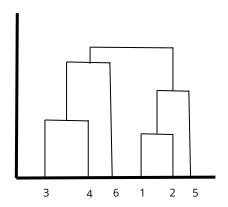
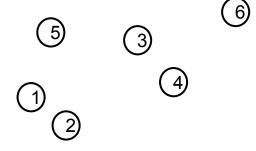
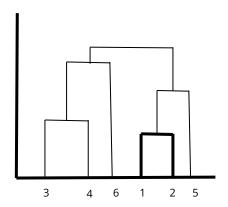
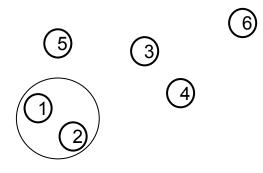
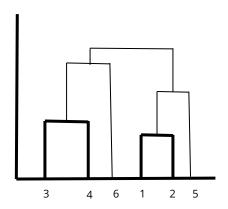
Boston University CS 506 - Lance Galletti

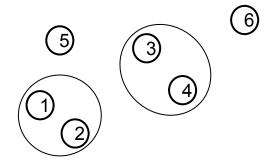


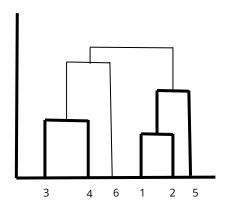


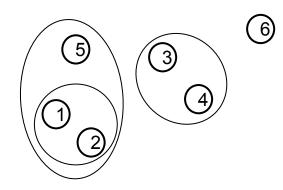


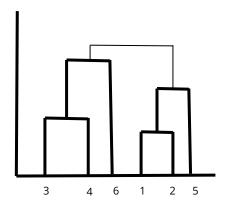


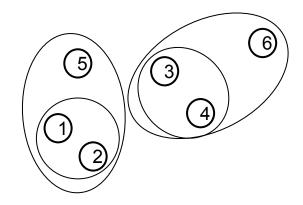


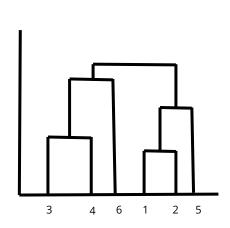


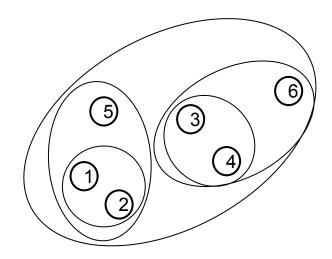




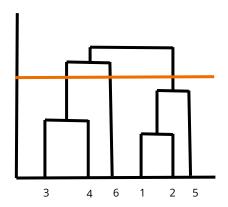


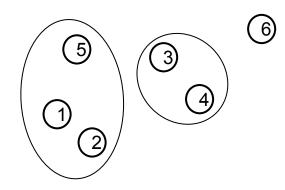




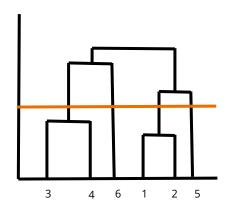


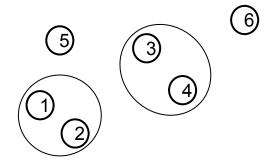
We can "cut" the dendrogram at any threshold to produce any number of clusters



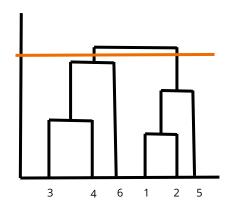


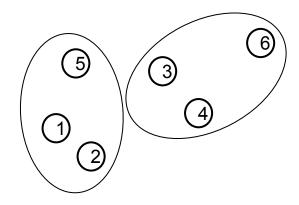
We can "cut" the dendrogram at any threshold to produce any number of clusters





We can "cut" the dendrogram at any threshold to produce any number of clusters





https://www.catalogueoflife.org/

Two types of hierarchical clustering:

### **Agglomerative**:

- 1. Start with every point in its own cluster
- 2. At each step, merge the two closest clusters
- 3. Stop when every point is in the same cluster

### Divisive:

- 1. Start with every point in the same cluster
- 2. At each step, split until every point is in its own cluster

### **Agglomerative Clustering Algorithm**

- 1. Let each point in the dataset be in its own cluster
- 2. Compute the distance between all pairs of clusters
- 3. Merge the two closest clusters
- 4. Repeat 3 & 4 until all points are in the same cluster

Can we implement this? Are we missing anything?

