

Deep Unsupervised Learning

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Supervised learning is effective, but it has some limitations:

- ▶ Needs a lot of labeled data to work well.
- ▶ Getting labels can be difficult or costly.
- ▶ Depends on experts to label the data.
- ▶ Not practical for many real-world situations where labeling is hard or impossible.

- ▶ Humans are good at:
 - Learning patterns from experience
 - Discovering hidden structures
- ▶ But:
 - They are slow and limited
 - Not always available
 - Can't always explain what they observe

- ▶ What if machines could learn to:
 - Find hidden patterns
 - Understand structures in data
 - Group and compare similar things

Without any human-provided labels?

Unsupervised Learning to the Rescue



- ▶ Learns **without labels**
- ▶ Discovers **structure within the data**
- ▶ Mimics how humans learn from **observation**
- ▶ Useful for:
 - Clustering
 - Dimensionality reduction
 - Representation learning

- ▶ Simple models can't handle:
 - High variability in real-world data
 - Complex abstract features
- ▶ We need:
 - Neural networks
 - With many layers → “Deep”
 - To learn hierarchical patterns

Deep Unsupervised Learning — The Goal

- ▶ Discover hidden patterns
- ▶ Learn rich representations
- ▶ Group and distinguish data points
- ▶ Match similar structures

Deep Unsupervised Learning aims to discover **hidden patterns** and **structures** in raw data using deep neural networks, **without any human-provided labels**.

It focuses on **capturing rich patterns in raw data with deep networks in a label-free way**.

- ▶ **Learns from observation** — mimics how humans learn from experience
- ▶ **Discovers structure** — finds groups, similarities, and representations
- ▶ **Scales to complex data** — uses deep models to capture abstract features
- ▶ **Generative Models** — recreate raw data distribution
- ▶ **Self-supervised Learning** — “puzzle” tasks that require semantic understanding

Why do we care?



Geoffrey Hinton
(in his 2014 AMA on Reddit)

"The brain has about 10^{14} synapses and we only live for about 10^9 seconds. So we have a lot more parameters than data. This motivates the idea that we must do a lot of unsupervised learning since the perceptual input (including proprioception) is the only place we can get 10^5 dimensions of constraint per second."



Yann LeCun

Need tremendous amount of information to build machines that have common sense and generalize well.

[LeCun-20161205-
NeurIPS-keynote]

■ “Pure” Reinforcement Learning (**cherry**)

- ▶ The machine predicts a scalar reward given once in a while.
- ▶ **A few bits for some samples**

■ Supervised Learning (**icing**)

- ▶ The machine predicts a category or a few numbers for each input
- ▶ Predicting human-supplied data
- ▶ **10→10,000 bits per sample**

■ Unsupervised/Predictive Learning (**cake**)

- ▶ The machine predicts any part of its input for any observed part.
- ▶ Predicts future frames in videos
- ▶ **Millions of bits per sample**

■ (Yes, I know, this picture is slightly offensive to RL folks. But I'll make it up)



- ▶ "Ideal Intelligence" is all about compression (finding all patterns)
- ▶ Finding all patterns = short description of raw data (*low Kolmogorov Complexity*)
- ▶ Shortest code-length = optimal inference (*Solomonoff Induction*)
- ▶ Extensible to optimal action-making agents (*AIXI*)

Transfer Learning via Compression:

- ▶ Assume we pretrain unsupervised on Data Distribution D_1 and then finetune on Data Distribution D_2
- ▶ If D_1 and D_2 are related, compressing D_2 conditioned on D_1 should be more efficient than compressing D_2 outright
- ▶ **Hence:** pretraining on D_1 should aid faster learning of D_2

By the end of this session, you will be able to:

1. **Define** deep unsupervised learning and **differentiate** it from supervised and semi-supervised approaches.
2. **Understand** the importance and real-world applications of unsupervised learning in:
 - Natural language processing
 - Computer vision
 - Fraud detection
3. **Identify** key challenges in unsupervised learning:
 - Model evaluation
 - Lack of labeled ground truth

⇒ Learning Outcomes (cont.)

4. Classify main types of unsupervised learning tasks:

- Clustering
- Dimensionality reduction
- Anomaly detection

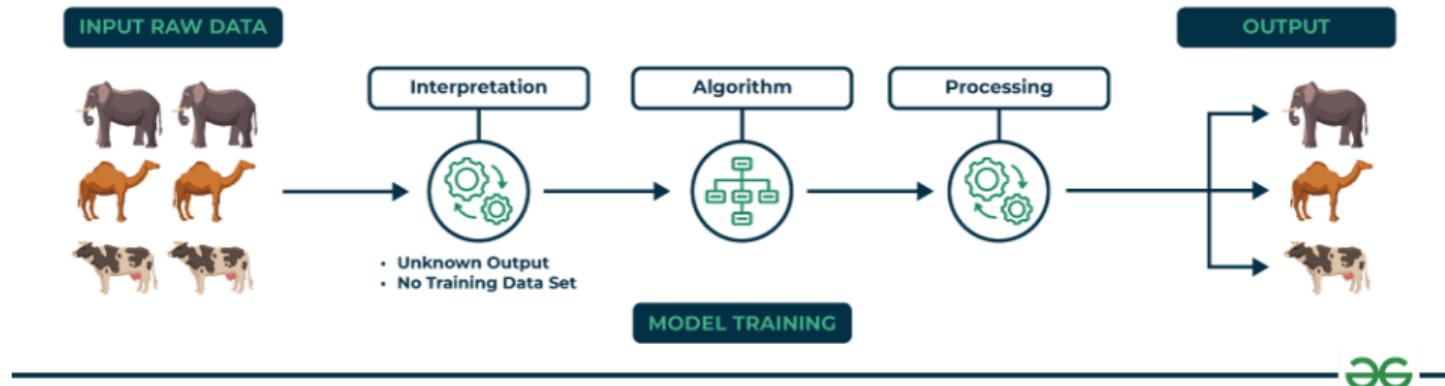
5. Explain core dimensionality reduction techniques:

- Principal Component Analysis (PCA)
- t-Distributed Stochastic Neighbor Embedding (t-SNE)
- Uniform Manifold Approximation and Projection (UMAP)

- ▶ **Data:** Unlabeled data, e.g., images, text, or sensor readings.
- ▶ **Model:** A mathematical representation of the data, e.g., a mixture model or a neural network.
- ▶ **Objective function:** A measure of how well the model fits the data, e.g., likelihood or reconstruction error.
- ▶ **Optimization algorithm:** An algorithm to minimize the objective function, e.g., gradient descent or expectation-maximization.
- ▶ **Evaluation metrics:** Measures to assess the quality of the learned model, e.g., silhouette score or clustering accuracy.

Applications: Use cases for unsupervised learning, e.g., clustering, dimensionality reduction, or anomaly detection.

Unsupervised Learning



Source: geeksforgeeks.org

Supervised vs Unsupervised Learning

Aspect	Supervised Learning	Unsupervised Learning
Objective	Learn a function f from labeled input–output pairs.	Discover structure or representations in unlabeled data.
Evaluation	Accuracy, precision/recall on held-out labels.	Clustering validity indices (e.g. silhouette), reconstruction error.
Cost	Methods range from $\mathcal{O}(n)$ to $\mathcal{O}(n^3)$ per fit.	k-means $\mathcal{O}(nkd)$, hierarchical $\mathcal{O}(n^2)$, PCA $\mathcal{O}(nd^2)$.
Labels/Clusters	Fixed, known set of classes.	Number of clusters unknown; must be chosen or inferred.
Output	Classifier or regressor for new inputs.	Cluster assignments, embeddings, density models, or generative samples.

Table 1: Key differences between Supervised and Unsupervised Learning

Deep Unsupervised Learning has many powerful applications:

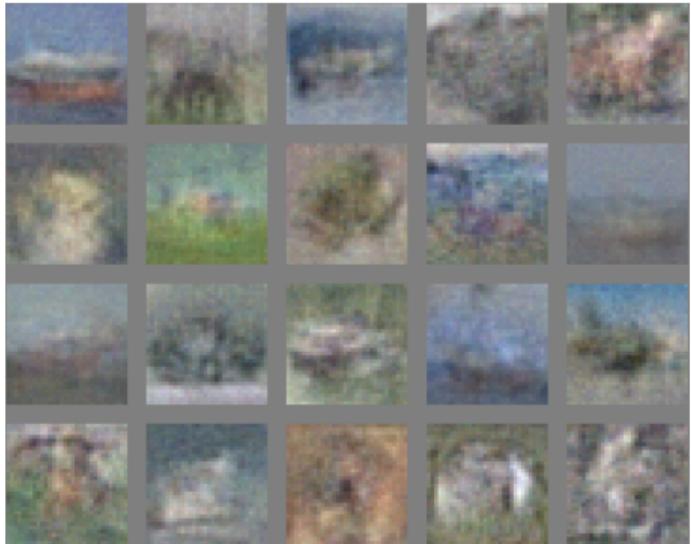
- ▶ **Generate Novel Data:** Create new data samples similar to the training set.
- ▶ **Conditional Synthesis Technology:** Enable advanced applications such as WaveNet for audio generation and GAN-based models like pix2pix for image-to-image translation.
- ▶ **Compression:** Learn compact representations for efficient data storage and transmission.
- ▶ **Improve Downstream Tasks:** Enhance performance of supervised tasks through unsupervised or self-supervised pre-training.
- ▶ **Production-Level Impact:** Power real-world systems, e.g., Google Search improvements with BERT pre-training.
- ▶ **Flexible Building Blocks:** Provide reusable components for a wide range of machine learning pipelines.

Application: Generate Images



Figure 2: [Deep Belief Nets, Hinton, Osindero, Teh, 2006]

Application: Generate Images (cont.)



[GAN, Goodfellow et al. 2014]

Application: Discovering Structure in Digits

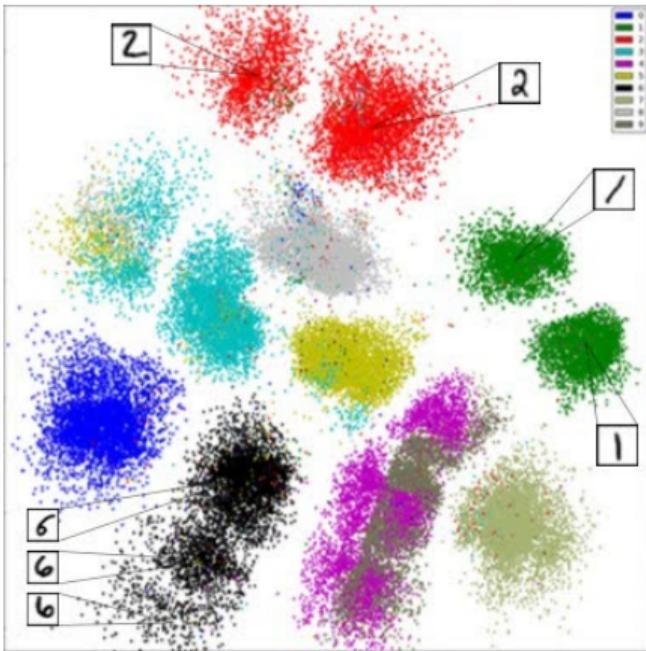


Figure 3: Unsupervised learning can discover structure in digits without any labels.

Application: DNA Analysis

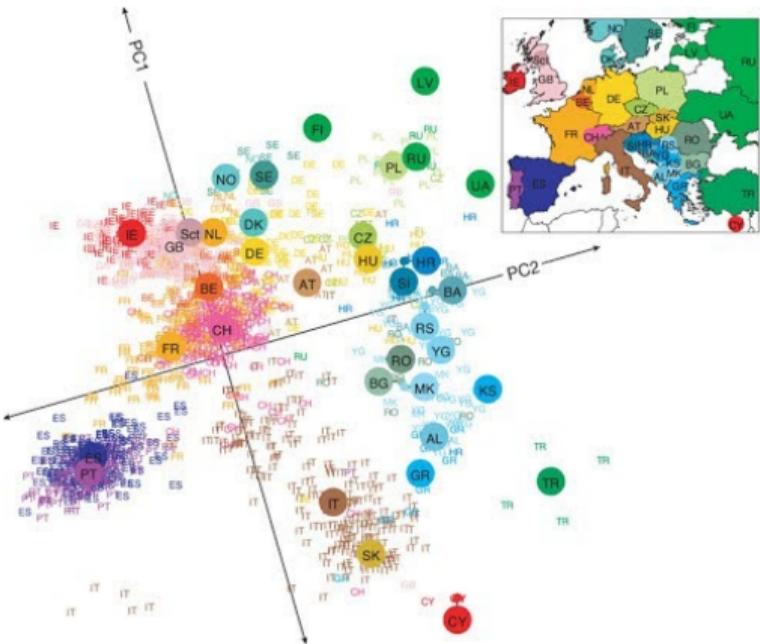


Figure 4: Dimensionality reduction applied to DNA reveal the geography of European countries.

Application: Text to Image Generation

“a masterful oil painting a persian exotic cat discovering their astounding crypto losses while checking their phone”



Application: Text to Audio Generation

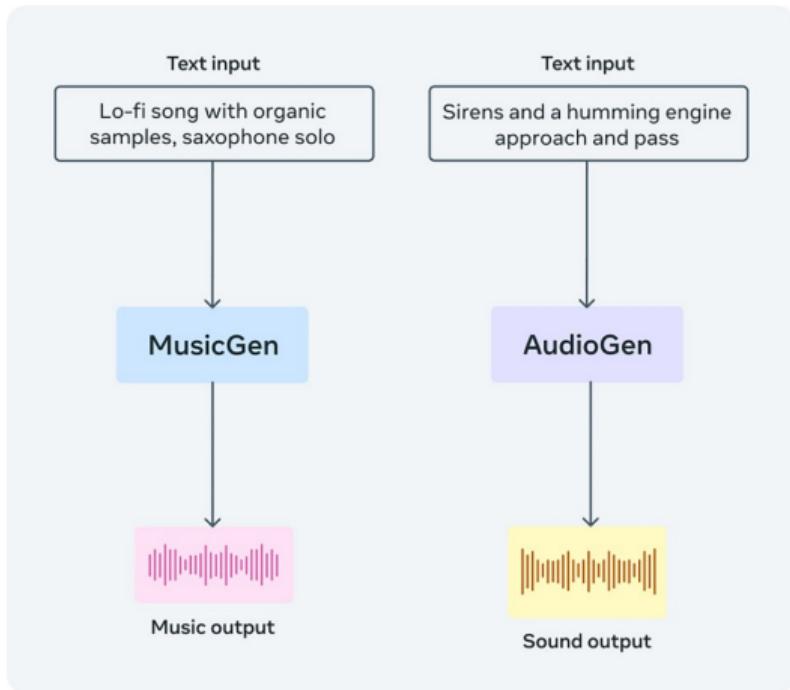


Figure 5: [AudioCraft, Copet et al., 2023]

Application: Text to Speech Generation

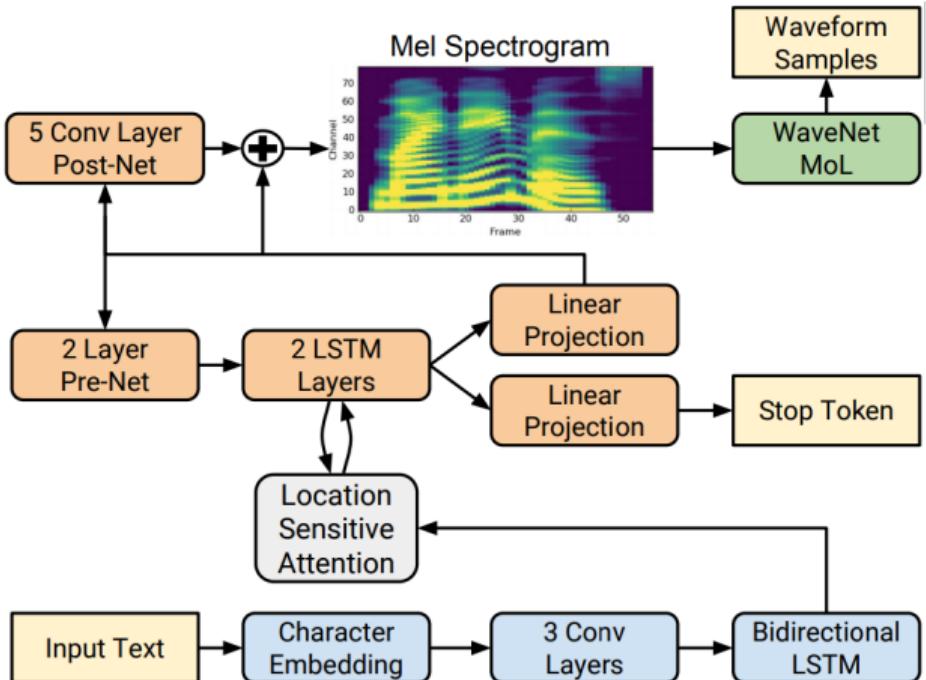


Figure 6: [Tacotron2 , Shen et al., 2018]

Application: Generate Math

For $\bigoplus_{n=1,\dots,m} \mathcal{L}_{m,n} = 0$, hence we can find a closed subset \mathcal{H} in \mathcal{H} and any sets \mathcal{F} on X , U is a closed immersion of S , then $U \rightarrow T$ is a separated algebraic space.

