CSE 258 – Lecture 5
Web Mining and Recommender Systems

Dimensionality Reduction
This week

How can we build low dimensional representations of high dimensional data?

e.g. how might we (compactly!) represent
1. The ratings I gave to every movie I’ve watched?
   2. The complete text of a document?
3. The set of my connections in a social network?
**Q1:** The ratings I gave to every movie I’ve watched (or product I’ve purchased)

**A1:** A (sparse) vector including all movies

\[ F_{\text{julian}} = [0.5, ?, 1.5, 2.5, ?, ?, ..., 5.0] \]

- A-team
- ABBA, the movie
- Zoolander
A1: A (sparse) vector including all movies

\[ F_{\text{julian}} = [0.5, ?, 1.5, 2.5, ?, ?, \ldots , 5.0] \]

- expensive
- missing values
- new items
- redundancy
A2: Describe my preferences using a low-dimensional vector.
Q2: How to represent the complete text of a document?

A1: A (sparse) vector counting all words

\[ F_{\text{text}} = [150, 0, 0, 0, 0, 0, 0, ..., 0] \]

- a
- aardvark
- zoetrope
A1: A (sparse) vector counting all **words**

\[ F_{text} = [150, 0, 0, 0, 0, 0, 0, \ldots, 0] \]

Incredibly high-dimensional...
- Costly to store and manipulate
- Many dimensions encode essentially the same thing
- Many dimensions devoted to the “long tail” of obscure words (technical terminology, proper nouns etc.)
A2: A low-dimensional vector describing the topics in the document

87 of 102 people found the following review helpful

⭐⭐⭐⭐⭐ You keep what you kill, December 27, 2004
By Schtinky "Schtinky" (Washington State) - See all my reviews

This review is from: The Chronicles of Riddick (Widescreen Unrated Director's Cut) (DVD)

Even if I have to apologize to my Friends and Favorites, and my family, I have to admit that I really liked this movie. It's a Sci-Fi movie with a "Mad Maxx" appeal that, while changing many things, left Riddick from 'Pitch Black' to be just Riddick. They did not change his attitude or soften him up or bring him out of his original character, which was very pleasing to 'Pitch Black' fans like myself.

First off, let me say that when playing the DVD, the first Convert or Fight, and no explanation of the choices. This I will mention off the bat that they are simply different menu has the very same options, simply different back either one and continue with the movie.

Week 5!

(review of “The Chronicles of Riddick”)
Q3: How to represent connections in a social network?

A1: An adjacency matrix!

\[
A = \begin{pmatrix}
1 & 0 & \cdots & 1 \\
0 & 0 & & 1 \\
\vdots & & \ddots & \vdots \\
1 & 1 & \cdots & 1
\end{pmatrix}
\]
Dimensionality reduction

A1: An adjacency matrix

\[ A = \begin{pmatrix}
1 & 0 & \cdots & 1 \\
0 & 0 & & 1 \\
& \ddots & \ddots & \ddots \\
1 & 1 & \cdots & 1
\end{pmatrix} \]

Seems almost reasonable, but...

- Becomes very large for real-world networks
- Very fine-grained – doesn’t straightforwardly encode which nodes are similar to each other
A2: Represent each node/user in terms of the **communities** they belong to

e.g. from a PPI network; Yang, McAuley, & Leskovec (2014)
Why dimensionality reduction?

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).
Why dimensionality reduction?

**Unsupervised learning**

- Today our goal is not to solve some specific predictive task, but rather to *understand* the important features of a dataset
- We are not trying to understand the process which generated labels from the data, but rather the process which generated the data itself
Why dimensionality reduction?

Unsupervised learning

• **But!** The models we learn will prove useful when it comes to solving predictive tasks later on, e.g.

• **Q1:** If we want to predict which users like which movies, we need to understand the important dimensions of opinions

• **Q2:** To estimate the category of a news article (sports, politics, etc.), we need to understand topics it discusses

• **Q3:** To predict who will be friends (or enemies), we need to understand the communities that people belong to
Today...

Dimensionality reduction, clustering, and community detection

- Principal Component Analysis
- K-means clustering
- Hierarchical clustering
- Next lecture: Community detection
  - Graph cuts
  - Clique percolation
  - Network modularity
Principal Component Analysis (PCA) is one of the oldest (1901!) techniques to understand which dimensions of a high-dimensional dataset are “important”

Why?
• To **select** a few important features
• To **compress** the data by ignoring components which aren’t meaningful
Principal Component Analysis

Motivating example:
Suppose we rate restaurants in terms of:
[value, service, quality, ambience, overall]

• Which dimensions are highly correlated (and how)?
• Which dimensions could we “throw away” without losing much information?
• How can we find which dimensions can be thrown away automatically?
• In other words, how could we come up with a “compressed representation” of a person’s 5-d opinion into (say) 2-d?
Suppose our data/signal is an $M \times N$ matrix

$N = \text{number of observations}$

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

$M = \text{number of features}$

(each column is a data point)
Principal Component Analysis

We’d like (somehow) to recover this signal using as few dimensions as possible.

\[ X \in \mathbb{R}^{M \times N} \quad Y' \in \mathbb{R}^{K \times N} \]

\[ f(Y') \approx X \]

(approximate) process to recover signal from its compressed version
E.g. suppose we have the following data:

The data (roughly) lies along a line

Idea: if we know the position of the point on the line (1D), we can approximately recover the original (2D) signal
But how to find the important dimensions?

