# CSE/STAT 416

**Hierarchical Clustering** 

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## Clustering





# Define Clusters

In their simplest form, a cluster is defined by

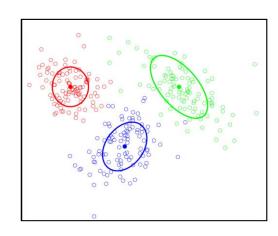
- The location of its center (centroid)
- Shape and size of its spread

**Clustering** is the process of finding these clusters and **assigning** each example to a particular cluster.

- $x_i$  gets assigned  $z_i \in [1, 2, ..., k]$
- Usually based on closest centroid

Will define some kind of score for a clustering that determines how good the assignments are

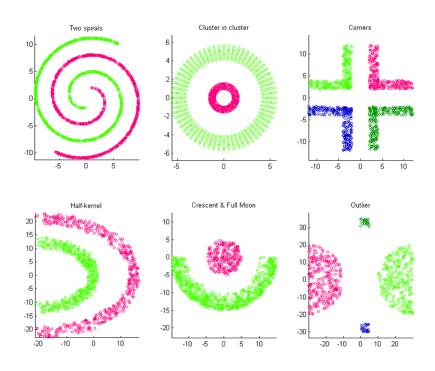
 Based on distance of assigned examples to each cluster



# Not Always Easy

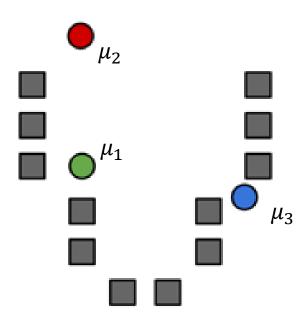
There are many clusters that are harder to learn with this setup

Distance does not determine clusters



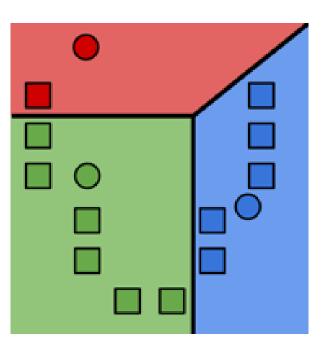
#### Start by choosing the initial cluster centroids

- A common default choice is to choose centroids at random
- Will see later that there are smarter ways of initializing



Assign each example to its closest cluster centroid

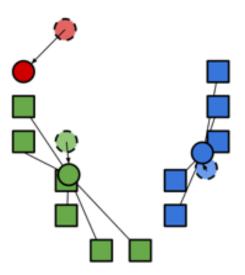
$$z_i \leftarrow \underset{j \in [k]}{\operatorname{argmin}} \left| \left| \mu_j - x_i \right| \right|^2$$



Update the centroids to be the mean of all the points assigned to that cluster.

$$\mu_j \leftarrow \frac{1}{n_j} \sum_{i: z_i = j} x_i$$

Computes center of mass for cluster!



## Smart Initializing w/ k-means++

Making sure the initialized centroids are "good" is critical to finding quality local optima. Our purely random approach was wasteful since it's very possible that initial centroids start close together.

Idea: Try to select a set of points farther away from each other.

**k-means++** does a slightly smarter random initialization

- L. Choose first cluster  $\mu_1$  from the data uniformly at random
- 2. For the current set of centroids (starting with just  $\mu_1$ ), compute the distance between each datapoint and its closest centroid
- 3. Choose a new centroid from the remaining data points with probability of  $x_i$  being chosen proportional to  $d(x_i)^2$
- 4. Repeat 2 and 3 until we have selected k centroids

# Problems with k-means

In real life, cluster assignments are not always clear cut

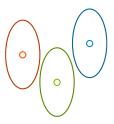
E.g. The moon landing: Science? World News? Conspiracy?

