# Special Topics in Biostatistics and Bioinformatics Week III

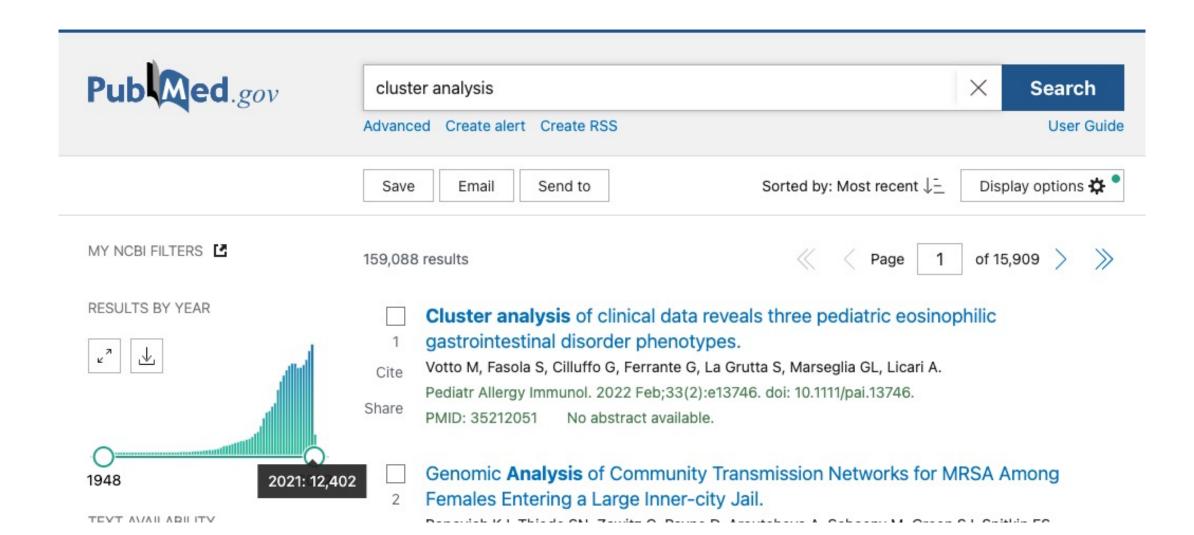
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17 March 2022



## Clustering

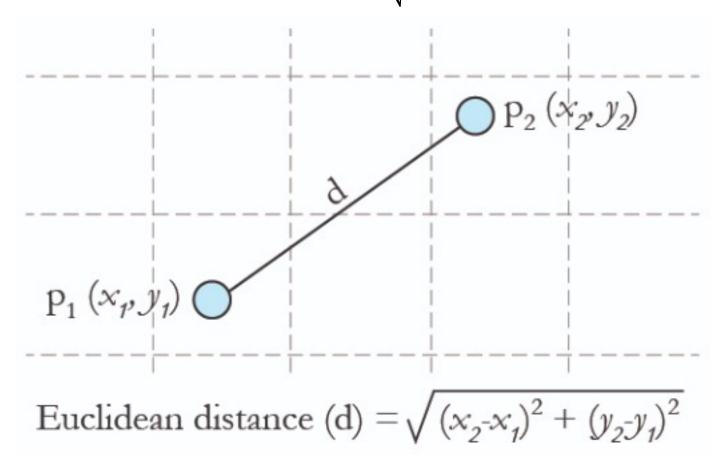
find "close" samples or genes etc. put them into groups



## Defining "distance"

#### **Eucledian distance**

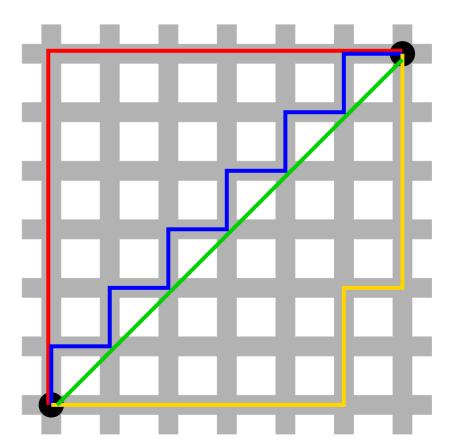
$$d_{euc}(x,y) = \sqrt{\sum_{i=1}^{n} (x_i - y_i)^2}$$