Find a new basis for the data (i.e., rotate it) such that

- **most** of the variance is along $x_0$,
- most of the “leftover” variance (not explained by $x_0$) is along $x_1$,
- most of the leftover variance (not explained by $x_0,x_1$) is along $x_2$,
- etc.
But how to find the important dimensions?

- Given an input \( X \in \mathbb{R}^{M \times N} \)
- Find a basis \( \varphi \in \mathbb{R}^{M \times M} \)

\[ \varphi_i \cdot \varphi_i = 1 \]
\[ \varphi_i \cdot \varphi_j = 0 \]
Principal Component Analysis

But how to find the important dimensions?

- Given an input $X \in \mathbb{R}^{M \times N}$
- Find a basis $\varphi \in \mathbb{R}^{M \times M}$
- Such that when $X$ is rotated $(Y = \varphi X)$
  - Dimension with highest variance is $y_0$
  - Dimension with 2nd highest variance is $y_1$
  - Dimension with 3rd highest variance is $y_2$
  - Etc.
Principal Component Analysis

\[ X \]  
\[ x_0 \quad x_1 \]  
\[ y_0 \quad y_1 \]  

\[ Y \]  
\[ y_0 \]  

\[ \varphi \]  
rotate  

discard lowest-variance dimensions  

\[ \varphi^{-1} = \varphi^T \]  
un-rotate
Principal Component Analysis

For a single data point: $y = \varphi x \quad x = \varphi^{-1} y = \varphi^T y$.

$$x = \ell_1 y_1 + \ell_2 y_2 + \ldots + \ell_m y_m$$

$$= \sum_{j=1}^{m} \ell_j y_j$$
Principal Component Analysis

\[ x = \varphi_1 y_1 + \varphi_2 y_2 + \ldots + \varphi_M y_M = \sum_{j=1}^{M} \varphi_j y_j \]

\[ x \approx \sum_{j=1}^{k} \varphi_j y_j + \sum_{j=k+1}^{M} \varphi_j y_j \]
Principal Component Analysis

We want to fit the “best” reconstruction:

\[ x = \varphi^T y \]

“complete” reconstruction

\[ x_i \approx \sum_{j=1}^{K} \varphi_j y_j + \sum_{j=K+1}^{M} \varphi_j b_j \]

approximate reconstruction

i.e., it should minimize the MSE:

\[ \frac{1}{N} \sum_{y} \left( \sum_{j=1}^{K} \varphi_j y_j + \sum_{j=K+1}^{M} \varphi_j b_j - \sum_{j=1}^{M} \varphi_j y_j \right)^2 \]
Principal Component Analysis

\[
\min_{\varphi, b} \frac{1}{N} \sum_y \left| \sum_{j=1}^{K} \varphi_j y_j + \sum_{j=K+1}^{M} \varphi_j b_j - \varphi^T y \right|^2
\]

Simplify...

\[
\frac{1}{N} \sum_{y} \left| \sum_{j=K+1}^{M} \varphi_j (y_j - 6_j) \right|^2
\]
Principal Component Analysis

\[ \min_{\varphi,b} \frac{1}{N} \sum_y \left\| \sum_{j=K+1}^{M} \varphi_j (y_j - b_j) \right\|_2^2 \]

Expand...

\[ = \frac{1}{N} \sum_{y} \sum_{j=K+1}^{M} (y_j - b_j)^2 \]

\[ = \frac{1}{N} \sum_{y} \sum_{j=K+1}^{M} (y_j - b_j)^2 \]

\[ = \frac{1}{N} \sum_{y} \sum_{j=K+1}^{M} (y_j - b_j)^2 \]

\[ = 1 \text{ if } i = j \]

\[ = 0 \text{ if } i \neq j \]
\[
\min_{\varphi,b} \frac{1}{N} \sum_{y} \sum_{j=K+1}^{M} (y_j - b_j)^2
\]

\[b_j = \bar{y}_i \]

ave. of \( j \)th
dim. of \( y \)
Principal Component Analysis

\[ \min_{\varphi} \frac{1}{N} \sum_y \sum_{j=K+1}^M (y_j - \bar{y}_j)^2 \]

Equal to the \textbf{variance} in the discarded dimensions
**PCA:** We want to keep the dimensions with the highest variance, and discard the dimensions with the lowest variance, in some sense to maximize the amount of “randomness” that gets preserved when we compress the data.
Principal Component Analysis

\[
\min_{\varphi} \frac{1}{N} \sum_{y} \sum_{j=K+1}^{M} (y_j - \bar{y}_j)^2 \quad \text{(subject to } \varphi \text{ orthonormal)}
\]

