

CSCI567 Machine Learning (Fall 2024)

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U of Southern California

November 1, 2024

Outline

- 1 Density estimation
- 2 Naive Bayes
- 3 Principal Component Analysis (PCA)

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 - Parametric methods
 - Nonparametric methods
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- 3 Principal Component Analysis (PCA)

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Useful for many downstream applications

- we have seen clustering already, will see more today
- these applications also *provide a way to measure quality of the density estimator*

Parametric methods: generative models

Parametric estimation assumes a generative model parametrized by θ :

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Examples:

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- **Multinomial**: a discrete variable with values in $\{1, 2, \dots, K\}$ s.t.

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where θ is a distribution over K elements.

Size of θ is independent of the training set size, so it's **parametric**.

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Again, we apply **MLE** to learn the parameters θ :

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For some other cases this admits a **simple closed-form solution** (e.g. multinomial).

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The solution is simply

$$\theta_k = \frac{z_k}{N} \propto z_k,$$

i.e. **the fraction of examples with value k** . (See HW4 Q1.1)

Nonparametric methods

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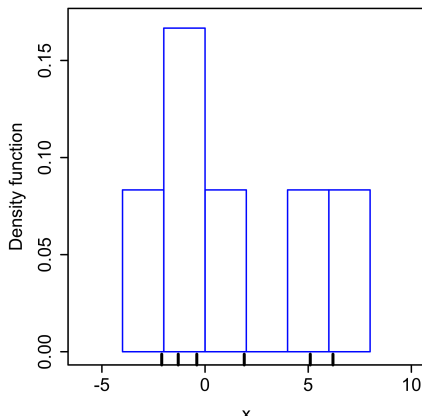
Yes, **kernel density estimation (KDE)** is a common approach

- here “kernel” means something different from what we have seen for “kernel function” (in fact it refers to several different things in ML)
- the approach is **nonparametric**: it keeps the entire training set
- we focus on the one-dimensional (continuous) case

High level idea

picture from Wikipedia

Construct something similar to a **histogram**:

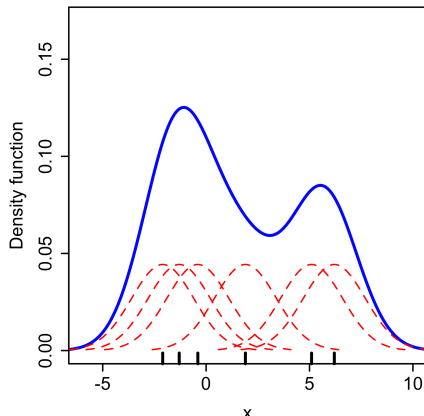
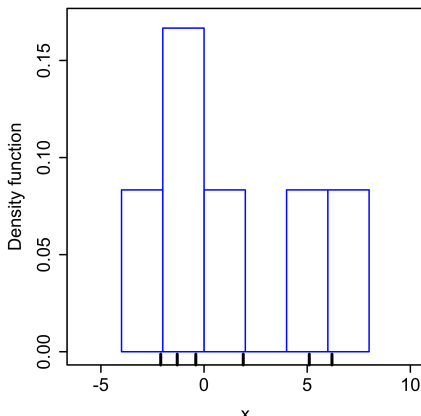


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- for each data point, create a “bump” (via a Kernel)

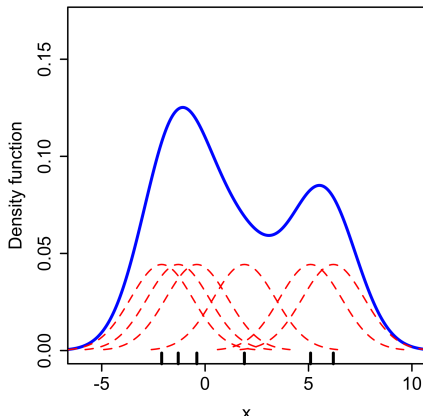
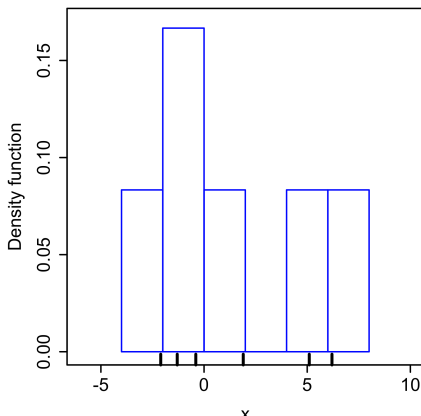