### How would you define distance between clusters?

### **Hierarchical Clustering - Distance Functions**

Let's first define:

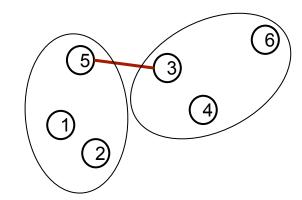
Distance between points:  $d(p_1, p_2)$ 

Distance between clusters:  $D(C_1, C_2)$ 

### **Single-Link Distance**

Is the **minimum** of all pairwise distances between a point from one cluster and a point from the other cluster.

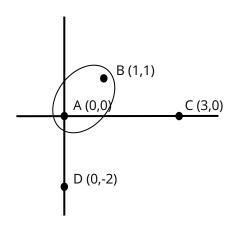
$$D_{SL}(C_1, C_2) = \min \{ d(p_1, p_2) \mid p_1 \in C_1, p_2 \in C_2 \}$$



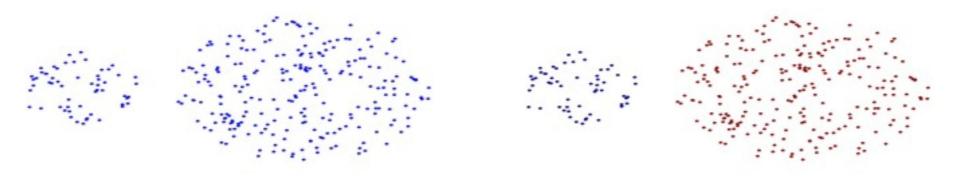
Depends on choice of **d** 

### Q: Single-Link Distance

Is C or D closer to {A, B}?

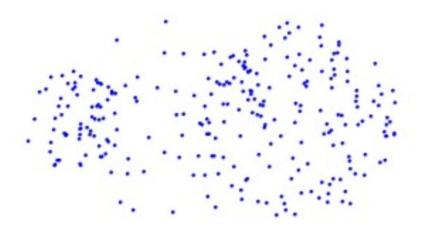


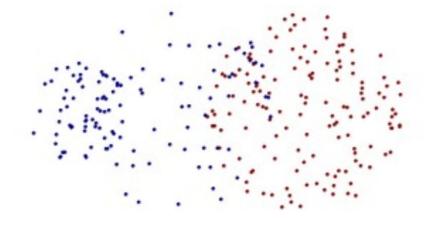
## **Single-Link Distance**



Can handle clusters of different sizes

## **Single-Link Distance**



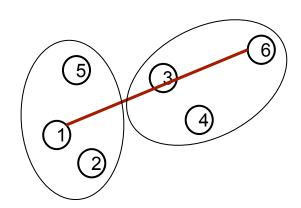


But... Sensitive to noise points Tends to create elongated clusters

### **Complete-Link Distance**

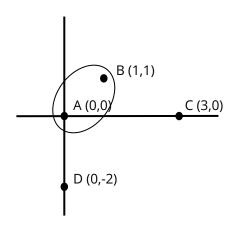
Is the **maximum** of all pairwise distances between a point from one cluster and a point from the other cluster.

$$D_{CL}(C_1, C_2) = \max \{d(p_1, p_2) \mid p_1 \in C_1, p_2 \in C_2\}$$

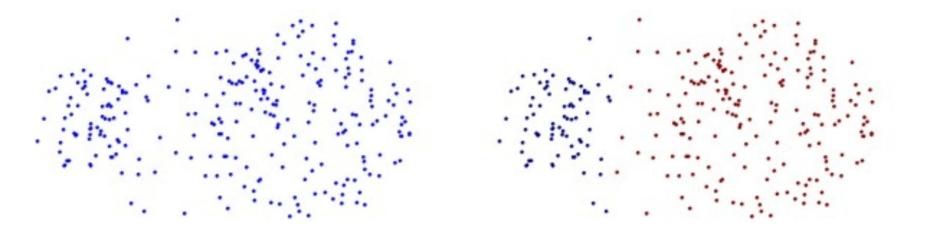


## **Q: Complete-Link Distance**

Is C or D closer to {A, B}?

