Network Analysis

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Community Detection

i.e. Clustering

Clustering in Graphs

- Can still use classical algorithms (**k-means**) in most cases
  - **Edge weights must reflect similarity** and not distance
  - Use the **adjacency matrix like a data matrix**
  - The "observations" and "variables" are the same entities, but you simply characterize an observation by its similarity to others.
- Families of algorithms designed specifically for graphs
  - **Spectral** (Eigenvector) methods
  - **Modularity**
  - Minimum Spanning Trees
- Theorem: Nothing works best all the time!

Spectral Clustering

(Spectral ➔ Eigenvalues/Eigenvectors. Yay!)

Not just for Graphs!

- Keep in mind the following methods operate on a similarity matrix (i.e. adjacency matrix).

- If you develop a notion of similarity using traditional data, these methods can be useful for clustering any data!

The Laplacian Matrix

- Spectral methods typically use a Laplacian Matrix.

- Let **A** be an adjacency matrix for a graph (or a similarity matrix for some data)
- Let **D** be a diagonal matrix containing the degrees of each node:
  - **D** = diag{d_1,d_2, … ,d_n}
- The **Laplacian matrix** is defined as **L** = **D**-**A**

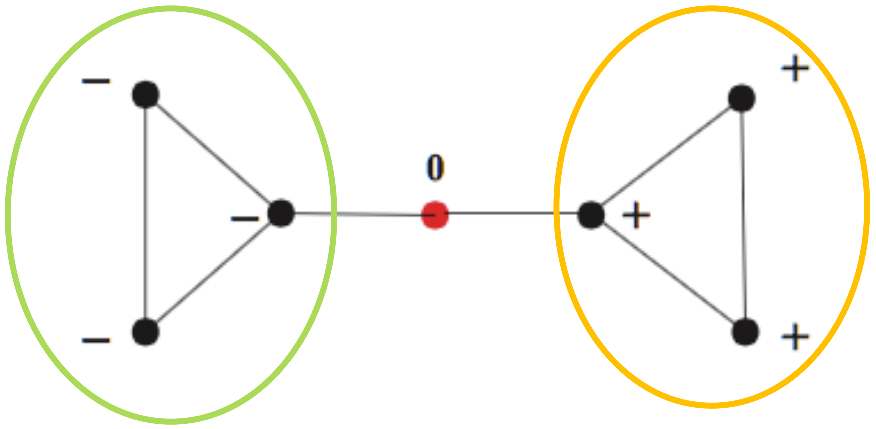
Simple Spectral Clustering

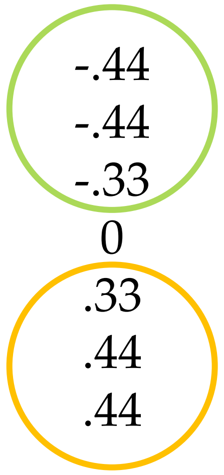
- The **Laplacian matrix** is defined as **L** = **D**-**A**
- The **Fiedler vector** is the eigenvector associated with the *second smallest* eigenvalue of **L**.

Baltimore Ravens' ex-Offensive Lineman John Urschel can tell you about it

Simple Spectral Clustering

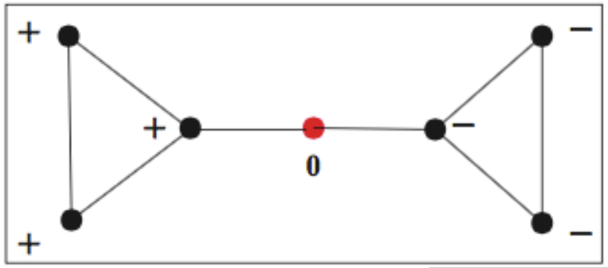
- Use the signs of the entries in the Fiedler vector.
  - Nodes associated with positive entries in one cluster
  - Nodes associated with negative entries in second cluster
  - Arbitrarily assign nodes associated with zero entries (often called **Articulation Points** – sometimes they are brokers)





