Goal: take **high-dimensional** data, and describe it compactly using a small number of dimensions.

Assumption: Data lies (approximately) on some **low-dimensional** manifold.
(a few dimensions of opinions, a small number of topics, or a small number of communities)
Principal Component Analysis

\[ X \]

\[ \begin{align*} x_1 & \quad x_0 \end{align*} \]

\[ \begin{align*} y_1 & \quad y_0 \end{align*} \]

\[ \begin{align*} y_0 & \quad Y, 0 \end{align*} \]

Rotate

Un-rotate

Discard lowest-variance dimensions
Q: What would PCA do with this data?
A: Not much, variance is about equal in all dimensions.
1. Input is still a matrix of features:

\[ X = \begin{pmatrix}
5 & 3 & \cdots & 1 \\
4 & 2 & 1 \\
3 & 1 & 3 \\
2 & 2 & 4 \\
1 & 5 & 2 \\
\vdots & \vdots & \vdots \\
1 & 2 & \cdots & 1
\end{pmatrix} \]

2. Output is a list of cluster "centroids":

\[
\text{centroids} = \begin{pmatrix}
1.1 & 2.1 \\
3.5 & 1.8 \\
0.2 & 0.1 \\
3.0 & -0.3
\end{pmatrix}
\]

3. From this we can describe each point in \( X \) by its cluster membership:

\[
f = [0,0,1,0] \quad f = [0,0,0,1]
\]

\[
Y = (1, 2, 4, 3, 4, 2, 4, 2, 2, 3, 3, 2, 1, 1, 3, \ldots, 2)
\]
Q: What if our clusters are hierarchical?
Q: What if our clusters are hierarchical?

A: We’d like a representation that encodes that points have **some features** in common but not others.
Hierarchical (agglomerative) clustering works by gradually fusing clusters whose points are closest together.

Assign every point to its own cluster:
Clusters = [[1],[2],[3],[4],[5],[6],..., [N]]

While len(Clusters) > 1:
    Compute the center of each cluster
    Combine the two clusters with the nearest centers
Hierarchical clustering (e.g.)
Hierarchical clustering

If we keep track of the order in which clusters were merged, we can build a “hierarchy” of clusters.

(“dendrogram”)

1 2 3 4 5 6 7 8

1 2 3 4

2 3 4

3 4

5 6 7

6 7

5 6 7

8

5 6 7 8

1 2 3 4 5 6 7 8
Hierarchical clustering

Splitting the dendrogram at different points defines cluster “levels” from which we can build our feature representation.

L1, L2, L3

1: [0,0,0,0,1,0]
2: [0,0,1,0,1,0]
3: [1,0,1,0,1,0]
4: [1,0,1,0,1,0]
5: [0,0,0,1,0,1]
6: [0,1,0,1,0,1]
7: [0,1,0,1,0,1]
8: [0,0,0,0,0,1]
• **Q:** How to choose K in K-means?

(or:
  • How to choose how many PCA dimensions to keep?
  • How to choose at what position to “cut” our hierarchical clusters?
  • (later) how to choose how many communities to look for in a network)
1) As a means of “compressing” our data

- Choose however many dimensions we can afford to obtain a given file size/compression ratio
- Keep adding dimensions until adding more no longer decreases the reconstruction error significantly
2) As a means of generating potentially useful features for some other predictive task (which is what we’re more interested in in a predictive analytics course!)

- Increasing the number of dimensions/number of clusters gives us additional features to work with, i.e., a longer feature vector
- In some settings, we may be running an algorithm whose complexity (either time or memory) scales with the feature dimensionality (such as we saw last week!); in this case we would just take however many dimensions we can afford
Model selection

• Otherwise, we should choose however many dimensions results in the best prediction performance on held out data
Further reading:
• Ricardo Gutierrez-Osuna’s PCA slides (slightly more mathsy than mine):
• Relationship between PCA and K-means:
  http://ranger.uta.edu/~chqding/papers/KmeansPCA1.pdf
  http://ranger.uta.edu/~chqding/papers/Zha-Kmeans.pdf
Community detection versus clustering

So far we have seen methods to reduce the dimension of points based on their **features**
Principal Component Analysis

\[
X \xrightarrow{\varphi} Y
\]

- rotate
- un-rotate
- discard lowest-variance dimensions

\[
X \rightarrow \varphi \rightarrow \varphi^T \rightarrow Y_0
\]
K-means Clustering

1. Input is still a matrix of features:

\[
X = \begin{pmatrix}
5 & 3 & \cdots & 1 \\
4 & 2 & 1 & 3 \\
2 & 2 & 4 & 1 \\
1 & 5 & 2 & \vdots \\
\vdots & \vdots & \vdots & \vdots \\
1 & 2 & \cdots & 1
\end{pmatrix}
\]