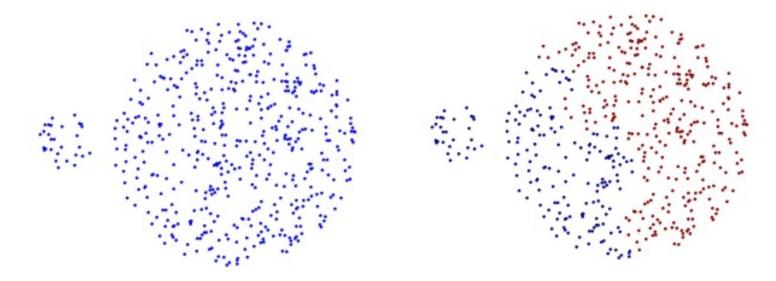


### **Complete-Link Distance**



Less susceptible to noise Creates more balanced (equal diameter) clusters

### **Complete-Link Distance**

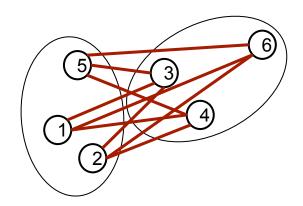


But... Tends to split up large clusters. All clusters tend to have the same diameter

### **Average-Link Distance**

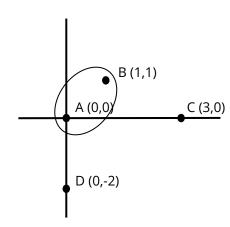
Is the **average** of all pairwise distances between a point from one cluster and a point from the other cluster.

$$D_{AL}(C_1, C_2) = \frac{1}{|C_1| \cdot |C_2|} \sum_{p_1 \in C_1, p_2 \in C_2} d(p_1, p_2)$$



### **Q: Average-Link Distance**

Is C or D closer to {A, B}?



### **Average-Link Distance**

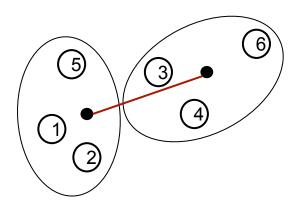
Less susceptible to noise and outliers.

But... Tends to be biased toward globular clusters

### **Centroid Distance**

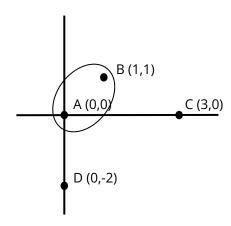
The distance between the centroids of clusters.

$$D_C(C_1, C_2) = d(\mu_1, \mu_2)$$



### **Q: Centroid Distance**

Is C or D closer to {A, B}?



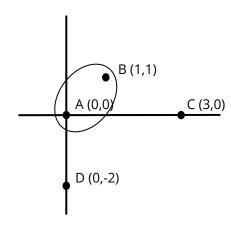
### **Ward's Distance**

Is the difference between the spread / variance of points in the merged cluster and the unmerged clusters.

$$D_{WD}(C_1,C_2) = \sum_{p \in C_{12}} d(p,\mu_{12}) - \sum_{p_1 \in C_1} d(p_1,\mu_1) - \sum_{p_2 \in C_2} d(p_2,\mu_2)$$

## Q: Ward's Distance

Is C or D closer to {A, B}?

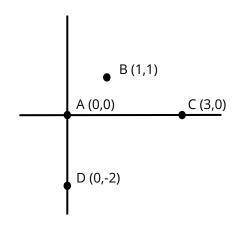


### **Agglomerative Clustering Algorithm**

- 1. Let each point in the dataset be in its own cluster
- 2. Compute the distance between all pairs of clusters
- 3. Merge the two closest clusters
- 4. Repeat 3 & 4 until all points are in the same cluster