Proof. Proof of (1). It also start we get

$$S = \text{Spec}(R) = U \times_X U \times_X U$$

and the comparicoly in the fibre product covering we have to prove the lemma generated by $\coprod Z \times_U U \rightarrow V$. Consider the maps M along the set of points Sch_{fppf} and $U \rightarrow U$ is the fibre category of S in U in Section ?? and the fact that any U affine, see Morphisms, Lemma ???. Hence we obtain a scheme S and any open subset $W \subset U$ in $\text{Sh}(G)$ such that $\text{Spec}(R') \rightarrow S$ is smooth or an

$$U = \bigcup U_i \times_{S_i} U_i$$

which has a nonzero morphism we may assume that f_i is of finite presentation over S . We claim that $\mathcal{O}_{X,x}$ is a scheme where $x, x', x'' \in S'$ such that $\mathcal{O}_{X,x'} \rightarrow \mathcal{O}'_{X',x'}$ is separated. By Algebra, Lemma ?? we can define a map of complexes $\text{GL}_{S'}(x'/S'')$ and we win. \square

To prove study we see that $\mathcal{F}|_U$ is a covering of \mathcal{X}' , and \mathcal{T}_i is an object of $\mathcal{F}_{X/S}$ for $i > 0$ and \mathcal{F}_p exists and let \mathcal{F}_i be a presheaf of \mathcal{O}_X -modules on \mathcal{C} as a \mathcal{F} -module. In particular $\mathcal{F} = U/\mathcal{F}$ we have to show that

$$\widetilde{\mathcal{M}}^\bullet = \mathcal{I}^\bullet \otimes_{\text{Spec}(k)} \mathcal{O}_{S,s} - i_X^{-1} \mathcal{F}$$

is a unique morphism of algebraic stacks. Note that

$$\text{Arrows} = (\text{Sch}/S)^{opp}_{fppf}, (\text{Sch}/S)_{fppf}$$

and

$$V = \Gamma(S, \mathcal{O}) \longrightarrow (U, \text{Spec}(A))$$

is an open subset of X . Thus U is affine. This is a continuous map of X is the inverse, the groupoid scheme S .

Proof. See discussion of sheaves of sets. \square

The result for prove any open covering follows from the less of Example ???. It may replace S by $X_{\text{spaces},\text{etale}}$ which gives an open subspace of X and T equal to S_{Zar} , see Descent, Lemma ???. Namely, by Lemma ?? we see that R is geometrically regular over S .

Lemma 0.1. Assume (3) and (3) by the construction in the description.

Suppose $X = \lim |X|$ (by the formal open covering X and a single map $\text{Proj}_X(\mathcal{A}) = \text{Spec}(B)$ over U compatible with the complex

$$\text{Set}(\mathcal{A}) = \Gamma(X, \mathcal{O}_{X,\mathcal{O}_X}).$$

When in this case of to show that $\mathcal{Q} \rightarrow \mathcal{C}_{Z/X}$ is stable under the following result in the second conditions of (1), and (3). This finishes the proof. By Definition ?? (without element is when the closed subschemes are catenary. If T is surjective we may assume that T is connected with residue fields of S . Moreover there exists a closed subspace $Z \subset X$ where U in X' is proper (some defining as a closed subset of the uniqueness it suffices to check the fact that the following theorem

(1) f is locally of finite type. Since $S = \text{Spec}(R)$ and $Y = \text{Spec}(R)$.

Proof. This is form all sheaves of sheaves on X . But given a scheme U and a surjective étale morphism $U \rightarrow X$. Let $U \cap U = \coprod_{i=1,\dots,n} U_i$ be the scheme X over S at the schemes $X_i \rightarrow X$ and $U = \lim_i X_i$. \square

The following lemma surjective resto-composes of this implies that $\mathcal{F}_{x_0} = \mathcal{F}_{x_0} = \mathcal{F}_{\mathcal{X},\dots,0}$.

Lemma 0.2. Let X be a locally Noetherian scheme over S , $E = \mathcal{F}_{X/S}$. Set $\mathcal{I} = \mathcal{J}_1 \subset \mathcal{I}'_n$. Since $\mathcal{I}^n \subset \mathcal{I}^n$ are nonzero over $i_0 \leq p$ is a subset of $\mathcal{J}_{n,0} \circ \widetilde{A}_2$ works.

Lemma 0.3. In Situation ???. Hence we may assume $q' = 0$.

Proof. We will use the property we see that p is the next functor (??). On the other hand, by Lemma ?? we see that

$$D(\mathcal{O}_{X'}) = \mathcal{O}_X(D)$$

where K is an F -algebra where δ_{n+1} is a scheme over S . \square

Figure 7: [Char-rnn, karpathy, 2015]

Prompt [human written]: A train carriage containing controlled nuclear materials was stolen in Cincinnati today. Its whereabouts are unknown.

GPT-2: The incident occurred on the downtown train line, which runs from Covington and Ashland stations. In an email to Ohio news outlets, the U.S. Department of Energy said it is working with the Federal Railroad Administration to find the thief. 'The theft of this nuclear material will have significant negative consequences on public and environmental health, our workforce and the economy of our nation,' said Tom Hicks, the U.S. Energy Secretary, in a statement. 'Our top priority is to secure the theft and ensure it doesn't happen again.' The stolen material was taken from the University of Cincinnati's Research Triangle Park nuclear research site, according to a news release from Department officials. The Nuclear Regulatory Commission did not immediately release any information. According to the release, the U.S. Department of Energy's Office of Nuclear Material Safety and Security is leading that team's investigation. 'The safety of people, the environment and the nation's nuclear stockpile is our highest priority,' Hicks said. 'We will get to the bottom of this and make no excuses.'

[OpenAI's GPT2 – Radford, Wu, Child, Luan, Amodei, Sutskever, 2019]

Why is unsupervised learning challenging?

▶ **Lack of labeled data:**

We don't have labels or answers to guide us—it's like solving a puzzle without a picture.

▶ **Difficult to assess performance:**

It's hard to know if our results are good, since there's nothing to compare them to.

▶ **Sensitivity to noise:**

The algorithms can get confused by noisy or unusual data points.

▶ **Curse of dimensionality:**

When there are too many features, it's tough to find real patterns—the data gets too spread out.

▶ **Interpretability issues:**

The results can be hard to understand or explain, making it tricky to use them effectively.

► Cluster Analysis:

- For identifying homogenous subgroups of samples.
- **Examples:** K-means, hierarchical clustering, DBSCAN.

► Dimensionality Reduction:

- For finding a low-dimensional representation to characterize and visualize the data.
- Reducing the number of features in a dataset while preserving important information.
- **Examples:** PCA, t-SNE, UMAP.

► Anomaly Detection:

- **Finding outliers in the dataset:** Identifying unusual (rare items, events, or observations) data points that do not conform to expected patterns.
- **Examples:** Isolation Forest, One-Class SVM, Autoencoders.

A set of methods for finding subgroups within the dataset.

- ▶ Observations should share common characteristics within the same group, but differ across groups.
- ▶ Groupings are determined from attributes of the data itself — differs from classification.

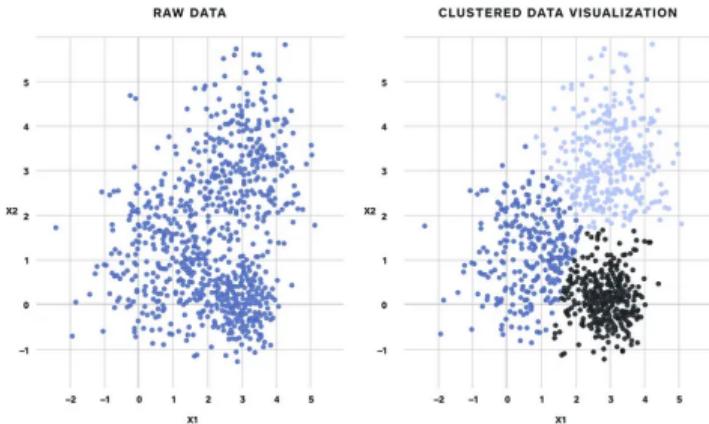


Figure 8: Taking a 2 dimensional dataset and separating it into 3 distinct clusters. [Source]

Clustering (cont.)

Input: Dataset $D = \{x_1, x_2, \dots, x_n\}$, number of clusters k

Output: Cluster assignments for each data point

Initialization: Randomly initialize k cluster centroids or seeds;

repeat

Assignment Step: Assign each data point x_i to the nearest cluster based on a distance metric;

Update Step: Recompute cluster centroids using current assignments;

until *convergence or maximum iterations reached*;

return Final cluster assignments;

Algorithm: Generic Clustering Algorithm

Clustering Vs Classification

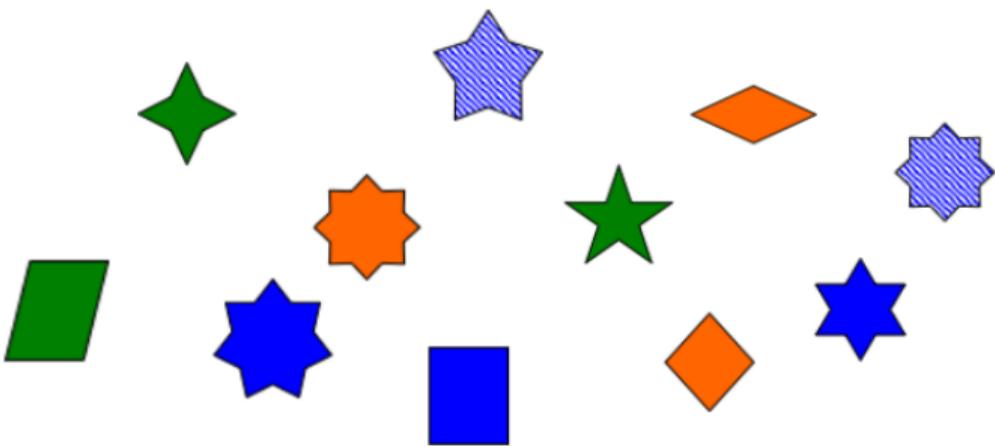


Figure 9: Sample data points.

Clustering Vs Classification (cont.)

Classification

- ▶ Labels available
- ▶ Assigning to known classes
- ▶ Supervised

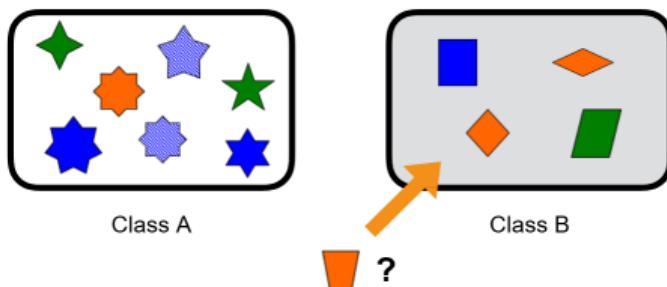
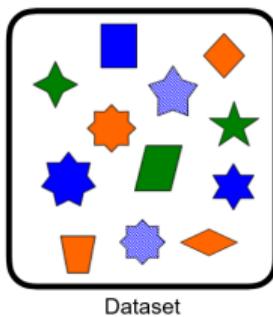


Figure 10: Classification result.

Clustering

- ▶ No labels
- ▶ Grouping based on similarity
- ▶ Unsupervised



Dataset

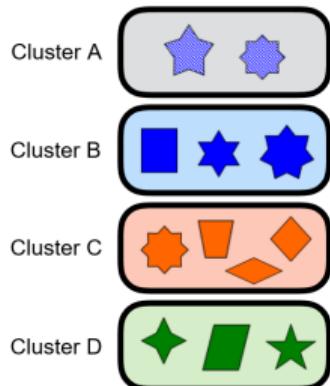


Figure 11: Clustering result.

- ▶ **Centroid-Based Clustering:** Groups data points based on their proximity to a central point, such as K-means or K-medoids.
- ▶ **Hierarchical Clustering:** Builds a hierarchy of clusters using either agglomerative (bottom-up) or divisive (top-down) approaches.
- ▶ **Model-Based Clustering:**
 - Each cluster is represented by a parametric distribution.
 - Dataset is a mixture of distributions.
 - Assumes a probabilistic model for the data and uses statistical methods to identify clusters, such as Gaussian Mixture Models (GMM).
- ▶ **Hard Clustering:**
 - Each data point is assigned exclusively to exactly one cluster.
 - **Example algorithms:** K-means, Hierarchical clustering.
 - **interpretation:** No ambiguity — clusters are crisp and non-overlapping.

► Soft/Fuzzy Clustering:

- Each data point can belong to multiple clusters simultaneously with varying degrees of membership (probabilities or weights).
- **Example algorithms:** Gaussian Mixture Models (GMM), Fuzzy C-means.
- **interpretation:** Reflects uncertainty or mixed membership — clusters can overlap.

Clustering - K-means

Groups data into K clusters that satisfy two properties.

1. Each observation belongs to at least one of the K clusters.
2. Clusters are non-overlapping.
No observation belongs to more than one cluster.

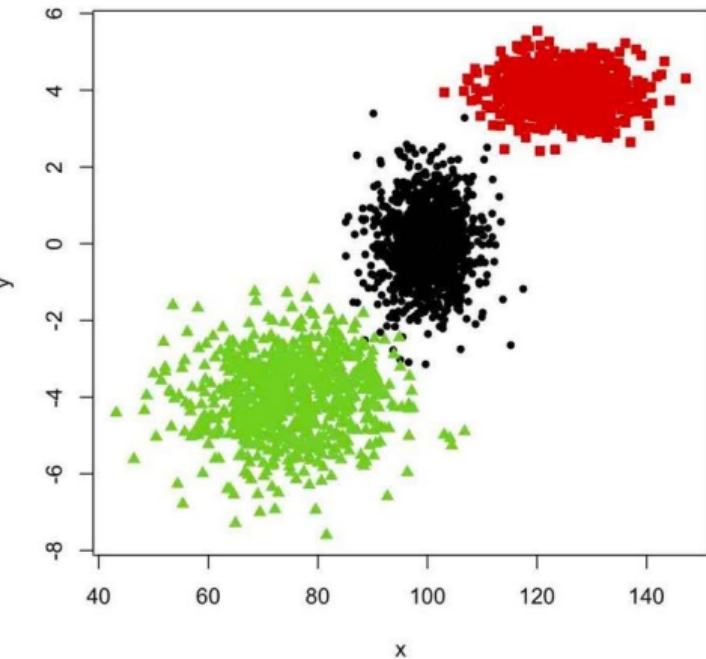


Figure 12: Clusters.

Clustering - K-means (cont.)

A good clustering is one for which the *within-cluster variation* is as small as possible.

Denote each cluster by C_k , and let $W(C_k)$ be a measure of the within-cluster variation.

K-means aims to solve the following optimization problem:

$$\underset{C_1, \dots, C_k}{\text{minimise}} \left\{ \sum_{k=1}^K W(C_k) \right\} \quad (1)$$

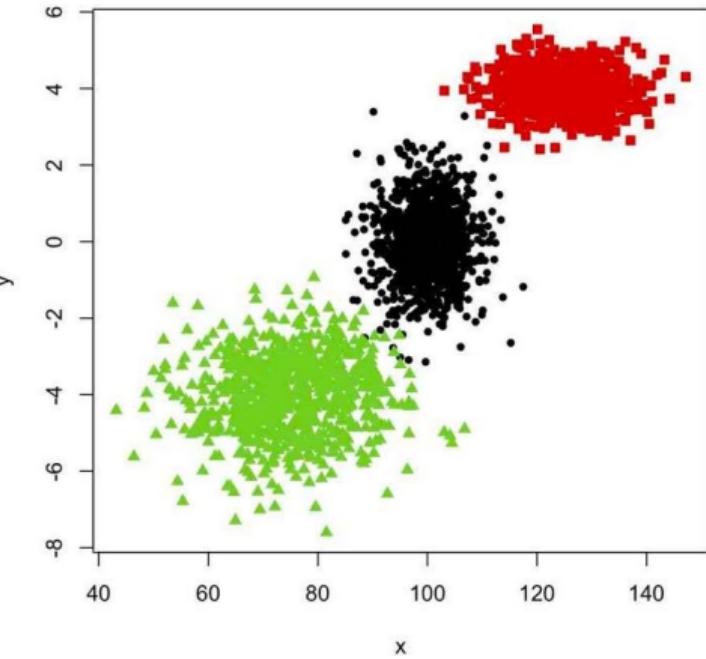


Figure 13: Clusters.

How to measure within-cluster variation?

The most common choice is squared Euclidean distance:

$$W(C_k) = \frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^p (x_{ij} - x_{i'j})^2 \quad (2)$$

where $|C_k|$ is the number of points in cluster C_k and x_{ij} is the j^{th} feature of the i^{th} point.

Which means overall we solve:

$$\underset{C_1, \dots, C_K}{\text{minimise}} \left\{ \sum_{k=1}^K \frac{1}{|C_k|} \sum_{i,i' \in C_k} \sum_{j=1}^p (x_{ij} - x_{i'j})^2 \right\} \quad (3)$$

Clustering - K-means (cont.)

- ▶ It turns out that this optimization problem is difficult to solve, as it is discrete and there are nearly K^n ways to split n samples into K clusters.
- ▶ In practice, use an iterative algorithm that finds a local minimum to this optimization.

