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Case study 1: Model selection for clustering

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Overview

- What is Model selection?
 - Challenges in model selection for clustering
 - Clustering algorithms
 - Colorectal Tissue Biopsy and Clustering
-
- Your task and dataset details
 - Expected results
 - Summary



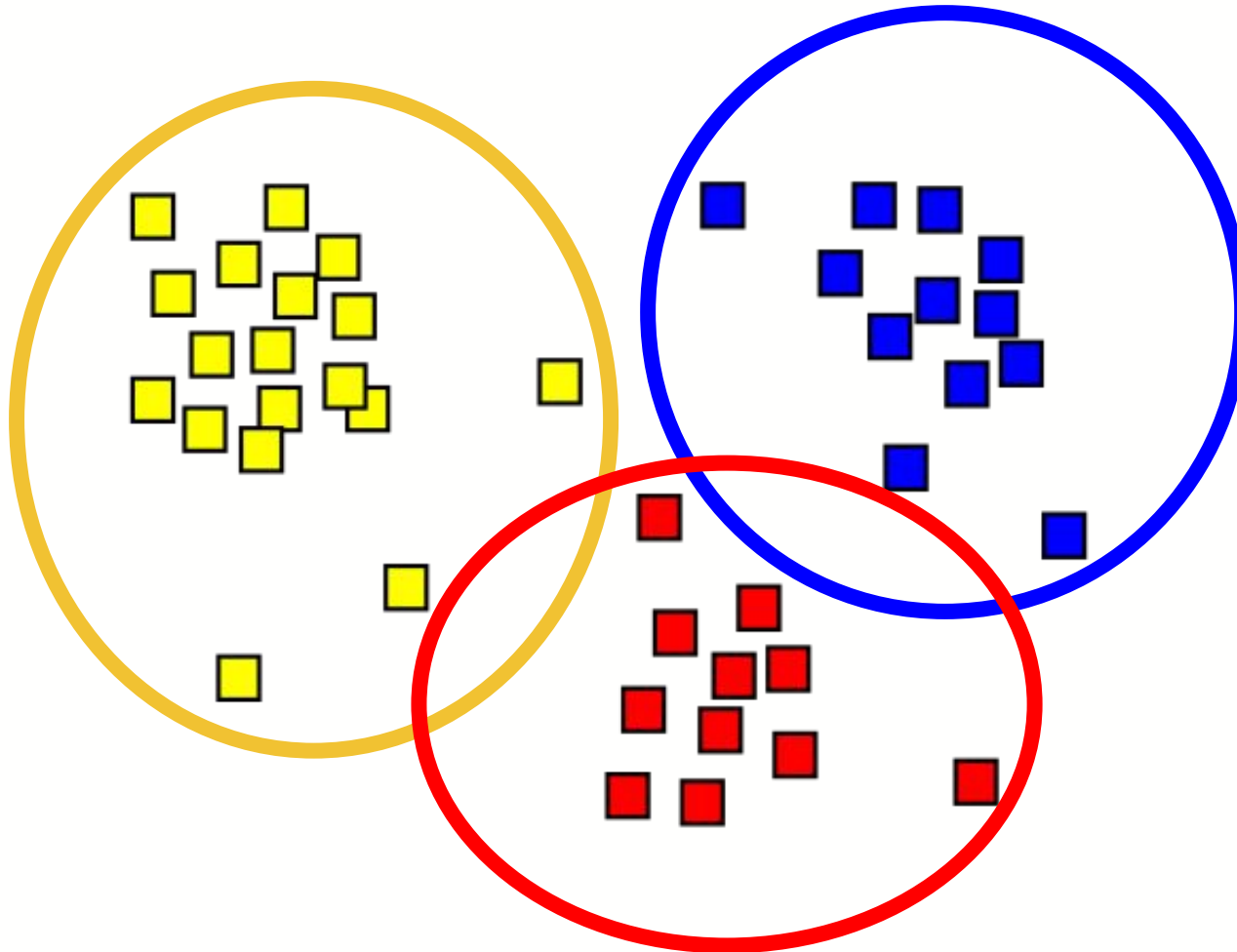
Model selection

- Choosing the best model candidate
 - family of algorithms (e.g. Logistic regression, KNN)
 - different hyperparameters (e.g. regularisation strength, number of neighbours)
- What is 'the best model'?
 - Define objective (e.g. accuracy, minimise false positives, etc)
 - Complexity
 - Computability
 - Ease of Implementation



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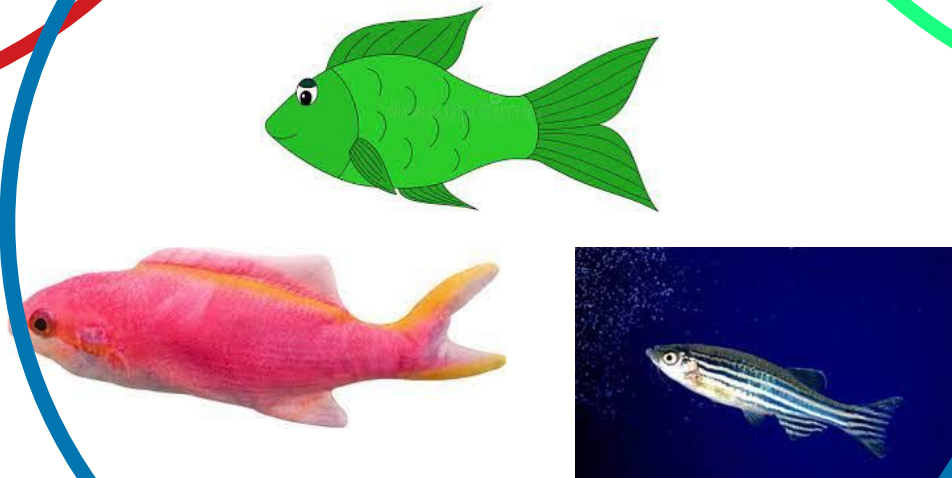
Why do we need model selection for clustering?





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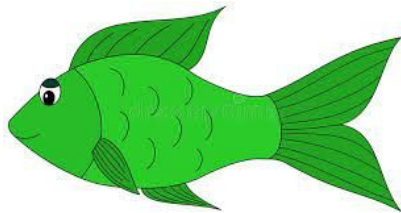
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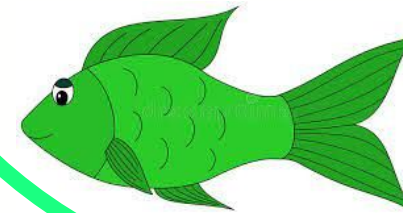
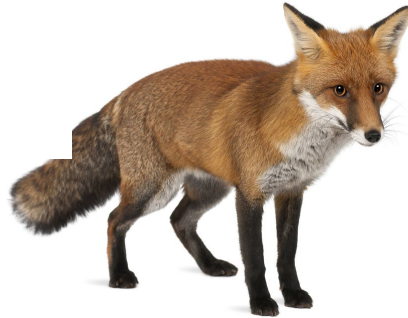
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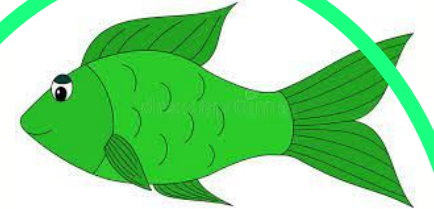
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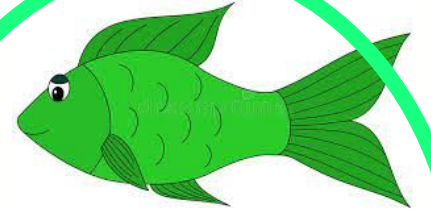
Why do we need model selection for clustering?





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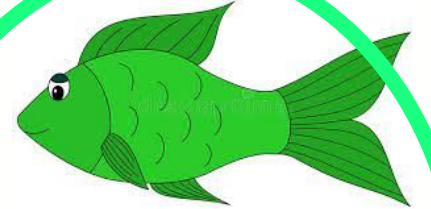
Why do we need model selection for clustering?





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Why do we need model selection for clustering?

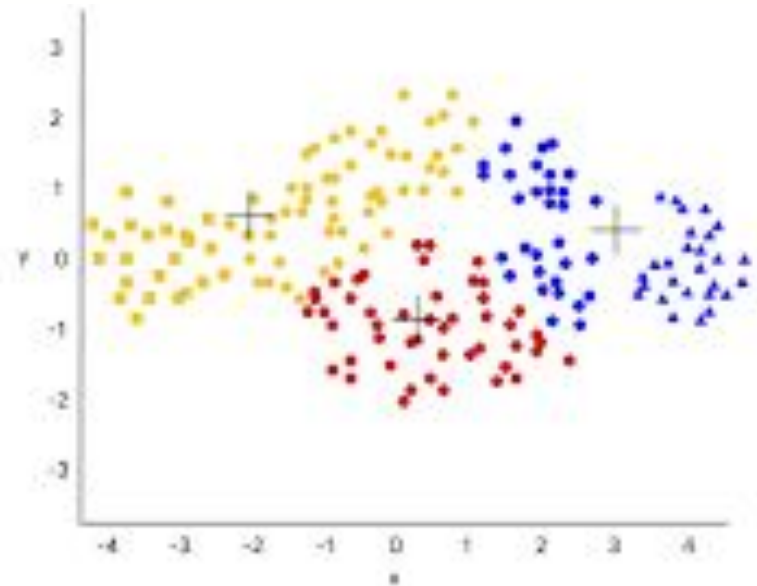
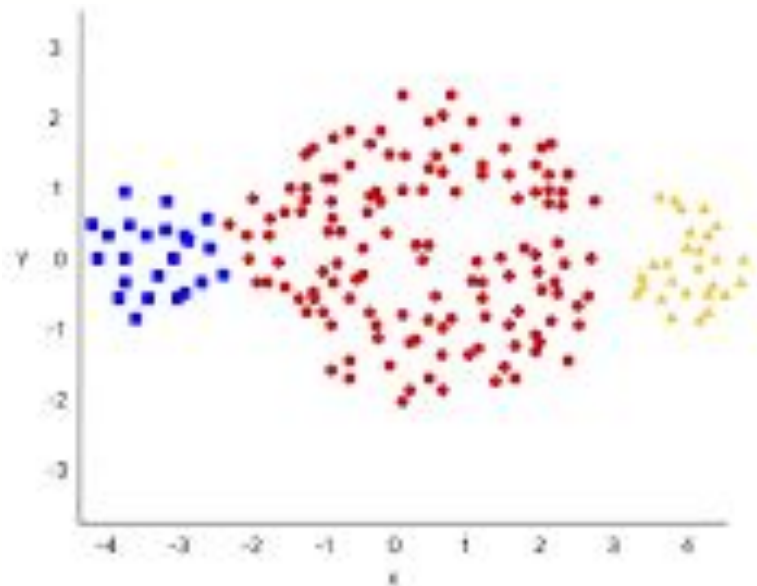




Why do we need model selection for clustering?

- Group similar objects together
- Constraints on clusters
- Understand the structure of a dataset

The best clustering model will best describe the structure of the data.





Examples of clustering algorithms

Cluster numbers can be explicitly specified:

1. K-means
2. Gaussian Mixture Model (GMM)

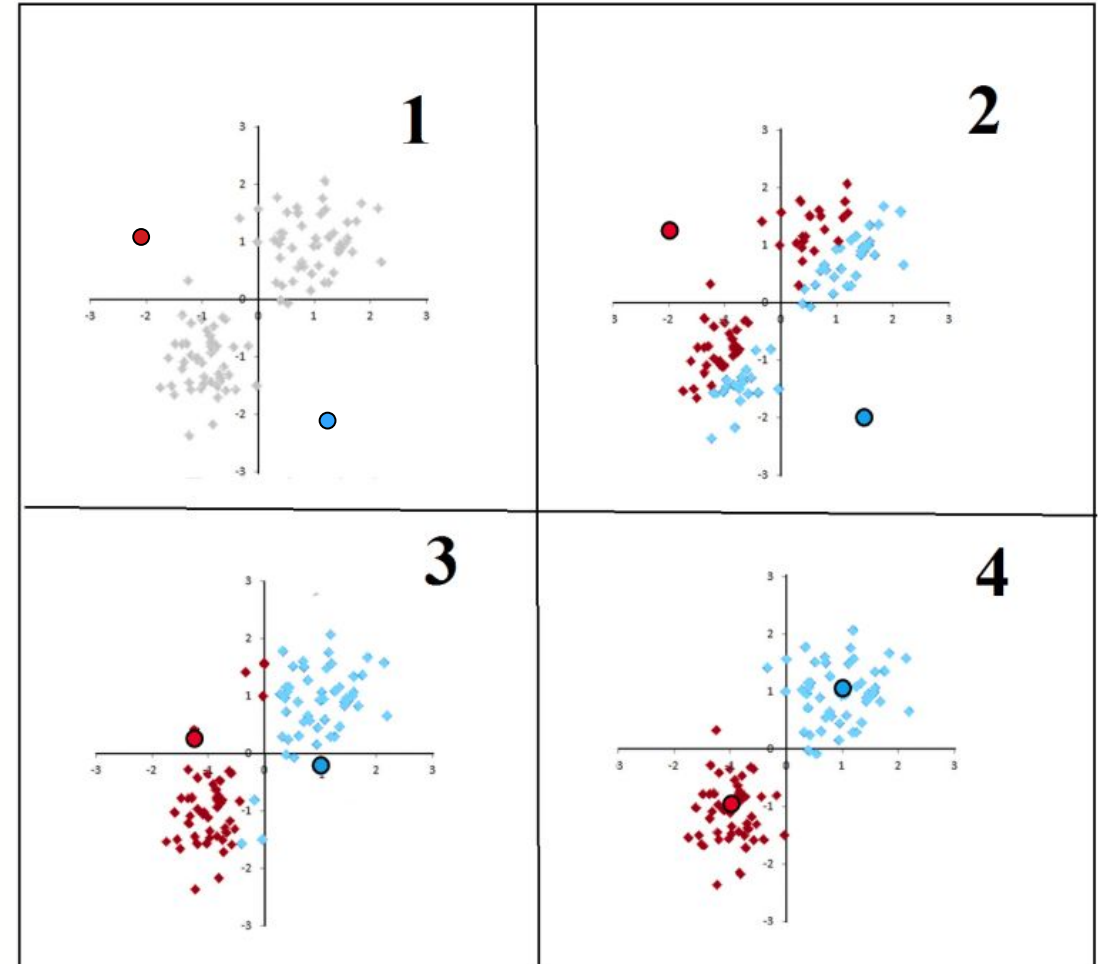
Or inferred:

1. Hierarchical clustering
2. Louvain Clustering



K-means

1. Choose k random points
2. Partition objects into k subset
3. Compute the new *centroids* (mean points) of the clusters
4. Repeat steps 2+3 until convergence

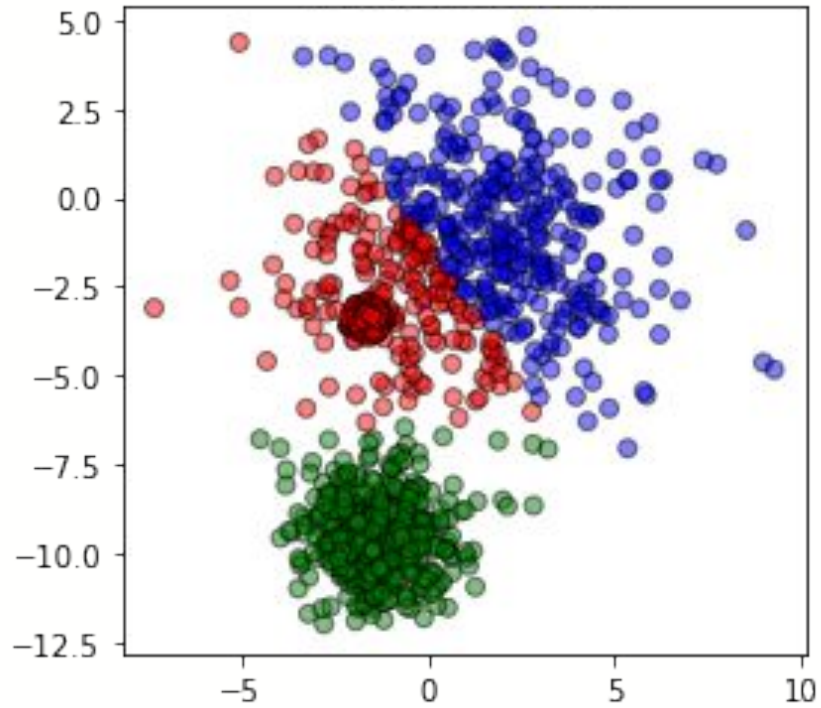




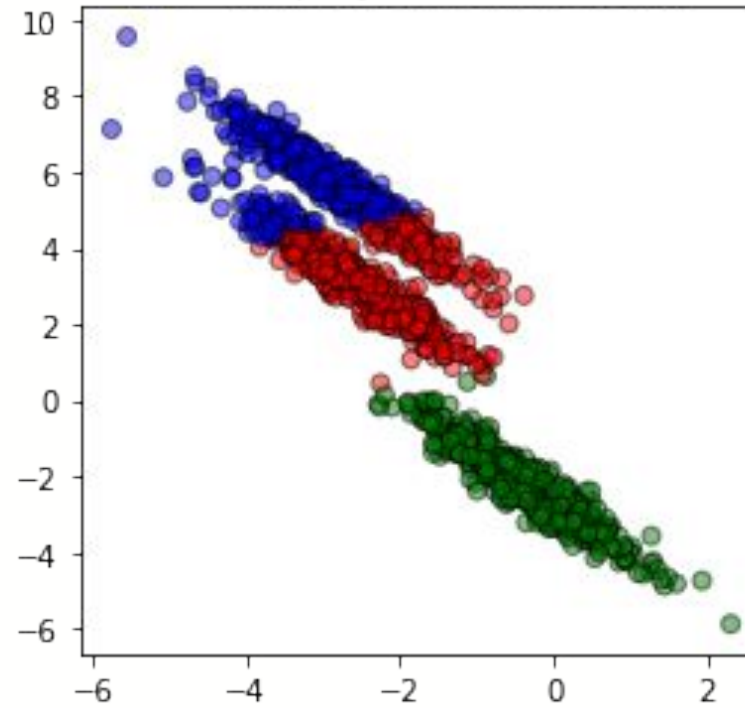
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K-means

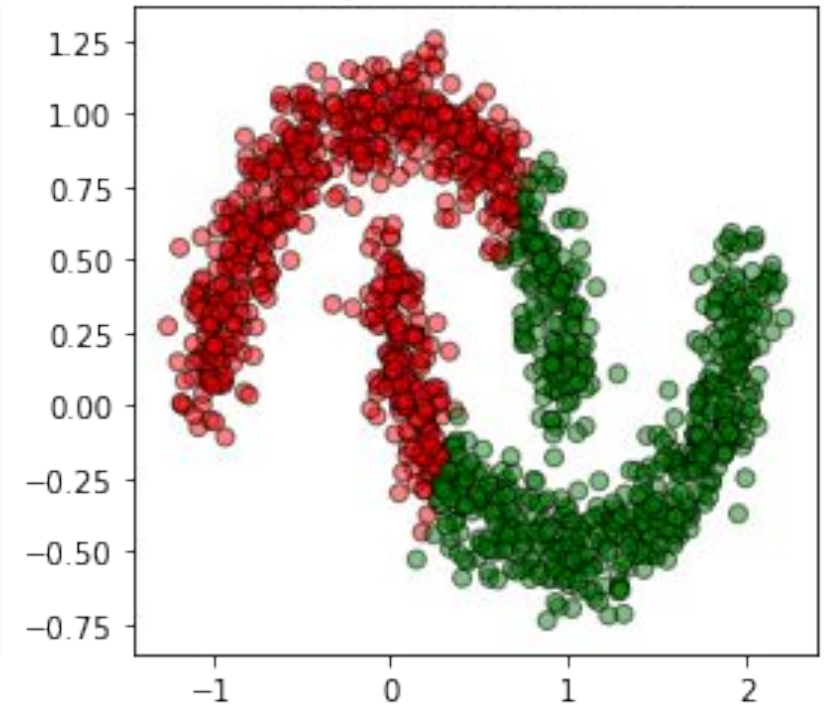
Unequal Variance



Anisotropically Distributed Blobs



Irregular Shaped Data





Gaussian Mixture Model (GMM)

- k-means only considers mean points
- GMM considers mean and (co-)variance
- Fit M Gaussian components by maximising log-likelihood

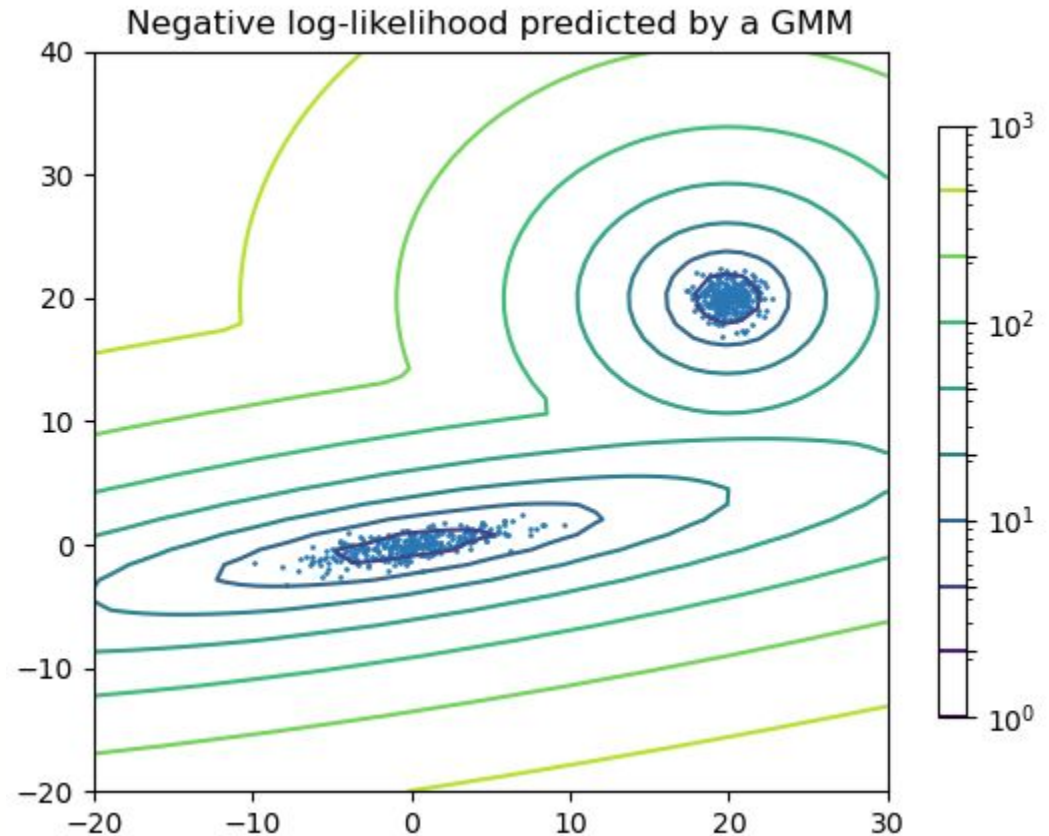
$$\ell(\theta|\mathbf{x}) = \sum_{i=1}^N \log \left(\sum_{m=1}^M \alpha_m \phi(x_i | \mu_m, \Sigma_m) \right)$$