Exploring Articulation Points

```
A=matrix(c(0,1,1,0,0,0,0,1,0,1,0,0,0,0,1,1,0,1,0,0,0,0,0,1,0,
1,0,0,0,0,0,1,0,1,1,0,0,0,0,1,0,1,0,0,0,0,1,1,0),nrow=7)
library("igraph")
g=graph_from_adjacency_matrix(A)
plot(g)
D=diag(rowSums(A))
L-D-A
spectrum=eigen(L)
spectrum$vectors[,6]
```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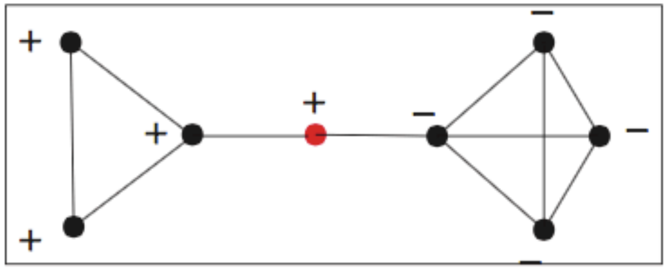
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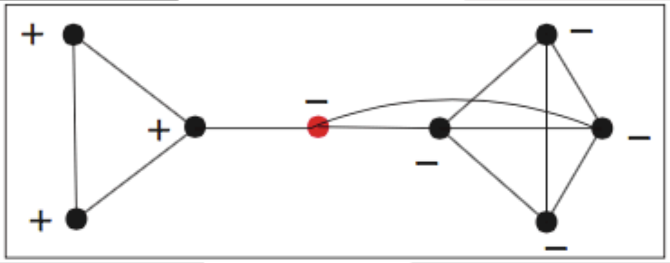
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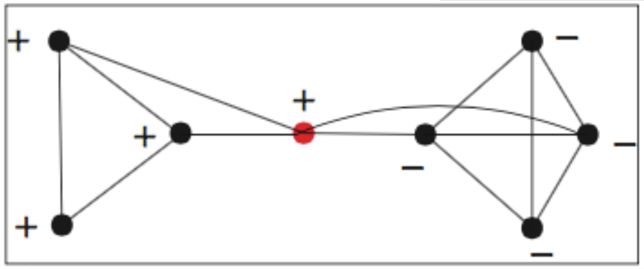
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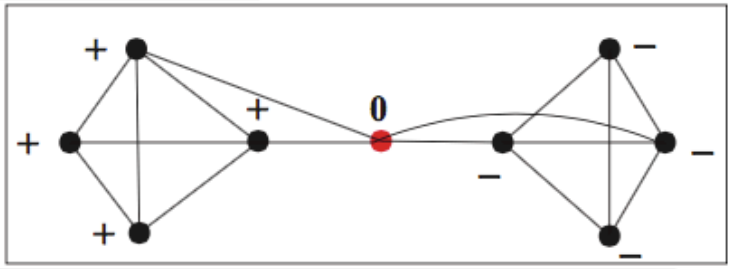
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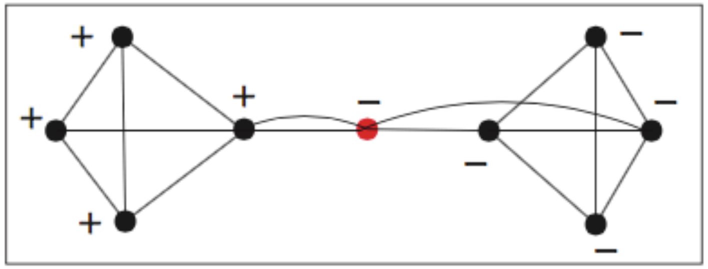
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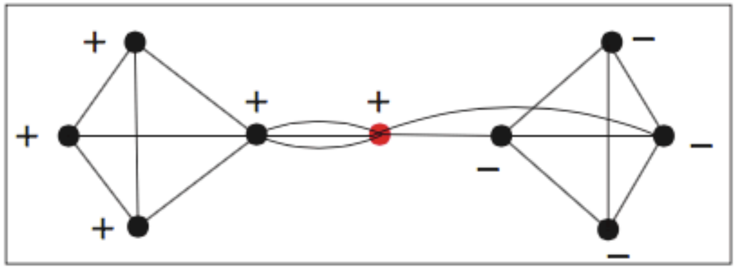
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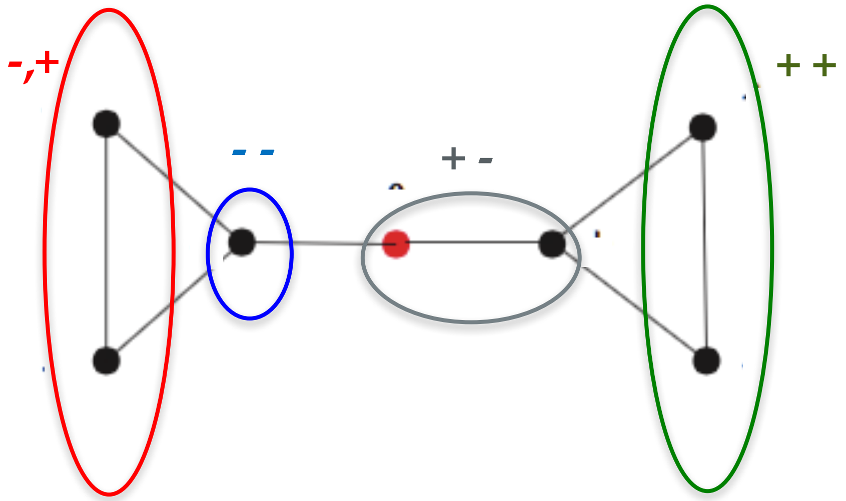
Simple Spectral Clustering

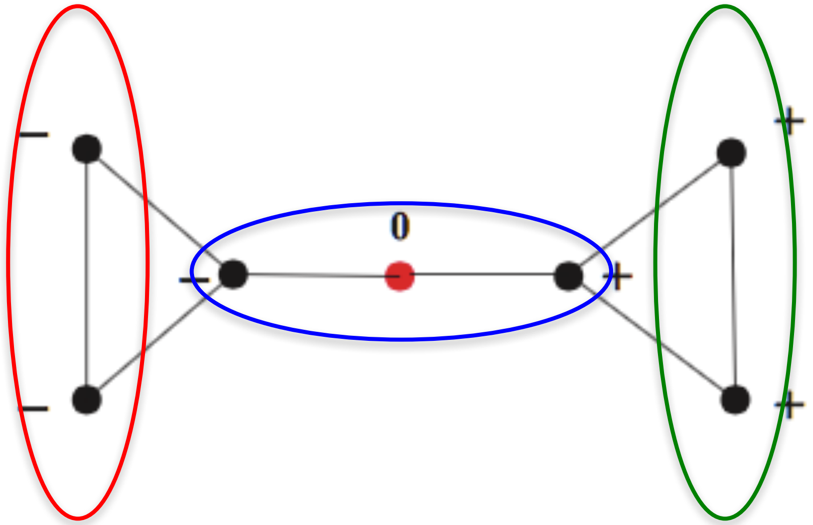
- How to get more than two clusters? (Two Ways)
  - Repeat process on each cluster.
  - Use additional eigenvectors (Two Ways)
    - Use the sign patterns (shown below)
    - Cluster the rows of the eigenvectors with k-means (Next Slide)



$\mathbf{v}_6$	$\mathbf{v}_5$
-.44	0.28
-.44	0.28
-.33	-0.16
0	-0.79
.33	-0.16
.44	0.28
.44	0.28

Simple Spectral Clustering

- Use k-means to cluster the rows of the eigenvectors
    - (Get to choose k in this case)



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Advanced Spectral Clustering