Input: Dataset $D = \{x_1, x_2, \dots, x_n\}$, number of clusters k

Output: Cluster assignments for each data point

Initialization: Randomly initialize k cluster centroids or seeds;

Repeat until convergence:

- ▶ **Assignment Step:** Assign each data point x_i to the nearest cluster based on a distance metric;
- ▶ **Update Step:** Recompute cluster centroids using current assignments;
- ▶ **Convergence Check:** Check if cluster assignments have changed or if centroids have stabilized;

Return: Final cluster assignments and centroids;

Algorithm: K-means Clustering Algorithm

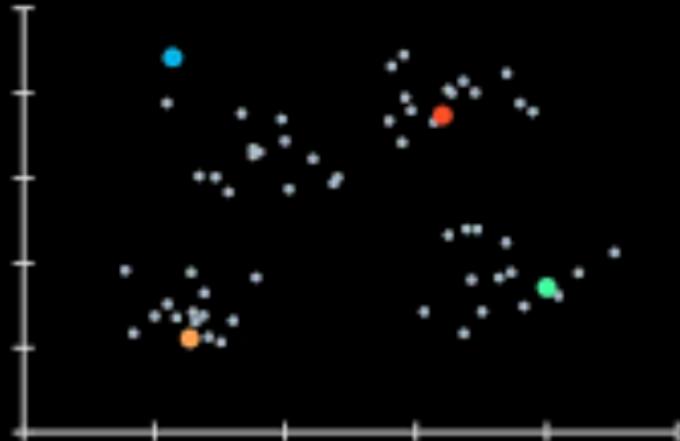
Clustering - K-means (cont.)

Watch the K-means clustering algorithm in action:

Clustering - K-means (cont.)

K-Means Algorithm

1. Initialize centroid positions ($k = 4$)
2. Assign labels (μ) to all data (X)
 $\mu_n = \underset{i}{\operatorname{argmin}} \|x_n - c_i\|$



Clustering - K-means (cont.)

1. It can be shown that the value of the objective function will never increase at each iteration of k -means.
2. Since the algorithm finds local minima, however, it will result in different clusters with different initializations.

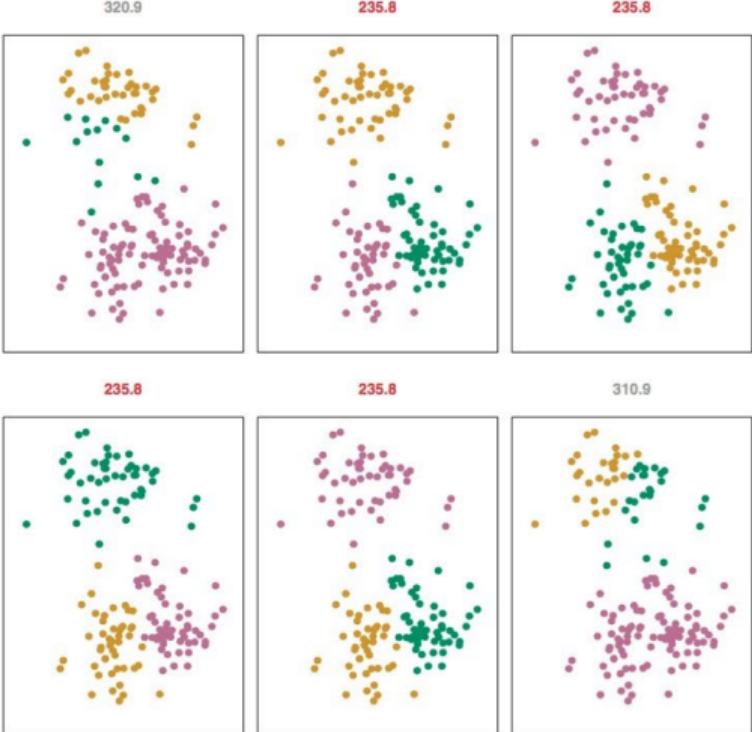


Figure 14: Different initializations of K-means.

Pros

- ▶ Simple and easy to implement
- ▶ Efficient for large datasets
- ▶ Works well with spherical clusters
- ▶ Scalable to large datasets

Cons

- ▶ Not robust to data perturbations and different initializations
- ▶ Sensitive to initial centroid placement
- ▶ Assumes spherical clusters
- ▶ Requires specifying the number ' K ' of clusters in advance
- ▶ Sensitive to outliers
- ▶ May converge to local minima
- ▶ Not suitable for non-convex shapes

Clustering - Hierarchical

Cluster based on distances between observations.

Represented as a tree hierarchy (*dendrogram*) rather than a partition of data.

Does not require committing to a choice of K .

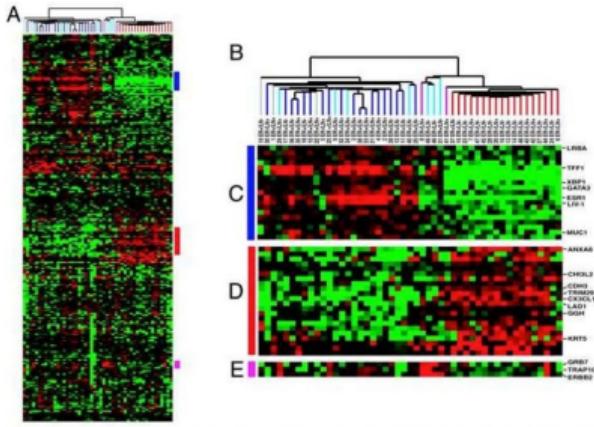


Figure 15: Sørlie, Therese, et al. (2003)
"Repeated observation of breast tumor subtypes in independent gene expression data sets,"
PNAS.

Clustering - Hierarchical: Dendrograms

- ▶ Each leaf in a dendrogram is a sample/ observation.
- ▶ As we move up the dendrogram, observations that are similar to each other begin to fuse into branches.
- ▶ Branches then fuse into bigger branches.
- ▶ Observations that fuse later (near the top of the tree, or root) are more different than observations that fuse earlier (near the leaves).

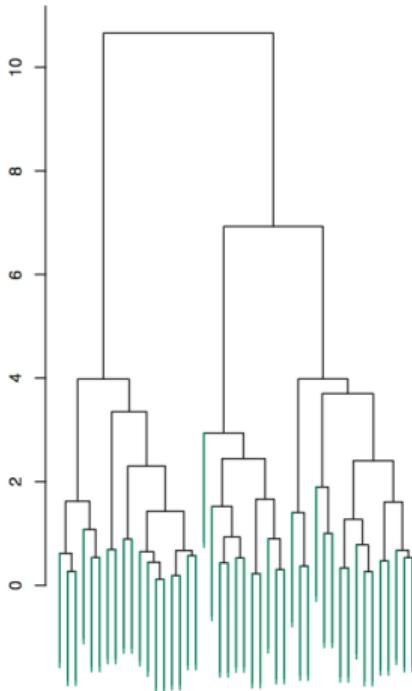


Figure 16: ISL (8th printing 2017)

Clustering - Hierarchical: Dendrograms (cont.)

Note that the horizontal distance between observations on a dendrogram is not the appropriate assessment of observation similarity. Instead, look at vertical axis where branches are first fused.

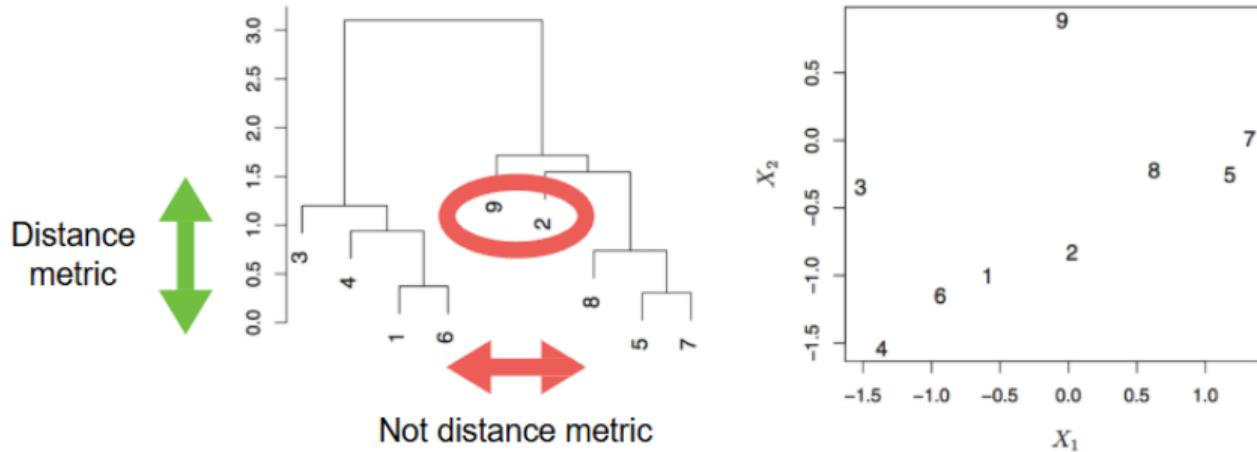


Figure 17: ISL (8th printing 2017)

Clustering - Hierarchical: Dendograms (cont.)

Clusters are created by making a horizontal cut across the dendrogram. Clusters are the separate trees below the cut.

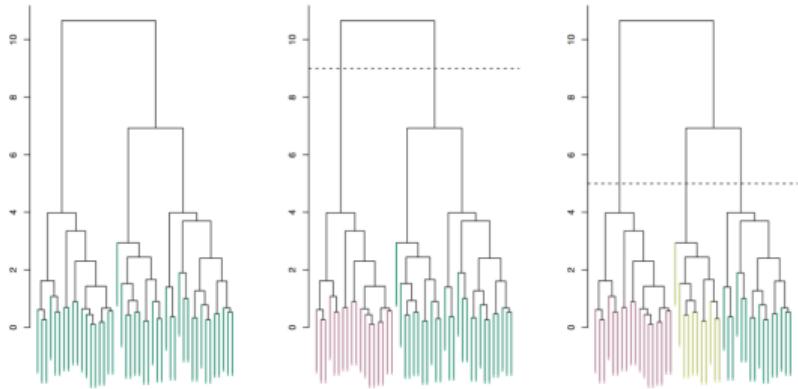


Figure 18: ISL (8th printing 2017)

Building a Dendrogram

A dendrogram is most commonly built using a bottom-up or agglomerative algorithm.

We start at the leaves and group observations until we reach the root containing the entire dataset.

Like in k -means, we need a measure of similarity. Again, the most common is Euclidean distance.

- ▶ Compute the distance between each pair of observations.
- ▶ Merge the two closest observations into a cluster.
- ▶ Compute the distance between the new cluster and all other observations.
- ▶ Repeat until all observations are in one cluster.
- ▶ The distance between clusters is computed using a linkage method.

Input: Dataset $D = \{x_1, x_2, \dots, x_n\}$

Output: Dendrogram representing the hierarchical structure of clusters

Initialization: Treat each data point as a separate cluster;

Compute distance matrix: Calculate pairwise distances between all clusters;

Repeat until only one cluster remains:

- ▶ Find the two closest clusters based on the distance matrix;
- ▶ Merge the two clusters into a new cluster;
- ▶ Update the distance matrix to reflect the new cluster;
- ▶ Recompute distances between the new cluster and all other clusters using a linkage method;

Return: Dendrogram representing the hierarchical structure of clusters;

Algorithm: Hierarchical Clustering Algorithm

w3schools: Codes and Playground

Clustering - Hierarchical: Dendrograms (cont.)

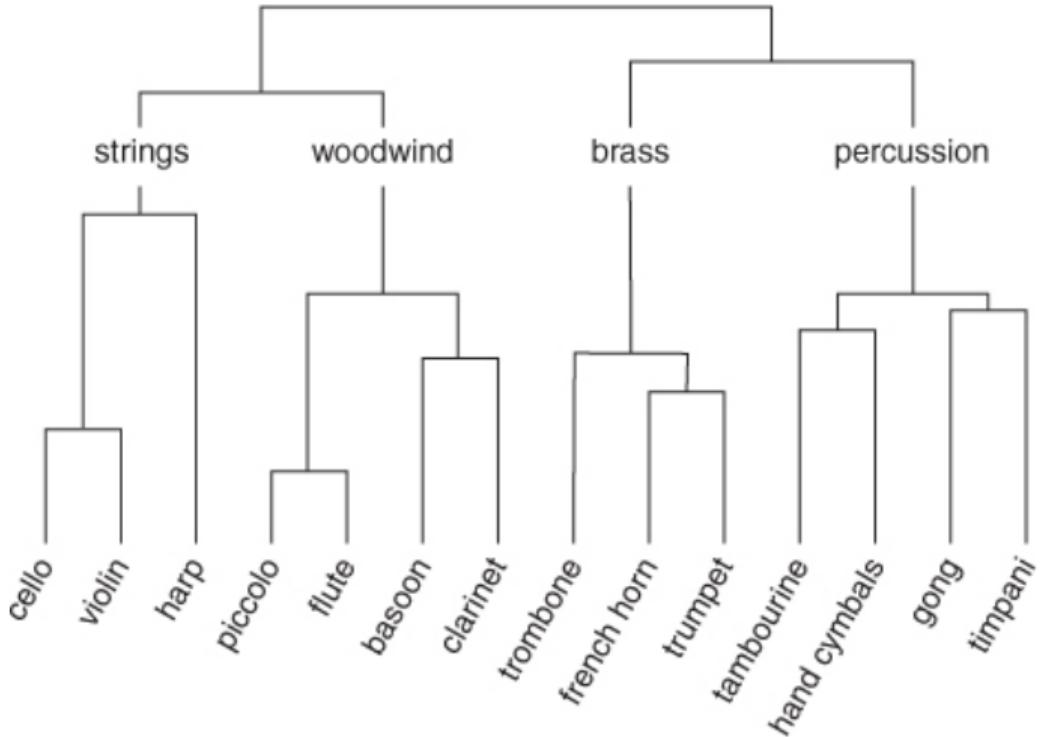


Figure 19: Dendrogram interpretation.

Clustering - Hierarchical: Dendrograms (cont.)



Distance between groups

It's easy to compute Euclidean distance between two observations. What is the distance or similarity between two groups or clusters of observations?

Linkage: defines the dissimilarity between two groups of observations. Most common types are *complete*, *average*, *single*, and *centroid*.

- ▶ **Single Linkage:** Distance between two clusters is the minimum distance between any two points in the clusters.
- ▶ **Complete Linkage:** Distance between two clusters is the maximum distance between any two points in the clusters.
- ▶ **Average Linkage:** Distance between two clusters is the average distance between all pairs of points in the clusters.
- ▶ **Centroid Linkage:** Distance between two clusters is the distance between their centroids.
- ▶ **Ward's Linkage:** Distance between two clusters is the increase in variance when the two clusters are merged.

Clustering - Hierarchical: Distance Metrics (cont.)

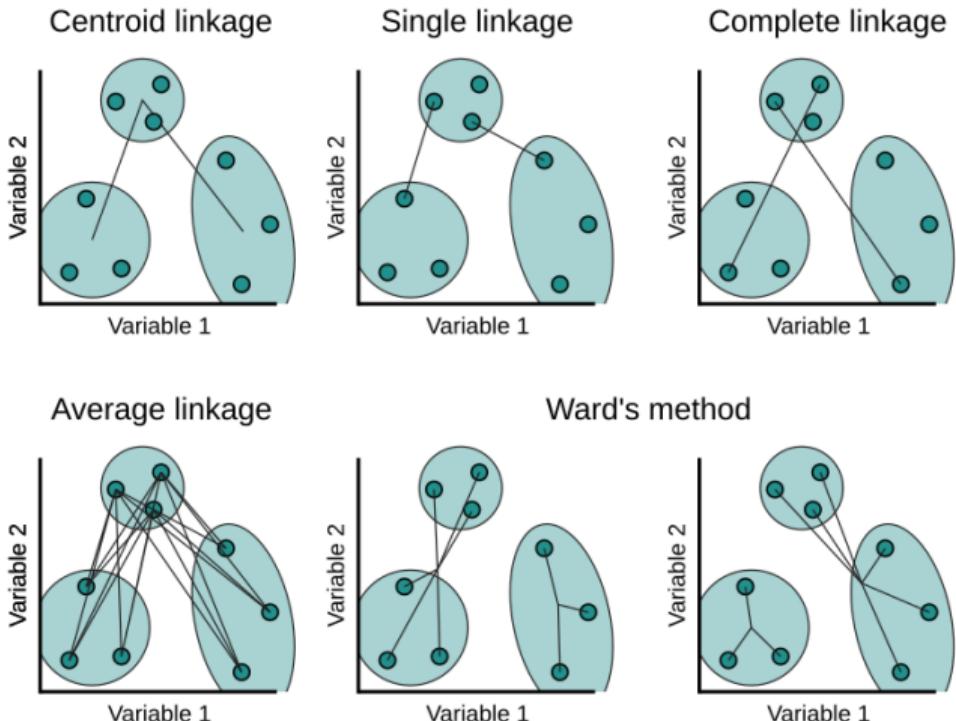


Figure 20: Linkage methods.

