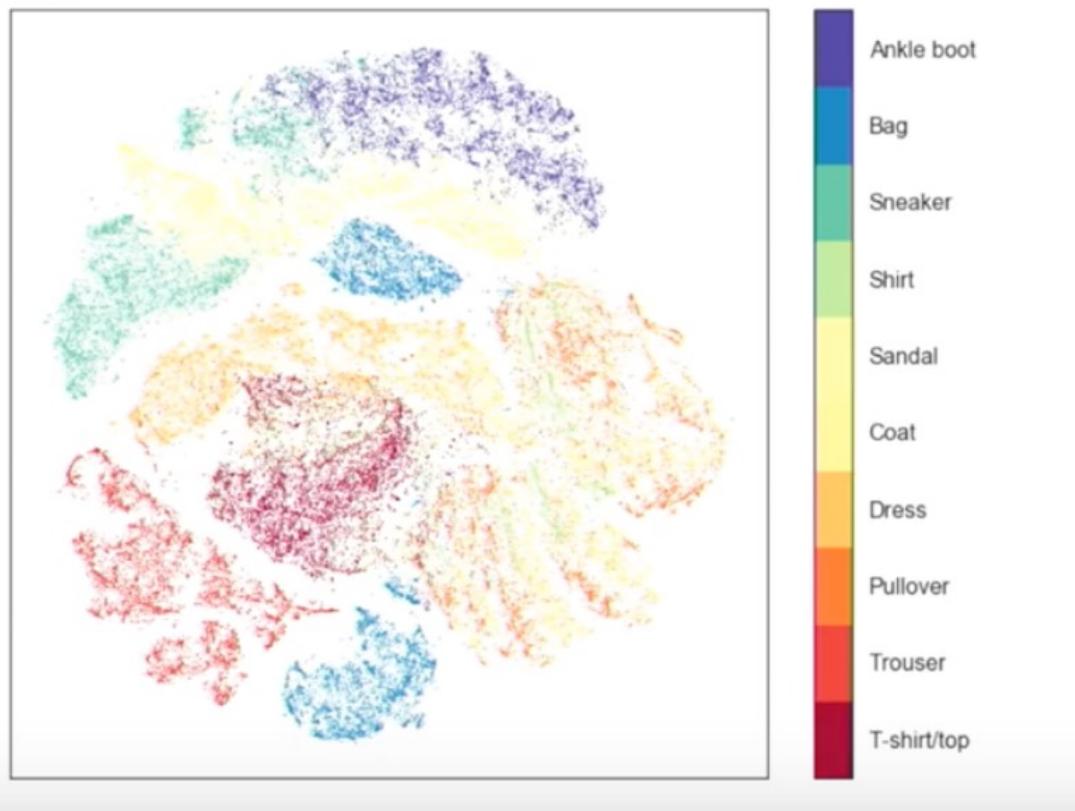
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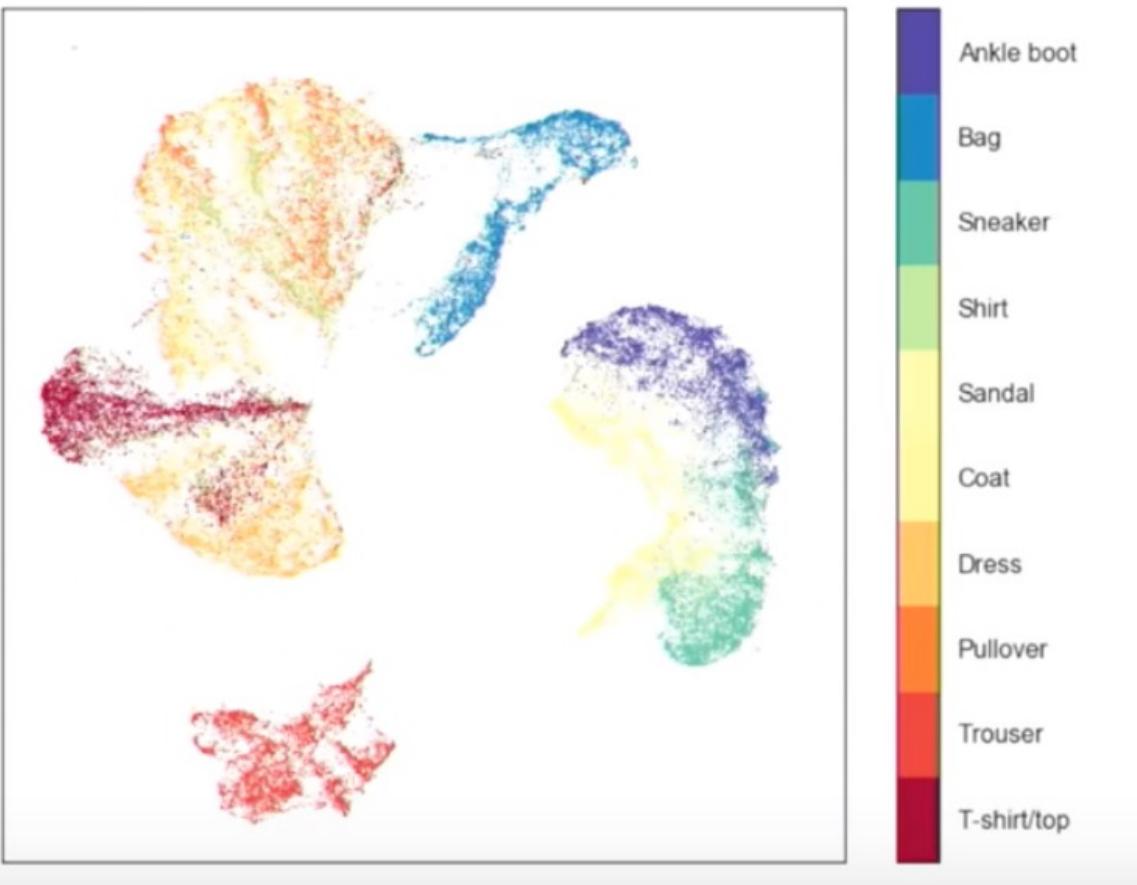


From L.McInnes, SciPy 2018

UMAP



UMAP on Fashion MNIST



	Seurat v3	Scater	Pagoda v2	Monocle v3
→	PCA ICA -	PCA - MDS	PCA - -	PCA ICA -
→	tSNE (BH, Flt) UMAP - Diff. Maps - PHATE -	tSNE (BH) UMAP - Diff. Maps - - -	tSNE (BH) - LargeVis Isomap - - -	tSNE (BH) UMAP - - DDRTree - SimplePPT

```
obj <- RunPCA( obj )
obj <- RunTSNE( obj )
obj <- RunUMAP( obj )
```