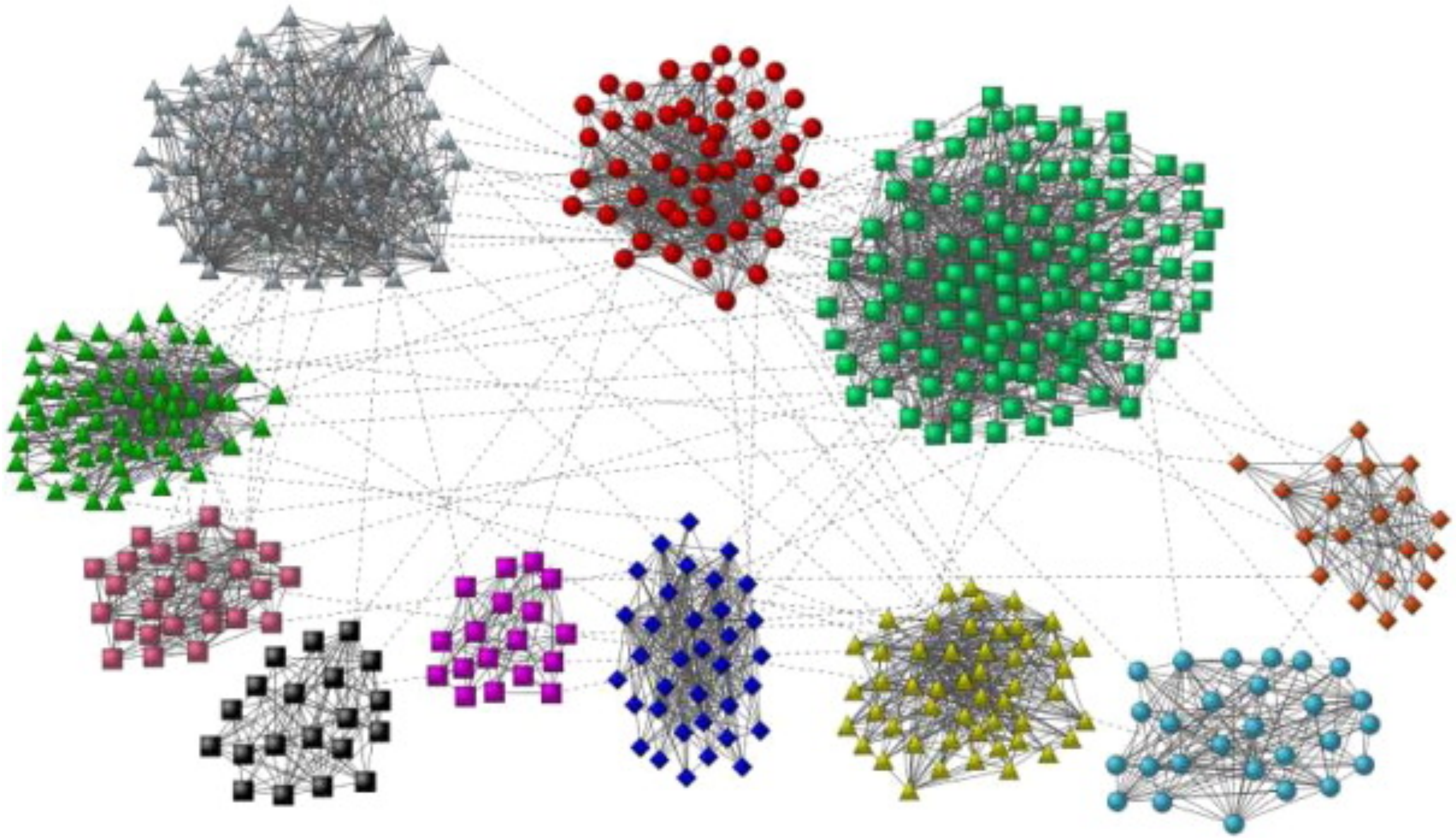
- NCUT
- Ratio Cut
- Normalized Spectral Clustering
- …Long list of algorithms

- All involve the Laplacian Matrix, typically normalized in different ways, and k-means run on Eigenvectors

Modularity Maximization

- Currently the **most popular** algorithm for community detection.
- Developed in 2006 by Mark Newman (UMichigan)
- Algorithm **Intuition**:
  - Compare the observed network to what you would expect to find at random.
  - Where are there more edges than expected?
  - These areas may define communities.

Modularity Maximization

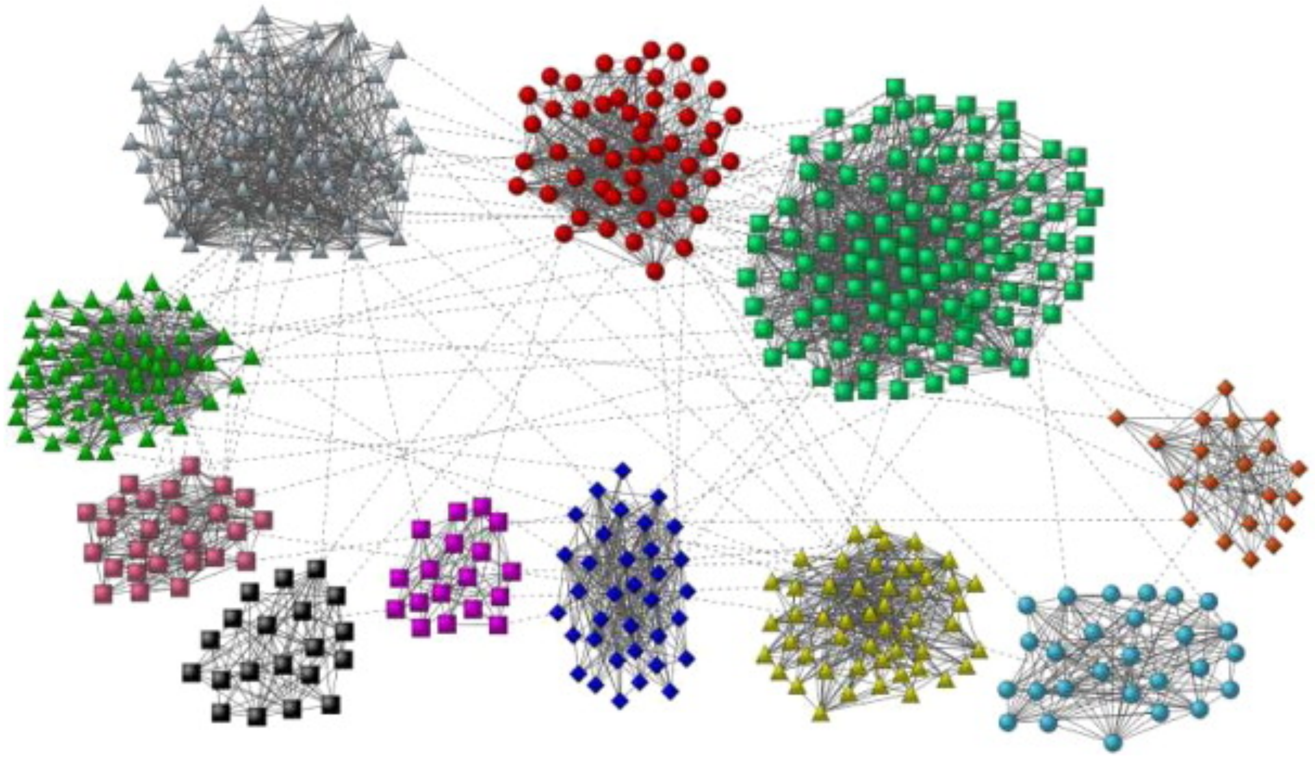


Modularity

- **Modularity** is a number that describes the ***extent to which given groups form communities in a graph***.
- Fraction of edges within groups minus the *expected* fraction if edges were distributed at random.
- Number in range [-1, 1)
  - **negative => random partition**
    - (We'd expect to find *more* edges within our groups if they were distributed at random)
  - **nearer 1 => better communities (components)**
    - (We see far more edges within our groups than we'd expect to find at random)

Modularity Maximization

Picks the partitioning of the vertices that maximizes the modularity.