x – datapoint

θ - gaussian parameters $\{(\mu_m, \Sigma_m): 0 \leq m \leq M\}$

α - mixing coefficient

Φ – probability density function





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Initial Random Guess

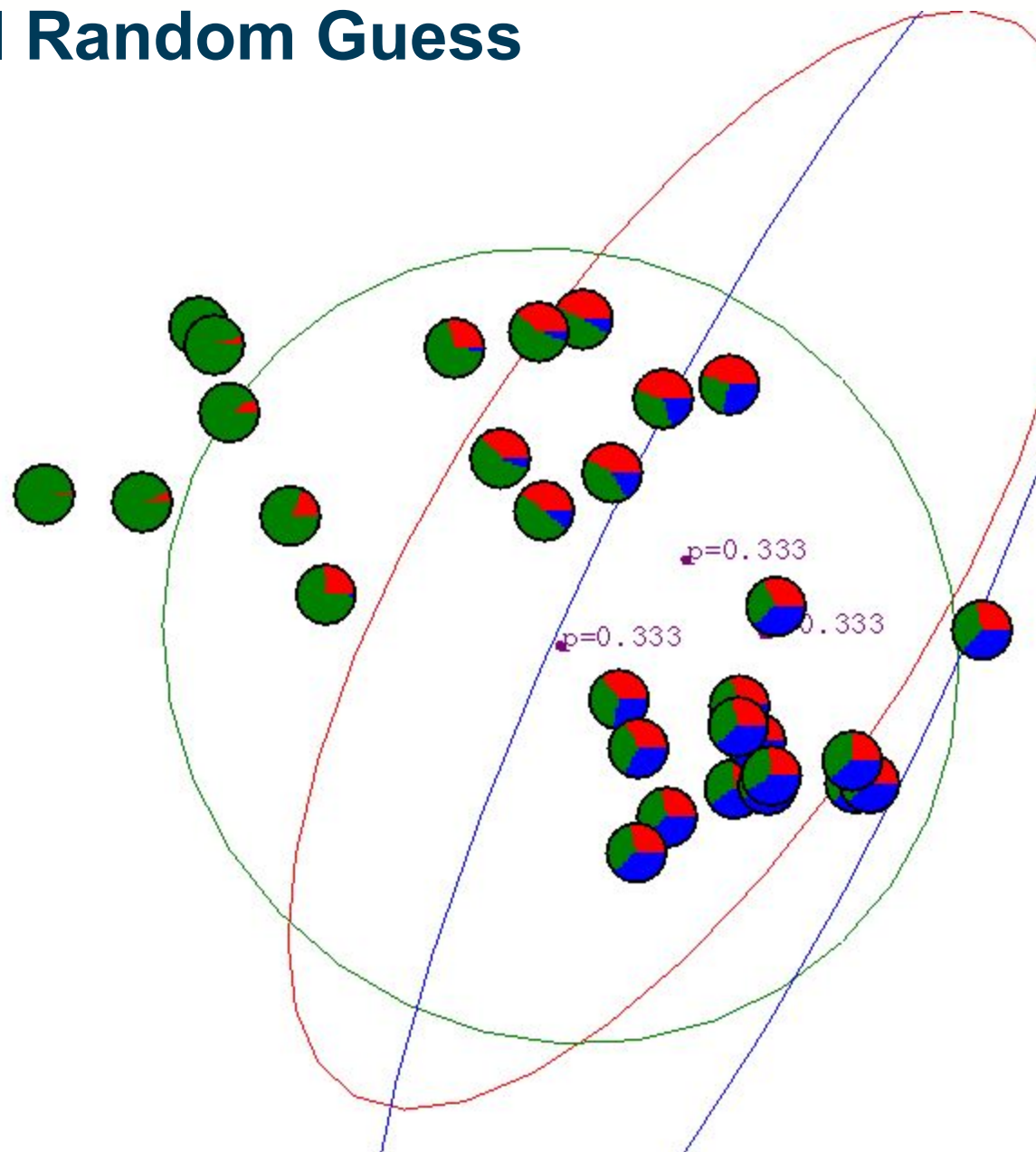
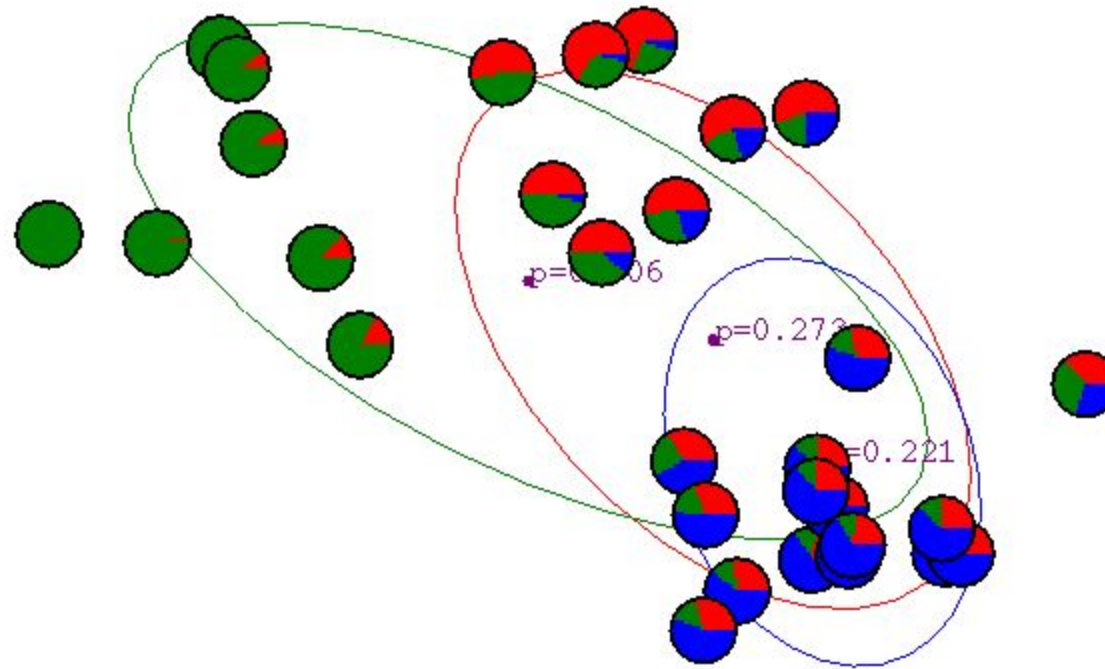


Image credit Prof A Moore, Carnegie Mellon University



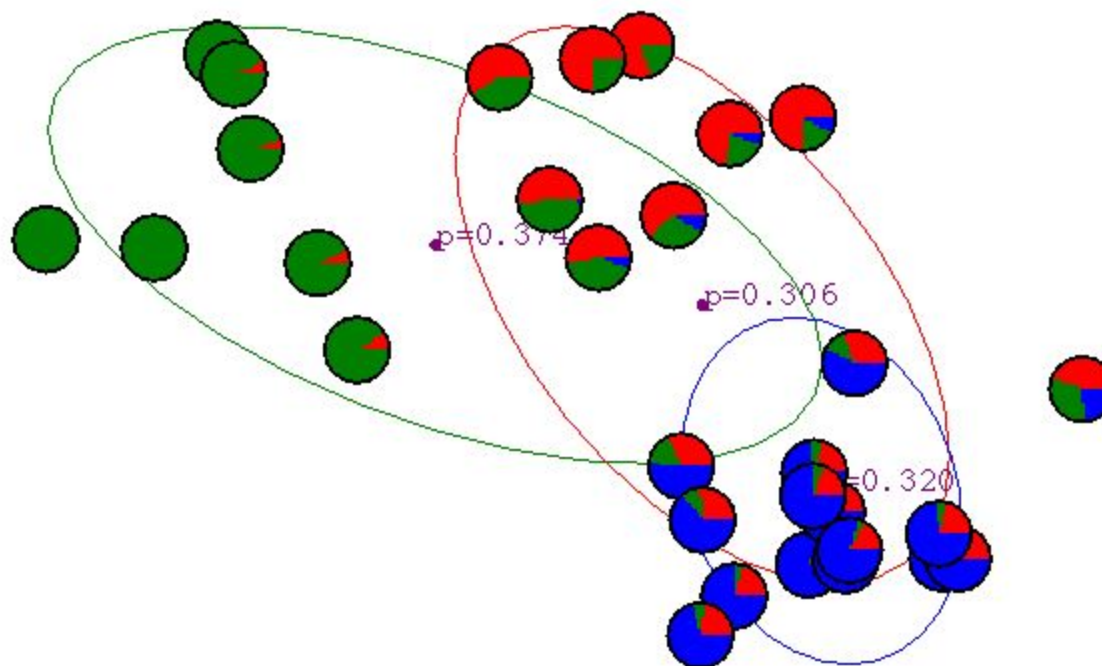
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1st Iteration