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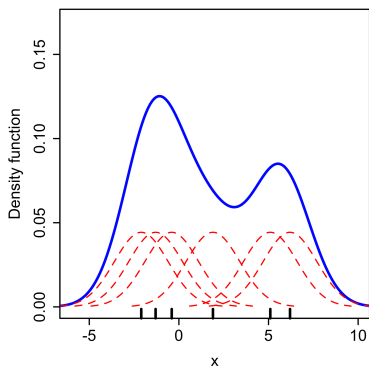
- for each data point, create a “bump” (via a Kernel)
- sum up or average all the bumps



Kernel

KDE with a kernel $K: \mathbb{R} \rightarrow \mathbb{R}$:

$$p(x) = \frac{1}{N} \sum_{n=1}^N K(x - x_n)$$

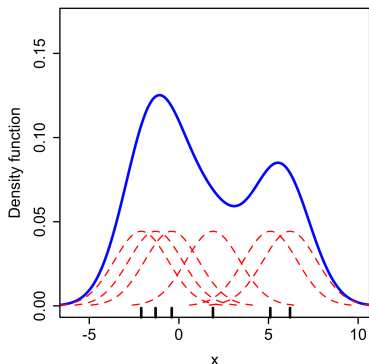


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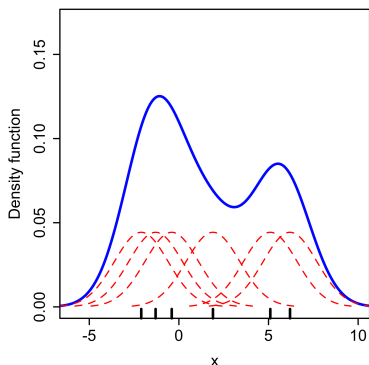
KDE with **a kernel** $K: \mathbb{R} \rightarrow \mathbb{R}$:

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Kernel needs to satisfy:

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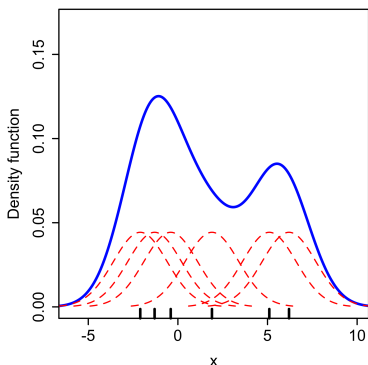
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Kernel needs to satisfy:

- **symmetry**: $K(u) = K(-u)$
- $\int_{-\infty}^{\infty} K(u) du = 1$, makes sure p is a density function.

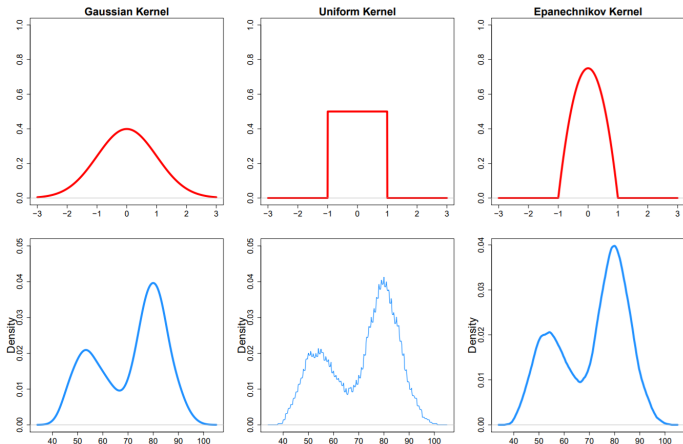


Different kernels $K(u)$

$$\frac{1}{\sqrt{2\pi}} e^{-\frac{u^2}{2}}$$

$$\frac{1}{2} \mathbb{I}[|u| \leq 1]$$

$$\frac{3}{4} \max\{1 - x^2, 0\}$$



Bandwidth

If $K(u)$ is a kernel, then for any $h > 0$

$$K_h(u) \triangleq \frac{1}{h} K\left(\frac{u}{h}\right) \quad (\text{stretching the kernel})$$