## Defining "distance"

#### Manhattan distance

$$d_{man}(x, y) = \sum_{i=1}^{n} |x_i - y_i|$$



## Defining "distance"

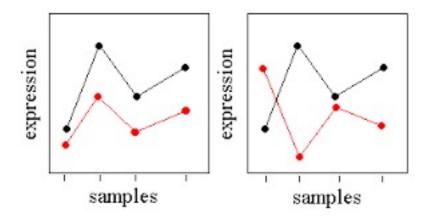
#### Minkowski distance

$$d_{mink}(x, y) = \left(\sum_{i=1}^{n} |x_i - y_i|^p\right)^{\frac{1}{p}}$$

## Other "dissimilarity" measures

#### **Pearson correlation distance**

$$d_{cor}(x,y) = 1 - \frac{\sum_{i=1}^{n} (x_i - \bar{x}) (y_i - \bar{y})}{\sqrt{\sum_{i=1}^{n} (x_i - \bar{x})^2 \sum_{i=1}^{n} (y_i - \bar{y})^2}}$$



## Other "dissimilarity" measures

#### Eisen cosine correlation distance

$$d_{eisen}(x,y) = 1 - \frac{\sum_{i=1}^{n} x_i y_i}{\sqrt{\sum_{i=1}^{n} x_i^2 \sum_{i=1}^{n} y_i^2}}$$

#### **Spearman correlation distance**

$$d_{spear}(x,y) = 1 - \frac{\sum_{i=1}^{n} (x_i' - \bar{x'})(y_i' - \bar{y'})}{\sqrt{\sum_{i=1}^{n} (x_i' - \bar{x'})^2 \sum_{i=1}^{n} (y_i' - \bar{y'})^2}}$$

#### **Kendall correlation distance**

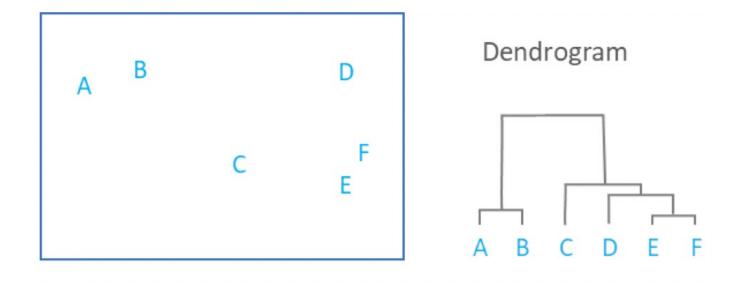
$$d_{kend}(x, y) = 1 - \frac{n_c - n_d}{\frac{1}{2}n(n-1)}$$

#### Clustering Methods

- Hierarchical clustering
- Centroid-based clustering
- Distribution-based clustering
- Density-based clustering
- Grid-based clustering
- Fuzzy clustering

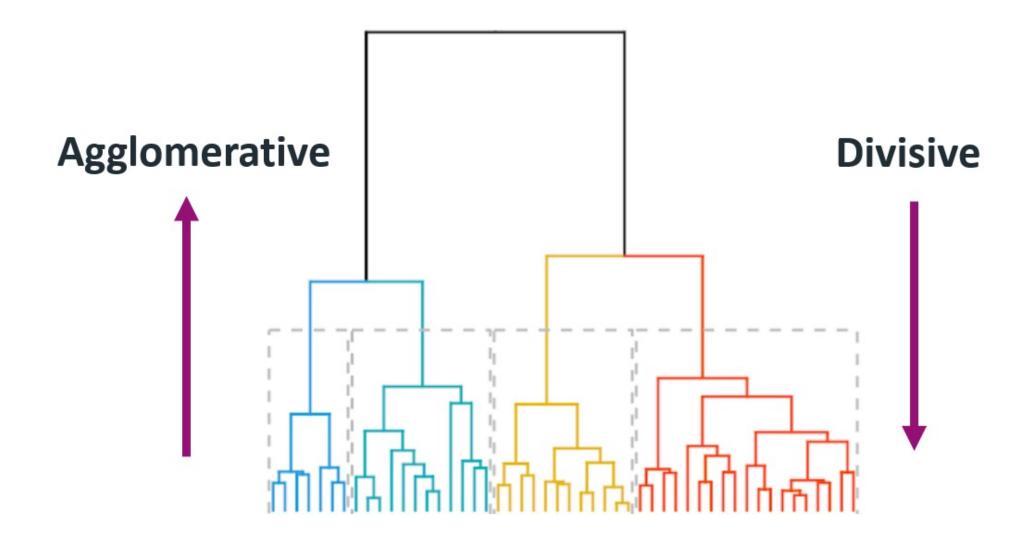
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## Hierarchical clustering