**d** = Euclidean

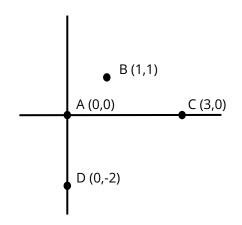
**D** = Single-Link



	Α	В	С	D
Α				
В				
С				
D				

**d** = Euclidean

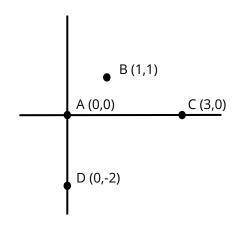
**D** = Single-Link



	Α	В	С	D
Α	0			
В		0		
С			0	
D				0

**d** = Euclidean

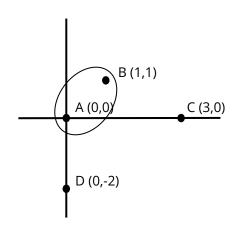
**D** = Single-Link



	Α	В	С	D
Α	0	√2	3	2
В	√2	0	√5	√10
С	3	√5	0	√13
D	2	√10	√13	0

**d** = Euclidean

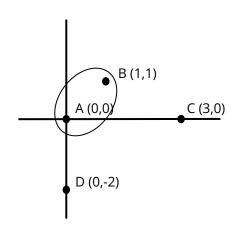
**D** = Single-Link



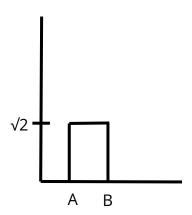
	Α	В	С	D
Α	0	√2	3	2
В	√2	0	√5	√10
С	3	√5	0	√13
D	2	√10	√13	0

**d** = Euclidean

**D** = Single-Link

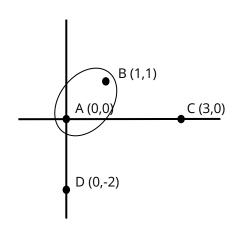


Dendrogram



**d** = Euclidean

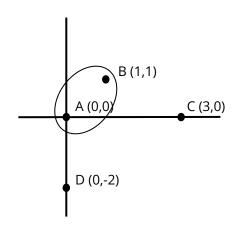
**D** = Single-Link



	A & B	С	D
A & B	0		
С		0	√13
D		√13	0

**d** = Euclidean

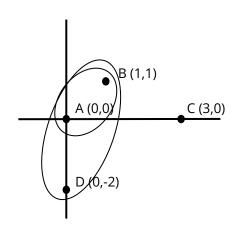
**D** = Single-Link



	A & B	С	D
A & B	0	√5	2
С	√5	0	√13
D	2	√13	0

**d** = Euclidean

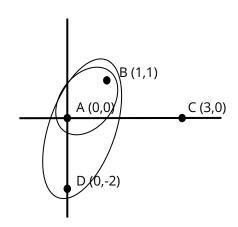
**D** = Single-Link



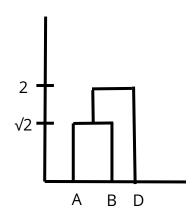
	A & B	С	D
A & B	0	√5	2
С	√5	0	√13
D	2	√13	0

**d** = Euclidean

**D** = Single-Link

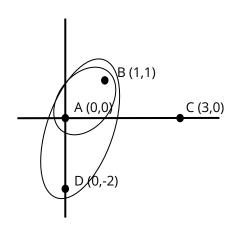


Dendrogram



**d** = Euclidean

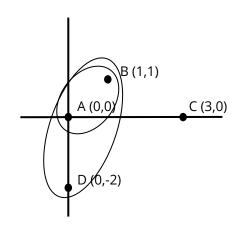
**D** = Single-Link



	A & B & D	С
A & B & D	0	
С		0

**d** = Euclidean

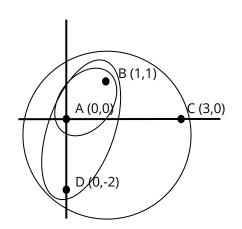
**D** = Single-Link



	A & B & D	С
A & B & D	0	√5
С	√5	0

**d** = Euclidean

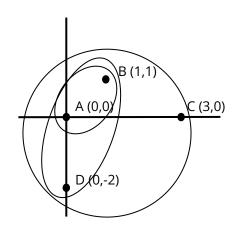
**D** = Single-Link



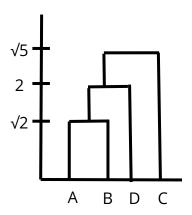
	A & B & D	С
A & B & D	0	√5
С	√5	0

**d** = Euclidean

**D** = Single-Link



Dendrogram



Finding the threshold with which to cut the dendrogram requires exploration and tuning. But in general hierarchical clustering is used to expose a hierarchy in the data (ex: finding/defining species via DNA similarity).

To capture the difference between clusterings you can use a cost function, or methods that we will discuss later when we look at clustering aggregation.