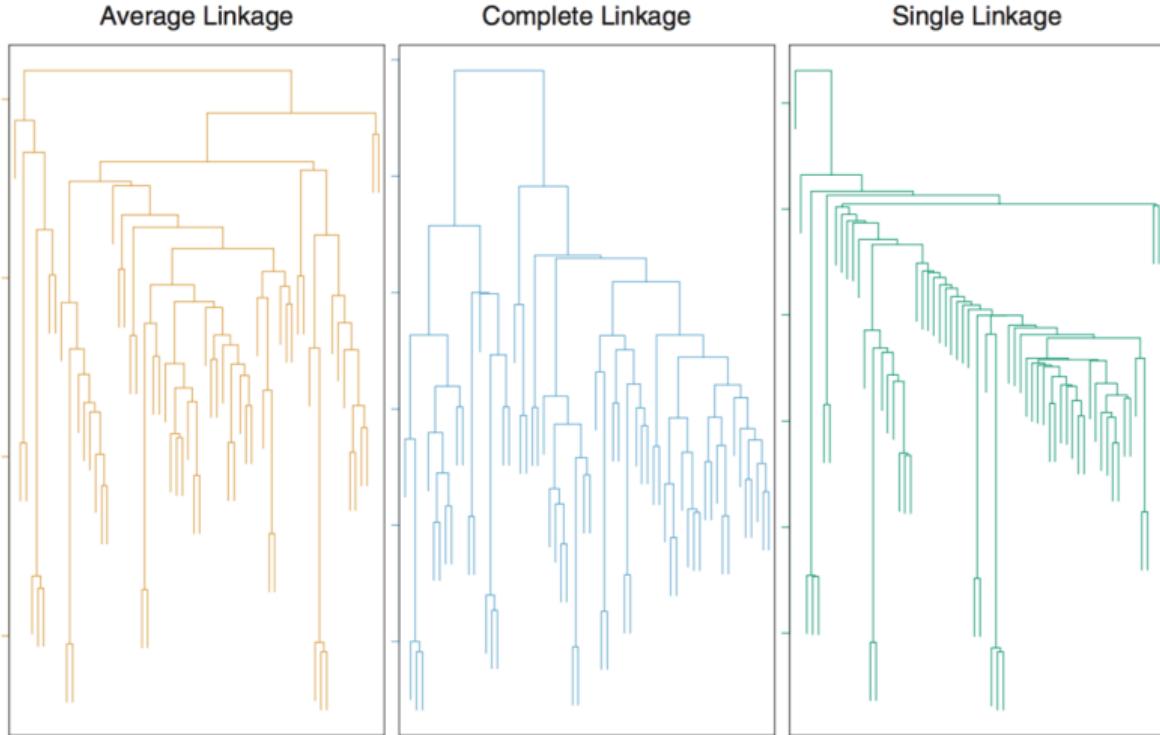


Figure 21: Dendrogram with different linkage types.

Clustering - Hierarchical: Distance Metrics (cont.)



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KAUST ACADEMY

Pros

- ▶ No need to specify the number of clusters K in advance.
- ▶ Dendograms provide a visual representation of the clustering process.
- ▶ Can capture complex cluster shapes and relationships.

Cons

- ▶ Computationally expensive for large datasets.
- ▶ Do have to pick where to cut the dendrogram to obtain clusters
- ▶ Sensitive to similarity measure and type of linkage used.
- ▶ Sensitive to noise and outliers.
- ▶ Difficult to interpret and choose the optimal number of clusters.

- ▶ Clustering based on density (local cluster criterion), such as density-connected points or based on an explicitly constructed density function.
- ▶ **Major features:**
 - Discover clusters of arbitrary shape
 - Handle noise
 - One scan
 - Need density parameters

► Major algorithms:

- DBSCAN (Density-Based Spatial Clustering of Applications with Noise): Ester, et al. (KDD'96)
- OPTICS (Ordering Points to Identify the Clustering Structure): Ankerst, et al. (SIGMOD'99)
- HDBSCAN (Hierarchical Density-Based Spatial Clustering of Applications with Noise): Campello, et al. (ACM TIST'15)
- DENCLUE (DENsity-based CLUstEring): Hinneburg and Gabriel (KDD'97)
- CLIQUE (CLustering In QUEst): Karypis, Han, and Kumar (SIGMOD'98)

► DBSCAN (Density-Based Spatial Clustering of Applications with Noise):

- Density = number of points within a specified radius ϵ .
- A point is a core point if it has more than a specified number of points (MinPts) within ϵ . These are points that are at the interior of a cluster.
- A border point has fewer than MinPts within ϵ , but is in the neighborhood of a core point
- A noise point is any point that is not a core point or a border point.
- Groups together points that are closely packed together, marking as outliers points that lie alone in low-density regions.
- Parameters:
 - ▶ ϵ : Maximum distance between two points for them to be considered as in the same neighborhood.
 - ▶ MinPts: Minimum number of points required to form a dense region.

Clustering - DBSCAN (cont.)

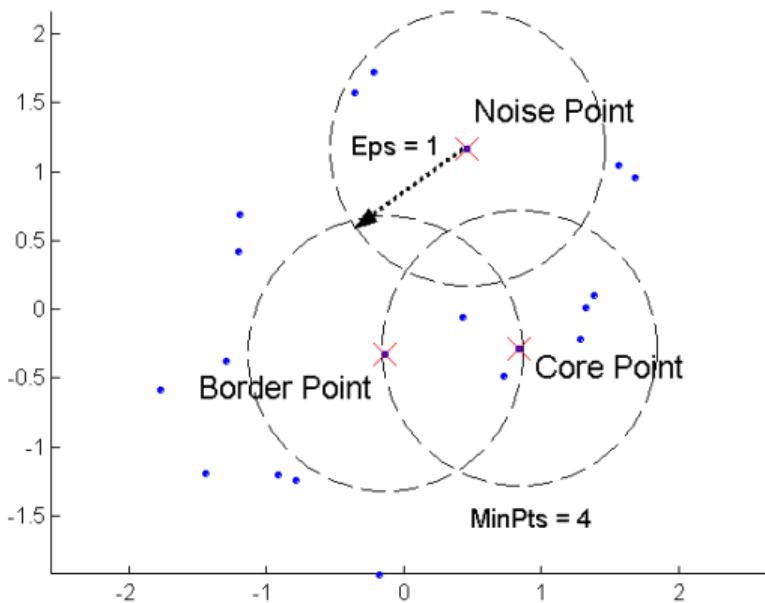


Figure 22: DBSCAN features: Core, Border, and Noise Points

Input: Set of points P , distance threshold ε , minimum number of points $minPts$

Output: A set of clusters

Construct a directed graph $G = (V, E)$ where each node in V corresponds to a point in P ;

foreach point $c \in P$ **do**

if c is a core point (i.e., $|\mathcal{N}_\varepsilon(c)| \geq minPts$) **then**

foreach point $p \in \mathcal{N}_\varepsilon(c)$ **do**

 Add a directed edge $(c \rightarrow p)$ to E ;

end

end

end

$N \leftarrow V$;

while there exists a core point $c \in N$ **do**

 Let X be the set of nodes reachable from c via directed edges in G ;

 Form a cluster $C = X \cup \{c\}$;

 Remove all nodes in C from N ;

end

Clustering - DBSCAN: Core, Border, and Noise Points



Figure 23: Original Points

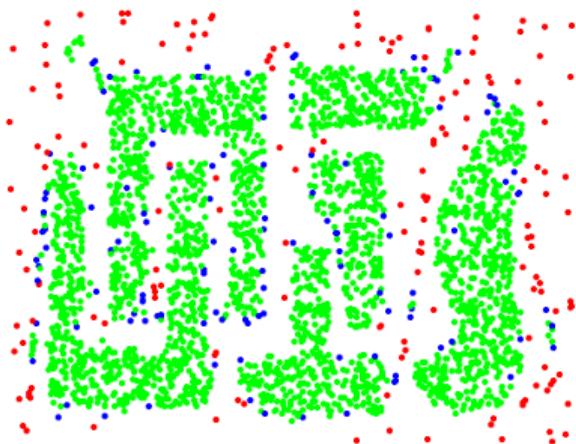


Figure 24: Point types: **Core**, **Border**, and **Noise** Points

Clustering - DBSCAN: Core, Border, and Noise Points (cont.)

Eps = 10, MinPts = 4

When DBSCAN Works Well

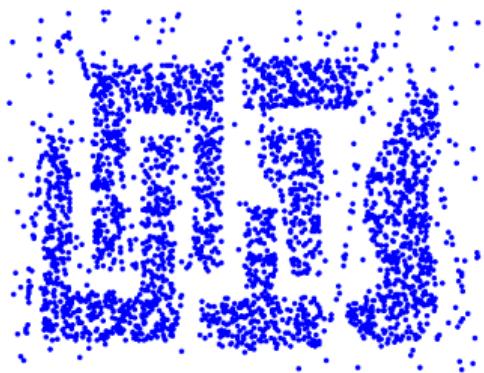


Figure 25: Original Points

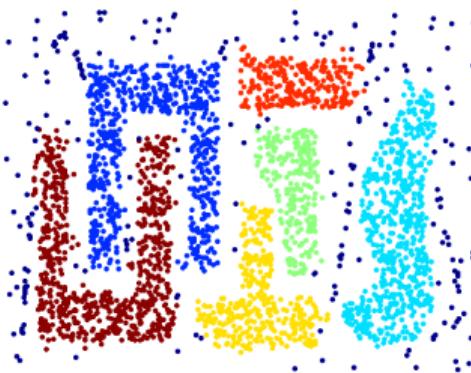


Figure 26: Clusters identified by DBSCAN

DBSCAN works well when:

- ▶ Clusters are of varying shapes and sizes.
- ▶ There is a clear distinction between dense and sparse regions.

When DBSCAN Works Well (cont.)



- ▶ The data contains noise or outliers.

When DBSCAN Doesn't Works Well

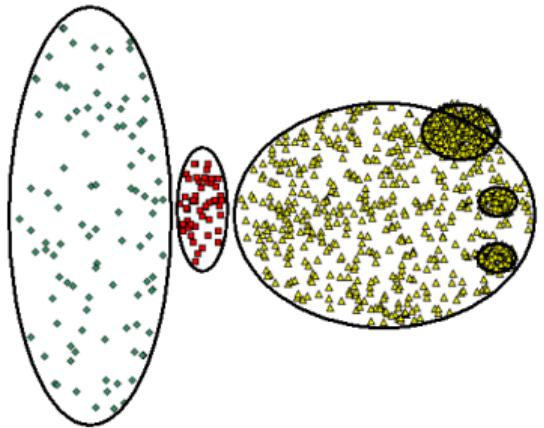


Figure 27: Original Points

DBSCAN does not work well when:

- ▶ Clusters are of varying densities.
- ▶ The data has varying scales or dimensions.
- ▶ There are overlapping clusters.

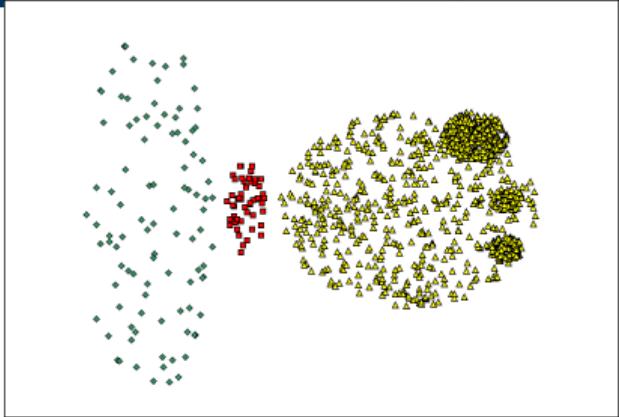
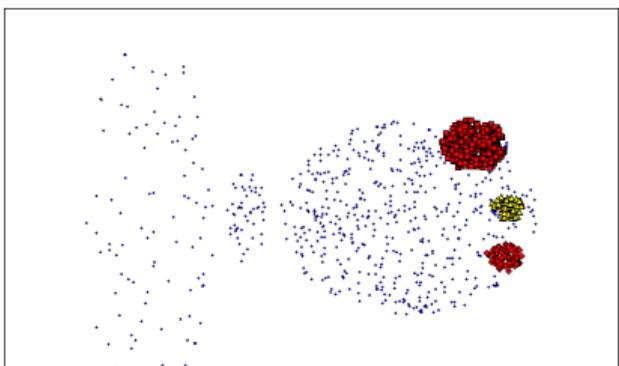


Figure 28: $\text{MinPts}=4$, $\epsilon=9.75$



- ▶ A common approach to determine ϵ is to use a k-distance graph:
 - For each point, compute the distance to its k-th nearest neighbor.
 - Plot these distances in ascending order.
 - Look for a "knee" in the plot, which indicates a suitable value for ϵ .
- ▶ MinPts is often set based on domain knowledge or heuristics:
 - A common rule of thumb is to set MinPts to at least the dimensionality of the data plus one (e.g., for 2D data, MinPts = 3).
 - Higher values of MinPts can lead to fewer clusters and more noise points.

DBSCAN: Determining ϵ and MinPts (cont.)

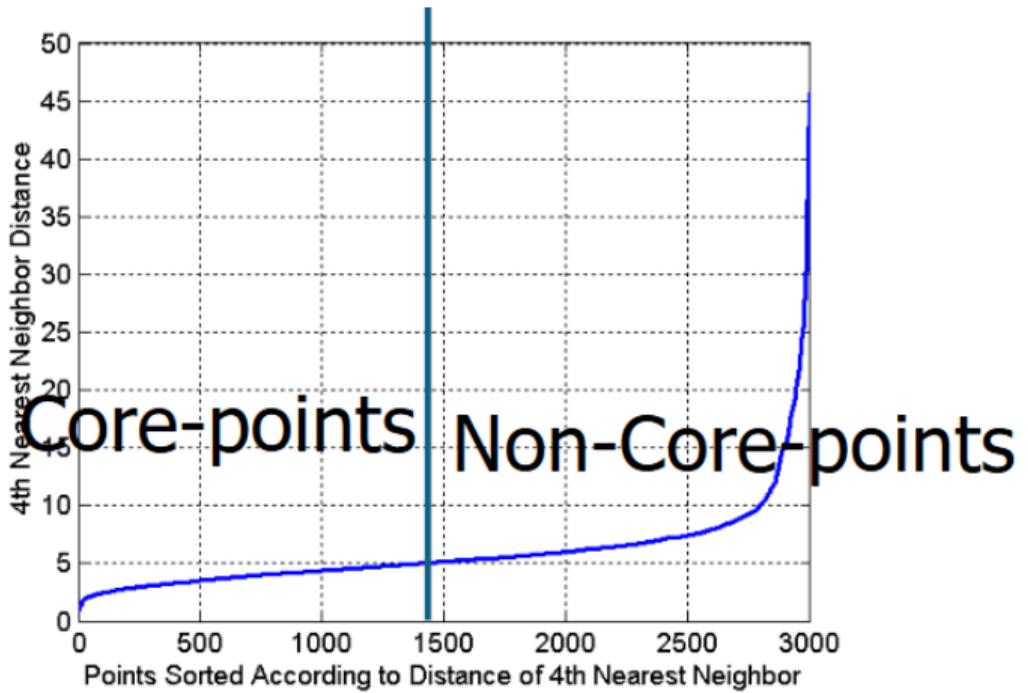


Figure 30: Run K-means for Minp=4 and not fixed ϵ

► Complexity:

- The time complexity of DBSCAN is $O(n \log n)$ for spatial data structures like KD-trees or R-trees, where n is the number of points.
- Without spatial indexing, the complexity can degrade to $O(n^2)$.
- Space complexity is $O(n)$, as it needs to store the points and their cluster assignments.

► Limitations:

- Sensitive to the choice of ϵ and MinPts parameters.
- Struggles with clusters of varying densities.
- Not suitable for high-dimensional data due to the curse of dimensionality.
- Cannot handle clusters that are not well-separated in terms of density.

► **Good:**

- Can discover clusters of arbitrary shape.
- Effectively handles noise and outliers.
- Requires only one scan of the data.
- Suitable for datasets with varying densities.
- Does not require prior knowledge of the number of clusters.

► **Bad:**

- Does not work well in high-dimensional datasets.
- Parameter selection is tricky.
- Has problems identifying clusters of varying densities (\rightarrow SSN algorithm).
- Density estimation is simplistic (\rightarrow does not create a real density function, but rather a graph of density-connected points).

```
current_cluster_label ← 1
for all core points do
    if the core point has no cluster label then
        current_cluster_label ← current_cluster_label + 1
        Label the current core point with cluster label current_cluster_label
    end if
    for all points in the  $Eps$ -neighborhood, except  $i^{th}$  the point itself do
        if the point does not have a cluster label then
            Label the point with cluster label current_cluster_label
        end if
    end for
end for
```

Figure 31: DBSCAN Algorithm Steps

Where are we heading?