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$$p(x) = \frac{1}{N} \sum_{n=1}^N K_h(x - x_n) = \frac{1}{Nh} \sum_{n=1}^N K\left(\frac{x - x_n}{h}\right)$$

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- x_n controls the center of each bump
- h controls the width/variance of the bumps

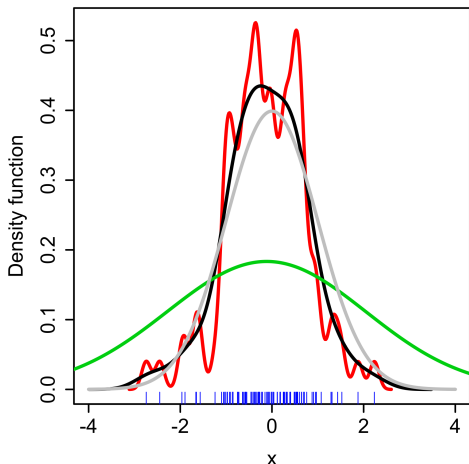
Effect of bandwidth

picture from Wikipedia

Larger h means larger variance and also smoother density

Gray curve is ground-truth

- Red: $h = 0.05$
- Black: $h = 0.337$
- Green: $h = 2$



Bandwidth selection

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- one can also do **cross-validation** based on downstream applications

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- 1 Density estimation
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 - Setup and assumption
 - Estimation and prediction
 - Connection to logistic regression
- 3 Principal Component Analysis (PCA)

Naive Bayes

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- a simple yet surprisingly powerful **classification** algorithm
- **density estimation** is one important part of the algorithm

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

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This is *not a 1D problem* in general.

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

Example: discrete features

Height: $\leq 3'$, $3'-4'$, $4'-5'$, $5'-6'$, $\geq 6'$

Vocabulary: $\leq 5K$, $5K-10K$, $10K-15K$, $15K-20K$, $\geq 20K$

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For each possible value k of a discrete feature d ,

$$p(x_d = k \mid y = c) = \frac{|\{n : x_{nd} = k, y_n = c\}|}{|\{n : y_n = c\}|}$$

Continuous features

If the feature is continuous, we can do

- **parametric estimation**, e.g. via a Gaussian

$$p(x_d = x \mid y = c) = \frac{1}{\sqrt{2\pi}\sigma_{cd}} \exp\left(-\frac{(x - \mu_{cd})^2}{2\sigma_{cd}^2}\right)$$

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- or **nonparametric estimation**, e.g. via a Kernel K and bandwidth h :

$$p(x_d = x \mid y = c) = \frac{1}{|\{n : y_n = c\}|} \sum_{n:y_n=c} K_h(x - x_{nd})$$

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Examples

For **discrete features**, plugging in previous MLE estimations gives

$$\begin{aligned} & \operatorname{argmax}_{c \in [C]} p(y = c \mid \mathbf{x}) \\ &= \operatorname{argmax}_{c \in [C]} \left(\ln p(y = c) + \sum_{d=1}^D \ln p(x_d \mid y = c) \right) \\ &= \operatorname{argmax}_{c \in [C]} \left(\ln |\{n : y_n = c\}| + \sum_{d=1}^D \ln \frac{|\{n : x_{nd} = x_d, y_n = c\}|}{|\{n : y_n = c\}|} \right) \end{aligned}$$

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For **continuous features** with a Gaussian model,

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which is *quadratic* in the feature \mathbf{x} .

What naive Bayes is learning?