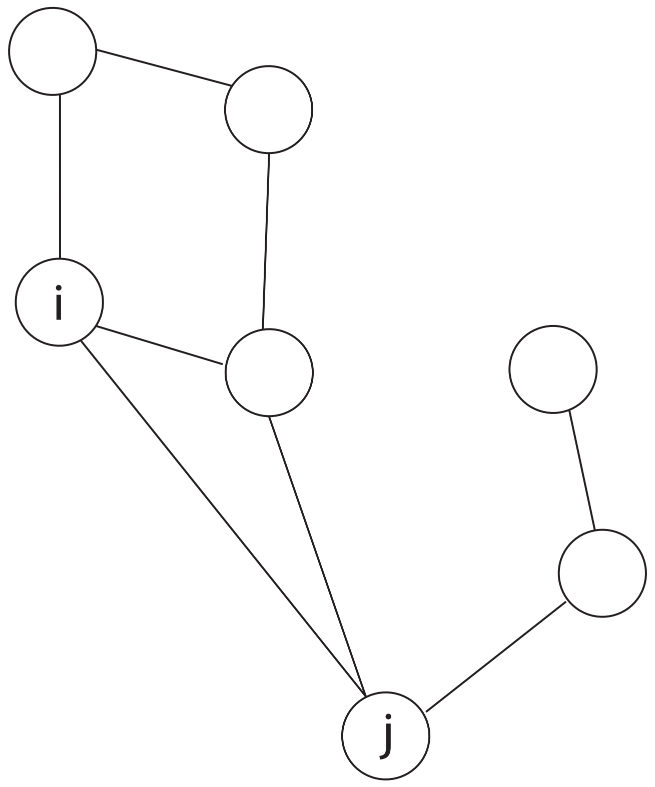


Modularity Maximization

- Let **A** be the adjacency matrix of the graph
- Let **P** be a matrix containing the expected number of edges between each vertex.

$$P_{ij} = \frac{d_i d_j}{\sum_k d_k}$$

Modularity Maximization



P(stub is connected to i) = 3/16
P(stub is connected to j) = 3/16

If i and j are independent,
P(i <-> j) = P(i) • P(j)

So the expected value of the number of complete edges between i and j is
P(i)•P(j) • 16.

Modularity Maximization

$$P_{ij} = \frac{d_i d_j}{\sum_k d_k}$$

- **B** = **A-P** is the modularity matrix
- The first eigenvector of the modularity matrix partitions the graph in two components.
- Repeat procedure on each component until the first eigenvalue is negative.

Algorithm 13 Modularity Procedure for Network Community Detection (Newman) [94]

```
**Input:** $n \times n$ adjacency matrix $\mathbf{A}$ for an undirected graph to be partitioned
1. Let $d_i$ be the $i^{th}$ row sum of $\mathbf{A}$. Let $d = \sum_{i=1}^{n} d_i$
2. Form the matrix $\mathbf{P}$ with $\mathbf{P}_{ij} = d_i d_j / d$.
3. Form the modularity matrix $\mathbf{B} = \mathbf{A} - \mathbf{P}$.
4. Compute the largest eigenvalue $\lambda_1$ and corresponding eigenvector $\mathbf{u}_1$ of $\mathbf{B}$.
5. If $\lambda_1 < 0$, stop. There is no partition of this graph.
6. Otherwise partition the vertices of the graph into 2 clusters as follows
       $C_1 = \{i : \mathbf{u}_1(i) < 0\}$
       $C_2 = \{i : \mathbf{u}_1(i) \geq 0\}$        (3.11)
7. Determine further partitions by extracting the rows and columns of the original adjacency matrix corresponding to the vertices in each cluster to form $\mathbf{A}'$ and repeat the algorithm with $\mathbf{A}'$ until each created cluster fails to partition in step 5.
**Output:** Final clusters.
```

Modularity Maximization

- Advantages
  - **Automatically determines number of clusters**
  - **Intuitive** rationale for/definition of a community
  - **Easy** to program and compute
- Disadvantages
  - Node can belong to only one community **(hard clustering)**
  - If first eigenvalue of modularity matrix is negative – no clusters.
    - (could be advantage)