2. Output is a list of cluster “centroids”:

\[
\text{centroids} = \begin{pmatrix}
1.1 & 2.1 \\
3.5 & 1.8 \\
0.2 & 0.1 \\
3.0 & -0.3
\end{pmatrix}
\]

3. From this we can describe each point in \( X \) by its cluster membership:

\[
f = [0, 0, 1, 0] \quad \text{for cluster 1}
\]

\[
f = [0, 0, 0, 1] \quad \text{for cluster 2}
\]

\[
f = [0, 1, 0, 0] \quad \text{for cluster 3}
\]

\[
f = [1, 0, 0, 0] \quad \text{for cluster 4}
\]

\[
Y = (1, 2, 4, 3, 4, 2, 4, 2, 2, 3, 3, 2, 1, 1, 3, \ldots, 2)
\]
Community detection versus clustering

So far we have seen methods to reduce the dimension of points based on their features.

What if points are not defined by features but by their relationships to each other?
Q: how can we compactly represent the set of relationships in a graph?
A: by representing the nodes in terms of the **communities** they belong to
Community detection

(from previous lecture)

f = [0,0,1,1] (A,B,C,D)

communities

f = [0,0,0,1] (A,B,C,D)

e.g. from a PPI network; Yang, McAuley, & Leskovec (2014)
Community detection versus clustering

Part 1 – Clustering
Group sets of points based on their **features**

Part 2 – Community detection
Group sets of points based on their **connectivity**

**Warning:** These are **rough** distinctions that don’t cover all cases. E.g. if I treat a row of an adjacency matrix as a "feature" and run hierarchical clustering on it, am I doing clustering or community detection?
Community detection

How should a “community” be defined?
Community detection

How should a “community” be defined?

1. Members should be connected
2. Few edges between communities
3. “Cliqueishness”
4. Dense inside, few edges outside
1. Connected components
   (members should be connected)
2. Minimum cut
   (few edges between communities)
3. Clique percolation
   ("cliqueishness")
4. Network modularity
   (dense inside, few edges outside)
1. Connected components

Define communities in terms of sets of nodes which are reachable from each other

- If \( a \) and \( b \) belong to a **strongly connected component** then there must be a path from \( a \rightarrow b \) and a path from \( b \rightarrow a \)
- A **weakly connected component** is a set of nodes that would be strongly connected, if the graph were undirected
1. Connected components

• Captures about the roughest notion of “community” that we could imagine
• Not useful for (most) real graphs: there will usually be a “giant component” containing almost all nodes, which is not really a community in any reasonable sense
What if the separation between communities isn’t so clear?

e.g. “Zachary’s Karate Club” (1970)

Picture from http://spaghetti-os.blogspot.com/2014/05/zacharys-karate-club.html
2. Graph cuts

Aside: Zachary’s Karate Club Club Club

http://networkkarate.tumblr.com/
2. Graph cuts

**Cut** the network into two partitions such that the number of edges crossed by the cut is minimal.

Solution will be degenerate – we need additional constraints.
2. Graph cuts

We’d like a cut that favors large communities over small ones

\[ \text{Ratio Cut}(C) = \frac{1}{|C|} \sum_{c \in C} \frac{\text{cut}(c, \bar{c})}{|c|} \]

- # of edges that separate $c$ from the rest of the network
- Proposed set of communities
- Size of this community
2. Graph cuts

What is the **Ratio Cut** cost of the following two cuts?

\[
\text{Ratio Cut}(\cdots) = \frac{1}{2} \left( \frac{3}{33} + \frac{3}{1} \right) = 1.54545 \\
\text{Ratio Cut}(\cdots) = \frac{1}{2} \left( \frac{9}{16} + \frac{9}{18} \right) = 0.53125
\]
2. Graph cuts

But what about...

\[
\text{Ratio Cut}(\rightarrow) = \frac{1}{2} \left( \frac{1}{33} + \frac{1}{1} \right) = 0.51515
\]
2. Graph cuts

Maybe rather than counting all nodes equally in a community, we should give additional weight to “influential”, or high-degree nodes.

\[
\text{Normalized Cut}(C) = \frac{1}{|C|} \sum_{c \in C} \frac{\text{cut}(c, \bar{c})}{\sum \text{degrees in } c}
\]

Nodes of high degree will have more influence in the denominator.
2. Graph cuts

What is the **Normalized Cut** cost of the following two cuts?

\[
\text{Norm. Cut}(\cdots) = \frac{1}{2} \left( \frac{1}{155} + \frac{1}{1} \right) = 0.50322
\]
\[
\text{Norm. Cut}(\cdots) = \frac{1}{2} \left( \frac{9}{76} + \frac{9}{80} \right) = 0.11546
\]
2. Graph cuts

```python
>>> Import networkx as nx
>>> G = nx.karate_club_graph()
>>> c1 = [1,2,3,4,5,6,7,8,11,12,13,14,17,18,20,22]
>>> c2 = [9,10,15,16,19,21,23,24,25,26,27,28,29,30,31,32,33,34]
>>> Sum([G.degree(v-1) for v in c1])
76
>>> sum([G.degree(v-1) for v in c2])
80
```

Nodes are indexed from 0 in the networkx dataset, 1 in the figure
So what actually happened?