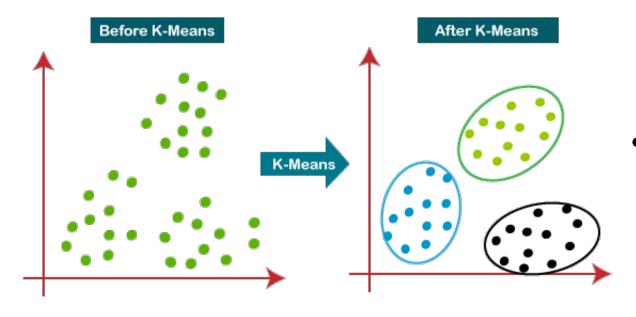


- Find the "closest" points
  - Merge
  - Repeat

## Hierarchical clustering



#### K-means clustering

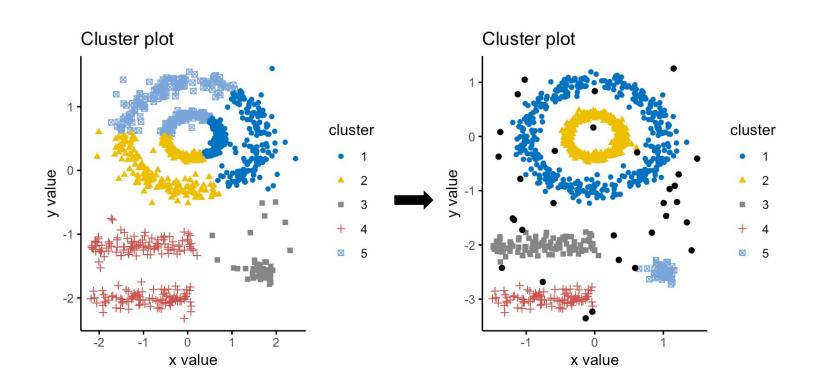


- Initialize k cluster "centers" (random seeds)
- Assign each value to the closest center
  - Update centers
  - Reassign values
    - Repeat

#### Other Approaches

- Hierarchical K-means Clustering
- Hierarchical clustering on principal components

- Fuzzy Clustering
  - Fuzzy c-means
- DBSCAN



#### Determining the optimal number of clusters

Visualization

- Elbow method
  - location of a bend in total within-cluster sum of square
- Average silhouette method
  - Maximum average silhouette
- Gap statistic method
  - the smallest value of k such that the gap statistic is within one standard deviation of the gap at k+1:  $Gap(k) \ge Gap(k + 1) s_{k+1}$ .

## Dimensionality Reduction

Overcoming the curse of dimensionality

## Curse of dimensionality

Cannot visualize observations

- Overfitting terrible out of sample performance.
- Observations become harder to cluster too many dimensions causes every observation to appear equidistant from all the others