Minimum Spanning Trees

An alternative

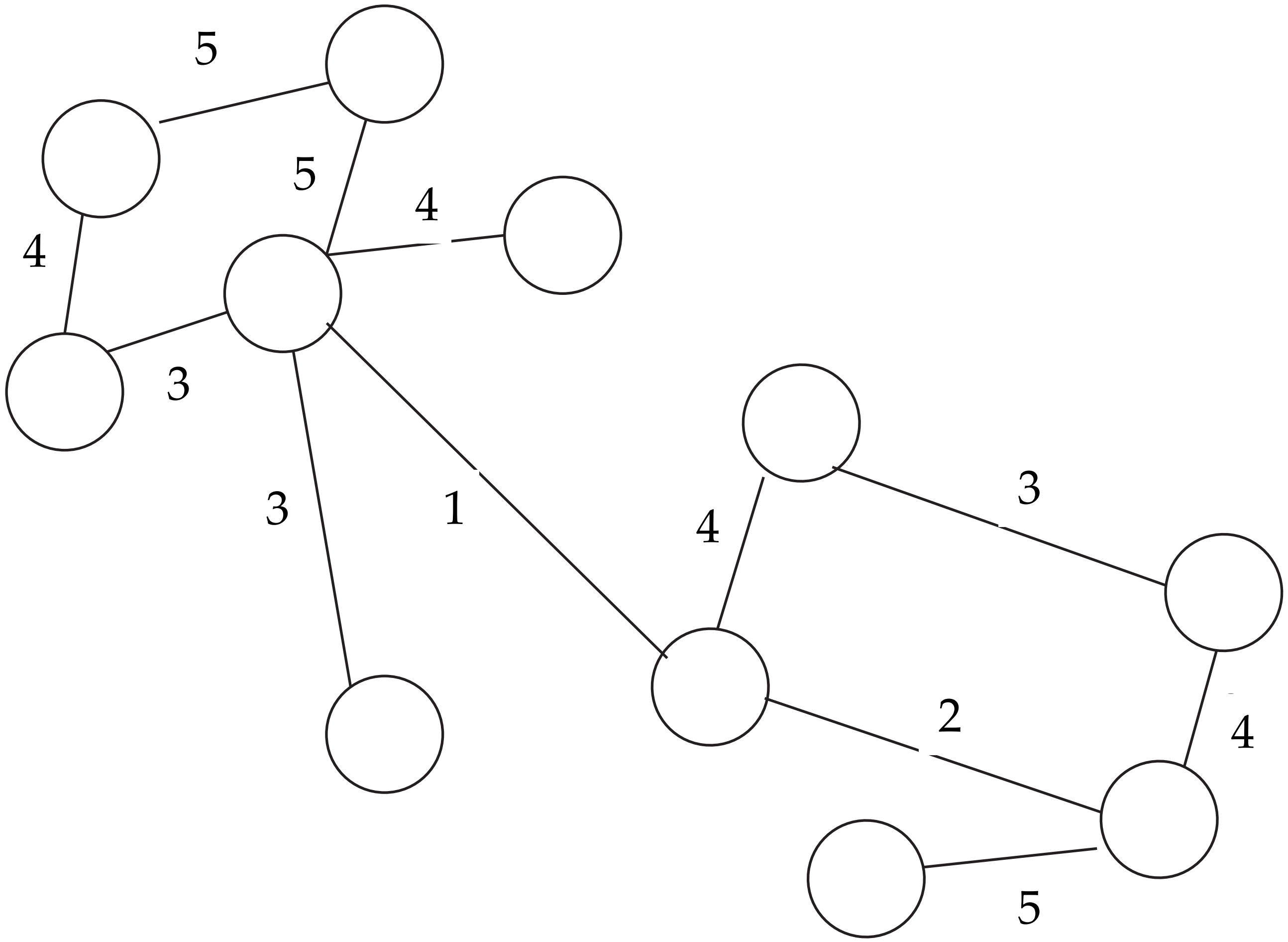
Minimum Spanning Trees

(or maximal spanning trees in the case of network similarity)

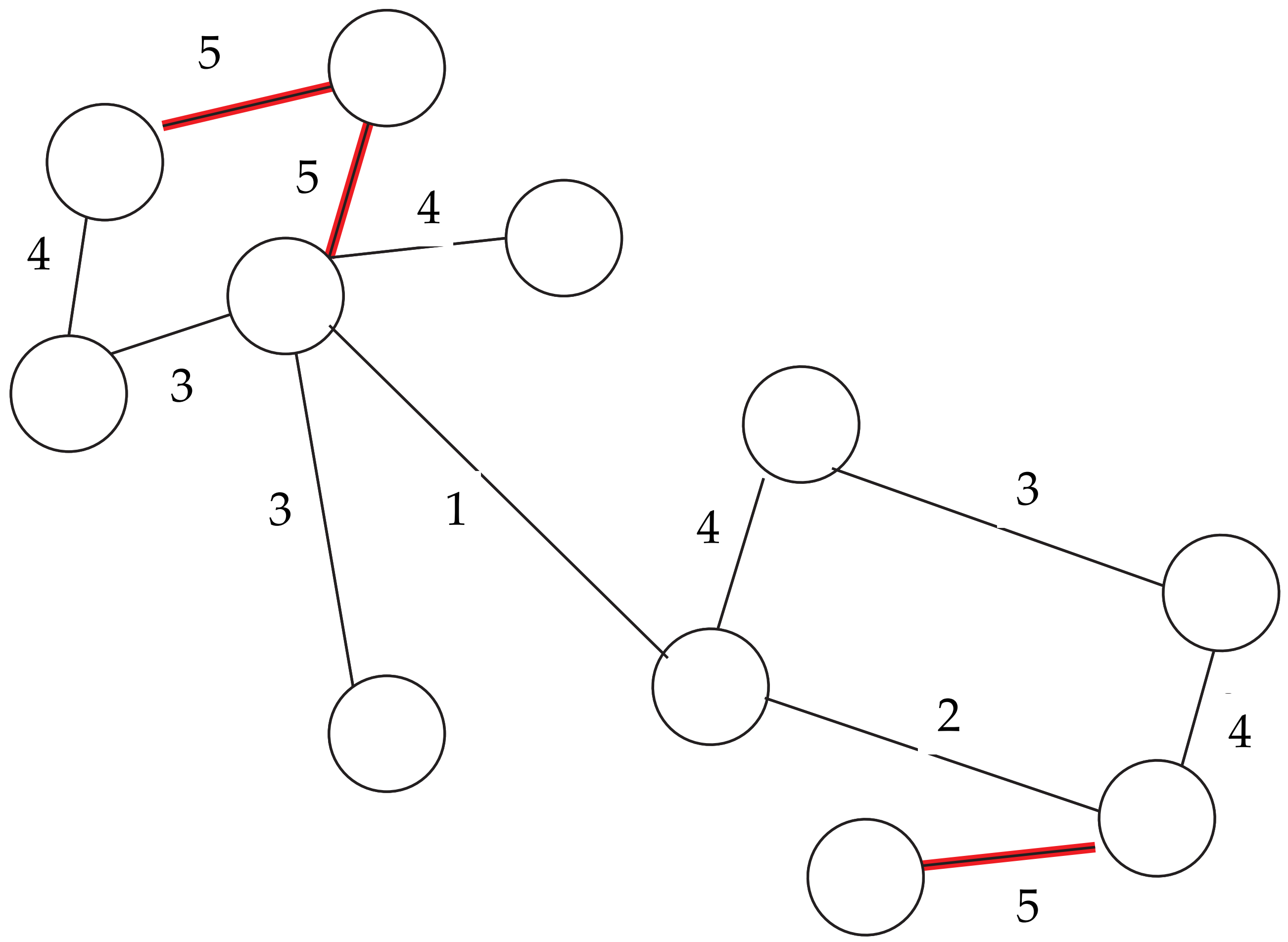
- Equivalent to **Single Linkage hierarchical clustering**.
- Creates a **tree** (graph with no cycles) that connects every node.
- Cutting all edges of the tree whose weight doesn't meet a pre-specified threshold will result in clusters.
- Changing threshold changes the number of clusters.

Building the *Maximum* Spanning Tree

(When edge weights reflect similarity)



Add the most similar edges to the spanning tree, as long as no cycles are created. Repeat.