Observe again for the case of continuous features with a Gaussian model, if we **fix the variance for each feature to be σ** (i.e. not a parameter of the model any more), then the prediction becomes

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where we denote $w_{c0} = \ln |\{n : y_n = c\}| - \sum_{d=1}^D \frac{\mu_{cd}^2}{2\sigma^2}$ and $w_{cd} = \frac{\mu_{cd}}{\sigma^2}$.

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So what is different then? They **learn the parameters in different ways**:

- both via MLE, **one on $p(y = c \mid \mathbf{x})$** , **the other on $p(\mathbf{x}, y)$**
- solutions are different: **logistic regression has no closed-form**, **naive Bayes admits a simple closed-form**

Generative model v.s discriminative model

	Discriminative model	Generative model
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Remark		more flexible, can generate data after learning

Outline

- 1 Density estimation
- 2 Naive Bayes
- 3 Principal Component Analysis (PCA)
 - PCA
 - Kernel PCA

Dimensionality reduction

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

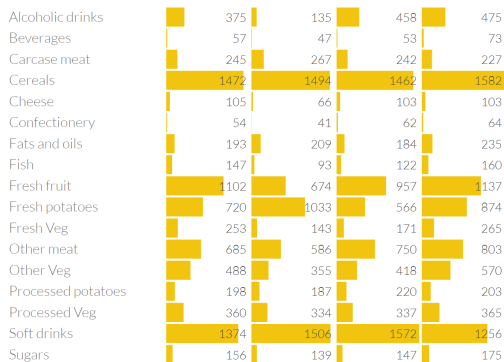
Principal Component Analysis (PCA)

Example

picture from here

Consider the following dataset:

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



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- 4 data points, each represents some country

Alcoholic drinks	375	135	458	475
Beverages	57	47	53	73
Carcass 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
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Hard to say anything looking at all these 17 features.

Example

picture from here

PCA can help us!

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PCA can help us! The **first principal component** of this dataset:

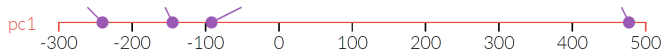


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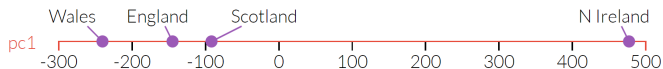
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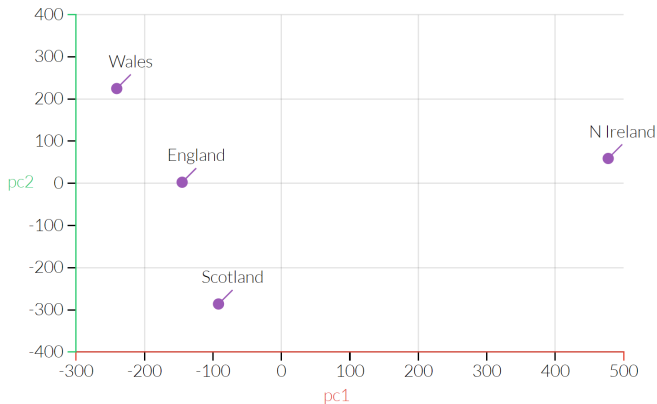
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That turns out to be data from **Northern Ireland**, *the only country not on the island of Great Britain out of the 4 samples.*

Example

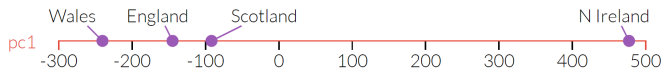
[picture from here](#)

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



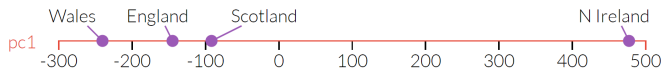
High level idea

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 $\mathbf{v} \in \mathbb{R}^D$ with $\|\mathbf{v}\|_2 = 1$, so that the **projection of the dataset on this direction has the most variance**,

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

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

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

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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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where $\lambda_1 \geq \dots \geq \lambda_N$ are sorted eigenvalues.