Because we minimize Euclidean distance, k-means assumes all the clusters are spherical



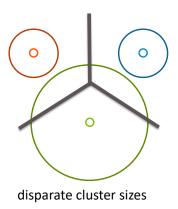
We can change this with weighted Euclidean distance

Still assumes every cluster is the same shape/orientation

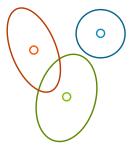


## Failure Modes of k-means

If we don't meet the assumption of spherical clusters, we will get unexpected results







different shaped/oriented clusters

### Mixture Models

A much more flexible approach is modeling with a **mixture model** 

Model each cluster as a different probability distribution and learn their parameters

- E.g. Mixture of Gaussians
- Allows for different cluster shapes and sizes
- Typically learned using Expectation Maximization (EM) algorithm

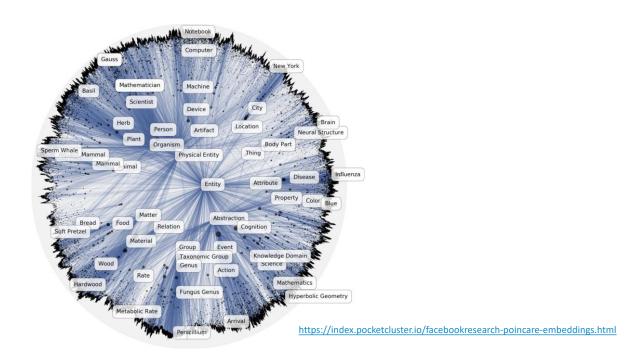
#### Allows **soft assignments** to clusters

54% chance document is about world news, 45% science, 1% conspiracy theory, 0% other

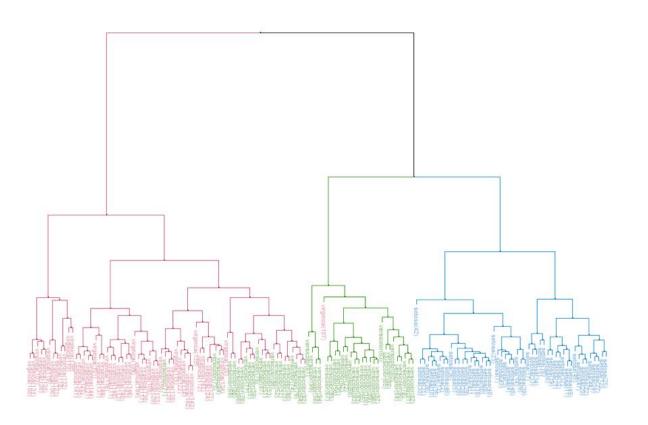
# Hierarchical Clustering

### Nouns

### Lots of data is hierarchical by nature



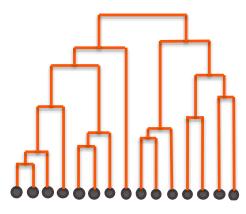
## Species



### Motivation

If we try to learn clusters in hierarchies, we can

- Avoid choosing the # of clusters beforehand
- Use dendrograms to help visualize different granularities of clusters
- Allow us to use any distance metric
  - K-means requires Euclidean distance
- Can often find more complex shapes than k-means

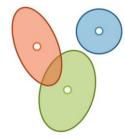


# Finding Shapes

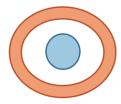
#### k-means



#### **Mixture Models**



**Hierarchical Clustering** 





# Types of Algorithms

#### Divisive, a.k.a. top-down

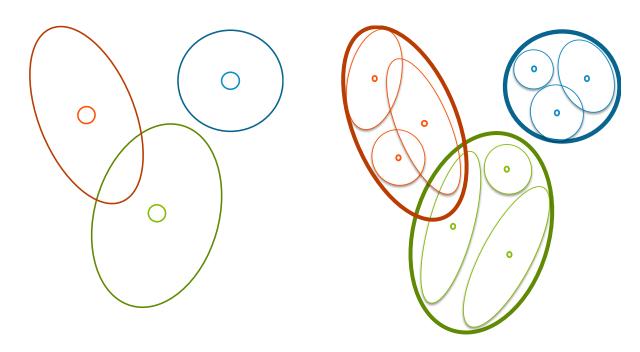
- Start with all the data in one big cluster and then recursively split the data into smaller clusters
  - Example: **recursive k-means**

#### **Agglomerative,** a.k.a. bottom-up:

- Start with each data point in its own cluster. Merge clusters until all points are in one big cluster.
  - Example: single linkage