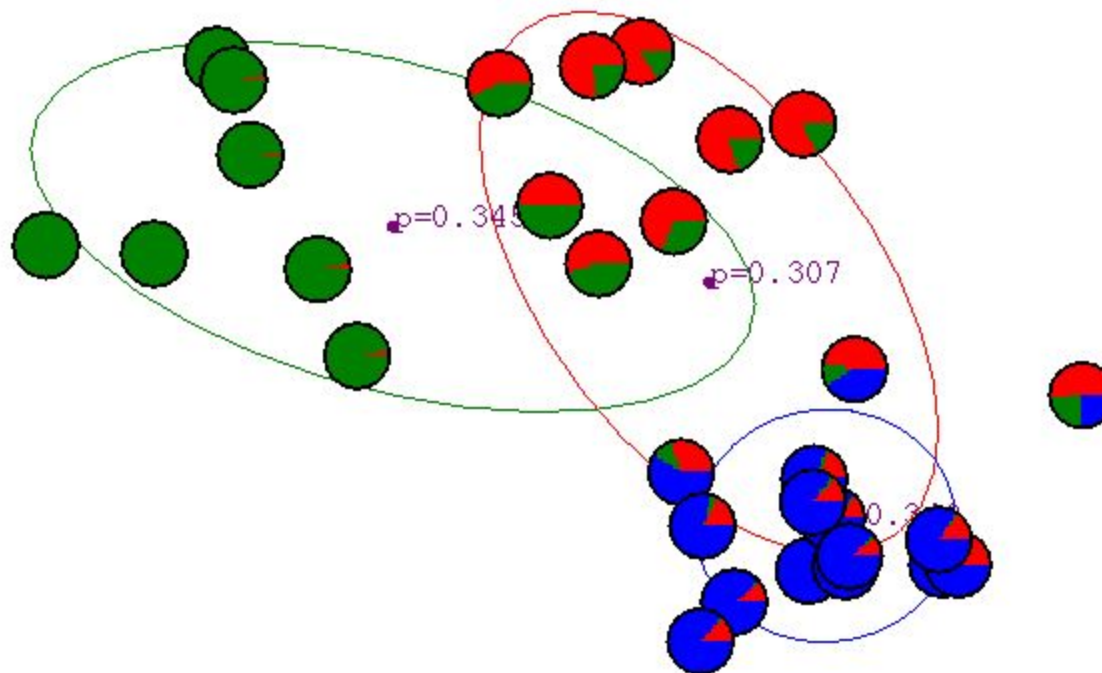


2nd Iteration



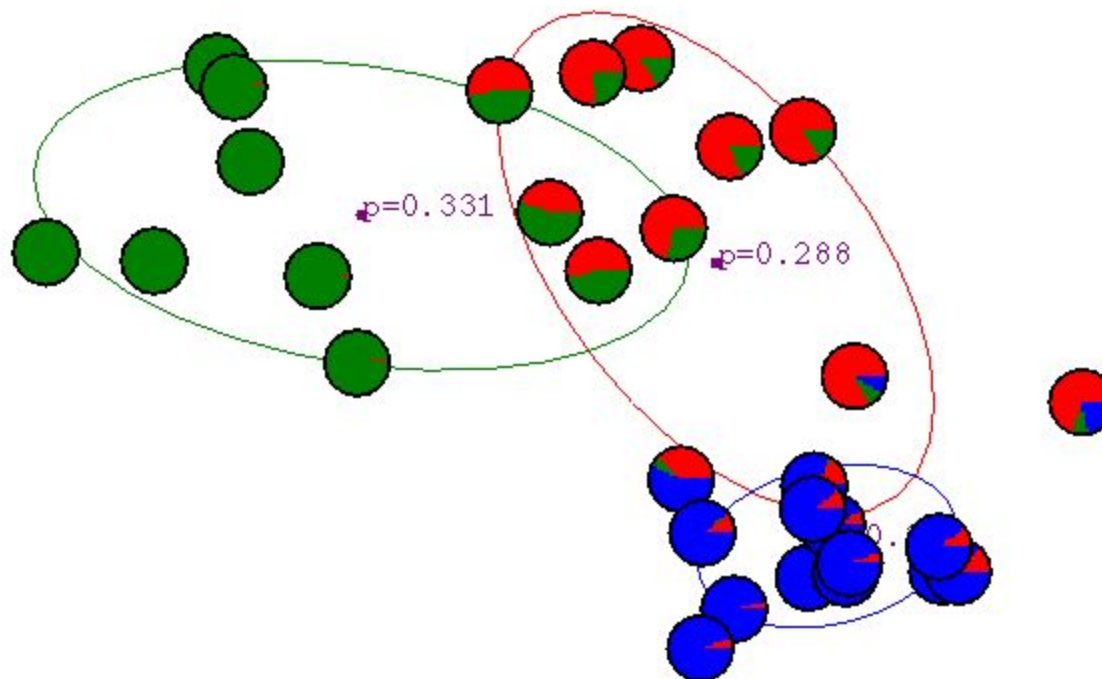


3rd Iteration





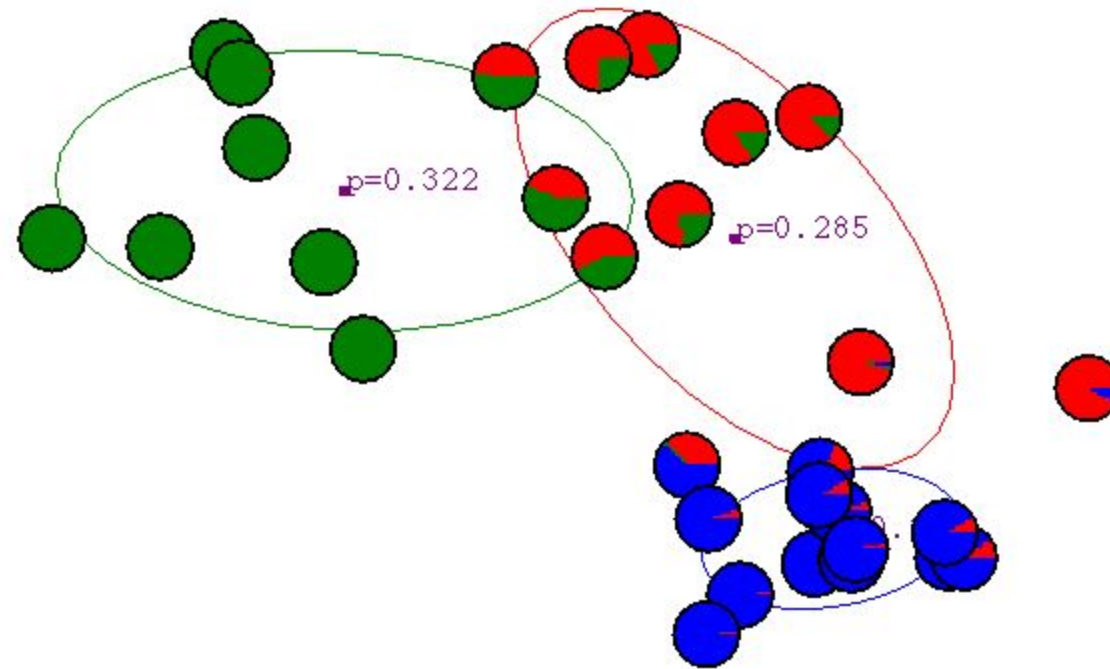
4th Iteration





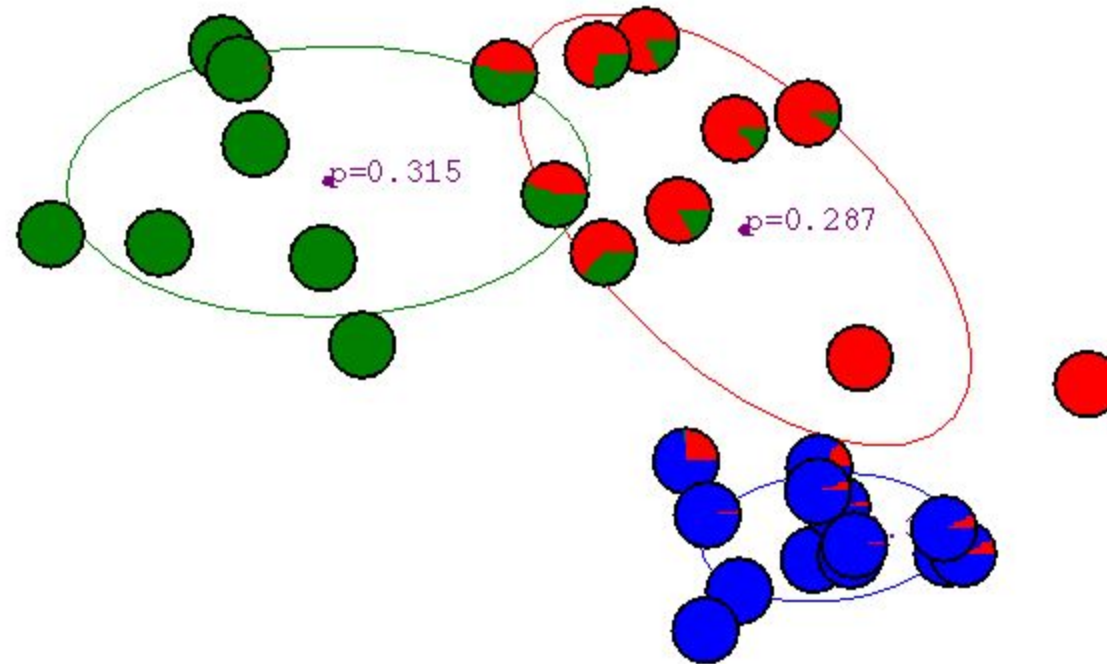
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5th Iteration





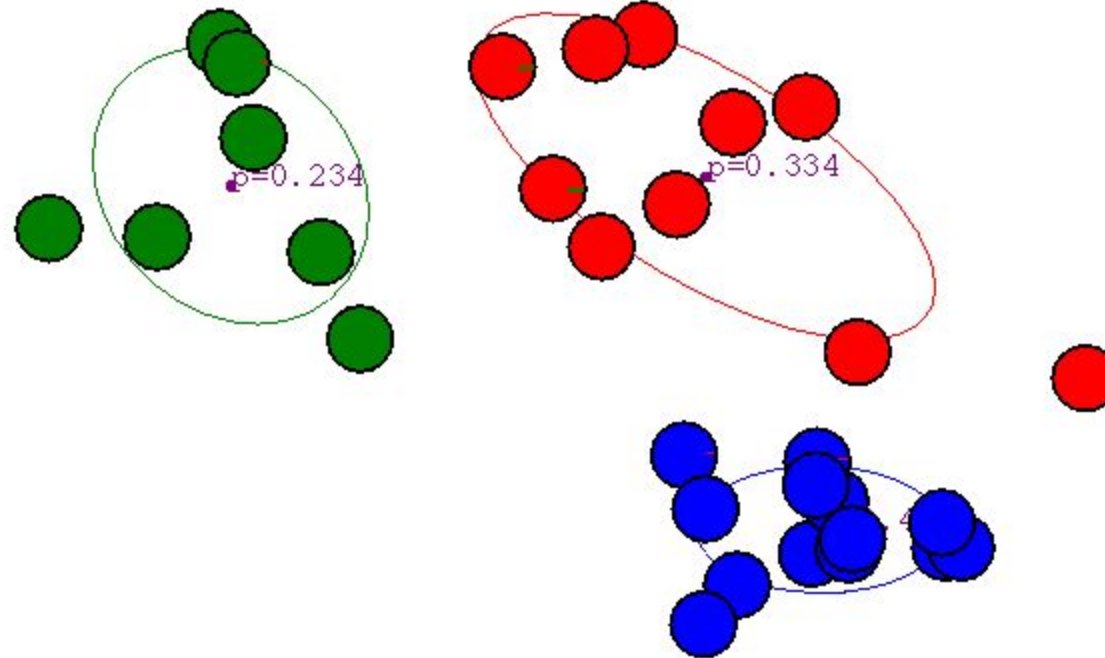
6th Iteration...





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...20th Iteration





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Gaussian Mixture Model (GMM)

Bio Assay Data

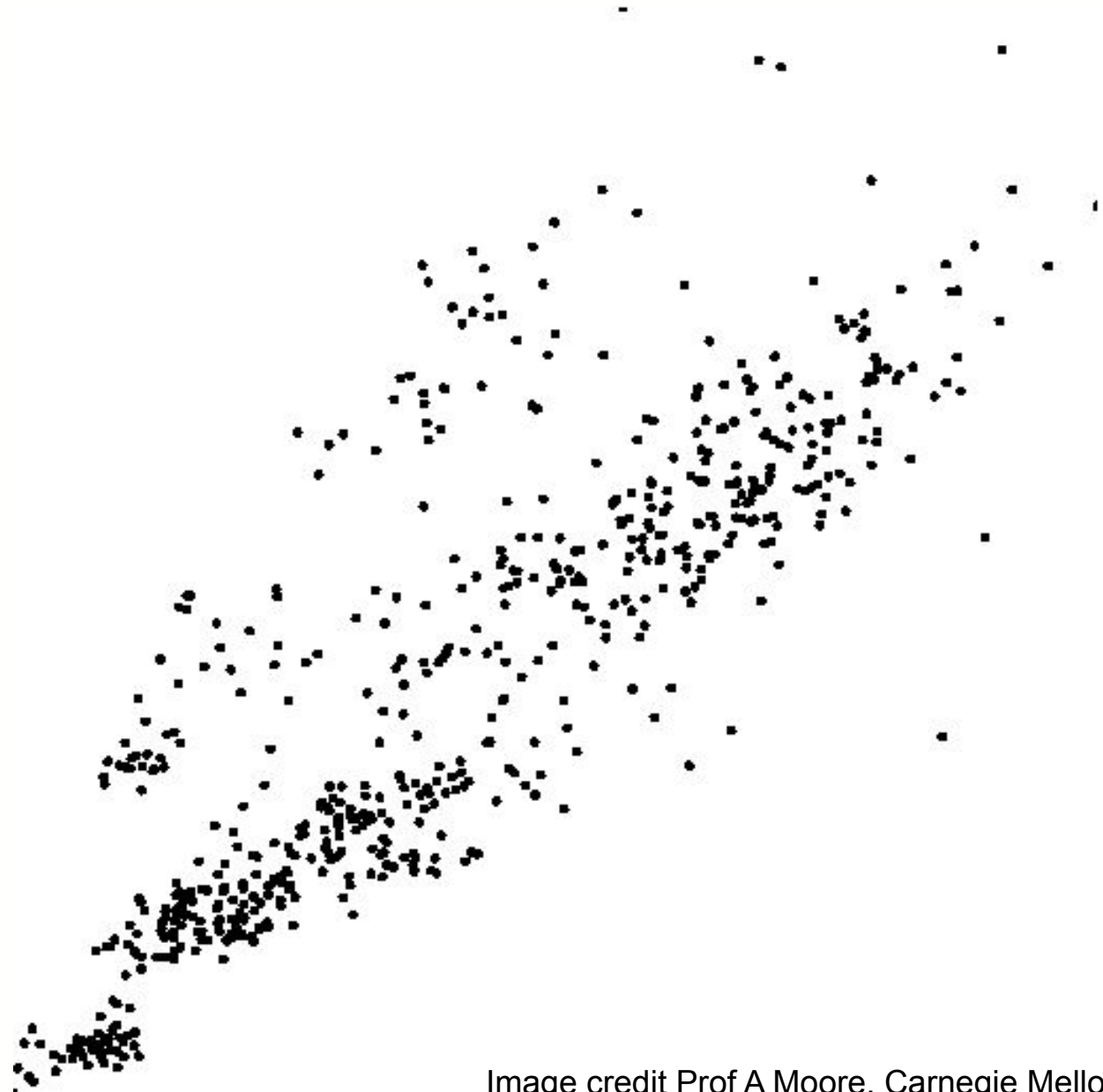


Image credit Prof A Moore, Carnegie Mellon University



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Gaussian Mixture Model (GMM)