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

Another visualization example

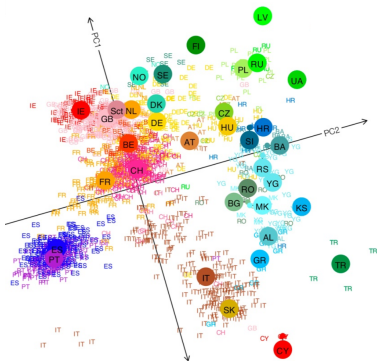
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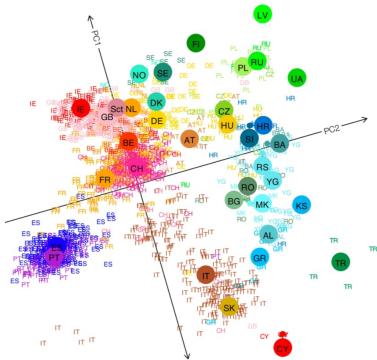
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Another visualization example

A famous study of **genetic map**

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Does PCA always work?

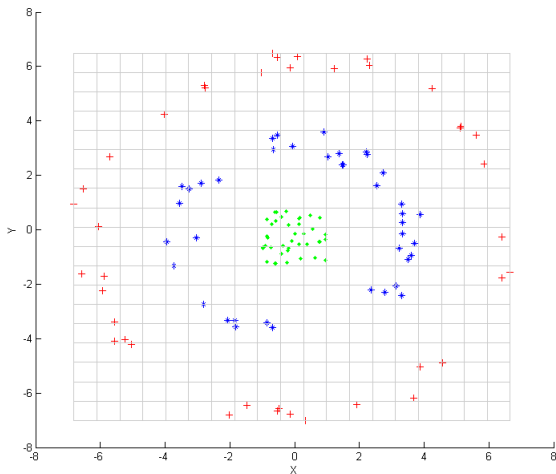
picture from Wikipedia

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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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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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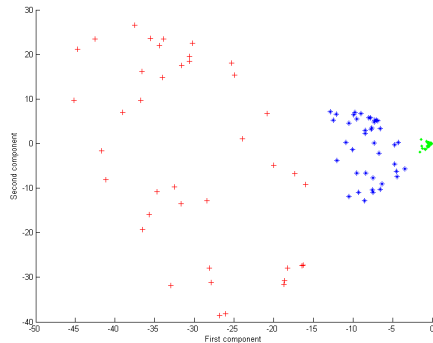
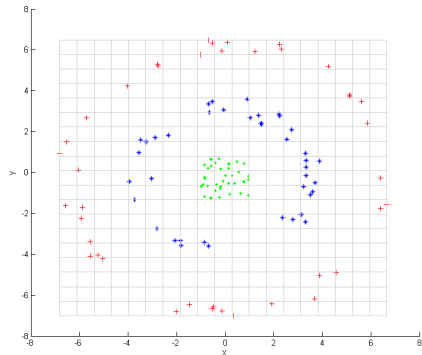
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Example

picture from Wikipedia

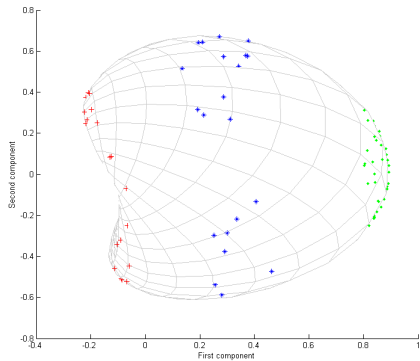
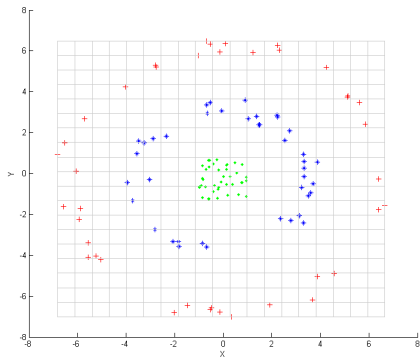
Applying kernel $k(\mathbf{x}, \mathbf{x}') = (\mathbf{x}^T \mathbf{x}' + 1)^2$:



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