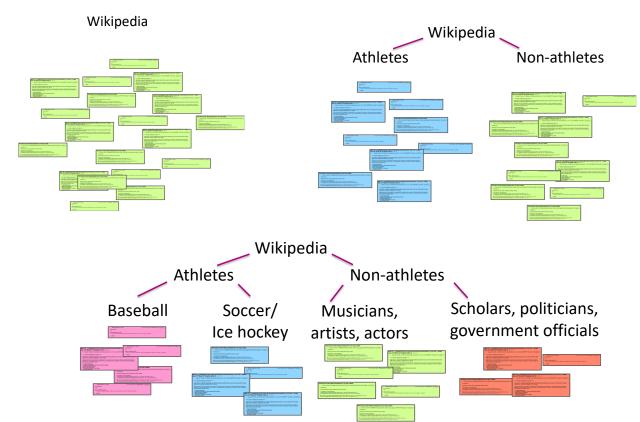
# Divisive Clustering

Start with all the data in one cluster, and then run k-means to divide the data into smaller clusters. Repeatedly run k-means on each cluster to make sub-clusters.



### Example

### Using Wikipedia



# Choices to Make

For decisive clustering, you need to make the following choices:

- Which algorithm to use
- How many clusters per split
- When to split vs when to stop
  - Max cluster size
     Number of points in cluster falls below threshold
  - Max cluster radius
    distance to furthest point falls below threshold
  - Specified # of clusterssplit until pre-specified # of clusters is reached

# Agglomerative Clustering

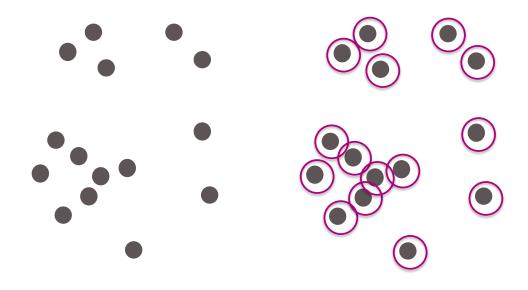
#### Algorithm at a glance

- 1. Initialize each point in its own cluster
- 2. Define a distance metric between clusters

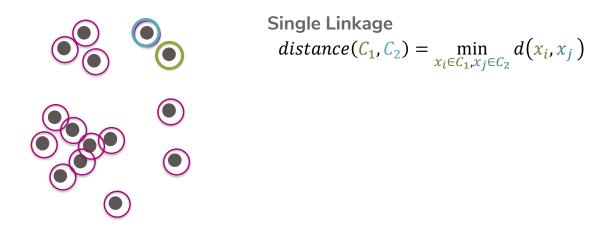
While there is more than one cluster

3. Merge the two closest clusters

1. Initialize each point to be its own cluster

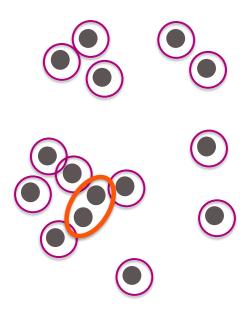


#### 2. Define a distance metric between clusters

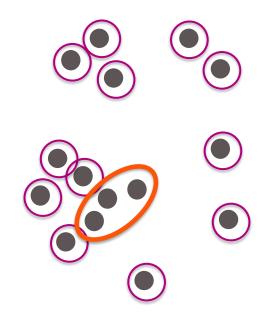


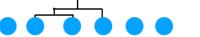
This formula means we are defining the distance between two clusters as the smallest distance between any pair of points between the clusters.

Merge closest pair of clusters

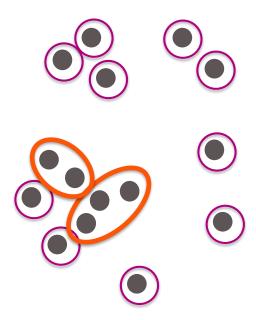


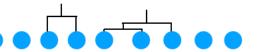


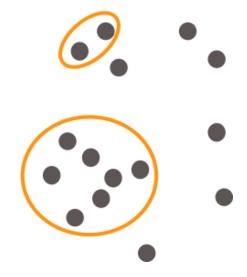


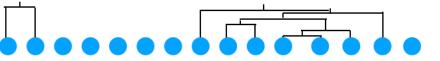


Notice that the height of the dendrogram is growing as we group points farther from each other