Gene	Description	Cell 1	Cell 2	Cell 3	Cell 4	Cell 5
Inpp5d	inositol polyphosphate-5-phosphatase D	7.00	5.45	5.89	6.03	5.75
Aim2	absent in melanoma 2	3.01	4.37	4.59	4.38	4.18
Gldn	gliomedin	3.48	3.63	4.61	4.70	4.74
Frem2	Fras1 related extracellular matrix protein 2	4.75	4.66	3.46	3.74	3.45
Rps3a1	ribosomal protein S3A1	6.10	7.23	7.44	7.36	7.34
Slc38a3	solute carrier family 38, member 3	1.90	3.16	3.52	3.61	3.19
Mt1	metallothionein 1	5.07	6.49	6.46	6.04	6.05
C1s1	complement component 1, s subcomponent 1	2.74	3.02	3.86	4.10	4.10
Cds1	CDP-diacylglycerol synthase 1	4.55	4.22	3.80	3.16	3.12
Ifi44	interferon-induced protein 44	4.82	4.52	3.87	3.42	3.59
Lefty2	left-right determination factor 2	6.95	6.28	5.88	5.60	5.61
Fmr1nb	fragile X mental retardation 1 neighbor	4.28	2.78	3.10	3.25	2.57
Tagln	transgelin	7.93	7.91	7.20	7.02	6.68

Figure 32: Original Points

- ▶ Each dot is a cell.
- ▶ Groups of dots are similar cells.
- ▶ Separation of groups could be interesting biology.

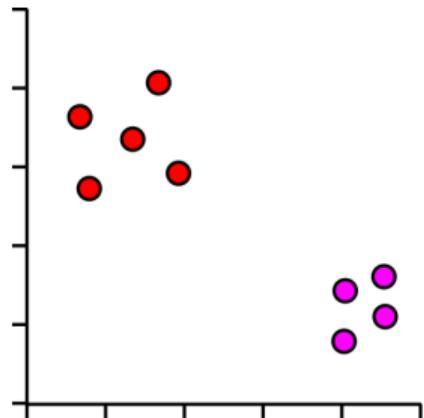
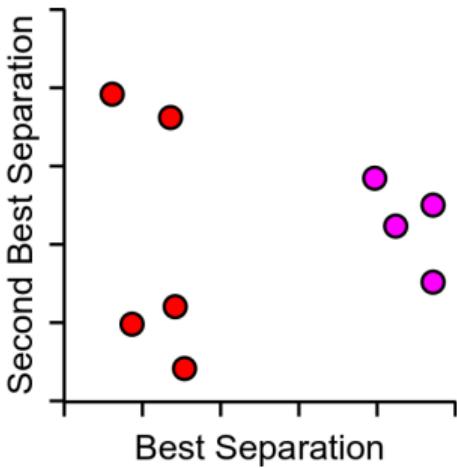
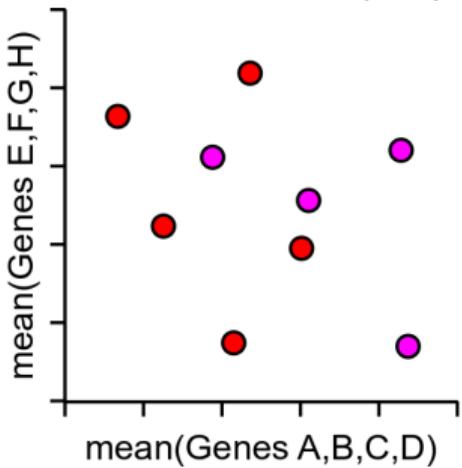
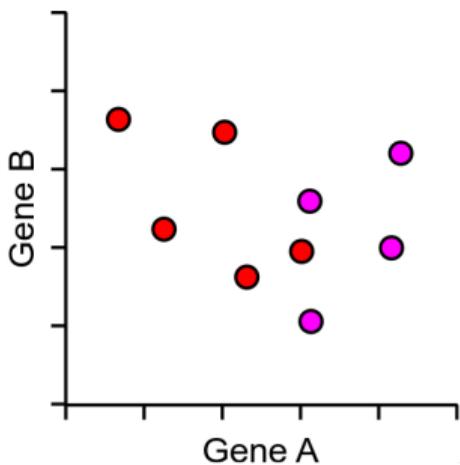


Figure 33: Clusters identified by DBSCAN

Too much data!

- ▶ 5000 cells and 2500 measured genes
- ▶ Realistically only 2 dimensions we can plot (x, y)



- ▶ Principal Component Analysis (PCA) is a method for optimally summarizing large, multi-dimensional datasets.
- ▶ PCA identifies a smaller number of dimensions (ideally 2) that retain most of the useful information present in the original data.
- ▶ The technique constructs a set of new variables, called Principal Components (PCs), which are linear combinations of the original variables.
- ▶ Each Principal Component represents a specific weighted sum of the original features. For example:

$$\text{PC} = (10 \times \text{GeneA}) + (3 \times \text{GeneB}) + (-4 \times \text{GeneC}) + (-20 \times \text{GeneD}) + \dots$$

- ▶ By projecting the data onto these principal components, PCA reduces dimensionality while preserving as much variance (information) as possible.

Principal Component Analysis (PCA) (cont.)

- ▶ Principal Component Analysis (PCA) is a method for optimally summarizing large, multi-dimensional datasets.
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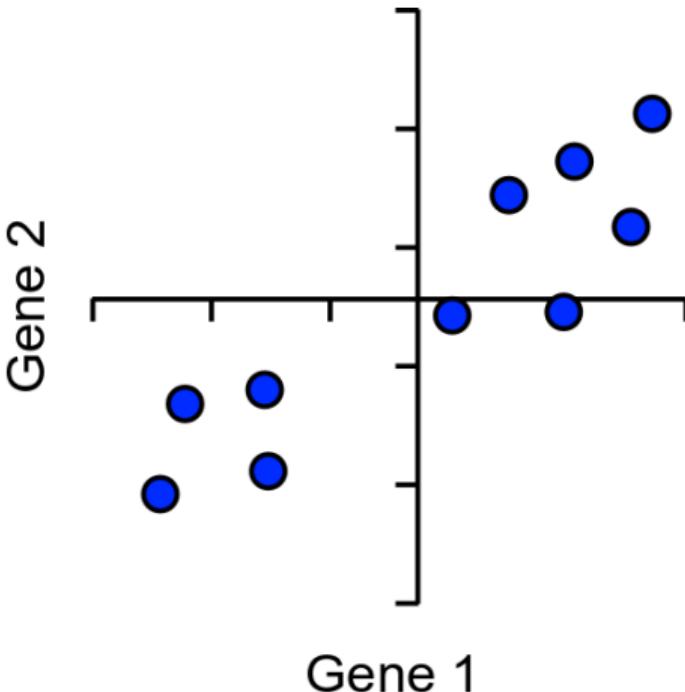
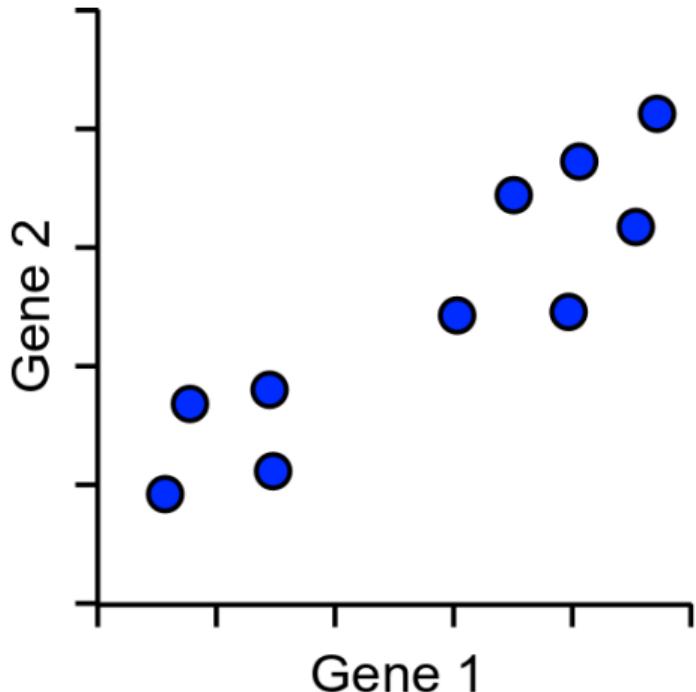
$$\text{PC} = (10 \times \text{GeneA}) + (3 \times \text{GeneB}) + (-4 \times \text{GeneC}) + (-20 \times \text{GeneD}) + \dots$$

- ▶ By projecting the data onto these principal components, PCA reduces dimensionality while preserving as much variance (information) as possible.

Simple example using 2 genes and 10 cells

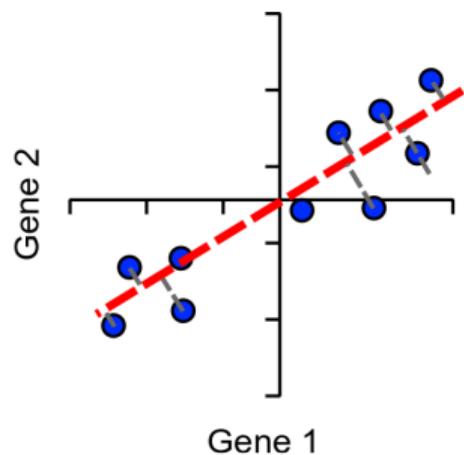
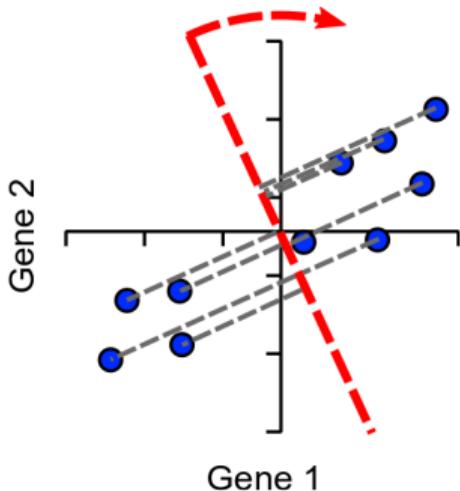
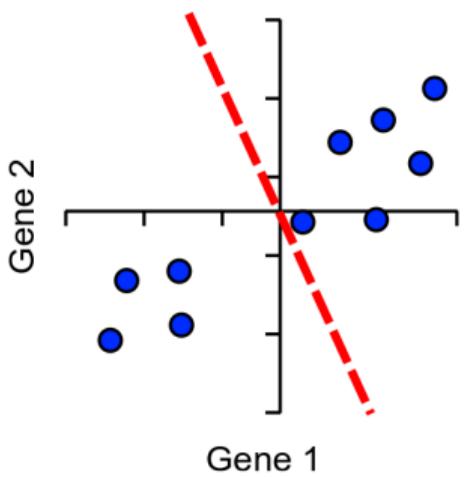
How does PCA work?

Simple example using 2 genes and 10 cells



How does PCA work? (cont.)

Find line of best fit, passing through the origin



Assigning Loadings to Genes

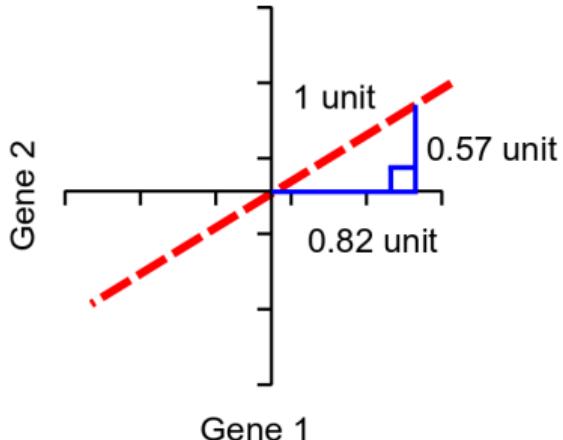
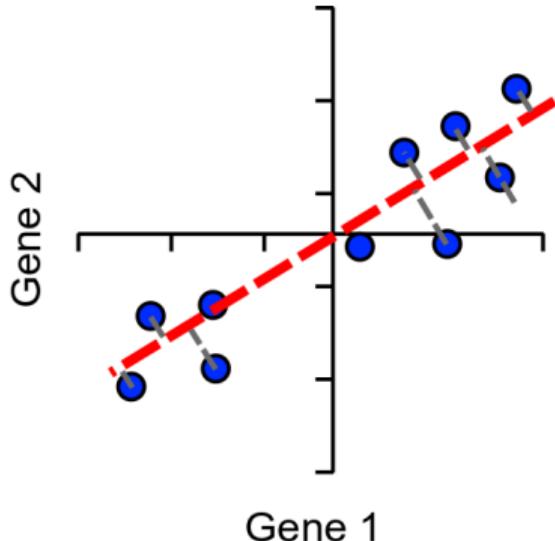


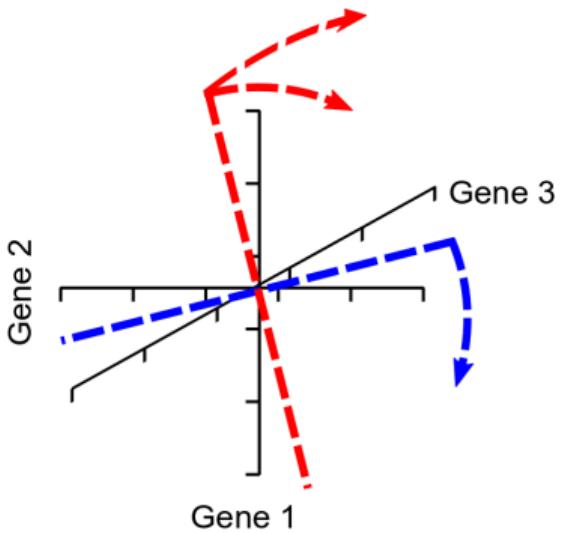
Figure 34: Eigenvector or Single Vector

- ▶ **Loadings** represent the contribution of each gene to the principal component.
- ▶ For this example using 2 genes and 10 cells:
 - Gene1 loading: 0.82
 - Gene2 loading: 0.57

Assigning Loadings to Genes (cont.)



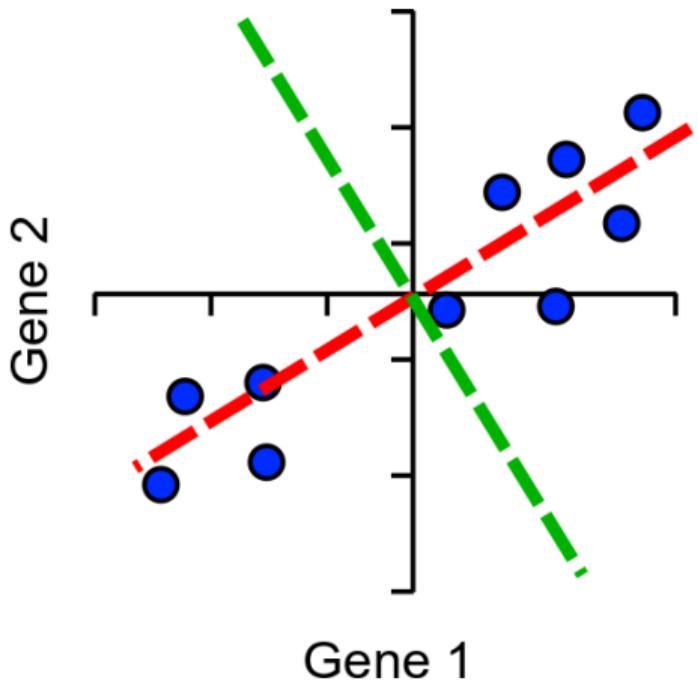
- ▶ A higher loading means the gene has a greater influence on the principal component.



- ▶ The same idea extends to datasets with more dimensions (n genes).
- ▶ The first principal component (PC1) finds the direction of maximum variance, rotating in $(n - 1)$ dimensions.
- ▶ The next principal component (PC2) is perpendicular to PC1 and rotates in the remaining $(n - 2)$ dimensions.
- ▶ Each subsequent principal component is always perpendicular to the previous ones, capturing the next largest variance.
- ▶ The last principal component is the only remaining perpendicular direction.
- ▶ The number of principal components always equals the number of original genes (features).