- \( = \) Optimal cut
- \( \text{Red/blue} = \) actual split
Normalized cuts in Computer Vision

“Normalized Cuts and Image Segmentation”
Shi and Malik, 1998
Disjoint communities

Separating networks into disjoint subsets seems to make sense when communities are somehow “adversarial”

E.g. links between democratic/republican political blogs (from Adamic, 2004)

Graph data from Adamic (2004). Visualization from allthingsgraphed.com
Social communities

But what about communities in social networks (for example)?

e.g. the graph of my facebook friends:

http://jmcauley.ucsd.edu/cse158/data/facebook/egonet.txt
Social communities

Such graphs might have:

- **Disjoint** communities (i.e., groups of friends who don’t know each other)
  e.g. my American friends and my Australian friends
- **Overlapping** communities (i.e., groups with some intersection)
  e.g. my friends and my girlfriend’s friends
- **Nested** communities (i.e., one group within another)
  e.g. my UCSD friends and my CSE friends
3. Clique percolation

How can we define an algorithm that handles all three types of community (disjoint/overlapping/nested)?

**Clique percolation** is one such algorithm, that discovers communities based on their “cliqueishness”
3. Clique percolation

- Clique percolation searches for “cliques” in the network of a certain size (K). Initially each of these cliques is considered to be its own community.
- If two communities share a (K-1) clique in common, they are merged into a single community.
- This process repeats until no more communities can be merged.

1. Given a clique size K
2. Initialize every K-clique as its own community
3. While (two communities I and J have a (K-1)-clique in common):
   4. Merge I and J into a single community
3. Clique percolation
What is a “good” community algorithm?

• So far we’ve just defined algorithms to match some (hopefully reasonable) intuition of what communities should “look like”
• But how do we know if one definition is better than another? I.e., how do we evaluate a community detection algorithm?

• Can we define a probabilistic model and evaluate the likelihood of observing a certain set of communities compared to some null model
4. Network modularity

Null model:
Edges are equally likely between any pair of nodes, regardless of community structure ("Erdos-Renyi random model")
4. Network modularity

Null model:
Edges are equally likely between any pair of nodes, regardless of community structure ("Erdos-Renyi random model")

Q: How much does a proposed set of communities deviate from this null model?
4. Network modularity
4. Network modularity

\[ e_{kk} = \frac{\# {\text{edges with both endpoints in community } k}}{\# {\text{edges}}} \]

\[ a_k = \frac{\# {\text{edge endpoints in community } k}}{\# {\text{edge endpoints}}} \]

\[ Q = \sum_{k=1}^{K} \left( e_{kk} - a_k^2 \right) \]

Fraction of edges in community k  
Fraction that we would expect if edges were allocated randomly
4. Network modularity
4. Network modularity

\[ e_{kk} = \frac{\text{\# edges with both endpoints in community } k}{\text{\# edges}} \]

\[ a_k = \frac{\text{\# edge endpoints in community } k}{\text{\# edge endpoints}} \]

\[ Q = \sum_{k=1}^{K} (e_{kk} - a_k^2) \]
4. Network modularity
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\[ e_{kk} = \frac{\text{\# edges with both endpoints in community } k}{\text{\# edges}} \]

\[ a_k = \frac{\text{\# edge endpoints in community } k}{\text{\# edge endpoints}} \]

\[ Q = \sum_{k=1}^{K} \left( e_{kk} - a_k^2 \right) \]

\[ -\frac{1}{2} \leq Q < 1 \]

Far fewer edges in communities than we would expect at random

Far more edges in communities than we would expect at random
4. Network modularity

**Algorithm:** Choose communities so that the deviation from the null model is maximized

\[ Q = \sum_{k=1}^{K} (e_{kk} - a_{k}^2) \]

\[ \arg \max_{\text{communities}} Q(\text{communities}) \]

That is, choose communities such that **maximally** many edges are within communities and **minimally** many edges cross them

(NP Hard, have to approximate)
Summary

• Community detection aims to summarize the structure in networks
  (as opposed to clustering which aims to summarize feature dimensions)

• Communities can be defined in various ways, depending on the type of network in question
  1. Members should be connected (connected components)
  2. Few edges between communities (minimum cut)
  3. “Cliqueishness” (clique percolation)
  4. Dense inside, few edges outside (network modularity)
Assignment 1

Will be discussed next lecture when we introduce **Recommender Systems**
Further reading:

Just on modularity: http://www.cs.cmu.edu/~ckingsf/bioinfo-lectures/modularity.pdf

Various community detection algorithms, includes spectral formulation of ratio and normalized cuts:
http://dmml.asu.edu/cdm/slides/chapter3.pptx