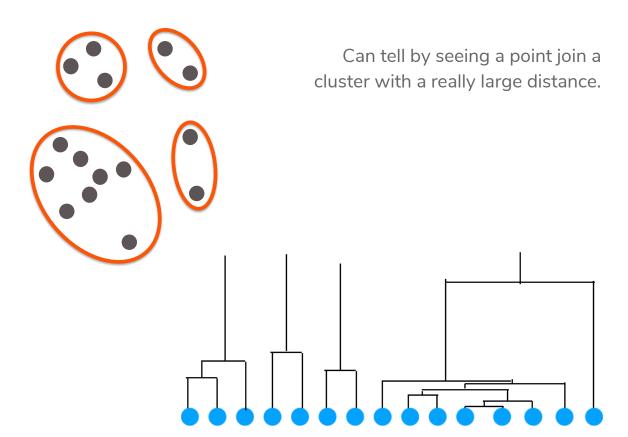




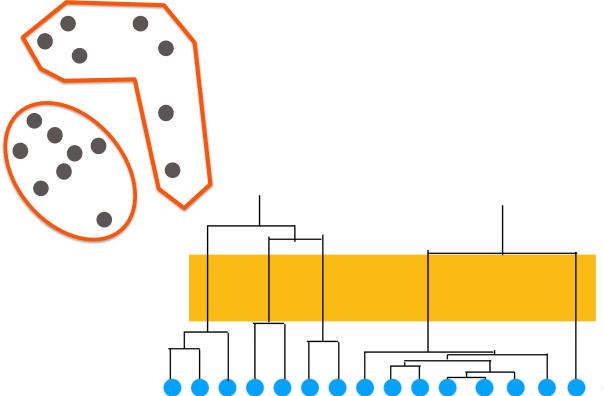




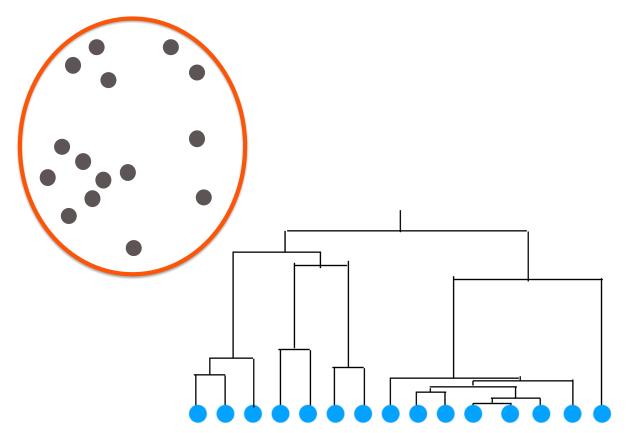
Looking at the dendrogram, we can see there is a bit of an outlier!



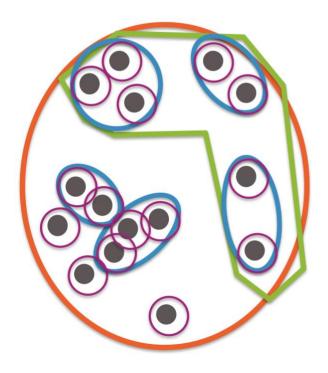
The tall links in the dendrogram show us we are merging clusters that are far away from each other

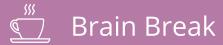


Final result after merging all clusters



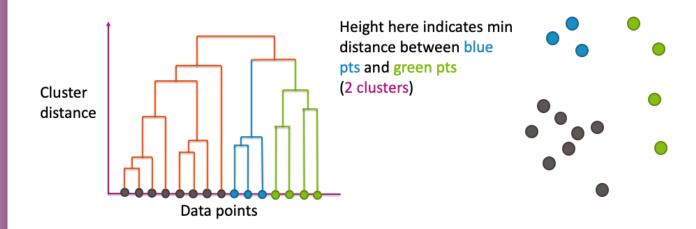
## Final Result





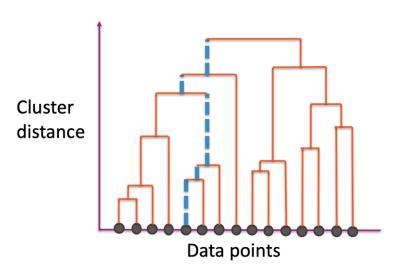
### Dendrogram

x-axis shows the datapoints (arranged in a very particular order) y-axis shows distance between pairs of clusters