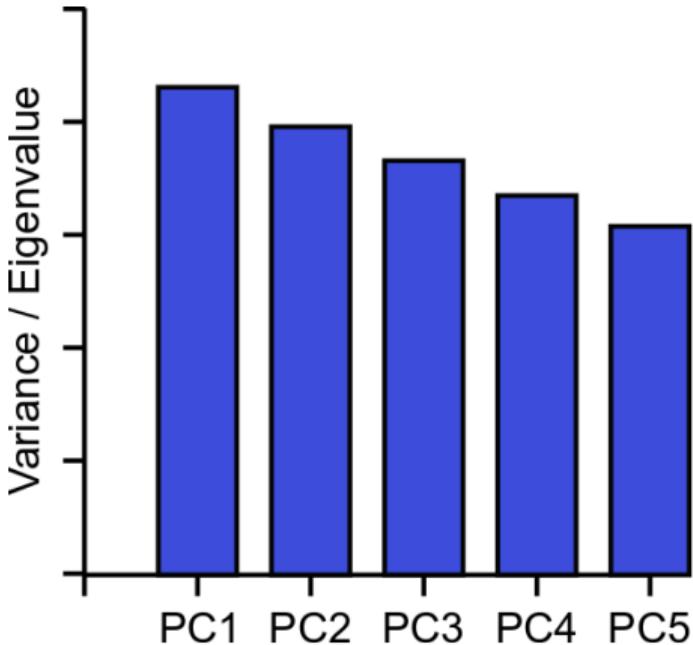
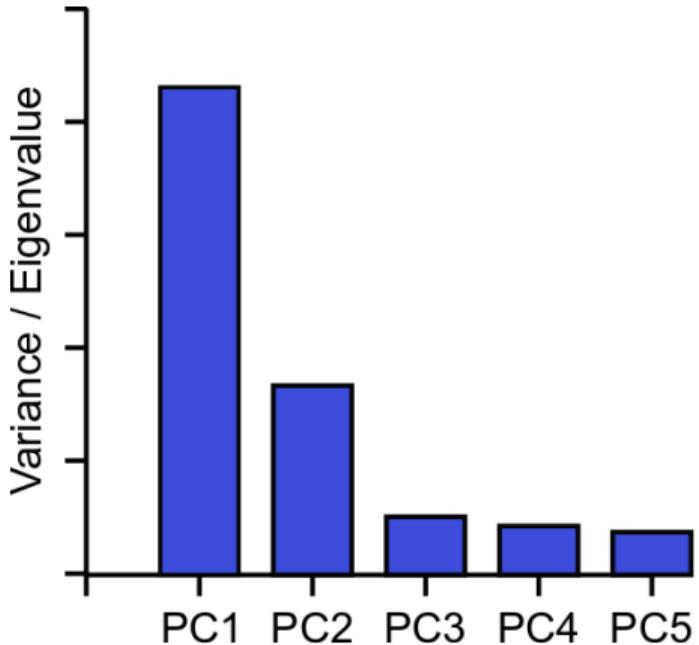
- ▶ Each principal component (PC) explains a certain proportion of the total variance in the data. Together, all PCs account for 100% of the variance.
- ▶ PC1 always explains the largest amount of variance.
- ▶ PC2 explains the next largest amount, and so on for subsequent PCs.
- ▶ Since we typically plot only 2 dimensions (PC1 and PC2), it's important to check how much of the total variance these two PCs explain.
- ▶ **How do we calculate this?**

Explaining Variance (cont.)

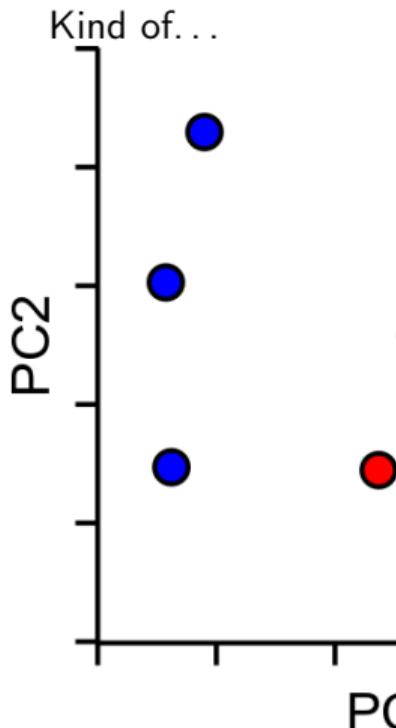


- ▶ Project each data point onto the principal component (PC).
- ▶ Calculate the distance of each projected point to the origin.
- ▶ Compute the sum of squared differences (SSD) from the origin.
- ▶ This SSD is a measure of variance, called the *eigenvalue*.
- ▶ Divide the SSD by $(\text{number of points} - 1)$ to obtain the actual variance explained by the PC.

Explaining Variance (cont.)

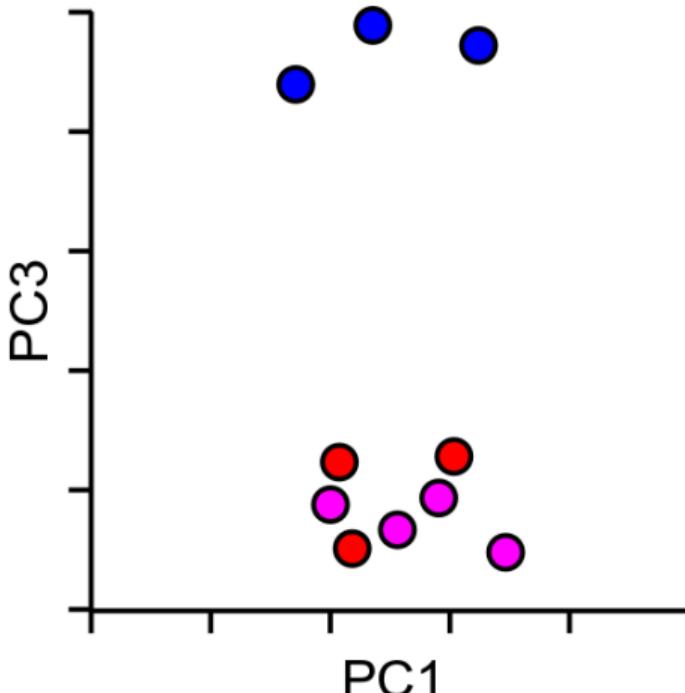
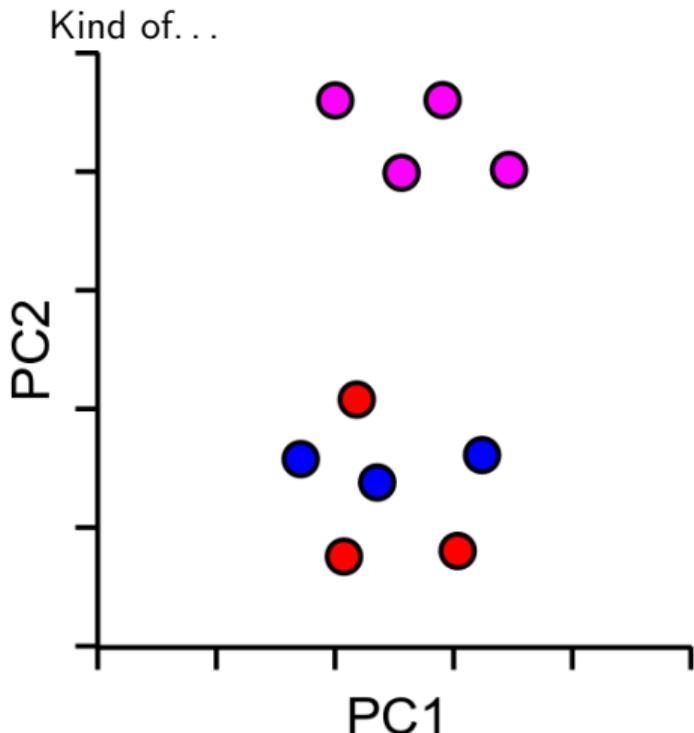


So PCA is great then?



Non-linear separation of values

So PCA is great then? (cont.)



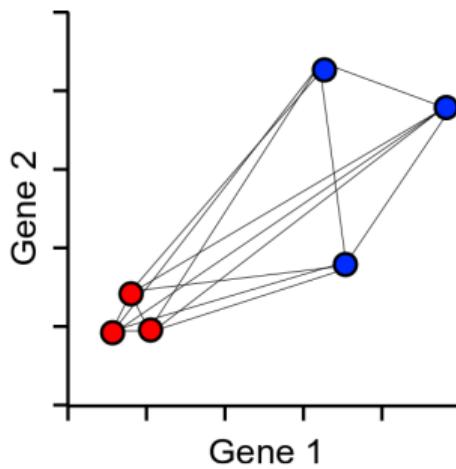
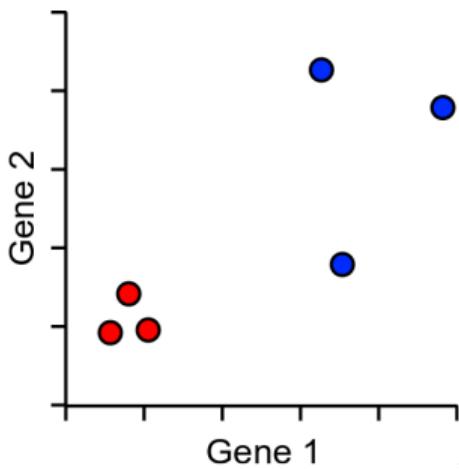
Not optimised for 2-dimensions

tSNE to the rescue...

- ▶ T-Distributed Stochastic Neighbour Embedding
- ▶ Aims to solve the problems of PCA
- ▶ Non-linear scaling to represent changes at different levels
- ▶ Optimal separation in 2-dimensions

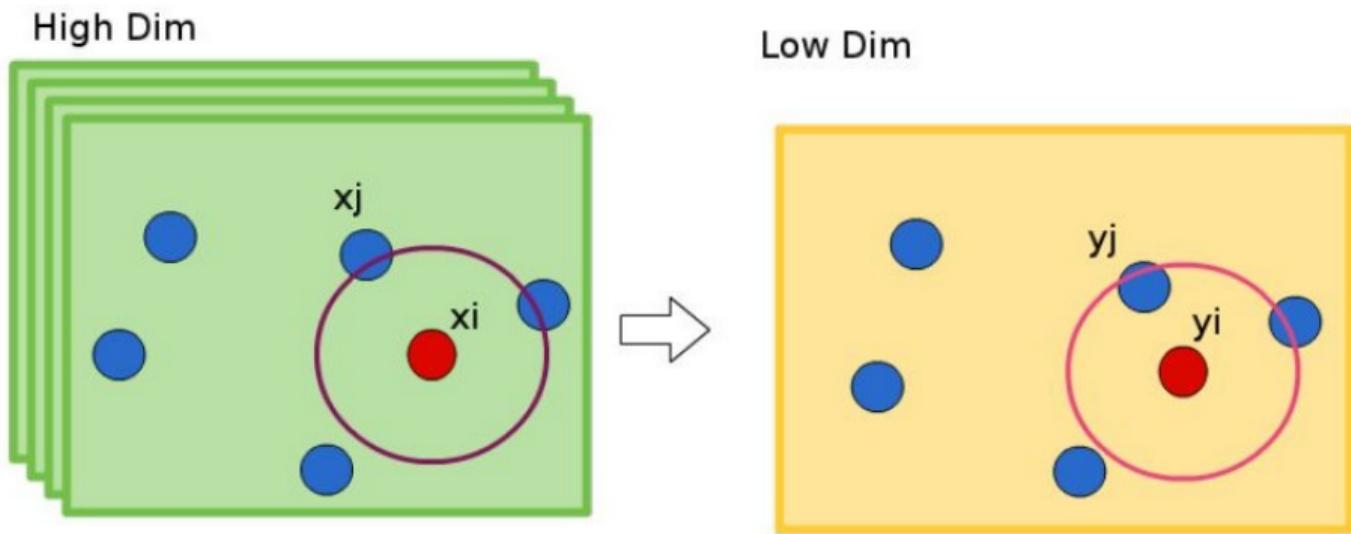
tSNE: How does it work?

- ▶ Based around all-vs-all table of pairwise cell to cell distances
- ▶ Each cell is represented as a point in a high-dimensional space
- ▶ The pairwise distances are converted into probabilities



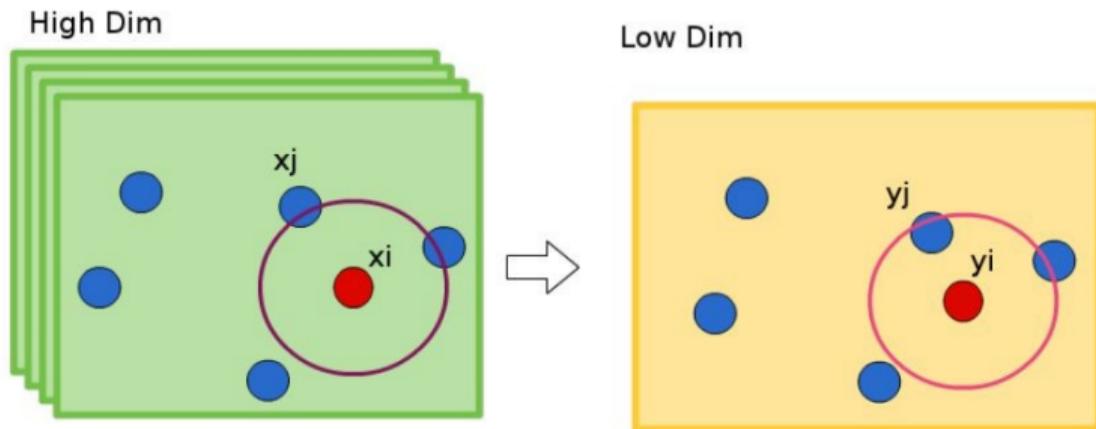
	0	10	10	295	158	153
0	9	0	1	217	227	213
10	1	8	0	154	225	238
295	205	189	260	0	23	45
158	248	227	246	44	0	54
153	233	176	184	41	36	0

tSNE: Underlying idea



tSNE: Stochastic Neighbor Embedding

Measure pairwise similarities between high-dimensional and low-dimensional objects



$$p_{j|i} = \frac{\exp(-||x_i - x_j||^2 / 2\sigma_i^2)}{\sum_{k \neq i} \exp(-||x_i - x_k||^2 / 2\sigma_i^2)}$$

Converting the high-dimensional Euclidean distances into conditional probabilities that represent similarities

- Similarity of datapoints in High Dimension

$$p_{j|i} = \frac{\exp(-||x_i - x_j||^2 / 2\sigma_i^2)}{\sum_{k \neq i} \exp(-||x_i - x_k||^2 / 2\sigma_i^2)}$$

- Similarity of datapoints in Low Dimension

$$q_{j|i} = \frac{\exp(-||y_i - y_j||^2)}{\sum_{k \neq i} \exp(-||y_i - y_k||^2)}$$

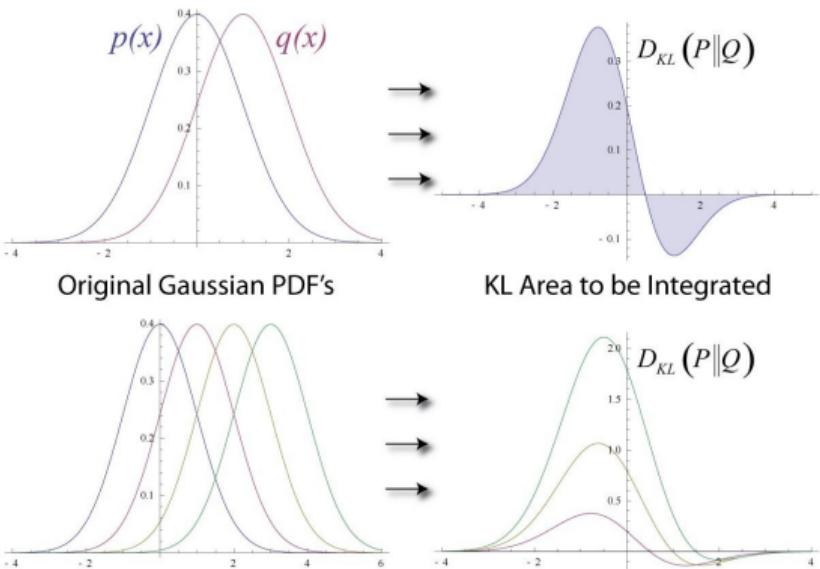
- Cost function

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

KL Divergence

Measures the similarity between two probability distributions it is asymmetric.

$$D_{\text{KL}}(P\|Q) = \sum_i P(i) \log \frac{P(i)}{Q(i)},$$



Gradient has a surprisingly simple form

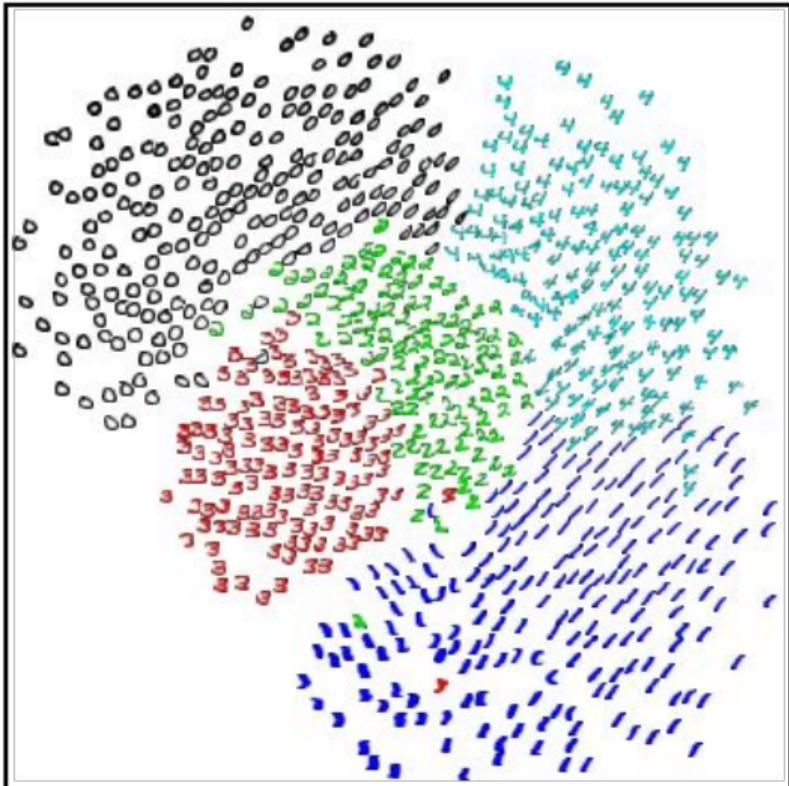
$$\frac{\partial C}{\partial y_i} = \sum_{j \neq i} (p_{j|i} - q_{j|i} + p_{i|j} - q_{i|j})(y_i - y_j)$$

The gradient update with momentum term is given by

$$Y^{(t)} = Y^{(t-1)} + \eta \frac{\partial C}{\partial y_i} + \beta(t)(Y^{(t-1)} - Y^{(t-2)})$$

tSNE: Stochastic Neighbor Embedding (cont.)