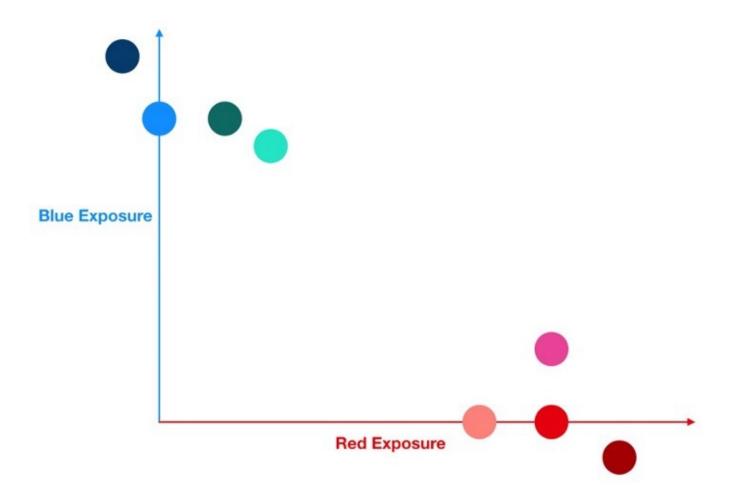
## Curse of dimensionality

Red	Maroon	Pink	Flamingo	Blue	Turquoise	Seaweed	Ocean
1	0	0	0	0	0	0	0
0	1	0	0	0	0	0	0
0	0	1	0	0	0	0	0
0	0	0	1	0	0	0	0
0	0	0	0	1	0	0	0
0	0	0	0	0	1	0	0
0	0	0	0	0	0	1	0
0	0	0	0	0	0	0	1

## Dimensionality Reduction

#### **Latent Features**

	Red	Blue
Red	1.00	0
Maroon	1.20	-0.10
Pink	1.00	0.20
Flamingo	0.80	0
Blue	0	1.00
Turquoise	0.25	0.90
Seaweed	0.15	1.00
Ocean	-0.10	1.20



#### Dimensionality Reduction

#### Projection

 Projecting every data point in high dimension onto a suitable lowerdimensional space, approximately preserving the distances

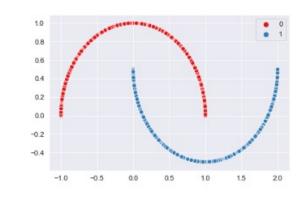
#### Manifold Learning

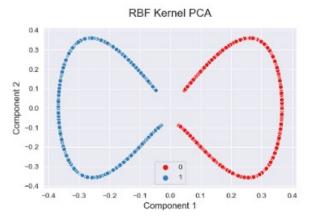
- Modelling the manifold on which the training instance lie
- Assumption: most real-world high-dimensional datasets lie close to a much lower-dimensional manifold

#### Use Cases

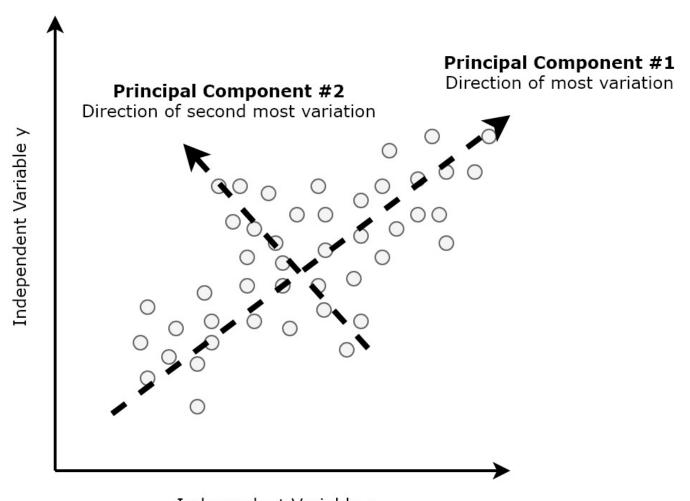
- Visualization to observe relationships 2D/3D
- Batch effect identification
- ...

- transforms non-linear data into a linearly-separable form
- removes multicollinearity
- reduces the training time of models
- improves the accuracy of models





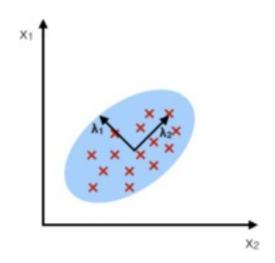
## Principal Component Analysis (PCA)



## Linear Discriminant Analysis (LDA)

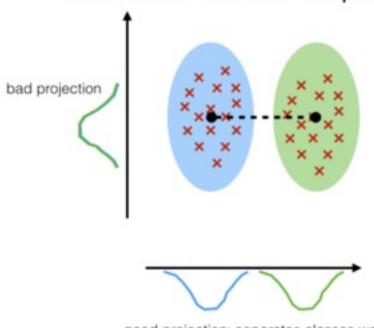
#### PCA:

component axes that maximize the variance



#### LDA:

maximizing the component axes for class-separation



good projection: separates classes well

## T-distributed stochastic neighbor embedding

(t-SNE)

