

CSCI567 Machine Learning (Spring 2021)

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Outline

- 1 Review of last lecture
- 2 Principal Component Analysis (PCA)

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Bayes optimal classifier

Suppose (\mathbf{x}, y) is drawn from a joint distribution p . The **Bayes optimal classifier** is

$$f^*(\mathbf{x}) = \operatorname{argmax}_{c \in [\mathcal{C}]} p(c \mid \mathbf{x})$$

i.e. predict the class with the largest conditional probability.

p is of course unknown, but we can estimate it, which is *exactly a density estimation problem!*

A “naive” assumption

Naive Bayes assumption:

conditioning on a label, features are independent, which means

$$p(\mathbf{x} \mid y = c) = \prod_{d=1}^D p(x_d \mid y = c)$$

Now for each d and c we have a simple **1D density estimation problem!**

Is this a reasonable assumption? Sometimes yes, e.g.

- use $x = (\text{Height}, \text{Vocabulary})$ to predict $y = \text{Age}$
- Height and Vocabulary are dependent
- but **condition on Age, they are independent!**

More often this assumption is **unrealistic and “naive”**, but still Naive Bayes can work very well even if the assumption is wrong.

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- 1 Review of last lecture
- 2 Principal Component Analysis (PCA)
 - PCA
 - Kernel PCA

Dimensionality reduction

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There are many approaches, we focus on a linear method:

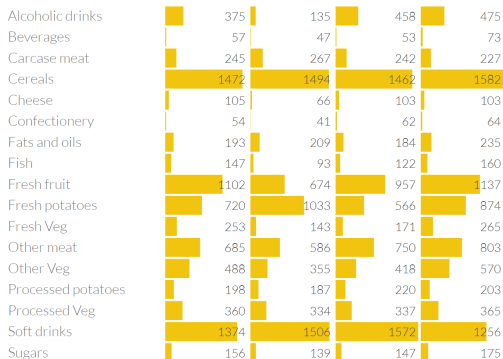
Principal Component Analysis (PCA)

Example

picture from here

Consider the following dataset:

- 17 features, each represents the average consumption of some food

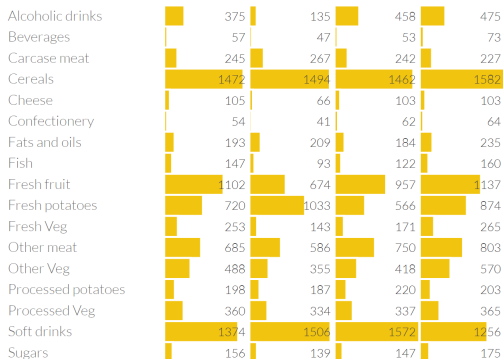


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Alcoholic drinks	375	135	458	475
Beverages	57	47	53	73
Carcase meat	245	267	242	227
Cereals	1472	1494	1462	1582
Cheese	105	66	103	103
Confectionery	54	41	62	64
Fats and oils	193	209	184	235
Fish	147	93	122	160
Fresh fruit	1102	674	957	1137
Fresh potatoes	720	1033	566	874
Fresh Veg	253	143	171	265
Other meat	685	586	750	803
Other Veg	488	355	418	570
Processed potatoes	198	187	220	203
Processed Veg	360	334	337	365
Soft drinks	1374	1506	1572	1256
Sugars	156	139	147	175

What can you tell?

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Hard to say anything looking at all these 17 features.

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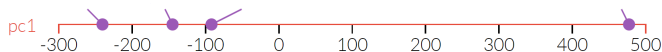
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PCA can help us! Plot along the **first principal component** of this dataset:

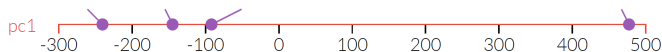


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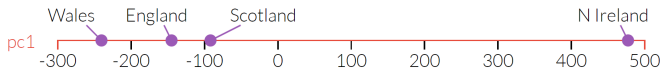
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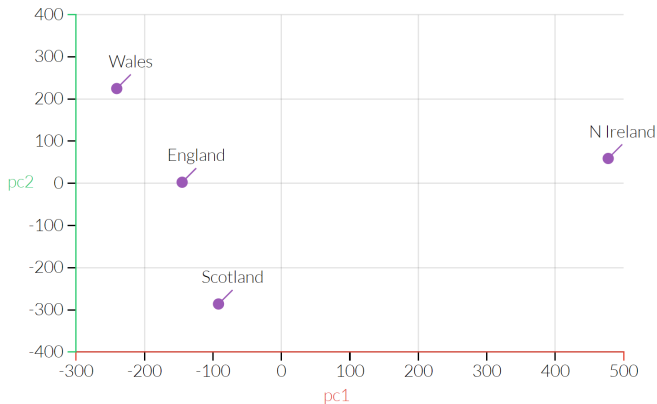
Now one data point is clearly different from the rest!

That turns out to be data from **Northern Ireland**, *the only country not on the island of Great Britain out of the 4 samples*.

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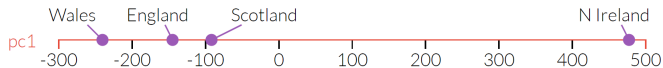
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PCA can find the **second (and more) principal component** of the data too:



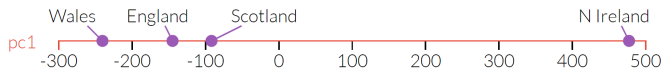
High level idea

How does PCA find these principal components (PC)?



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The first PC is in fact **the direction with the most variance**, i.e. the direction where the data is most spread out.

Finding the first PC

More formally, we want to find a direction $\boldsymbol{v} \in \mathbb{R}^D$ with $\|\boldsymbol{v}\|_2 = 1$, so that the **projection of the dataset on this direction has the most variance**,

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- if we **pre-center the data**, i.e. let $\mathbf{x}'_n = \mathbf{x}_n - \frac{1}{N} \sum_m \mathbf{x}_m$, then the objective simply becomes

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- we will simply assume $\{\mathbf{x}_n\}$ is centered (to avoid notation \mathbf{x}'_n)

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With $\mathbf{X} \in \mathbb{R}^{N \times D}$ being the data matrix, we want

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Conclusion: the first PC is the top eigenvector of the covariance matrix

Finding the other PCs

If v_1 is the first PC, then the **second PC** is found via

$$\max_{v_2: \|v_2\|_2=1, v_1^T v_2=0} v_2^T (X^T X) v_2$$

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Conclusion: the d -th principal component is the d -th eigenvector (sorted by the eigenvalue from largest to smallest).

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Step 3 Construct the new compressed dataset $\mathbf{XV} \in \mathbb{R}^{N \times p}$

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For **visualization**, also often pick $p = 1$ or $p = 2$.

Another visualization example

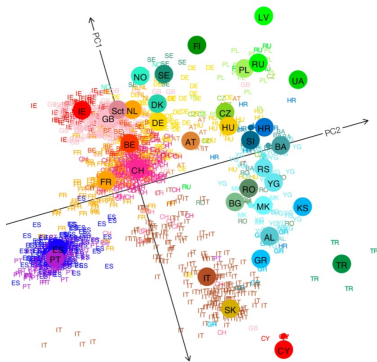
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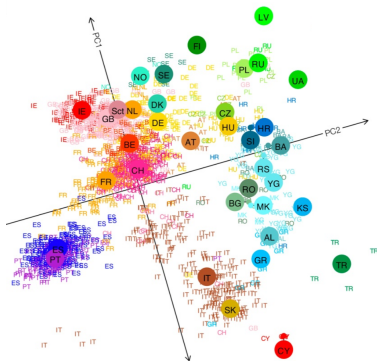
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Another visualization example

A famous study of **genetic map**

- dataset: **genomes of 1,387 Europeans**
- First 2 PCs shown below; *looks remarkably like the geographic map*



Does PCA always work?