- ▶ The result of running the SNE algorithm on 3000 256-dimensional grayscale images of handwritten digits.
- ▶ The classes are quite well separated even though SNE had no information about class labels.
- ▶ Furthermore, within each class, properties like orientation, skew, and stroke thickness tend to vary smoothly across the space.



Such that $p_{ij} = p_{ji}$, $q_{ij} = q_{ji}$, the main advantage is simplifying the gradient

$$\frac{\partial C}{\partial y_i} = 2 \sum_j (p_{ij} - q_{ij})(y_i - y_j)$$

However, in practice we symmetrize (or average) the conditionals

$$p_{ij} = \frac{p_{j|i} + p_{i|j}}{2N}$$

Set the bandwidth σ_i such that the conditional has a fixed perplexity (effective number of neighbors) $Perp(P_i) = 2^{H(P_i)}$, typical value is about 5 to 50

Use heavier tail distribution than Gaussian in low-dim space, we choose

$$q_{ij} \propto (1 + \|y_i - y_j\|^2)^{-1}$$

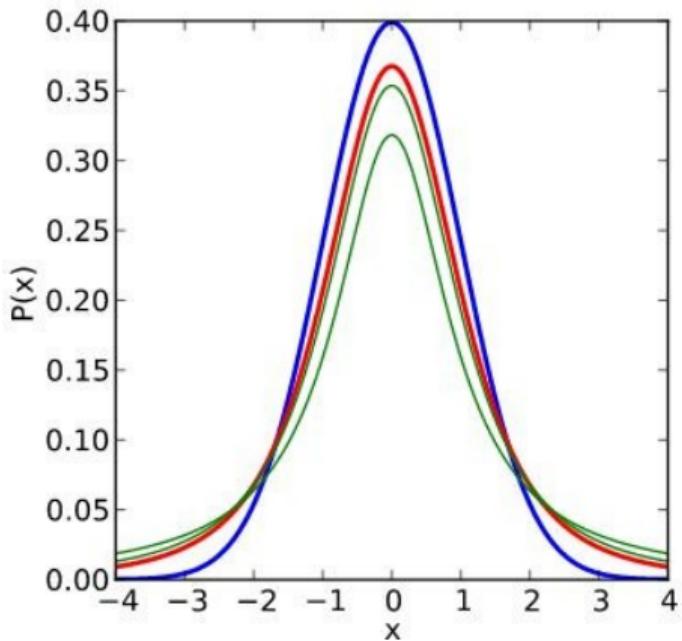
Then the gradient could be

$$\frac{\partial C}{\partial y_i} = 4 \sum_{j \neq i} (p_{ij} - q_{ij})(1 + \|y_i - y_j\|^2)^{-1}(y_i - y_j)$$

- ▶ Why do we define map similarities as:

$$q_{ij} = \frac{(1 + \|y_i - y_j\|^2)^{-1}}{\sum_{k \neq i} (1 + \|y_k - y_i\|^2)^{-1}}$$

- ▶ Suppose data is intrinsically high dimensional
- ▶ We try to model the local structure of this data in the map
- ▶ Result: Dissimilar points have to be modeled as too far apart in the map!



- Similarity of datapoints in High Dimension

$$p_{ij} = \frac{\exp(-\|x_i - x_j\|^2 / 2\sigma^2)}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2 / 2\sigma^2)}$$

- Similarity of datapoints in Low Dimension

$$q_{ij} = \frac{(1 + \|y_i - y_j\|^2)^{-1}}{\sum_{k \neq i} (1 + \|y_k - y_i\|^2)^{-1}}$$

- Cost function

$$C = KL(P||Q) = \sum_i \sum_j p_{ij} \log \frac{p_{ij}}{q_{ij}}$$

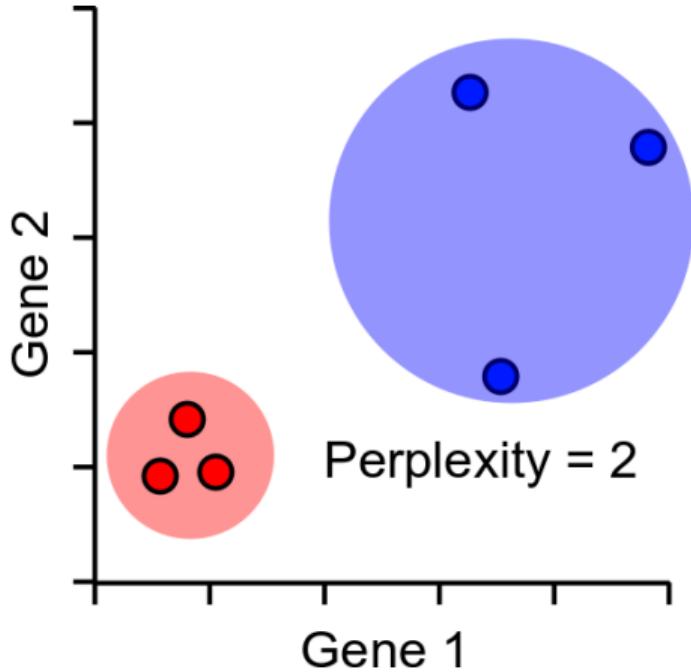
- Large p_{ij} modeled by small q_{ij} : Large penalty
- Small p_{ij} modeled by large q_{ij} : Small penalty
- t-SNE mainly preserves local similarity structure of the data

- Gradient

$$\frac{\partial C}{\partial y_i} = 4 \sum_{j \neq i} (p_{ij} - q_{ij})(1 + \|y_i - y_j\|^2)^{-1}(y_i - y_j)$$

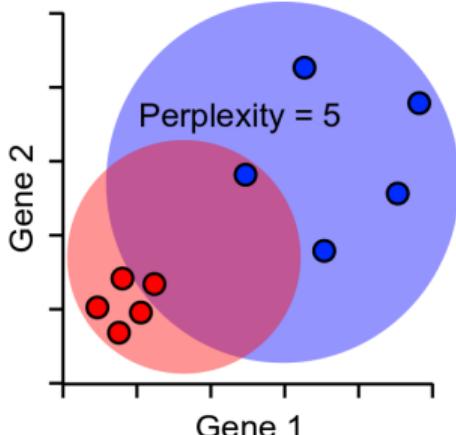
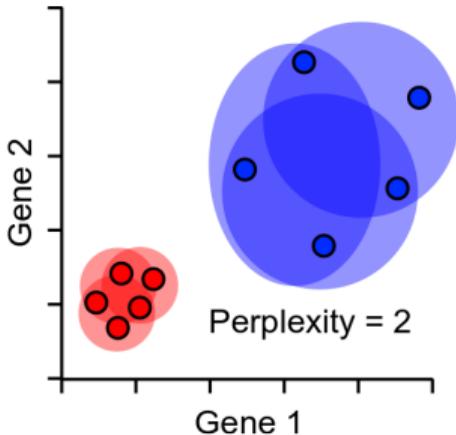
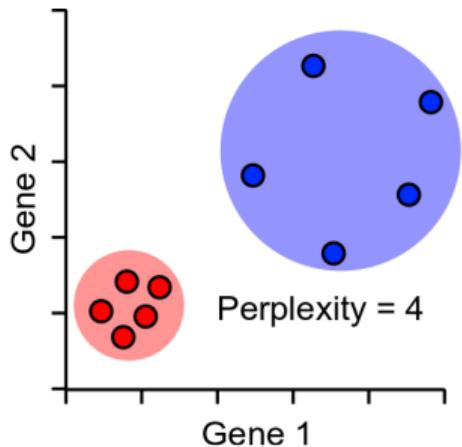
Distance scaling and perplexity

- ▶ Perplexity = expected number of neighbours within a cluster
- ▶ Distances scaled relative to perplexity neighbours



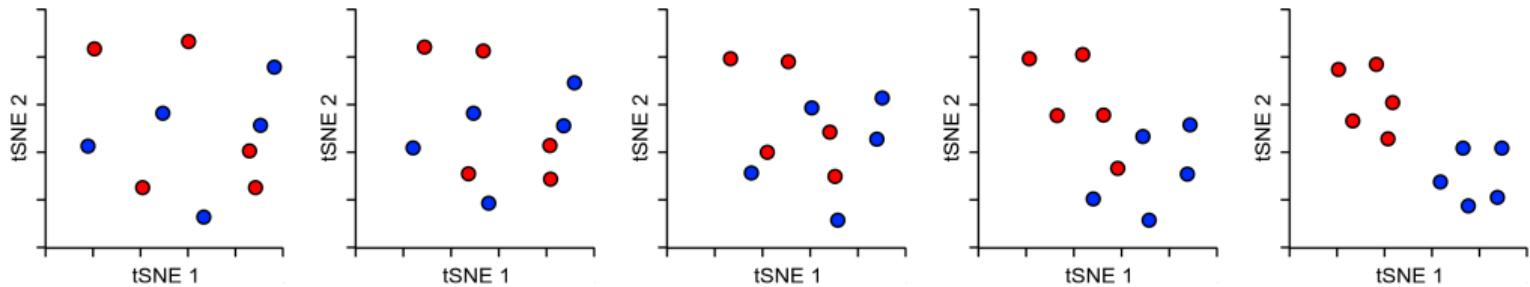
	0	4	6	586	657	836
0	0	4	815	527	776	
4	9	3	0	752	656	732
6	31	28	29	0	4	7
586	31	24	25	4	0	7
657	40	37	32	8	8	0
836						

Perplexity Robustness



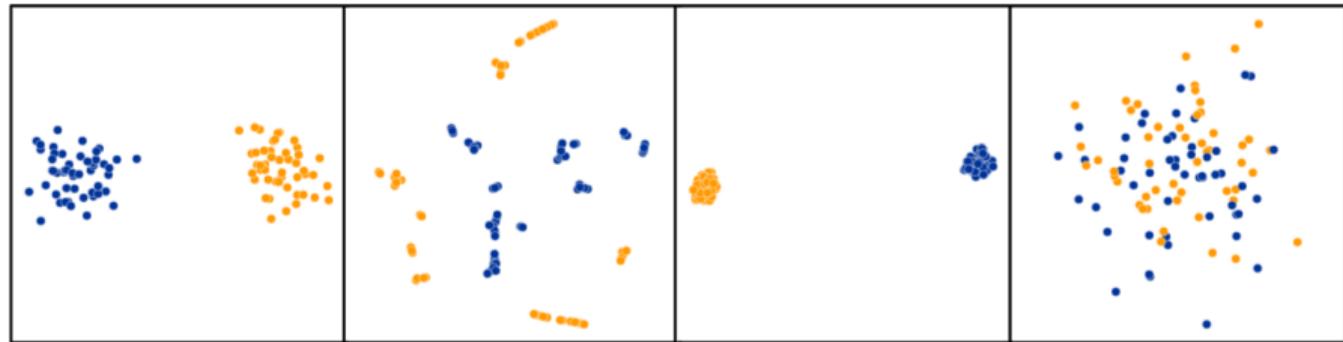
- ▶ Randomly scatter all points within the space (normally 2D)
- ▶ Start a simulation
 - Aim is to make the point distances match the distance matrix
 - Shuffle points based on how well they match
 - Stop after fixed number of iterations, or
 - Stop after distances have converged

tSNE Projection (cont.)



- ▶ X and Y don't mean anything (unlike PCA)
- ▶ Distance doesn't mean anything (unlike PCA)
- ▶ Close proximity is highly informative
- ▶ Distant proximity isn't very interesting
- ▶ Can't rationalise distances, or add in more data