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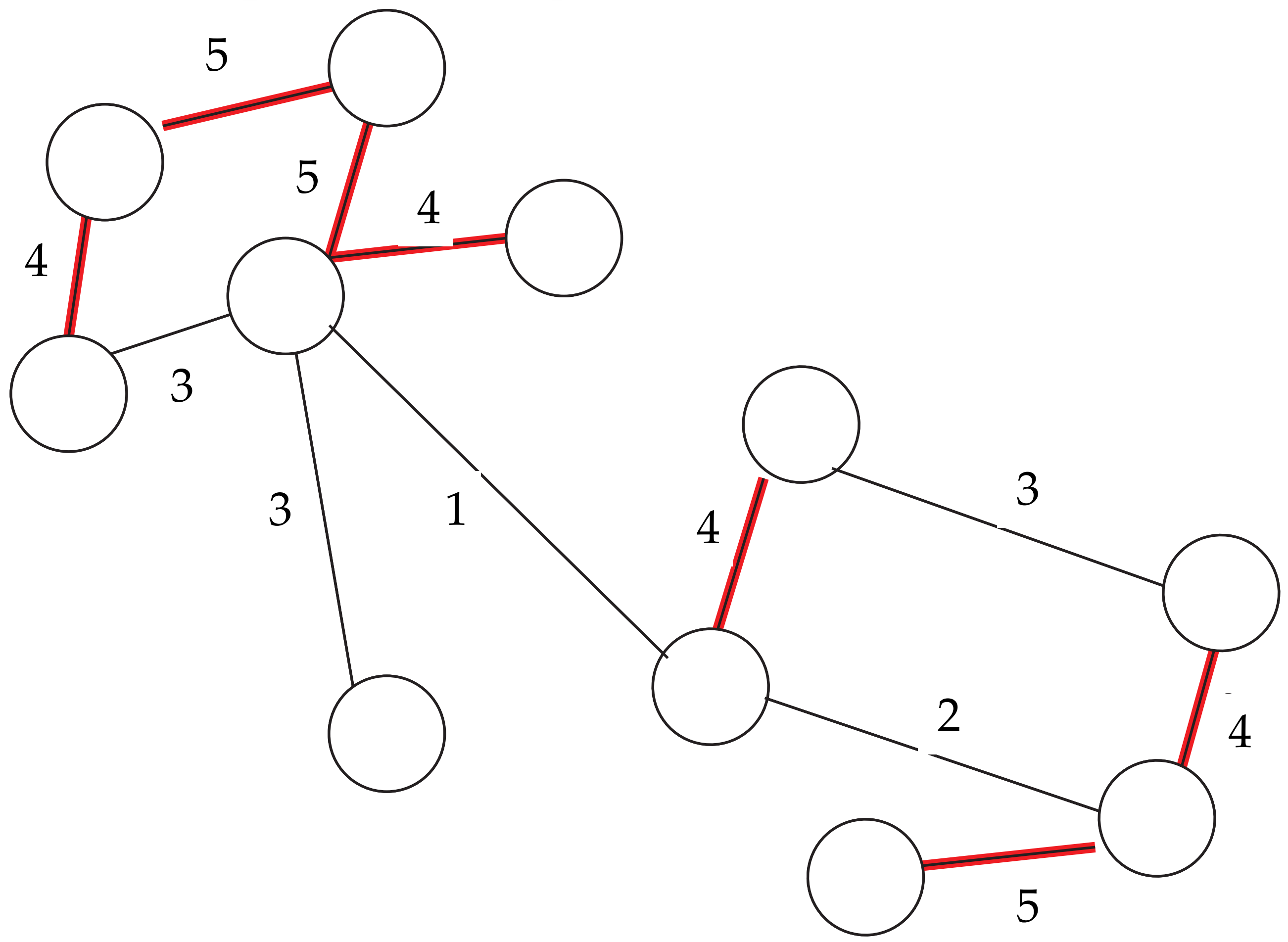