Bio Assay Data

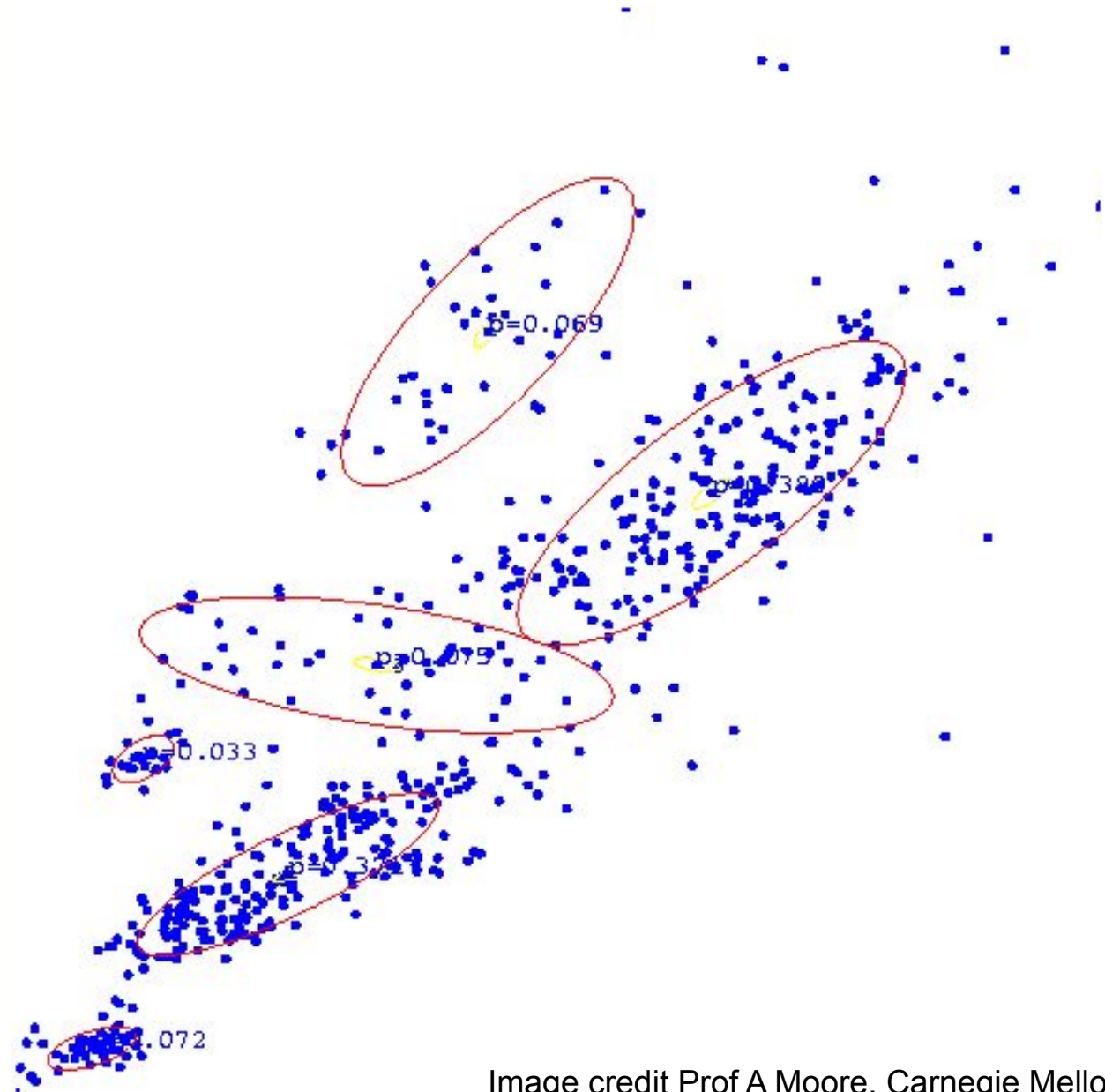


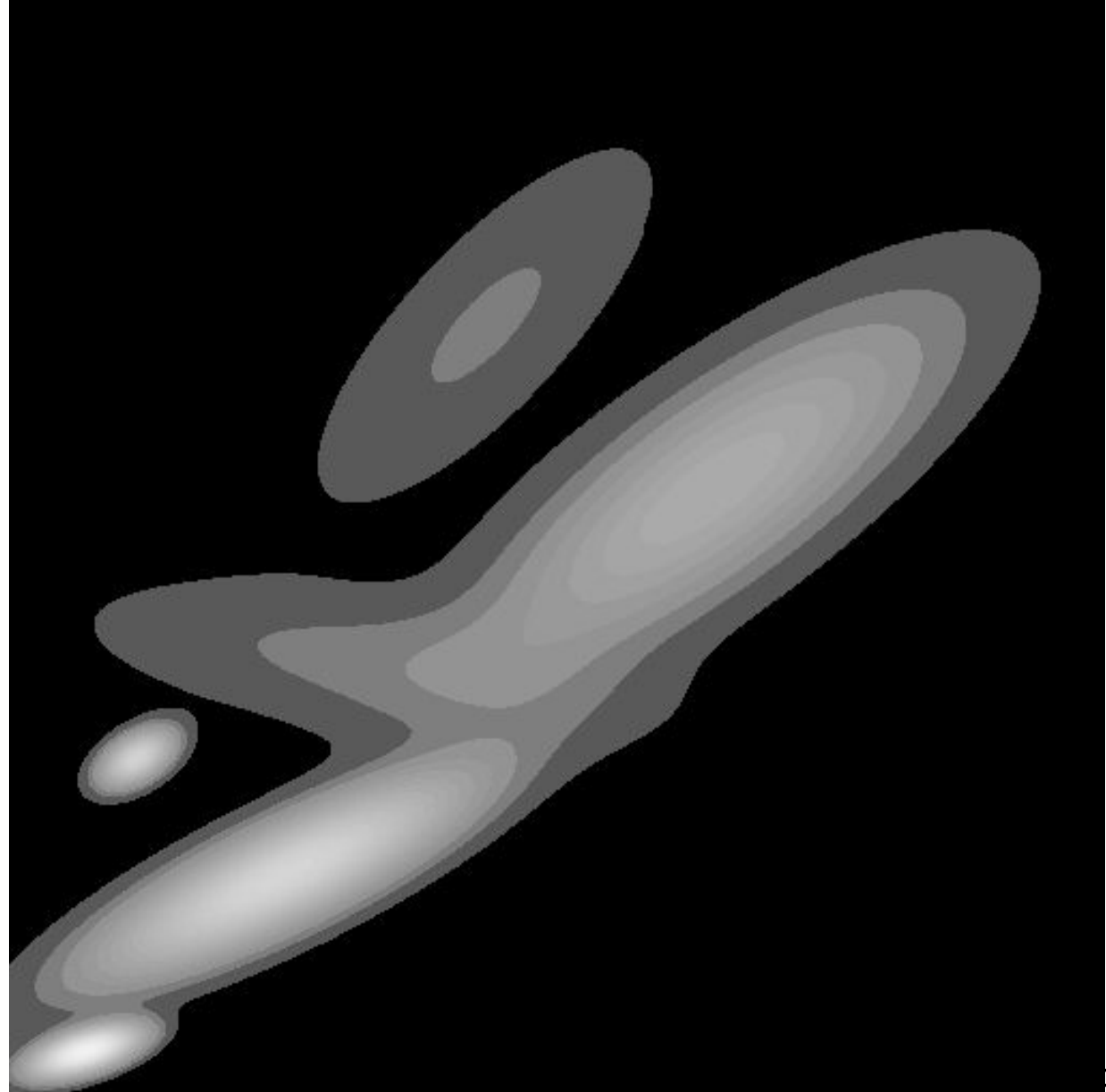
Image credit Prof A Moore, Carnegie Mellon University



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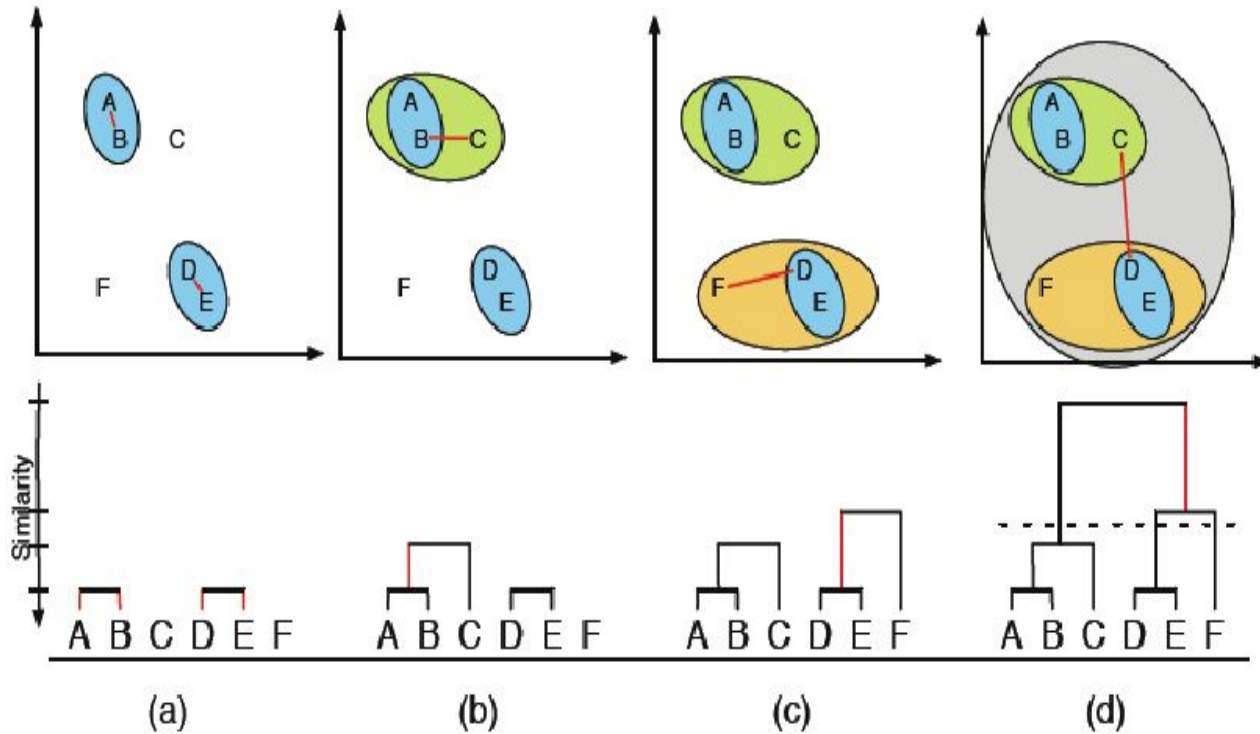
Gaussian Mixture Model (GMM)

Bio Assay Data





Hierarchical Clustering (HC)



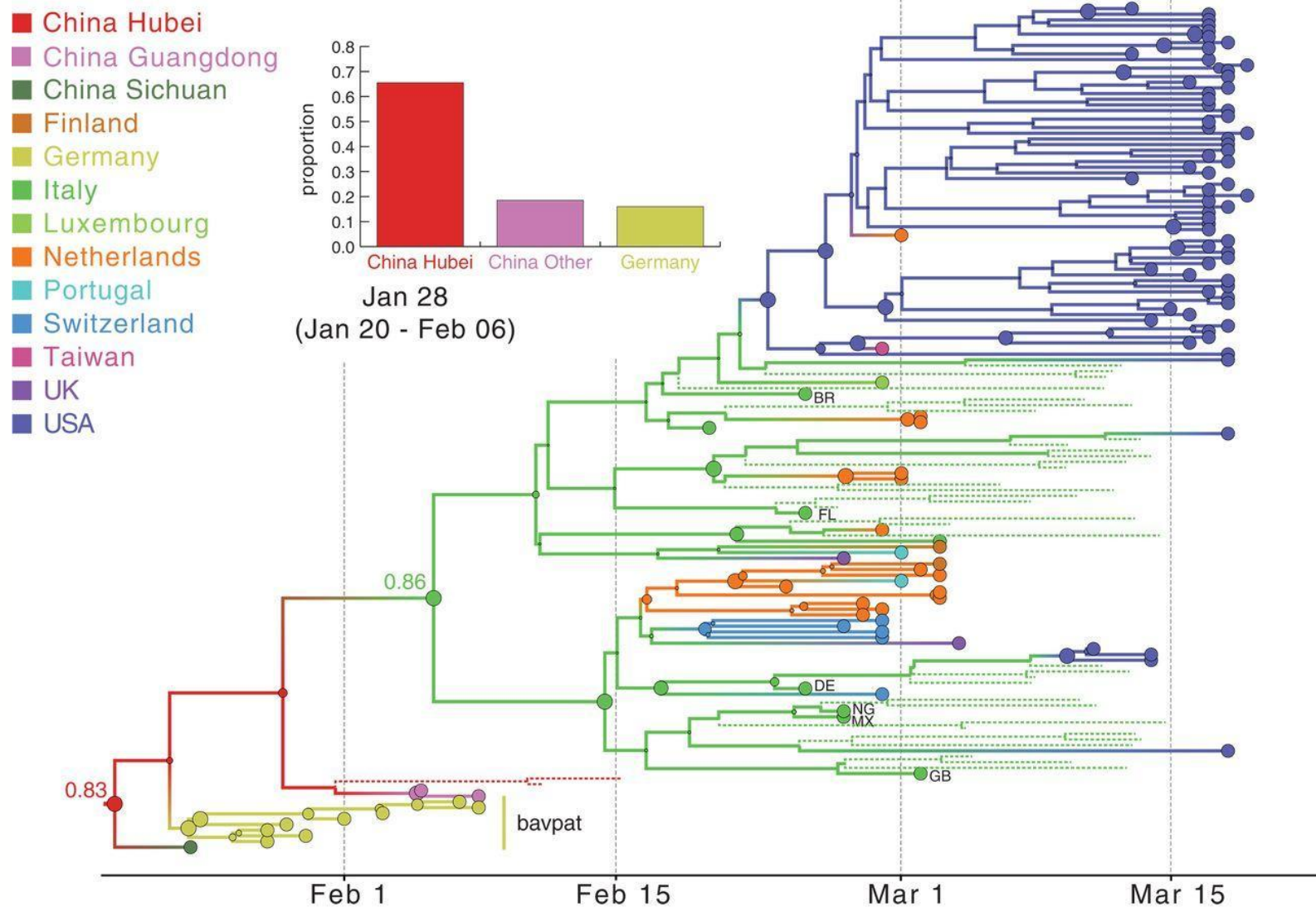
- Consider each data point as separate cluster.
- Consecutively merge clusters until all clusters are connected or specified number of clusters are obtained.

Dendrograms illustrate distance between clusters.

No assumption on number of clusters



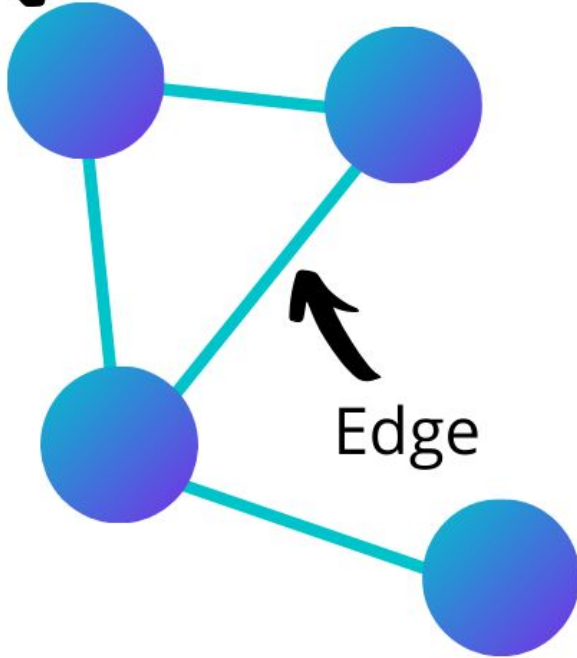
Hierarchical Clustering (HC)



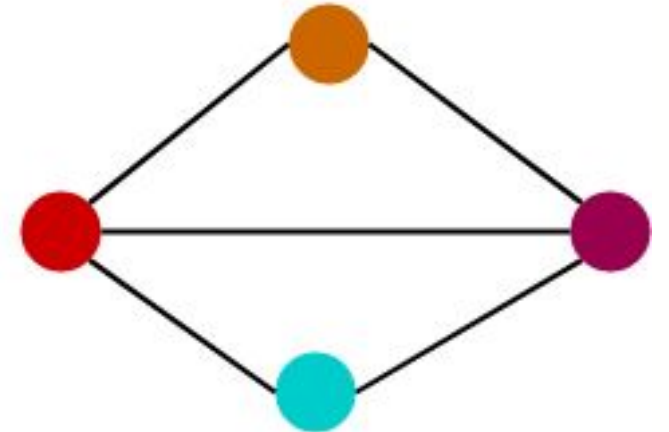
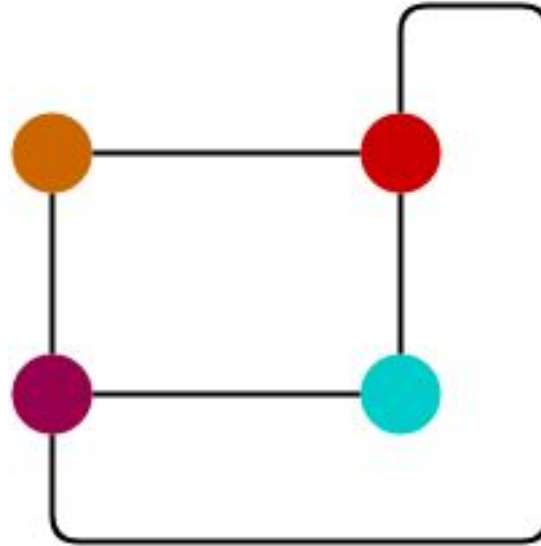
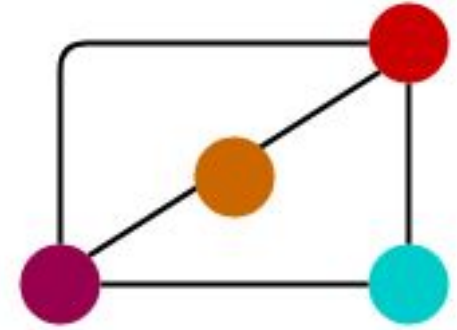
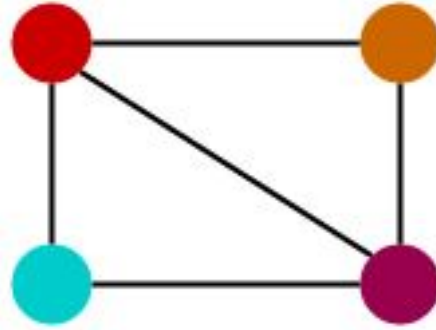