Perplexity Settings Matter



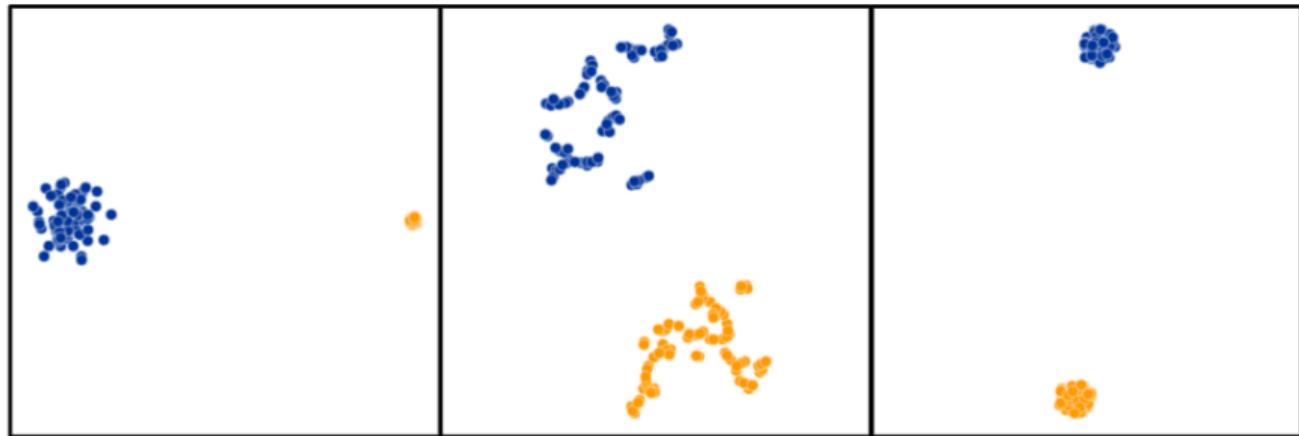
Original

Perplexity = 2

Perplexity = 30

Perplexity = 100

Cluster Sizes are Meaningless

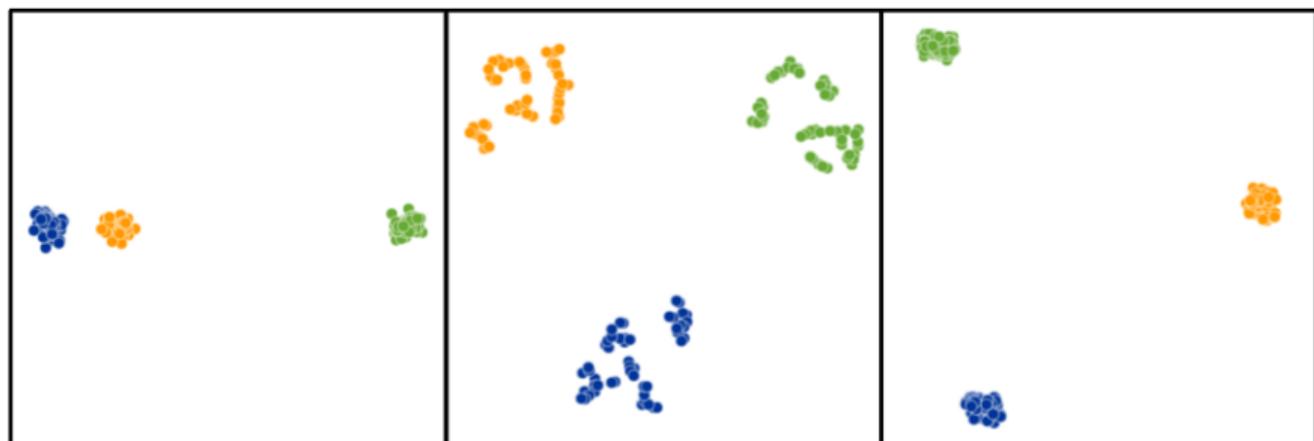


Original

Perplexity = 5

Perplexity = 50

Distances between clusters can't be trusted



Original

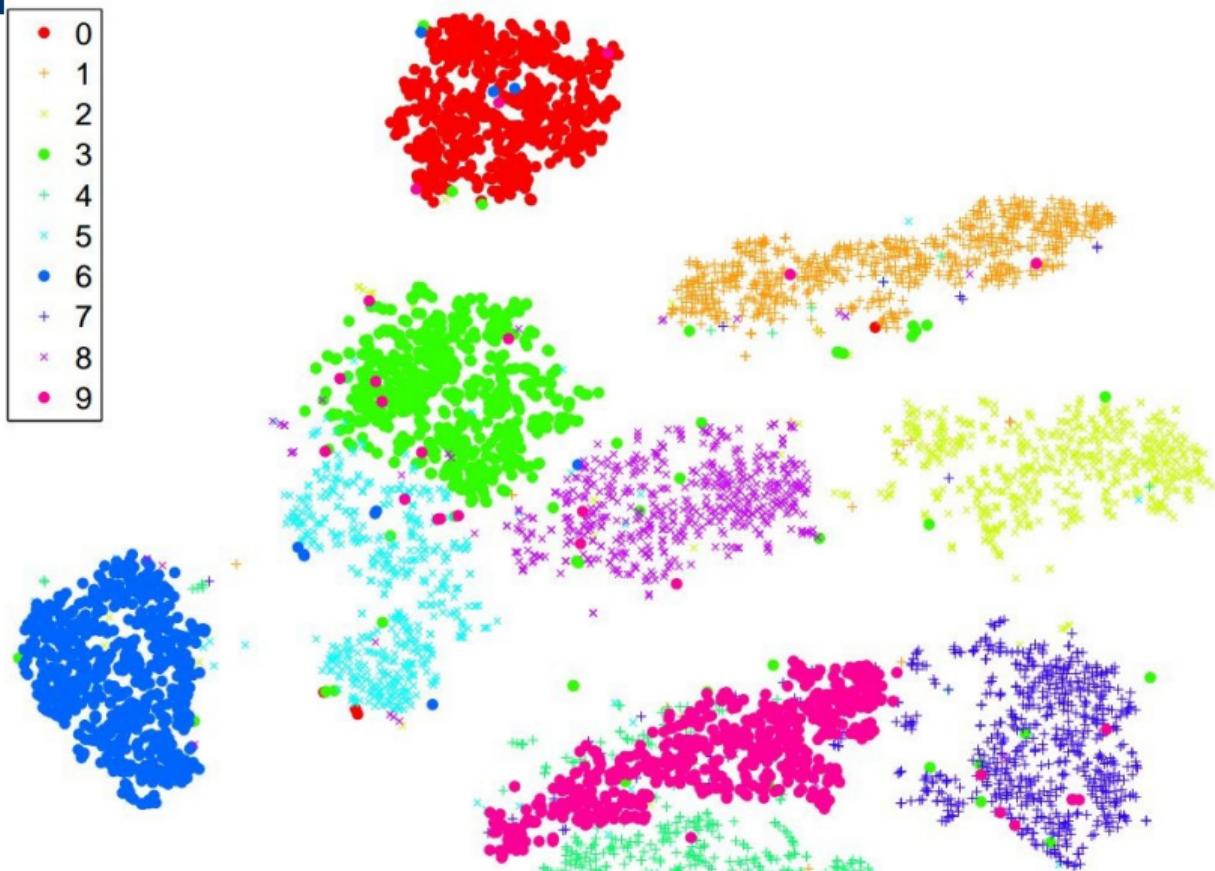
Perplexity = 5

Perplexity = 30

tSNE: Results on MNIST



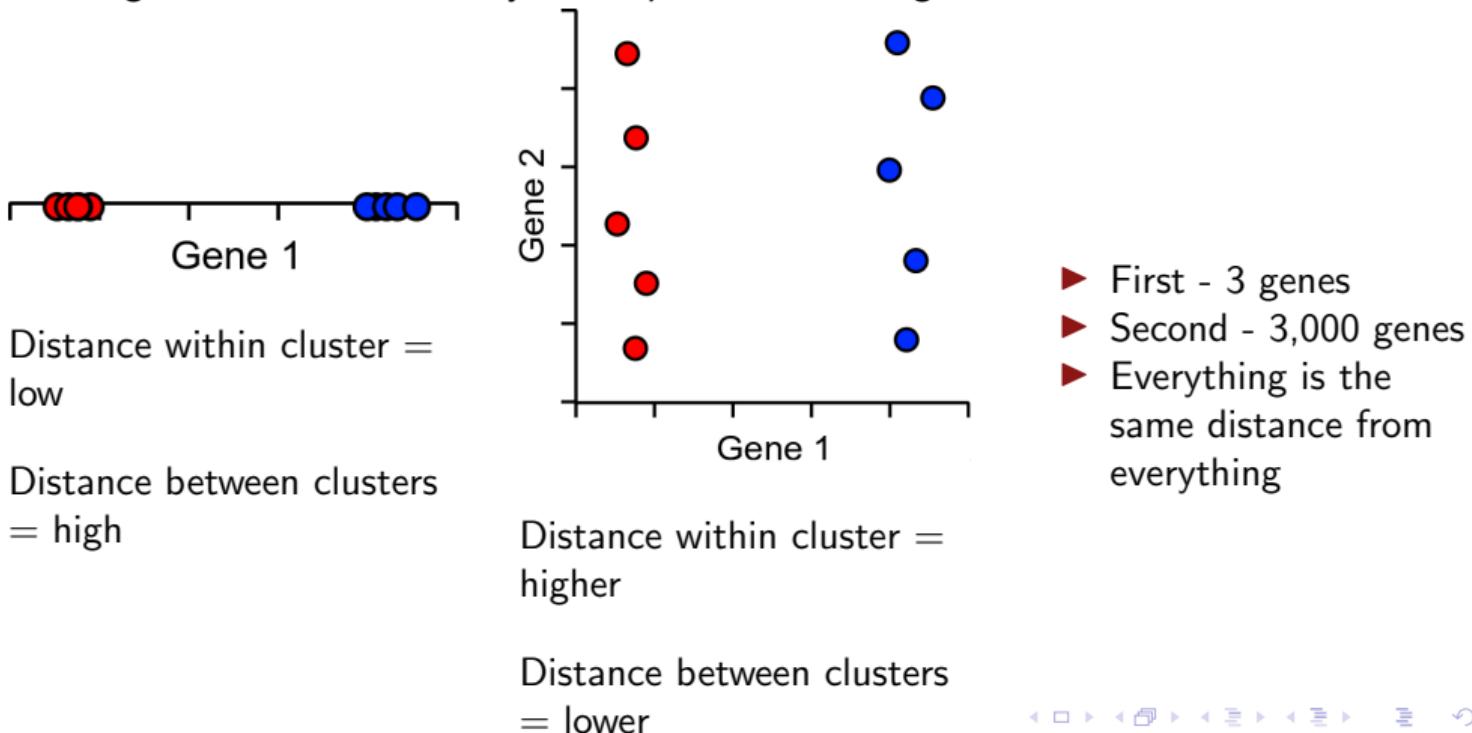
tSNE: Results on MNIST (cont.)



So tSNE is great then?

Kind of...

Imagine a dataset with only one super informative gene



So there is no clear solution?

PCA:

- ▶ Requires more than 2 dimensions
- ▶ Expects linear relationships

tSNE:

- ▶ Can't cope with noisy data
- ▶ Loses the ability to cluster

So there is no clear solution? (cont.)

PCA:

- ▶ Requires more than 2 dimensions
- ▶ Expects linear relationships

tSNE:

- ▶ Can't cope with noisy data
- ▶ Loses the ability to cluster

Answer: Combine the two methods, get the best of both worlds!

PCA:

- ▶ Good at extracting signal from noise
- ▶ Extracts informative dimensions

tSNE:

- ▶ Can reduce to 2D well
- ▶ Can cope with non-linear scaling

This is what many pipelines do in their default analysis!

So PCA + tSNE is great then?

Kind of...

- ▶ tSNE is slow—this is its biggest drawback.
 - tSNE does not scale well to large datasets (10,000+ samples).
- ▶ tSNE provides reliable information only about the closest neighbors; large distance information is mostly irrelevant.

- ▶ UMAP is a replacement for t-SNE, designed to fulfill the same role in dimensionality reduction.
- ▶ It is conceptually very similar to t-SNE, but introduces several relevant (and somewhat technical) changes.
- ▶ In practice, UMAP offers several advantages:
 - UMAP is significantly faster than t-SNE.
 - It can preserve more global structure compared to t-SNE.¹
 - UMAP can operate directly on raw data without requiring PCA preprocessing.²
 - It allows new data points to be added to an existing projection, enabling incremental updates.

¹Preservation of global structure may depend on the dataset and parameter choices.

²Although PCA preprocessing can still be beneficial in some cases.

- ▶ Unlike t-SNE, which uses a single perplexity parameter, UMAP introduces two key parameters:
 - **Number of Nearest Neighbours:** Specifies how many nearest neighbours are considered for each point. This is conceptually similar to perplexity in t-SNE and controls the balance between local and global structure in the embedding.
 - **Minimum Distance:** Determines how closely UMAP packs points together in the low-dimensional space. Lower values allow points to be closer, resulting in more compact clusters, while higher values spread points apart.
- ▶ The **nearest neighbours** parameter influences the trade-off between preserving local versus global structure in the data.
- ▶ The **minimum distance** parameter affects the density and compactness of clusters in the resulting visualization.
- ▶ Together, these parameters provide more flexibility and control over the embedding compared to t-SNE's single perplexity value.

UMAP differences (cont.)

Structure preservation – mostly in the 2D projection scoring

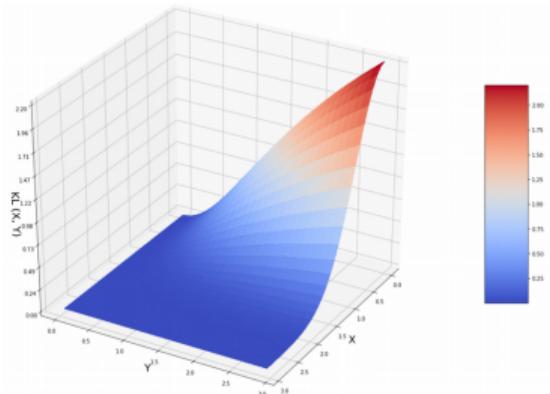


Figure 35: t-SNE

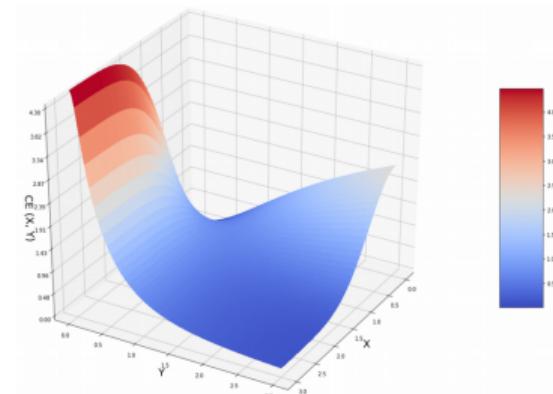
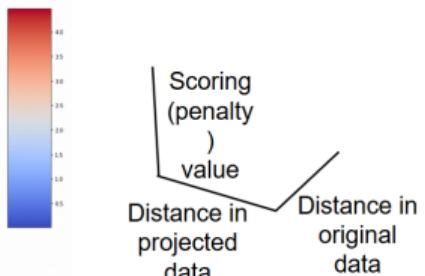
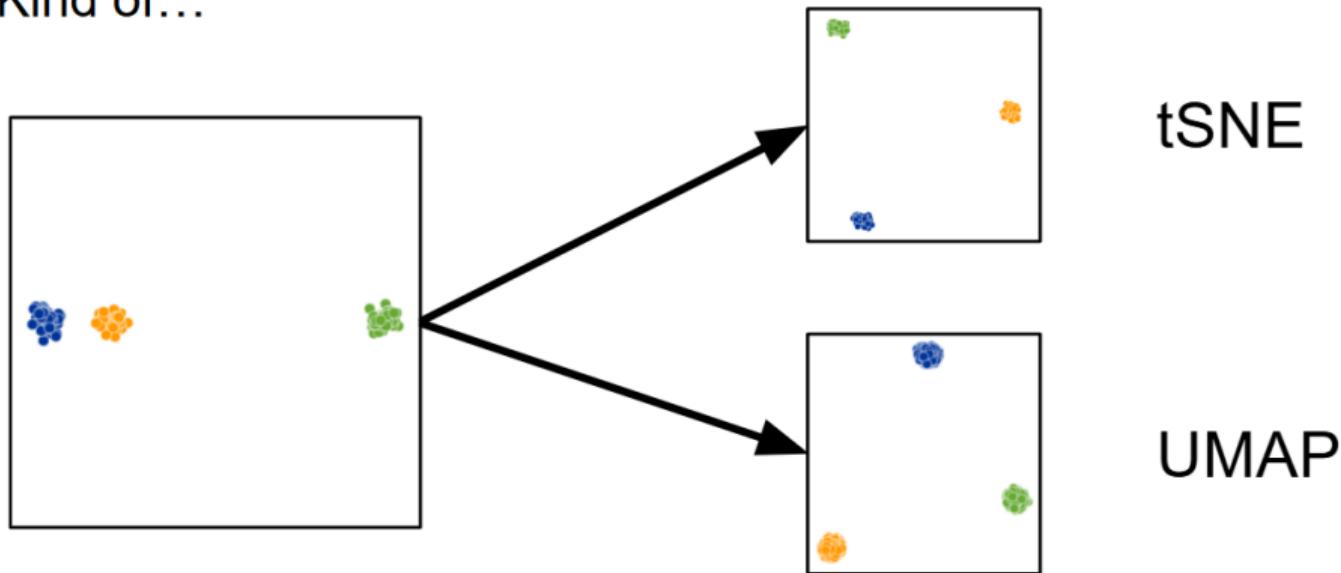


Figure 36: UMAP



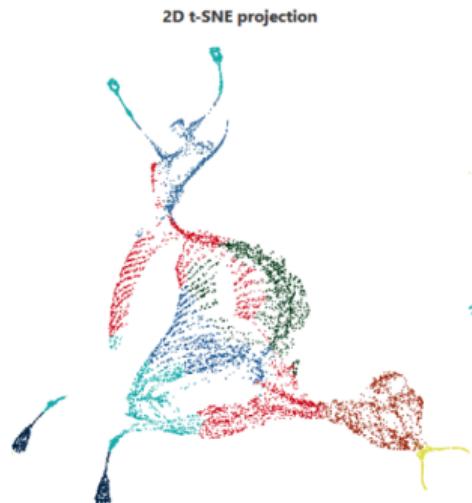
So UMAP is great then?

Kind of...



So UMAP is all hype then?

No, it really does better for some datasets...



3D mammoth skeleton projected into 2D

tSNE: Perplexity 2000 2h 5min

UMAP: Neigh 200, mindist 0.25, 3min

<https://pair-code.github.io/understanding-umap/>

► **Filter the data:**

- Remove poorly behaving cells to ensure data quality.
- Select only expressed genes for further analysis.
- Identify and retain variable genes to focus on informative features.

► **Apply PCA (Principal Component Analysis):**

- Extract the most interesting and informative signals from the data.
- Select the top principal components (PCs) to reduce dimensionality, but do not reduce directly to 2 dimensions.

► **Run t-SNE or UMAP:**

- Calculate distances between samples using the PCA projections.
- Scale these distances appropriately.
- Project the data into 2 dimensions for visualization using t-SNE or UMAP.

So PCA + UMAP is great then?

- ▶ Kind of... as long as you only have one dataset.
 - In 10X experiments, each library is considered a **batch**.
 - Over time or distance, additional biases can be introduced.
 - These biases make direct comparisons between datasets challenging.
 - To enable meaningful comparisons, it is necessary to align the datasets and correct for batch effects.

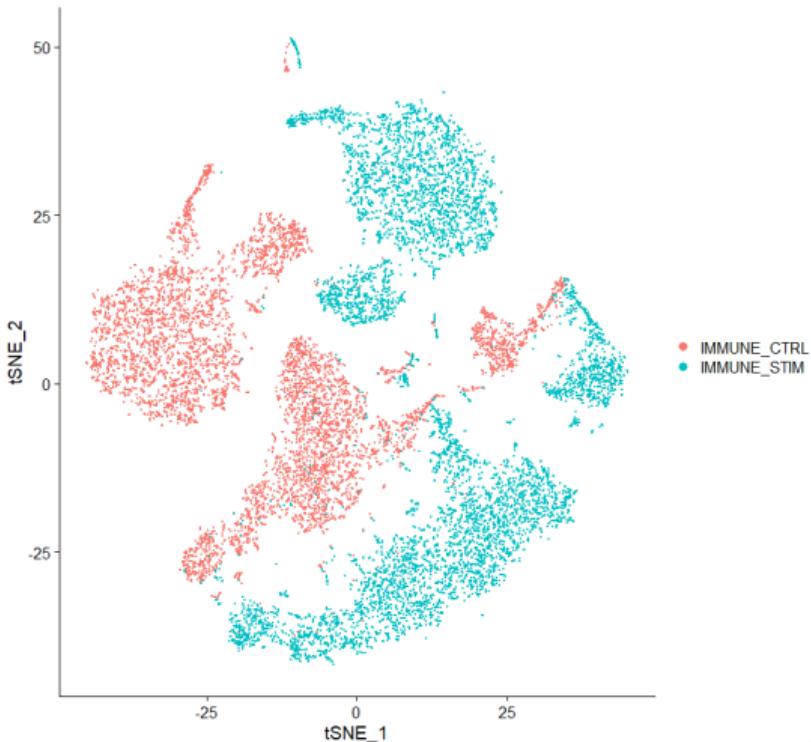


Figure 37: UMAP

- ▶ Sherrie Wang, CME 250: Introduction to Machine Learning, Stanford University. <https://web.stanford.edu/class/cme250/>
- ▶ Volodymyr Kuleshov, CS 5785: Applied Machine Learning, Cornell University. https://www.cs.cmu.edu/~arielpro/15381f16/slides/NLP_guest_lecture.pdf
- ▶ Aykut Erdem, COMP547: Deep Unsupervised Learning, Koç University. <https://aykuterdem.github.io/classes/comp547.s24/>
- ▶ Christoph F. Eick, Machine Learning, University of Houston. <http://www2.cs.uh.edu/~ceick/ML/Topic9.ppt>
- ▶ Zaur Fataliyev, Seoul AI. <https://seoulai.com/presentations/t-SNE.pdf>
- ▶ Simon Andrews, "Dimensionality Reduction", Babraham Bioinformatics. <https://www.bioinformatics.babraham.ac.uk/training/10XRNASeq/Dimension%20Reduction.pptx>

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