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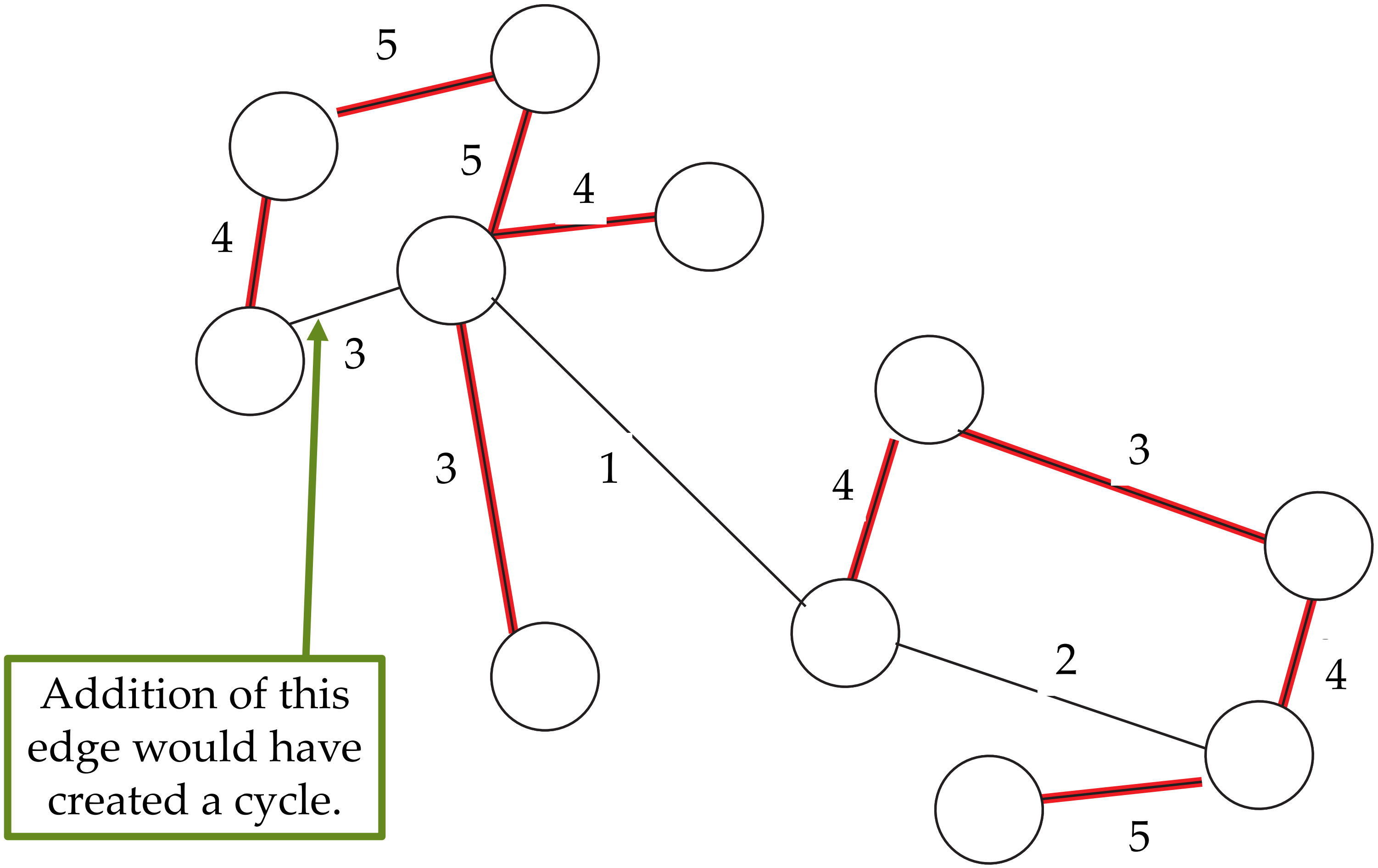
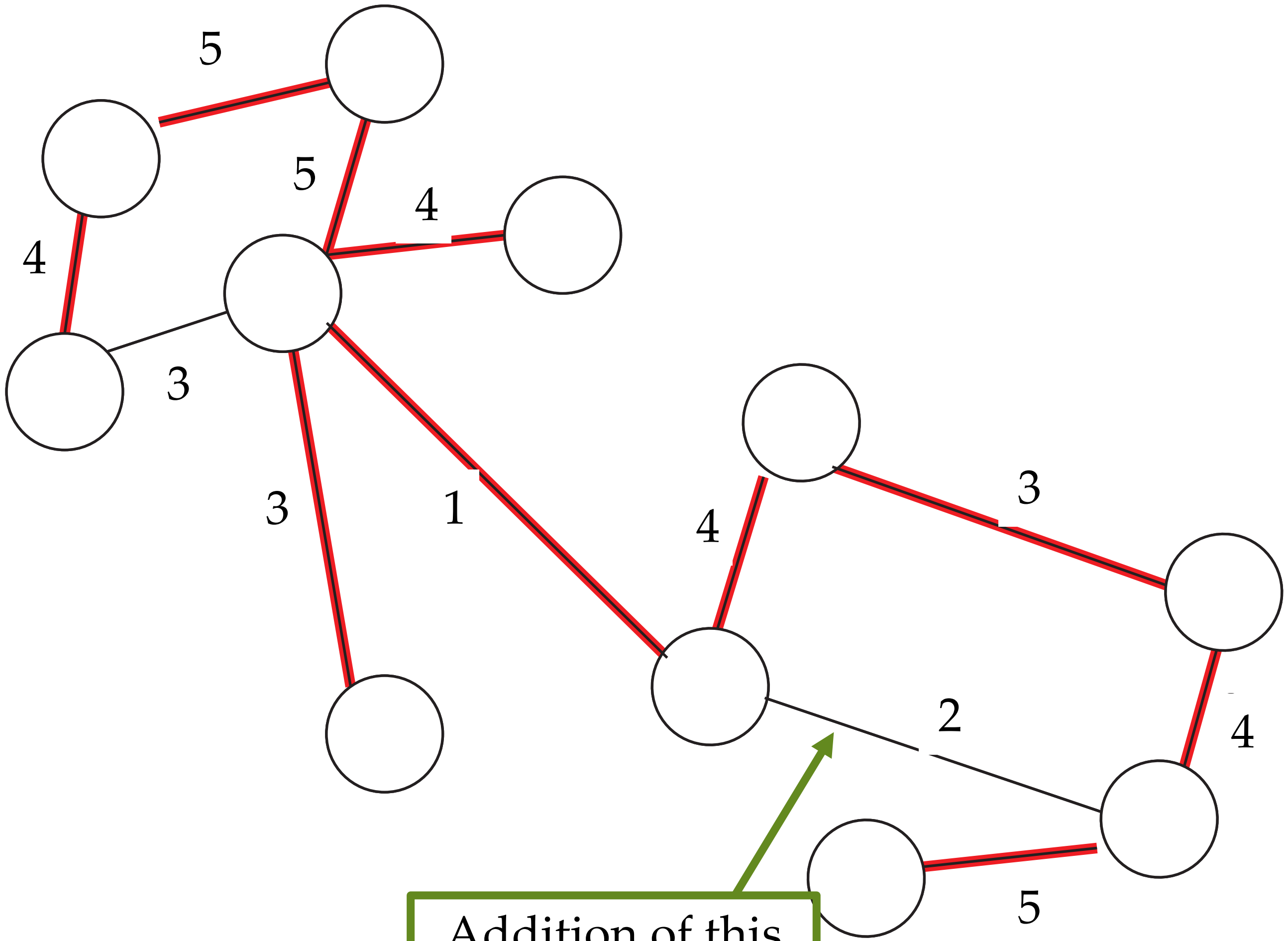