Graph Theory

Node



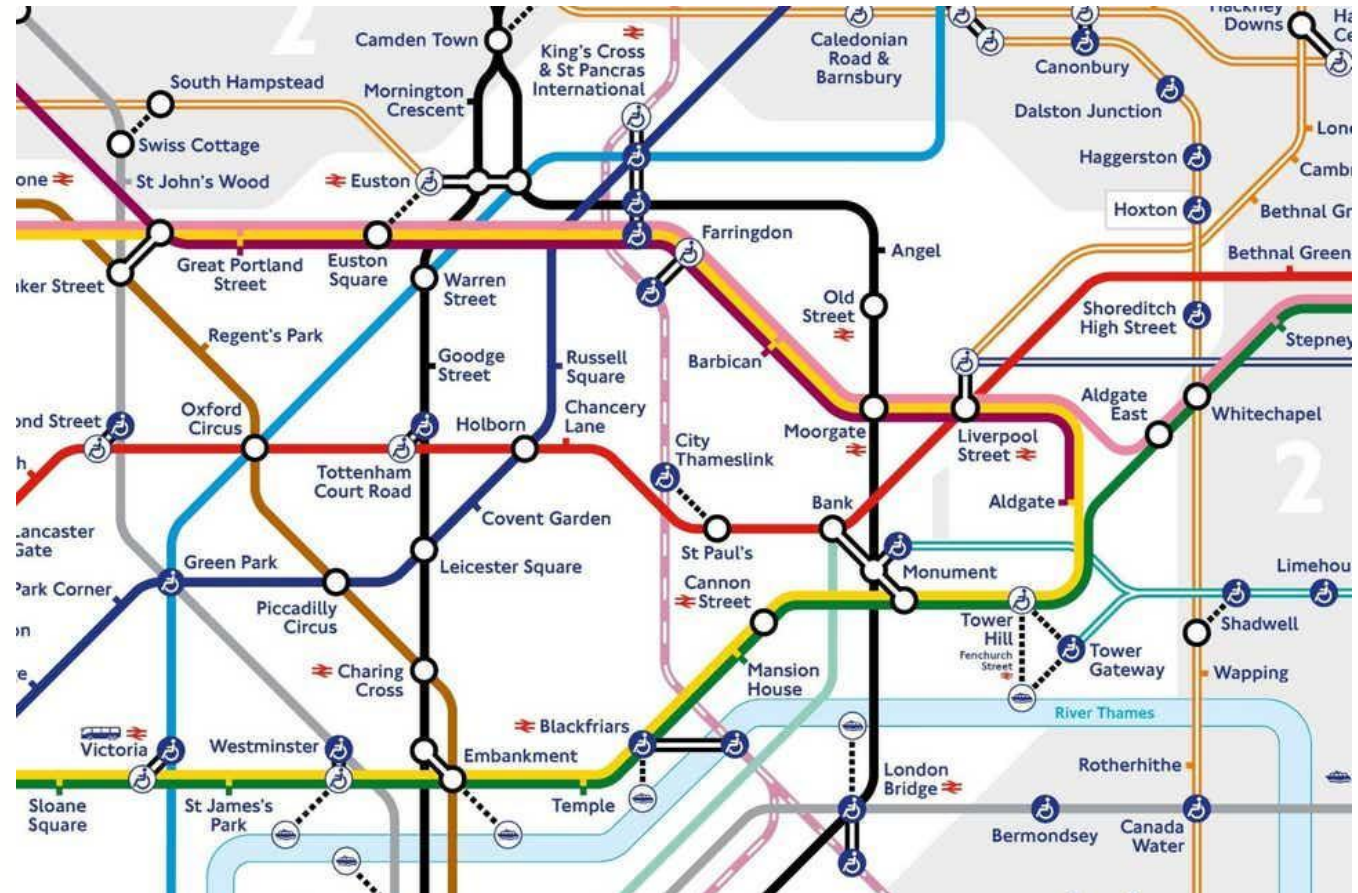
Edge





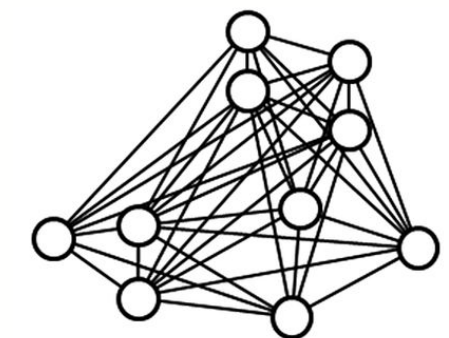
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Making Sense of Arbitrary Shapes

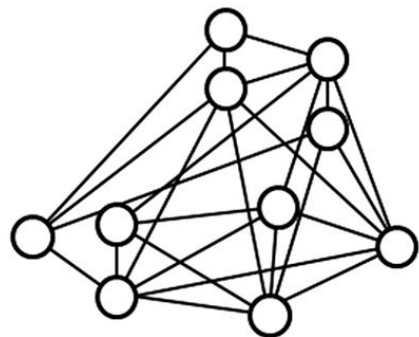




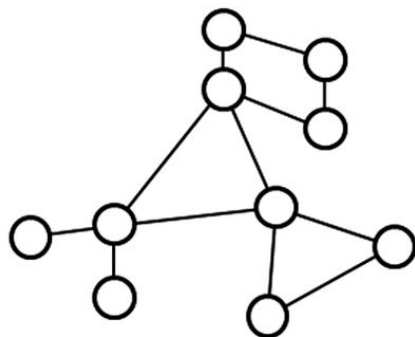
Graph-based clustering



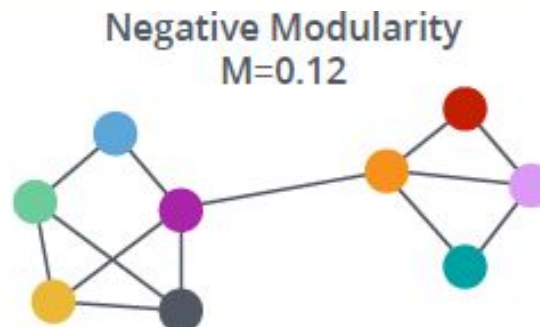
Modularity ≈ -1
(almost complete network)



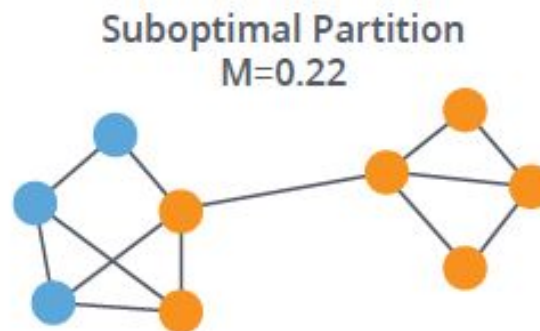
Modularity ≈ 0
(random network)



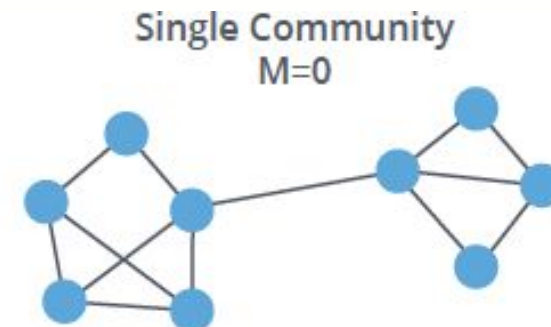
Modularity ≈ 1
(modular network)



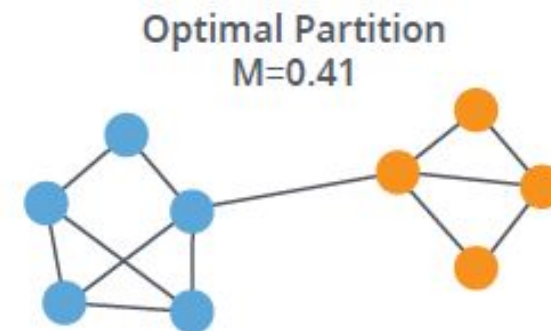
Negative Modularity
 $M=0.12$



Suboptimal Partition
 $M=0.22$



Single Community
 $M=0$



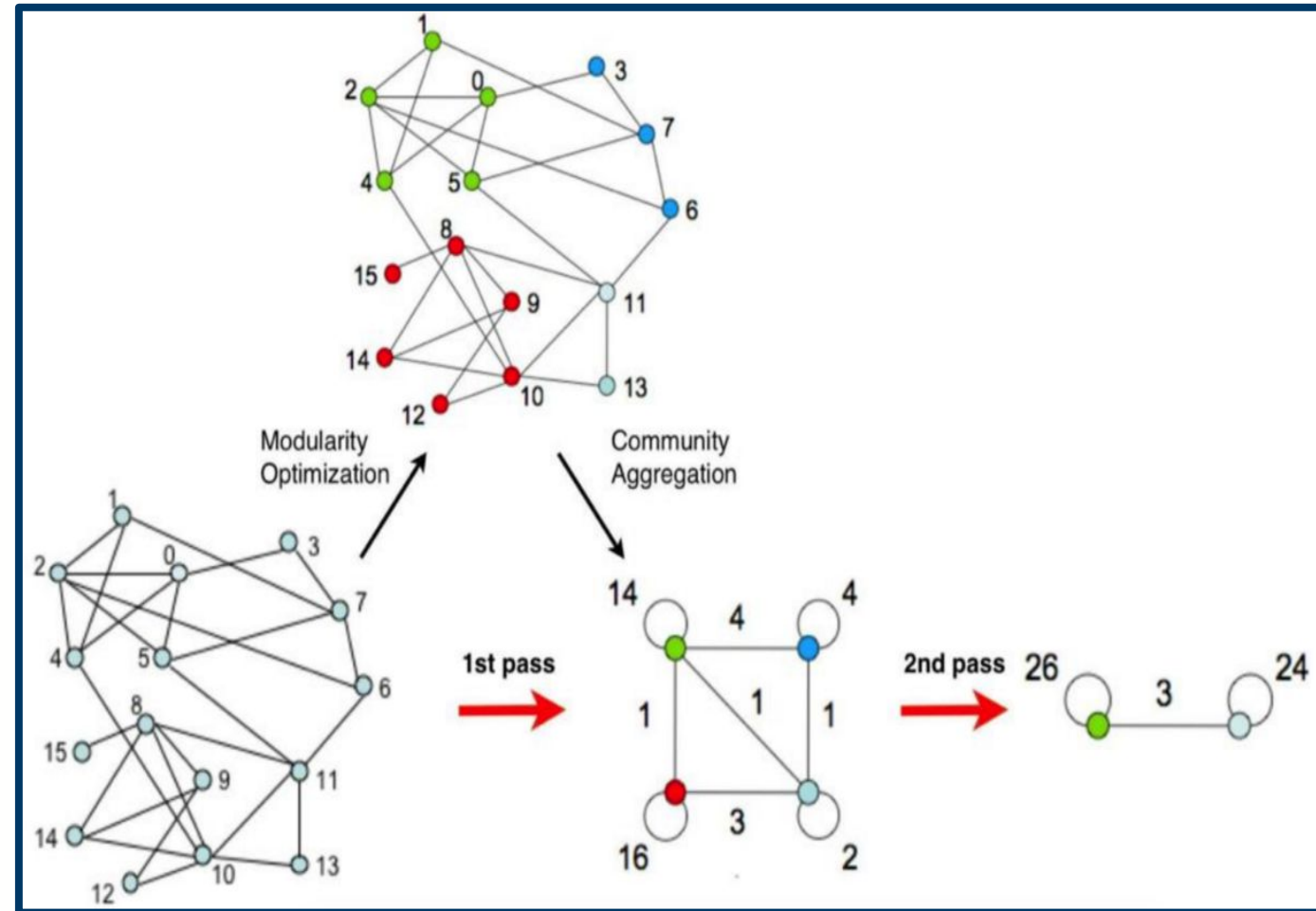
Optimal Partition
 $M=0.41$



Louvain Clustering

- Each data point represented as a node
- Similarity between two data points represented by an edge
- Assign nodes to different clusters by Modularity
- Clusters repeatedly combined until no improvement in modularity

Resolution parameter in modularity function determines number of clusters.





What make model selection for clustering challenging?

- No labels
- Outcomes are subjective
- Hard to define model performance (cluster quality)
- Sensitive to different clustering algorithms and different feature spaces

How do we evaluate then?



