## ESS2222

## Lecture 8 - Mining of Massive Data Dimensionality Reduction

Hosein Shahnas

University of Toronto, Department of Earth Sciences,

## Outline

- Principal Component Analysis
- Dimensionality Reduction



## Review of Lecture 7

| 0 | 0 | 0 | 0 | 0 | 0 | $\ldots$ |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 0 | 156 | 155 | 156 | 158 | 158 | $\ldots$ |
| 0 | 153 | 154 | 157 | 159 | 159 | $\ldots$ |
| 0 | 149 | 151 | 155 | 158 | 159 | $\ldots$ |
| 0 | 146 | 146 | 149 | 153 | 158 | $\ldots$ |
| 0 | 145 | 143 | 143 | 148 | 158 | $\ldots$ |
| $\ldots .$. | $\ldots$ | $\ldots$ | $\ldots$ | $\ldots$ | $\ldots$ | $\ldots$ |
| Input Channel \#1 (Red) |  |  |  |  |  |  |
|  |  |  |  |  |  |  |

Input Channel \#1 (Red)

| -1 | -1 | 1 |
| :---: | :---: | :---: |
| 0 | 1 | -1 |
| 0 | 1 | 1 |

Kernel Channel \#1
$\sqrt{6}$
$308+$

Input Channel \#2 (Green)

| 1 | 0 | 0 |
| :---: | :---: | :---: |
| 1 | -1 | -1 |
| 1 | 0 | -1 |

Kernel Channel \#2 ! $\sqrt{6}$
$-498$


Input Channel \#3 (Blue)


Test Image
$\xrightarrow{ }$

Prediction from our network

No idea!?!


Fully connected layers

## Principal Component Analysis

## Principal component analysis (PCA)

A statistical procedure that uses an orthogonal transformation to convert a set of observations of possibly correlated variables into a set of values of linearly uncorrelated variables called principal components.

Feature 1
Feature 2
Feature 3

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | 10 | 11 | 8 | 3 | 2 | 1 |
| Gene 2 | 6 | 4 | 5 | 3 | 2.8 | 1 |
| Gene 3 | 12 | 9 | 10 | 2.5 | 1.3 | 2 |

How can we take three or more features (three or more dimensional feature data) and make a lower $P C$ representation (lower dimension)?


## Principal Component Analysis

Let's assume we have only two genes (two features):

|  |  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Feature 1 | Gene 1 | 10 | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |
| Feature 2 | Gene 2 | 6 | 4 | 5 | 3 | $\mathbf{2 . 8}$ | $\mathbf{1}$ |



## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | 10 | 11 | 8 | 3 | 2 | 1 |
| Gene 2 | 6 | 4 | 5 | 3 | 2.8 | 1 |




## Principal Component Analysis

Let's assume we have only two genes (two features):

|  |  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Feature 1 <br> Feature 2 | Gene 1 | 10 | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |



## Principal Component Analysis

Let's assume we have only two genes (two features):

|  |  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Feature 1 <br> Feature 2 | Gene 1 | 10 | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |






## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | 10 | $\mathbf{1 1}$ | 8 | 3 | 2 | 1 |
| Gene 2 | 6 | 4 | 5 | 3 | 2.8 | 1 |

a) Find the center of mean


## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | $\mathbf{1 0}$ | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |
| Gene 2 | 6 | 4 | 5 | 3 | $\mathbf{2} .8$ | $\mathbf{1}$ |

a) Find the center of mean
b) Move the center to the origin


## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | 10 | $\mathbf{1 1}$ | 8 | 3 | 2 | 1 |
| Gene 2 | 6 | 4 | 5 | 3 | 2.8 | 1 |

and the center of mean
b) Move the center to the origin


## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | $\mathbf{1 0}$ | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |
| Gene 2 | 6 | 4 | 5 | 3 | $\mathbf{2} .8$ | $\mathbf{1}$ |

a) Find the center of mean
b) Move the center to the origin
c) Fit the data points to a line (minimize b or maximize c) $\operatorname{Max} \sum_{i} c_{i}^{2}$


## Principal Component Analysis

Let's assume we have only two genes (two features):

Feature 1
Feature 2

|  | Mouse 1 | Mouse | Mouse 3 | Mouse 4 | Mouse 5 | Mouse 6 |
| :--- | :--- | :--- | :--- | :--- | :--- | :--- |
| Gene 1 | $\mathbf{1 0}$ | $\mathbf{1 1}$ | 8 | 3 | $\mathbf{2}$ | $\mathbf{1}$ |
| Gene 2 | 6 | 4 | 5 | 3 | $\mathbf{2} .8$ | $\mathbf{1}$ |



A unit vector along PC1 is an Eigenvector for PC1. $\mathrm{SSD}=\operatorname{Max} \sum_{i} c_{i}^{2} \quad$ Eigenvalue for PC1 $\sqrt{S S D}$ Singular value for PC1

SSD: Sum of squares od distances


## Principal Component Analysis

$$
\begin{array}{ll}
\frac{S S D_{P C 1}}{n-1} & \text { variation for PC1 } \\
\frac{S S D_{P C 2}}{n-1} & \text { variation for PC2 }
\end{array}
$$





For example if: $\frac{S S D_{P C 1}}{n-1}=16, \quad \frac{S S D_{P C 2}}{n-1}=2 \quad \operatorname{Var}(P C 1)+\operatorname{Var}(P C 2)=18$,

PC1 accounts for $16 / 18=89 \%$ of variations (information) around PC's .