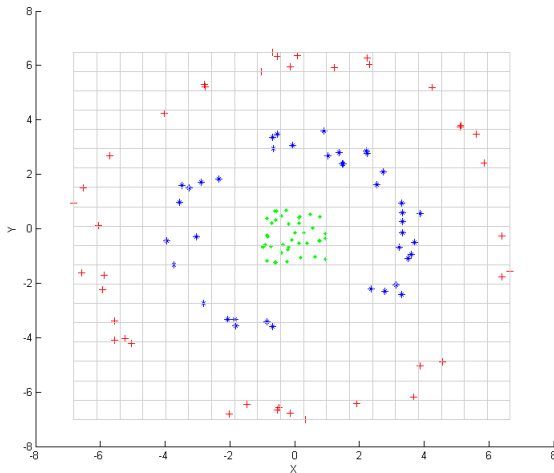
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PCA is a **linear method** (recall the new dataset is XV), it does not do much when **every direction has similar variance**.



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How to implement KPCA efficiently without actually working in \mathbb{R}^M ?

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Conclusion: KPCA is just finding top eigenvectors of the Gram matrix

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No. Recall we want $v = \Phi^T \alpha$ to have unit L2 norm, so

$$v^T v = \alpha^T \Phi \Phi^T \alpha = \lambda \|\alpha\|_2^2 = 1$$

In other words, we in fact need to **scale α so that its L2 norm is $1/\sqrt{\lambda}$** , where λ it's the corresponding eigenvalue.

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KPCA

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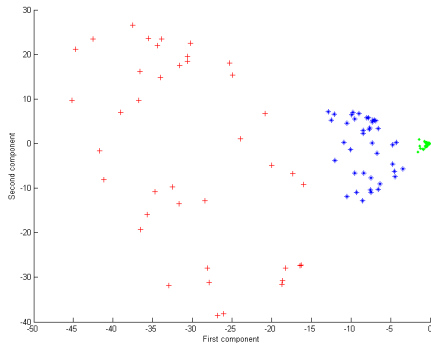
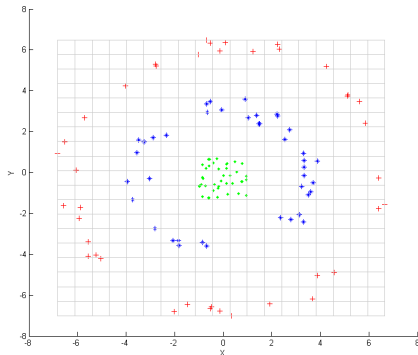
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Step 3 Construct the new dataset $(\Phi - \mathbf{E}\Phi)(\Phi - \mathbf{E}\Phi)^T \mathbf{A} = \bar{\mathbf{K}} \mathbf{A}$

Example

picture from Wikipedia

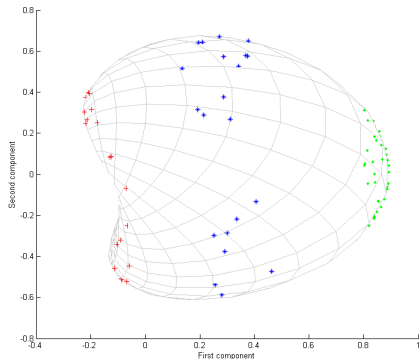
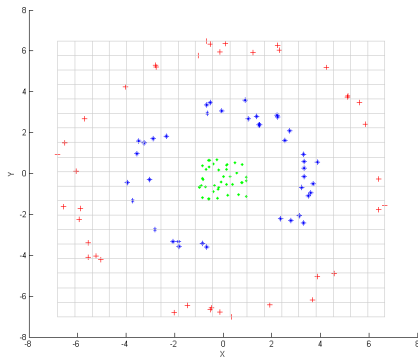
Applying kernel $k(\mathbf{x}, \mathbf{x}') = (\mathbf{x}^T \mathbf{x}' + 1)^2$:



Example

picture from Wikipedia

Applying Gaussian kernel $k(\mathbf{x}, \mathbf{x}') = \exp\left(\frac{-\|\mathbf{x} - \mathbf{x}'\|^2}{2\sigma^2}\right)$:



Denoising via PCA

Original data



Data corrupted with Gaussian noise



Result after linear PCA



Result after kernel PCA, Gaussian kernel