### Dendrogram

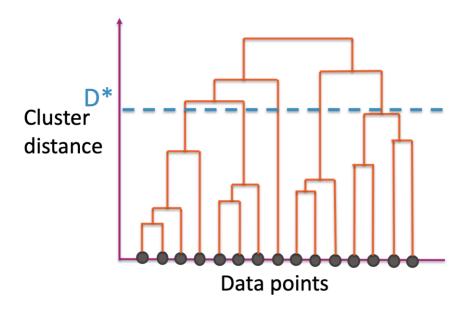
The path shows you all clusters that a single point belongs and the order in which its clusters merged



## Cut Dendrogram

#### Choose a distance $D^*$ to "cut" the dendrogram

- Use the largest clusters with distance  $< D^*$
- Usually ignore the idea of the nested clusters after cutting



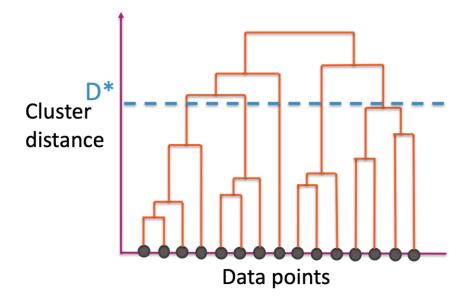


Think &

1 min

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How many clusters would we have if we use this threshold?





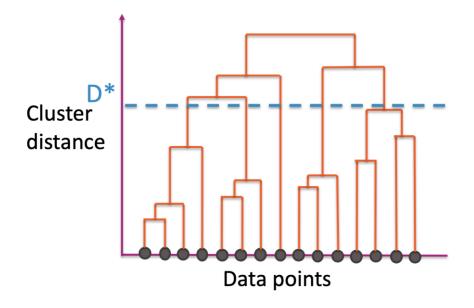


Pair 22

2 min

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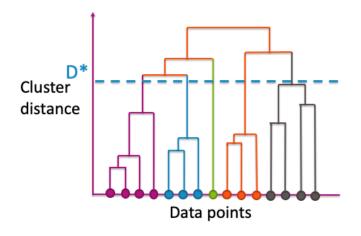
How many clusters would we have if we use this threshold?





# Cut Dendrogram

Every branch that crosses  $D^*$  becomes its own cluster





# Choices to Make

For agglomerative clustering, you need to make the following choices:

- Distance metric  $d(x_i, x_j)$
- Linkage function
  - Single Linkage:

$$\min_{x_i \in C_1, x_j \in C_2} d(x_i, x_j)$$

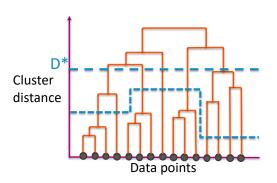
- Complete Linkage:

$$\max_{x_i \in C_1, x_j \in C_2} d(x_i, x_j)$$

Centroid Linkage

$$d(\mu_1, \mu_2)$$

- Others
- Where and how to cut dendrogram



# Practical Notes

For visualization, generally a smaller # of clusters is better

For tasks like outlier detection, cut based on:

- Distance threshold
- Or some other metric that tries to measure how big the distance increased after a merge

No matter what metric or what threshold you use, no method is "incorrect". Some are just more useful than others.

# Computational Cost

Computing all pairs of distances is pretty expensive!

A simple implementation takes  $\mathcal{O}(n^2 \log(n))$ 

Can be much implemented more cleverly by taking advantage of the **triangle inequality** 

"Any side of a triangle must be less than the sum of its sides"

Best known algorithm is  $\mathcal{O}(n^2)$ 

# Concept Inventory

This week we want to practice recalling vocabulary. Spend 10 minutes trying to write down all the terms for concepts we have learned in this class and try to bucket them into the following categories.

Regression

Classification

**Document Retrieval** 

**Misc** – For things that fit in multiple places

You don't need to define/explain the terms for this exercise, but you should know what they are!

Try to do this for at least 5 minutes before looking at your notes.