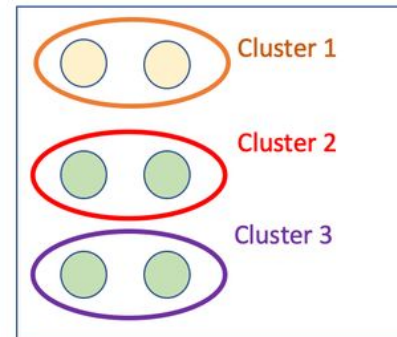
V-measure

Given ground truth labels: Use them!

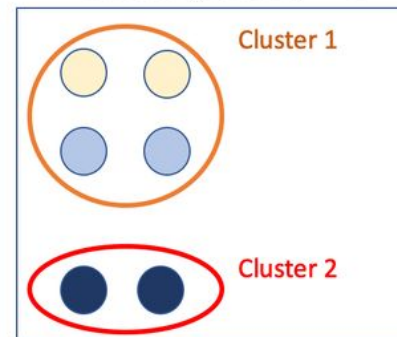
- homogeneity: each cluster contains only members of a single class
- completeness: members of a given class are assigned to the same cluster

V-measure is the average (harmonic mean) of the two metrics

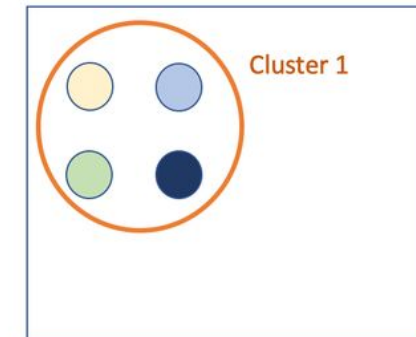
(a) Homogeneity = 1
Completeness < 1



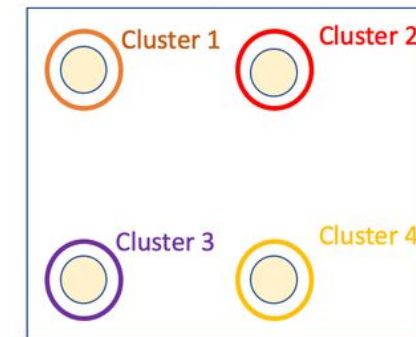
(c) Completeness = 1
Homogeneity < 1



(b) Homogeneity = 0
Completeness = 1



(d) Completeness = 0
Homogeneity = 1





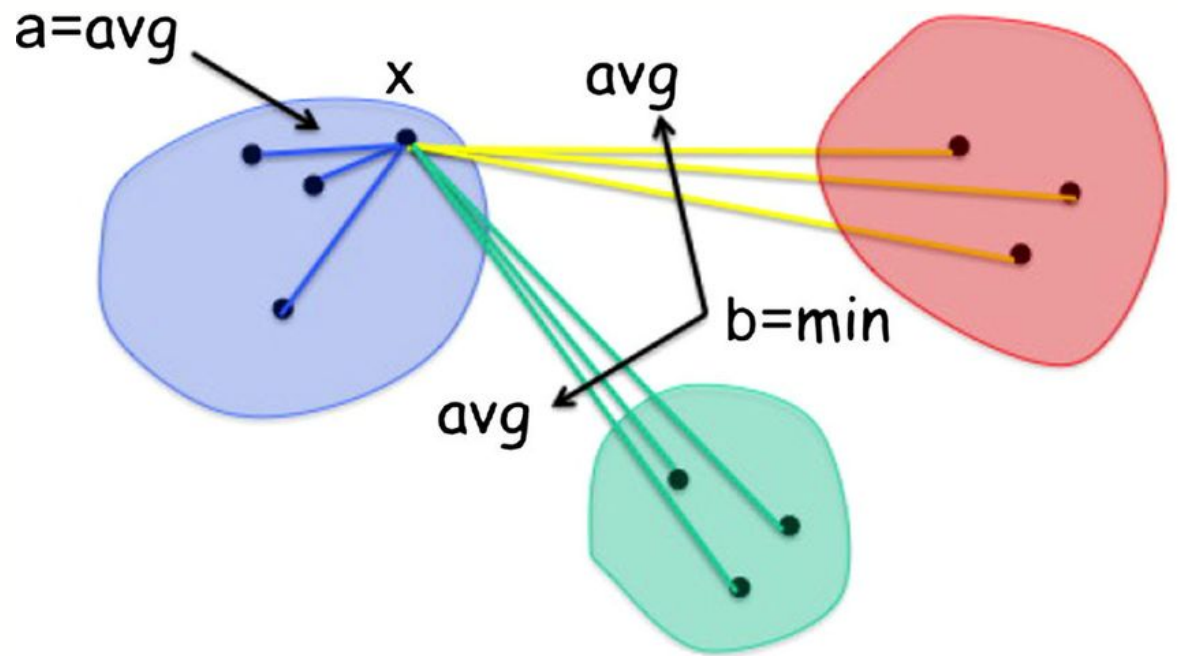
Silhouette Score

If the ground truth labels are not known:

Evaluate on structure

- -1: incorrect clustering
- ≈ 0 : overlapping clusters.
- +1: highly dense clustering

Higher score means clusters are dense and well separated



$$s = \frac{b - a}{\max(a, b)}$$

- a. Mean distance between a sample and all other points in the same class
- b. The mean distance between a sample and all other points in the next nearest cluster



Introduction to digital pathology

- Cancer diagnosed by biopsy
- Removed tissue analysed under digital microscope
- 20Gb on average $\sim 1000000 \times 100000$ pixels

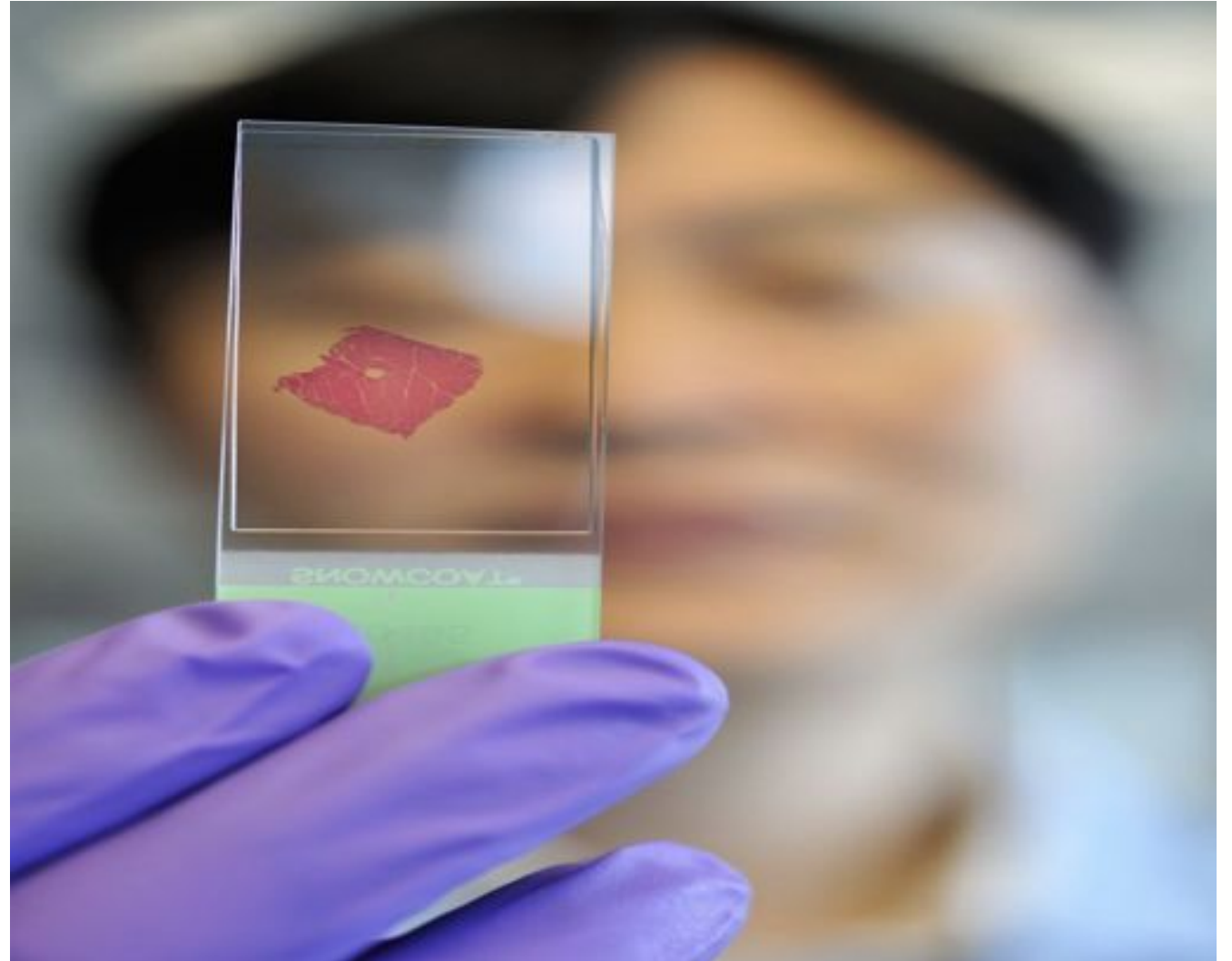
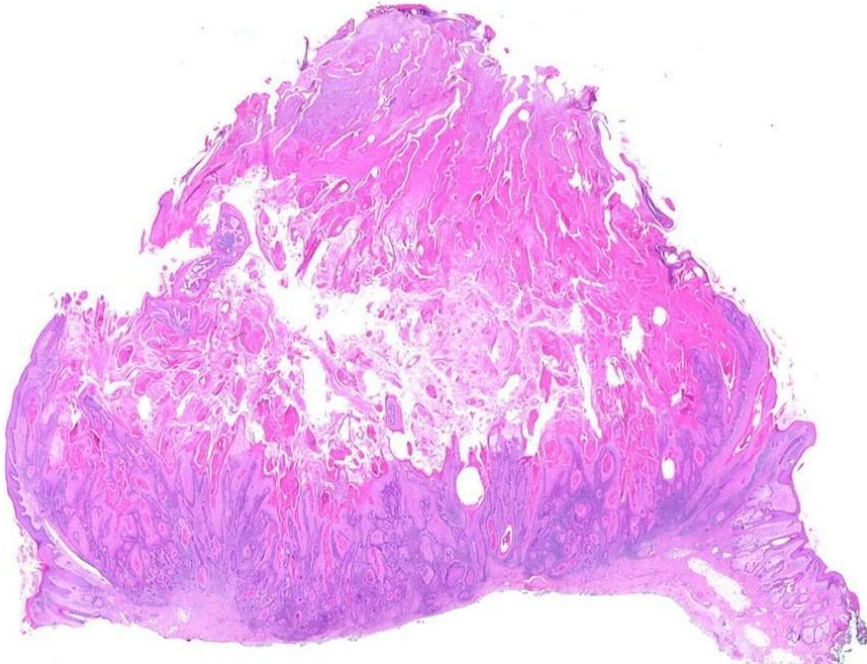




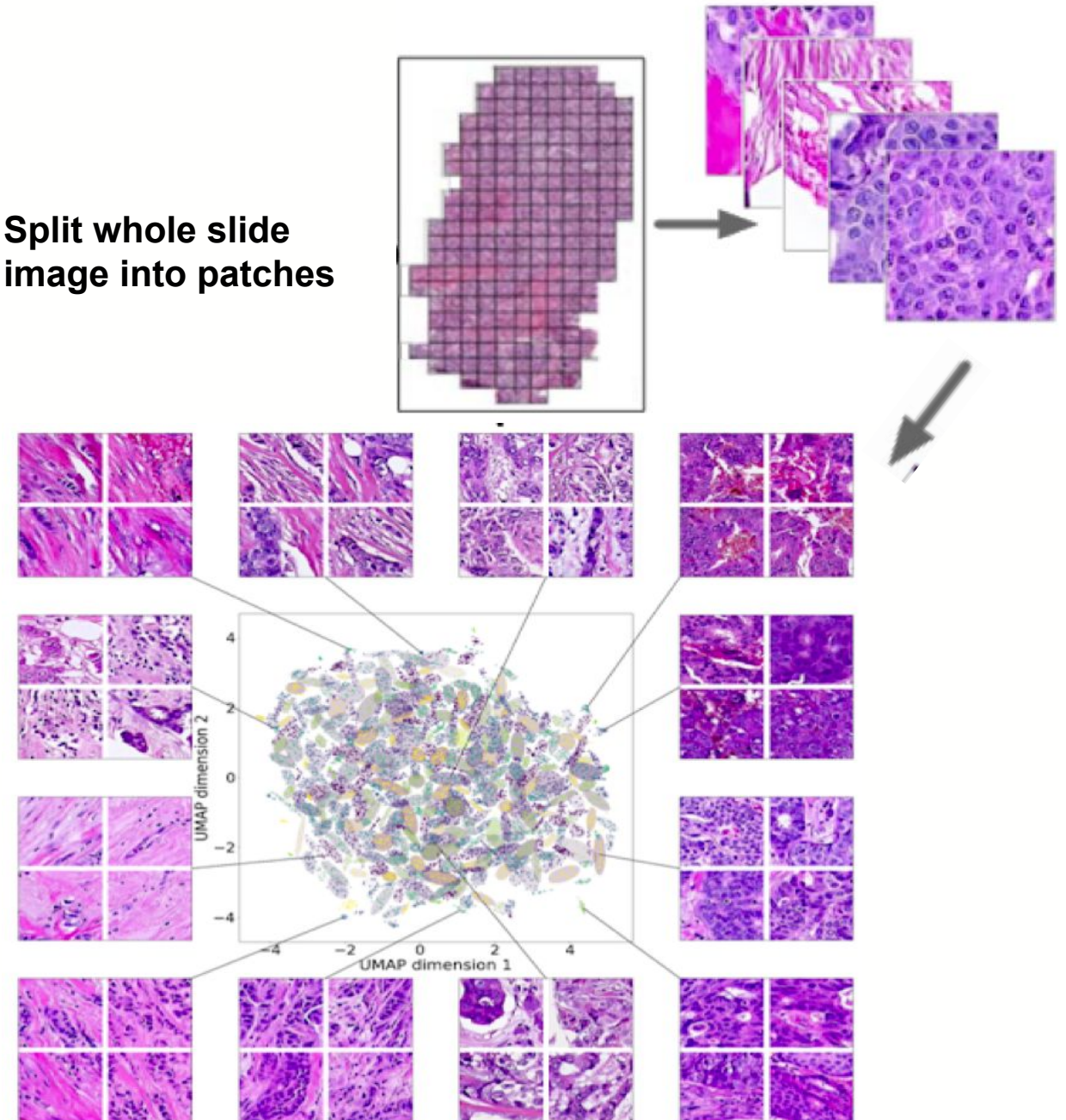
Image Processing

- Break whole slide images (WSIs) into small patches
- (Dimensionality reduction/feature extraction)
- Cluster tissue patches