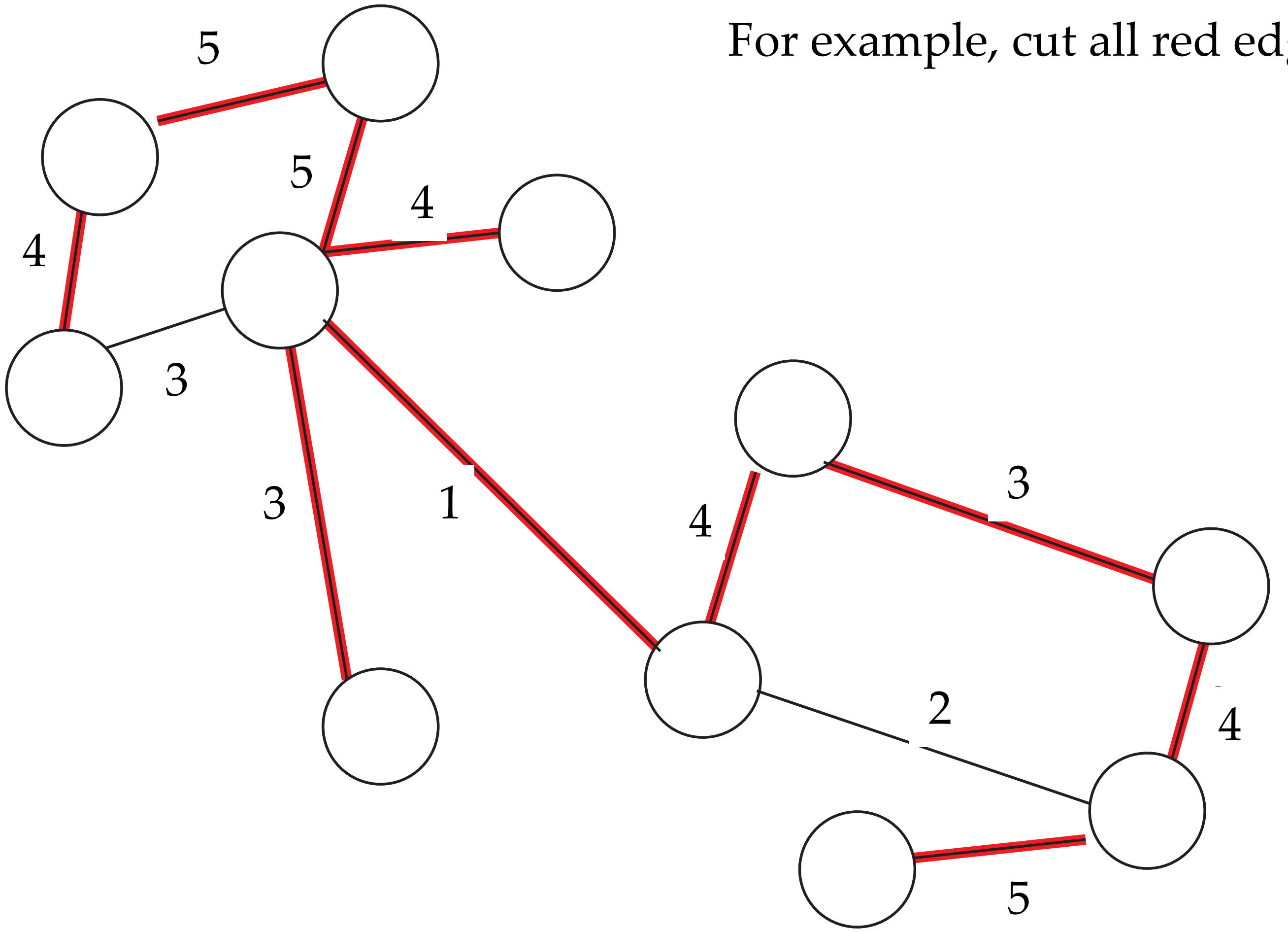
Add the most similar edges to the spanning tree, as long as no cycles are created. Repeat.



Addition of this edge would have created a cycle.

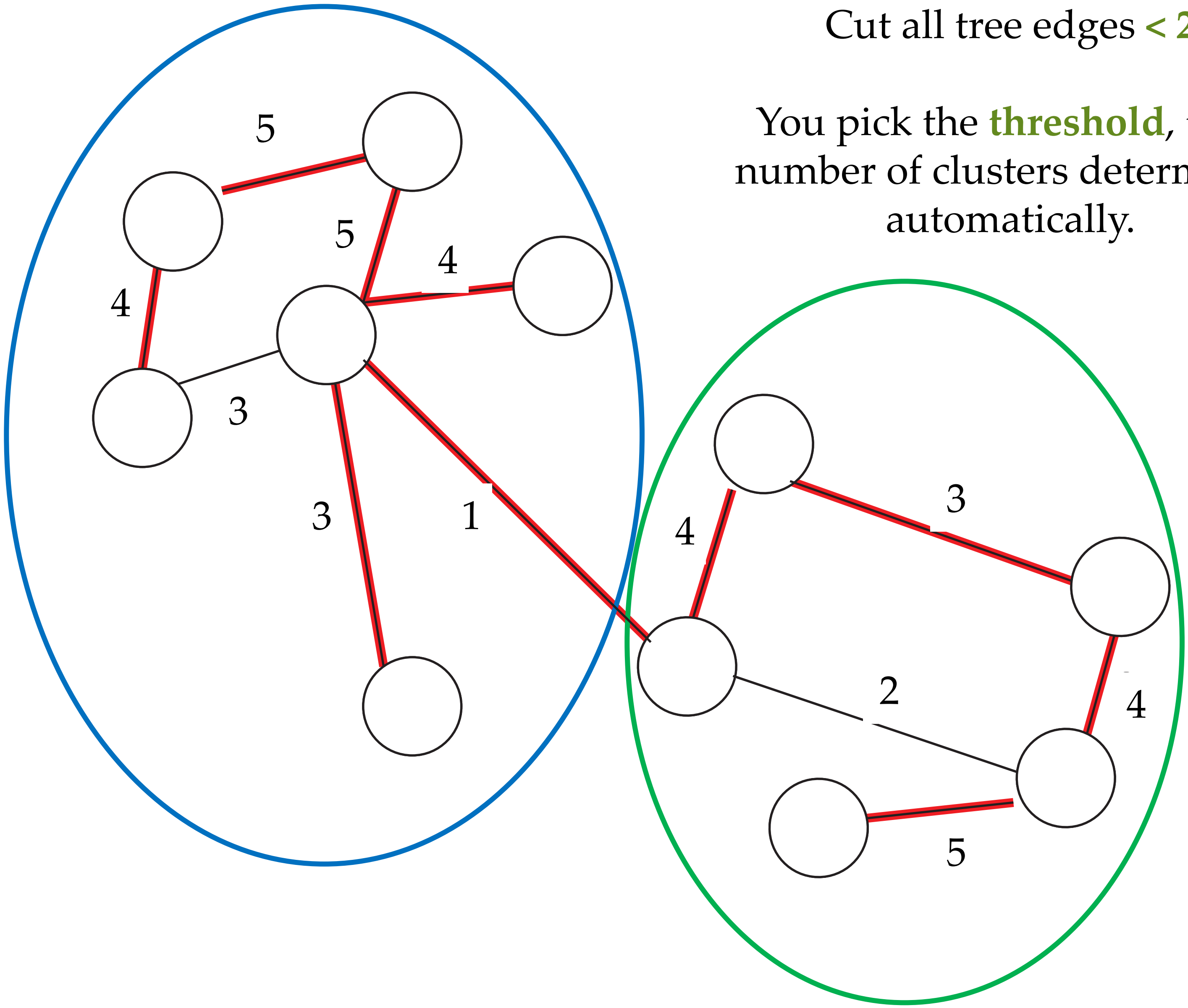
Cut the tree at some threshold.

For example, cut all red edges < 2



Cut all tree edges **< 2**

You pick the **threshold**, then number of clusters determined automatically.



Ensemble Clustering

- Try many different clustering algorithms
- (Or even k-means with different starting points)
- Create a network where the weight of the edge is the number of times that obs *i* was clustered with obs *j*.
- Partition the resulting network.