## Dimensionality Reduction

Singular Value Decomposition (SVD)

$$
A_{[m n]}=U_{[m r]} \Sigma_{[r r]} V_{[n r]}^{\top}
$$

m : number of rows n: number of columns


A: Input data
$U$ : The left-singular vectors of $A$ are a set of orthonormal eigenvectors of $A A^{T}$.
$V$ : The right-singular vectors of $A$ are a set of orthonormal eigenvectors of $A^{T} A$.
$\Sigma$ : Singular values
The non-zero singular values of $A$ (found on the diagonal entries of $\Sigma$ ) are the square roots of the non-zero eigenvalues of both $\mathrm{AA}^{\mathrm{T}}$ and $\mathrm{A}^{\mathrm{T}} \mathrm{A}$.


## Dimensionality Reduction

It is always possible to decompose a real matrix $A$ into $A=U \Sigma V^{\top}$, where
$\mathbf{U}, \boldsymbol{\Sigma}, \mathrm{V}$ : unique (decomposition is unique)
$\mathbf{U}, \mathbf{V}$ : orthonormal ( $\mathbf{U}^{\mathbf{T}} \mathbf{U}=\mathbf{I} ; \mathbf{V}^{\mathbf{T}} \mathbf{V}=\mathbf{I}$ )
$\mathbf{\Sigma}$ : diagonal
Entries are (singular values) are positive ( $\left.\sigma_{1} \geq \sigma_{2} \geq \ldots \sigma_{r} \geq 0\right)$.

## Example:

Netflix users ranking the movies


## Dimensionality Reduction

What do we learn from SVD decomposition?


The first four users strongly correspond to SciFi - concept, The last three users heavily correspond to Romance - concept,

U: "user-to-concept" similarity matrix
V: "movie-to-concept" similarity matrix

## Principal Component Analysis



## PCA for Visualization

Example 1: Reduction of the number of features in Iris-problem from 4 to 2:

## Standardization

|  | sepal length | sepal width | petal length | petal width |
| :--- | ---: | ---: | ---: | ---: |
| $\mathbf{0}$ | 5.1 | 3.5 | 1.4 | 0.2 |
| $\mathbf{1}$ | 4.9 | 3.0 | 1.4 | 0.2 |
| $\mathbf{2}$ | 4.7 | 3.2 | 1.3 | 0.2 |
| $\mathbf{3}$ | 4.6 | 3.1 | 1.5 | 0.2 |
| $\mathbf{4}$ | 5.0 | 3.6 | 1.4 | 0.2 |



## PCA

|  | sepal length | sepal width | petal length | petal width | PCA (2 components) |  | principal component 1 | princial component 2 |
| :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| 0 | -0.900681 | 1.032057 | -1.341272 | -1.312977 |  | 0 | -2.264542 | 0.505704 |
| 1 | -1.143017 | -0.124958 | -1.341272 | -1.312977 |  | 1 | -2.086426 | -0.655405 |
| 2 | -1.385353 | 0.337848 | -1.398138 | -1.312977 |  | 2 | -2.367950 | -0.318477 |
| 3 | -1.506521 | 0.106445 | -1.284407 | -1.312977 |  | 3 | -2.304197 | -0.575368 |
| 4 | -1.021849 | 1.263460 | -1.341272 | -1.312977 |  | 4 | -2.388777 | 0.674767 |

## Concatenating

|  | principal component 1 | principal component 2 |
| :--- | ---: | ---: |
| $\mathbf{0}$ | -2.264542 | 0.505704 |
| $\mathbf{1}$ | -2.086426 | -0.655405 |
| 2 | -2.367950 | -0.318477 |
| 3 | -2.304197 | -0.575368 |
| 4 | -2.388777 | 0.674767 |


|  |  | target |
| :---: | ---: | ---: |
| 0 | Iris-setosa |  |
| $\mathbf{1}$ | Iris-setosa |  |
| 2 | Iris-setosa |  |
| $\mathbf{3}$ | Iris-setosa |  |
| $\mathbf{4}$ | Iris-setosa |  |