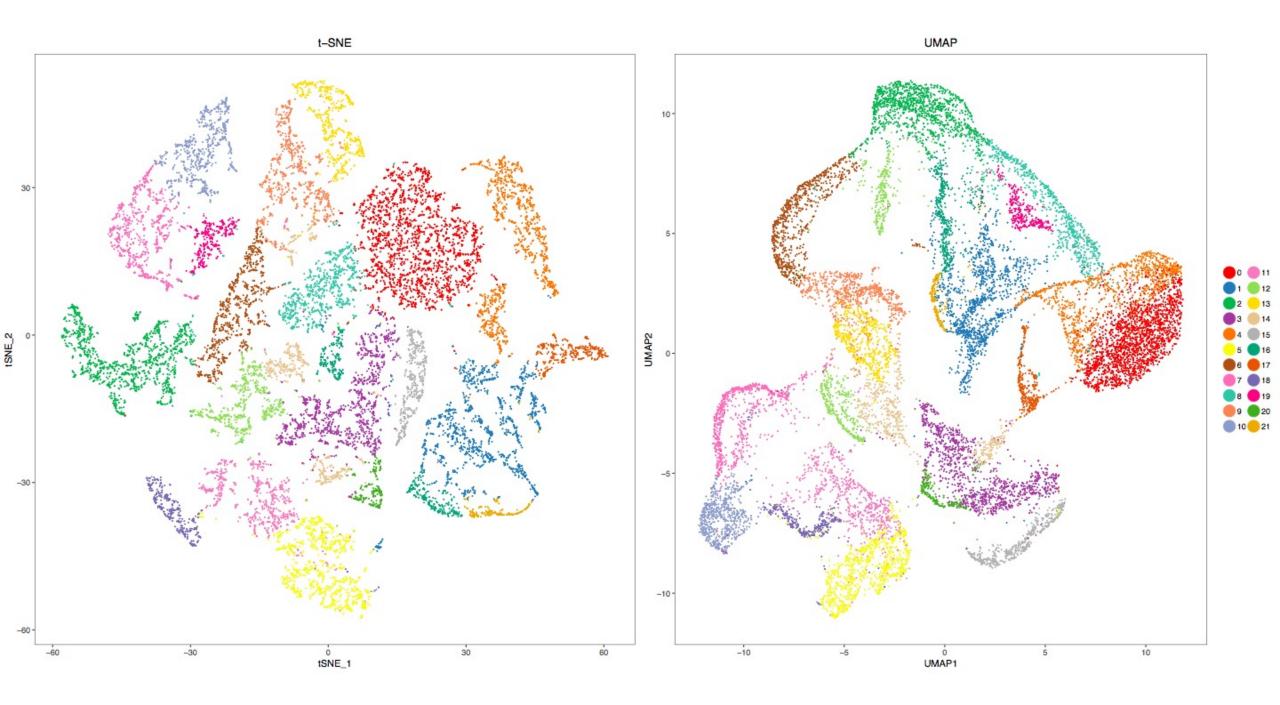
t-SNE reduces dimensionality while trying to keep similar instances close and dissimilar instances apart

van der Maaten, L.J.P.; Hinton, G.E. (Nov 2008). "Visualizing Data Using t-SNE" (PDF). Journal of Machine Learning Research. 9: 2579–2605.

## Uniform Manifold Approximation and Projection (UMAP) McInnes, L., & Healy, J. (2018). UMAP: Unit

McInnes, L., & Healy, J. (2018). UMAP: Uniform Manifold Approximation and Projection for Dimension Reduction. ArXiv e-prints.

- Similar to tSNE
- a number of advantages over tSNE
  - increased speed
  - scalability
  - better preservation of the data's global structure



#### More Techniques

- Multidimensional Scaling (MDS)
- Independent Component Analysis (ICA)
- Non-negative Matrix Factorization (NMF)

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