Clustering gives statistical summary of visual features

Group similar patches into the same clusters

Split whole slide image into patches

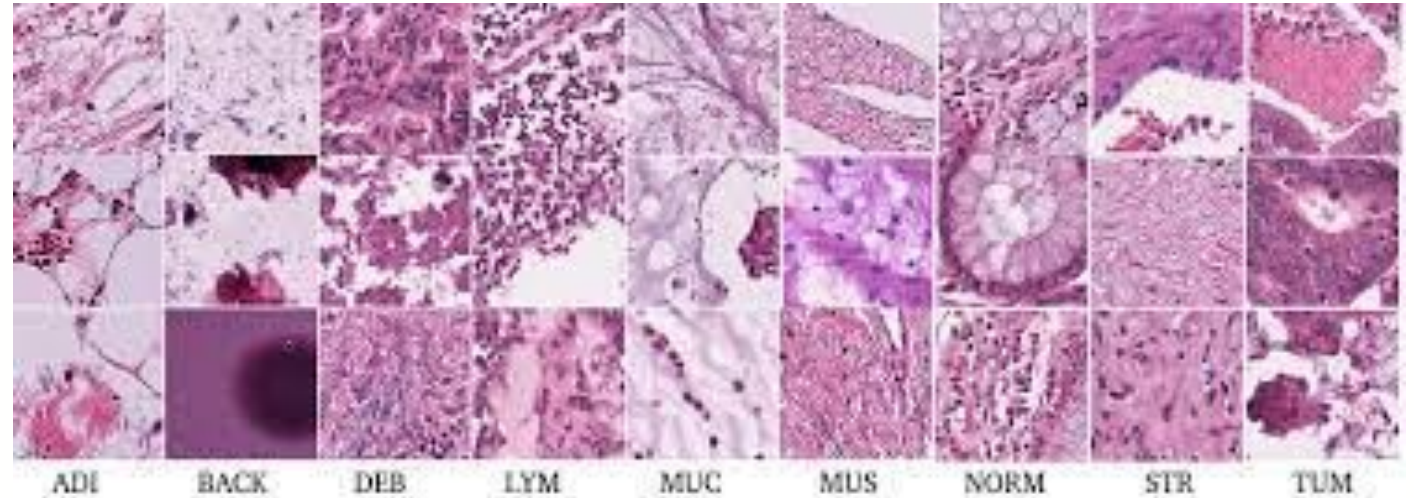




Your task: model selection for tissue patch clustering

Dataset:

- 5,000 colorectal cancer tissue patches.
- 9 tissue types:
 - Adipose (ADI)
 - background (BACK)
 - debris (DEB)
 - lymphocytes (LYM)
 - mucus (MUC)
 - smooth muscle (MUS)
 - normal colon mucosa (NORM)
 - cancer-associated stroma (STR)
 - colorectal adenocarcinoma epithelium (TUM)



Your task

- Select appropriate clustering algorithms (Kmeans, GMM, HC, and Louvain, or HDBScan, Leiden or any other algorithm)
- Apply to a cancer dataset
- Assess model performance (Silhouette score/V measure)

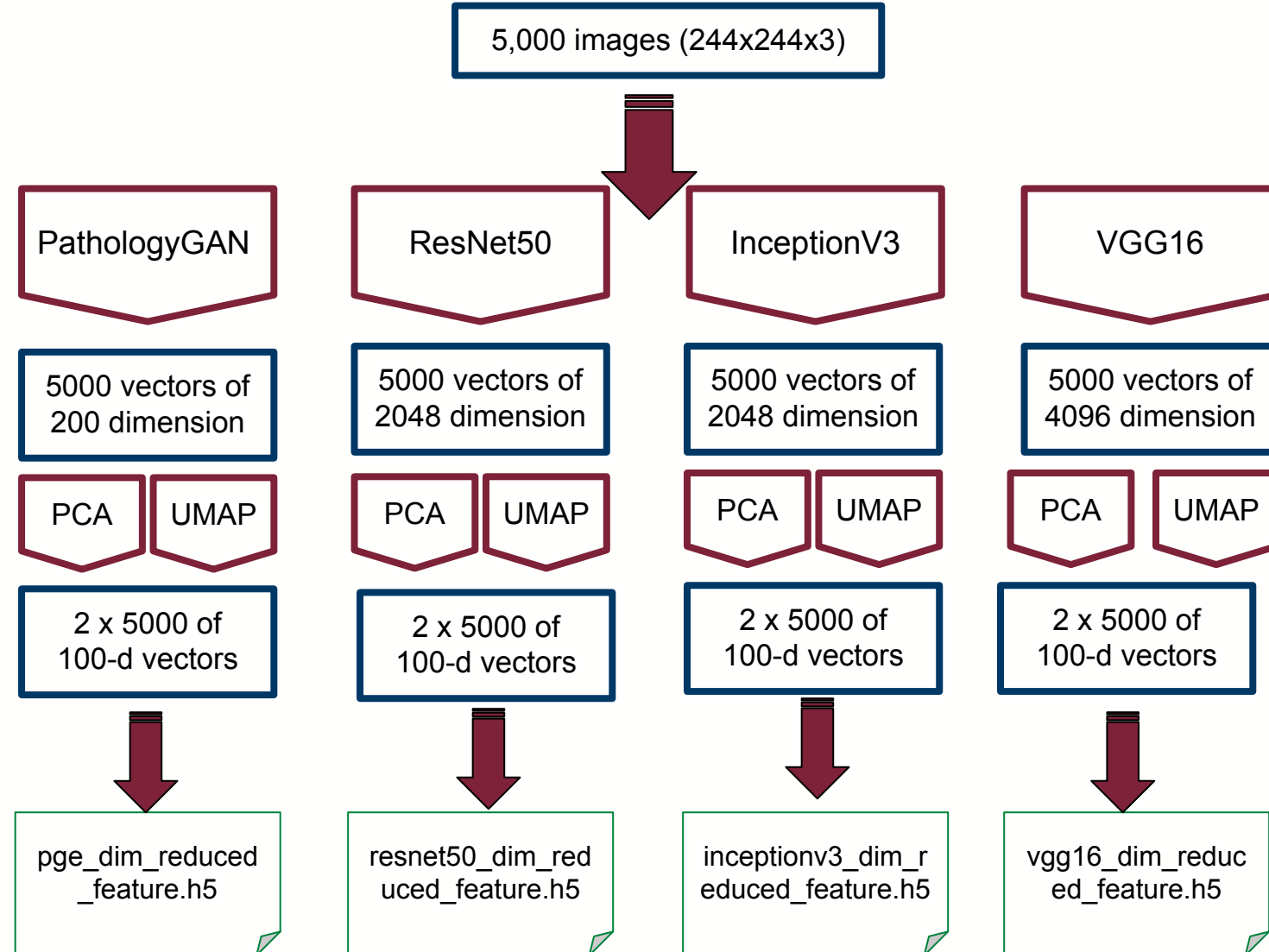


Feature extraction and preprocessing has been done for you

- **PathologyGAN:**
 - state-of-the-art model for tissue images
 - Trained on unlabelled data
- **ResNet50/InceptionV3/VGG16:**
 - Popular CNN classifiers
 - Trained on ImageNet dataset and achieve 74.9%, 77.9%, 71.3% accuracy

Dimensionality reduction methods reduce each representation size to 100

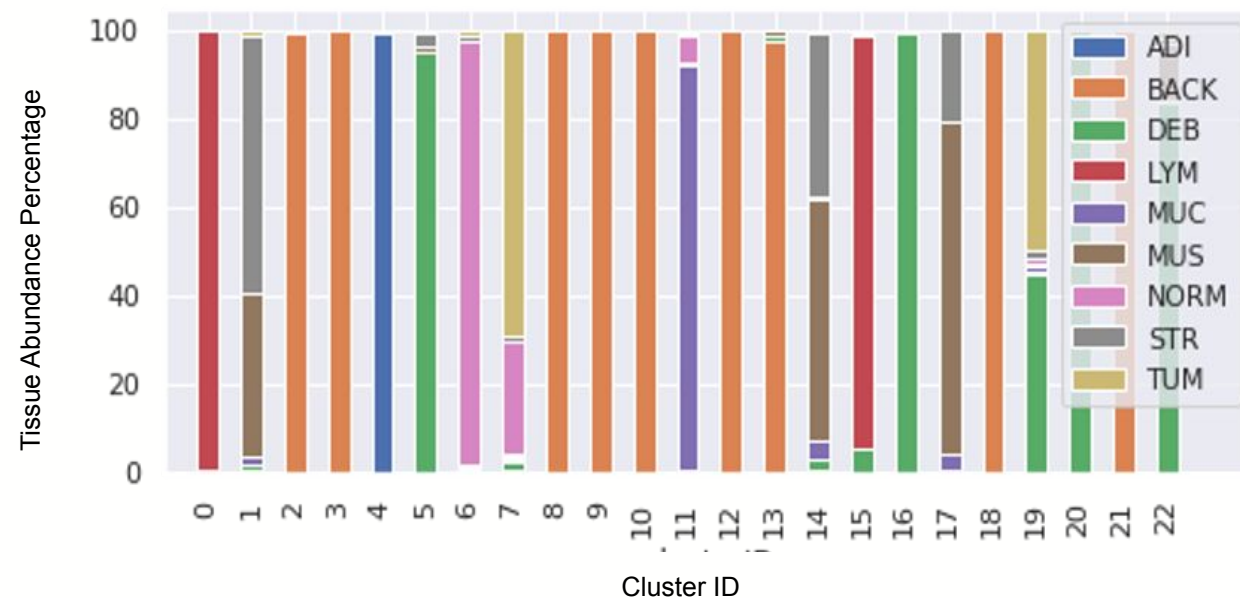
- **PCA:** the first 100 PCs with highest variance are obtained
- **UMAP:** 100 umap components





Example of cluster performance report

Measure A				
Representation	Kmeans	GMM	DBScan	Louvain
PathologyGAN	?	?	?	?
ResNet50	?	?	?	?
InceptionV3	?	?	?	?
VGG16	?	?	?	?





Report summary

Objective: test clustering algorithms and evaluate performance on real data

Include in your report:

1. **Introduction**

Clustering/background/data

2. **Methodology:**

Theory and intuition behind each algorithm and representation

3. **Experimental framework:**

Parameter searching and evaluation

4. **Results**

Report and discuss cluster qualities according to both qualitative and quantitative measures

5. **Conclusion**



Summary of Methods

K-means

- Fast, simple, guaranteed convergence, scales well with dataset size
- Manual number of clusters, sensitive to outliers, scales badly with dimensions

Hierarchical Clustering

- Simple, guaranteed convergence, scales well, no predetermined number of clusters, gives different resolutions of clustering
- Slow, limited meaningful clustering, can infer artificial relationships

Gaussian Mixture Model

- Handles outliers, more informative, guaranteed convergence
- Slow, same issues as k-means, computation time scales badly with dataset size

Louvain Community Detection

- Handles outliers, more informative, scales well with dataset size and dimension, no assumption on shape
- Computationally intensive for small datasets, pre-determined resolution



Summary

Model Selection

- What does *best* mean?
- Consider what outcomes are most important

Clustering

- Different models give very different results
- Use prior knowledge to select appropriate model
- Evaluate clusters based on structure or labels



Summary and extra hints!

1. The objective of this case study is **to test different clustering algorithms on 4 different deep neural network-based representations** extracted from colorectal tissue patches by reporting the cluster qualities according to both intrinsic and extrinsic measures
2. In your report, you are expected to present...
 - Introduction to tasks/backgrounds/data
 - Methodology:
 - Theory and Intuition behinds each algorithm and representation
 - Experimental framework:
 - Parameter searching and evaluation
 - Result discussion
 - Conclusion



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THANK YOU