df[['target']]


```
1#https://towardsdatascience.com/pca-using-python-scikit-Learn-e653f8989e60
    2#from sklearn.datasets import fetch_mldata
    3#mnist = fetch_mldata('MNIST original')
    4import sys
    5#================================================ PCA for Data Visualization
    6#=================================================== import data
    7 print(' ============================================== 1')
    8import pandas as pd
    9url = "https://archive.ics.uci.edu/ml/machine-learning-databases/iris/iris.data"
10# Load dataset into Pandas DataFrame
11df = pd.read_csv(url, names=['sepal length','sepal width','petal length','petal width','target'])
12#df = pd.read_csv(url, names=['sepal length','sepal width','target'])
13
14 print ('df = ', df)
15 print(' ============================================= 1')
16#===================================================== import data
17#================================================ set x and y and Standardize
18print(' =============================================== 2')
19 from sklearn.preprocessing import StandardScaler
20features = ['sepal length', 'sepal width', 'petal length', 'petal width']
21# Separating out the features
22x = df.loc[:, features].values
23# Separating out the target
24y = df.loc[:,['target']].values
25# Standardizing the features
26x = StandardScaler().fit_transform(x)
27#print ('y = ', y)
28#print ('x = ', x
29print ('y.shape = ', y.shape)
30print ('x.shape = ', x.shape)
31 print(' =============================================== 2')
32#================================================= set }X\mathrm{ and }y\mathrm{ and Standardize
33
34#=============================================================== Principal Component Analysis 1
35
36print(' =============================================== 3')
3 7 \text { from sklearn.decomposition import PCA}
38pca = PCA(n_components=2)
39principalComponents = pca.fit_transform(x)
40print('pca.explained_variance_ratio_ = ', pca.explained_variance_ratio_ )
```

```
41principalDf = pd.DataFrame(data = principalComponents
42 , columns = ['principal component 1', 'principal component 2'])
43#print('principalComponents = ',principalComponents)
44 print ('principalComponents.shape = ', principalComponents.shape)
45 print ('principalDf.shape = ', principalDf.shape)
46
47#print ('principalComponents = ', principalComponents)
48print ('principalDf.head(3) = ', principalDf.head(3))
4 9
50 print(' ============================================== 3')
51
52#=|=|=|=|=|=|=|=|=================|=|=|=========================== Principal Component Analysis 1
53
54#================================================================== Principal Component Analysis 2
55'''
56print(' =============================================== 4')
57# scikit-learn choose the minimum number of principal components such that 95% of the variance is retained.
58 from sklearn.decomposition import PCA
59pca = PCA(0.98)
60principalComponents = pca.fit transform(x)
61n_dim = principalComponents[1].shape
62print('pca.explained_variance_ratio_ = ', pca.explained_variance_ratio_ )
63Feature_size = int(principalComponents.size/y.size)
64print('Feature_size = ', Feature_size)
6 5
66if (Feature_size==1):
6 7 ~ c o l u m n s 0 ~ = ~ [ ' p r i n c i p a l ~ c o m p o n e n t ~ 1 ' ] ~
68if (Feature_size==2):
69 columns\overline{0}=['principal component 1', 'principal component 2']
70if (Feature_size==3):
71 columns0 = ['principal component 1', 'principal component 2', 'principal component 3']
72if (Feature_size==4):
73 columns\overline{0}= ['principal component 1', 'principal component 2', 'principal component 3', 'principal component 4']
74
75 principalDf = pd.DataFrame(data = principalComponents
76 , columns = columns0)
77#print('principalComponents = ',principalComponents)
78print ('principalComponents.shape = ', principalComponents.shape)
79print ('principalDf.shape = ', principalDf.shape)
```

```
81#print ('principalComponents = ', principalComponents)
82print ('principalDf.head(3) = ', principalDf.head(3))
83print('principalComponents.shape = ', len(principalDf.columns))
84print('=========================================== 4')
85'''
86#
88#=========================================== Concatenating along axis = 1 (column)
89print(' ======================================= 5')
90 # combine reduced features and targets (3 columns: 2 reduced features + 1 taget)
91finalDf = pd.concat([principalDf, df[['target']]], axis = 1)
92#print('finalDf = ', finalDf)
93print('finalDf.shape = ', finalDf.shape)
94print(' ======================================== 5')
```



```
96#====#==================================== Visualize 2D Projection
97import matplotlib.pyplot as plt
98fig = plt.figure(figsize = (8,8))
99ax = fig.add_subplot(1,1,1)
100ax.set_xlabel('Principal Component 1', fontsize = 15)
101ax.set_ylabel('Principal Component 2', fontsize = 15)
102ax.set_title('2 component PCA', fontsize = 20)
103targets = ['Iris-setosa', 'Iris-versicolor', 'Iris-virginica']
104colors = ['r', 'g', 'b']
105 for target, color in zip(targets, colors):
106 indicesToKeep = finalDf['target'] == target
107 ax.scatter(finalDf.loc[indicesToKeep, 'principal component 1']
108 , finalDf.loc[indicesToKeep, 'principal component 2']
109 , c = color
110 , s = 50)
111ax.legend(targets)
112ax.grid()
113#================================== Visualize 2D Projection
114explained_var = pca.explained_variance_ratio_
115 print('explained_var = ', explained_var)
116
1 1 7
```