Expand in terms of X

\[
\min_{\varphi} \frac{1}{N} \sum_{j=K+1}^{M} \varphi_j (X - \bar{X})(X - \bar{X})^T \varphi_j^T \quad \text{(subject to } \varphi \text{ orthonormal)}
\]
Principal Component Analysis

$$\min_{\varphi} \frac{1}{N} \sum_{j=K+1}^{M} \varphi_j (X - \bar{X})(X - \bar{X})^T \varphi_j^T$$

(subject to $\varphi$ orthonormal)

$$\min_{\varphi} \frac{1}{N} \sum_{j=K+1}^{M} \varphi_j \text{Cov}(X) \varphi_j^T - \lambda_j (\varphi_j \varphi_j^T - 1)$$

Lagrange multiplier

Lagrange multipliers: Bishop appendix E
Principal Component Analysis

Solve:

\[
\frac{\partial}{\partial \phi_j} \sum_{j=K+1}^{M} \varphi_j \text{Cov}(X) \varphi_j^T - \lambda_j (\varphi_j \varphi_j^T - 1) = 0
\]

(Cov(X) is symmetric)

\[
2(\text{Cov}(X) \varphi_j^T - \lambda_j \varphi_j^T) = 0
\]

- This expression can only be satisfied if \(\phi_j\) and \(\lambda_j\) are an eigenvectors/eigenvalues of the covariance matrix.
- So to minimize the original expression we’d discard \(\phi_j\)’s corresponding to the smallest eigenvalues.
Moral of the story: if we want to optimally (in terms of the MSE) project some data into a low dimensional space, we should choose the projection by taking the eigenvectors corresponding to the largest eigenvalues of the covariance matrix.
Example 1:
What are the principal components of people’s opinions on beer?

(code available on)
http://jmcauley.ucsd.edu/cse258/code/week3.py
Principal Component Analysis
Example 2: What are the principal dimensions of image patches?

\[(0.7, 0.5, 0.4, 0.6, 0.4, 0.3, 0.5, 0.3, 0.2)\]
Principal Component Analysis

Construct such vectors from 100,000 patches from real images and run PCA:

Black and white:
Principal Component Analysis

Construct such vectors from 100,000 patches from real images and run PCA:

Color:
Principal Component Analysis

From this we can build an algorithm to “denoise” images.

Idea: image patches should be more like the high-eigenvalue components and less like the low-eigenvalue components.

McAuley et. al (2006)
Principal Component Analysis

• We want to find a low-dimensional representation that best compresses or “summarizes” our data
• To do this we’d like to keep the dimensions with the highest variance (we proved this), and discard dimensions with lower variance. Essentially we’d like to capture the aspects of the data that are “hardest” to predict, while discard the parts that are “easy” to predict
• This can be done by taking the eigenvectors of the covariance matrix
Clustering – K-means
Q: What would PCA do with this data?

A: Not much, variance is about equal in all dimensions.
But: The data are highly **clustered**

Idea: can we compactly describe the data in terms of **cluster memberships**?
K-means Clustering

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:

\[
Y = (1, 2, 4, 3, 4, 2, 4, 2, 2, 3, 3, 2, 1, 1, 3, \ldots, 2)
\]

\[
f = [0, 0, 1, 0] \\
f = [0, 0, 0, 1]
\]
K-means Clustering

Given **features** \( (X) \) our goal is to choose \( K \) **centroids** \( (C) \) and **cluster assignments** \( (Y) \) so that the reconstruction error is minimized

\[
\text{reconstruction error} = \sum_i \| X_i - C_{y_i} \|^2_2
\]

\( (= \text{sum of squared distances from assigned centroids}) \)
Q: Can we solve this optimally?

\[
\min_{C, y} \sum_i \| X_i - C_{y_i} \|_2^2
\]

A: No. This is (in general) an **NP-Hard** optimization problem

K-means Clustering

**Greedy algorithm:**

1. Initialize $C$ (e.g. at random)
2. Do
3. Assign each $X_i$ to its nearest centroid
4. Update each centroid to be the mean of points assigned to it
5. While (assignments change between iterations)

(Also: reinitialize clusters at random should they become empty)

$$y_i = \arg\min_k \| X_i - C_k \|_2^2$$

$$C_k = \frac{\sum_i \delta(y_i=k)X_i}{\sum_i \delta(y_i=k)}$$
Further reading:

- **K-medians**: Replaces the mean with the median. Has the effect of minimizing the 1-norm (rather than the 2-norm) distance.
- **Soft** K-means: Replaces “hard” memberships to each cluster by a proportional membership to each cluster.
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Clustering – hierarchical clustering
Hierarchical clustering

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 clustering

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
Example
Hierarchical clustering

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

(“dendrogram”)
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]
Model selection

• **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?
  • (next week) 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
• Otherwise, we should choose however many dimensions results in the best prediction performance on held out data

• **Q:** Why does this happen? i.e., why doesn’t the validation performance continue to improve with more dimensions
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