

# CSCI567 Machine Learning (Fall 2018)

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U of Southern California

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# Administration

HW3 solution is available, HW4 is due on Sunday (11/4)

Minor typo in P4 for the formula of multivariate Gaussian density, see Piazza pinned post as well as the updated P4.pdf.

- the comment in gmm.py:

$$p = e^{(-0.5(x-\text{mean})*(\text{inv}(\text{variance}))*(\text{x-mean})'/\text{sqrt}(c))}$$

should be

$$p = e^{(-0.5(x-\text{mean})*(\text{inv}(\text{variance}))*(\text{x-mean})')/\text{sqrt}(c)}$$

# Outline

- 1 Review of last lecture
- 2 (Hidden) Markov models
- 3 Principal Component Analysis (PCA)

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# General EM algorithm

**Step 0** Initialize  $\theta^{(1)}$ ,  $t = 1$

**Step 1 (E-Step)** update the posterior of latent variables

$$q_n^{(t)}(\cdot) = p(\cdot \mid \mathbf{x}_n ; \theta^{(t)})$$

and obtain **Expectation** of complete likelihood

$$Q(\theta ; \theta^{(t)}) = \sum_{n=1}^N \mathbb{E}_{z_n \sim q_n^{(t)}} [\ln p(\mathbf{x}_n, z_n ; \theta)]$$

**Step 2 (M-Step)** update the model parameter via **Maximization**

$$\theta^{(t+1)} \leftarrow \underset{\theta}{\operatorname{argmax}} Q(\theta ; \theta^{(t)})$$

**Step 3**  $t \leftarrow t + 1$  and return to Step 1 if not converged

# Applying EM to learn GMMs

EM for clustering:

**Step 0** Initialize  $\omega_k, \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k$  for each  $k \in [K]$

**Step 1 (E-Step)** **update the “soft assignment”** (fixing parameters)

$$\gamma_{nk} = p(z_n = k \mid \mathbf{x}_n) \propto \omega_k N(\mathbf{x}_n \mid \boldsymbol{\mu}_k, \boldsymbol{\Sigma}_k)$$

**Step 2 (M-Step)** **update the model parameter** (fixing assignments)

$$\omega_k = \frac{\sum_n \gamma_{nk}}{N} \quad \boldsymbol{\mu}_k = \frac{\sum_n \gamma_{nk} \mathbf{x}_n}{\sum_n \gamma_{nk}}$$

$$\boldsymbol{\Sigma}_k = \frac{1}{\sum_n \gamma_{nk}} \sum_n \gamma_{nk} (\mathbf{x}_n - \boldsymbol{\mu}_k)(\mathbf{x}_n - \boldsymbol{\mu}_k)^T$$

**Step 3** return to Step 1 if not converged

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- 1 Review of last lecture
- 2 (Hidden) Markov models
  - Markov chain
  - Hidden Markov Model
  - Inferring HMMs
  - Learning HMMs
- 3 Principal Component Analysis (PCA)

# Markov Models

Markov models are powerful probabilistic tools to analyze **sequential data**:

- text or speech data
- stock market data
- gene data
- ...



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$$P(Z_{t+1} \mid Z_{1:t}) = P(Z_{t+1} \mid Z_t) \quad (\text{Markov property})$$

i.e. *the current state only depends on the most recent state* (notation  $Z_{1:t}$  denotes the sequence  $Z_1, \dots, Z_t$ ).

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- $P(Z_1 = s) = \pi_s$
- $(\{\pi_s\}, \{a_{s,s'}\}) = (\boldsymbol{\pi}, \mathbf{A})$  are **parameters of the model**

# Examples

- Example 1 (**Language model**)

States  $[S]$  represent a dictionary of words,

$$a_{\text{ice,cream}} = P(Z_{t+1} = \text{cream} \mid Z_t = \text{ice})$$

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- Example 2 (**Weather**)

States  $[S]$  represent weather at each day

$$a_{\text{sunny,rainy}} = P(Z_{t+1} = \text{rainy} \mid Z_t = \text{sunny})$$



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$$P(Z_{t+1} \mid Z_{1:t}) = P(Z_{t+1} \mid Z_t, Z_{t-1}) \quad (\text{second-order Markov})$$

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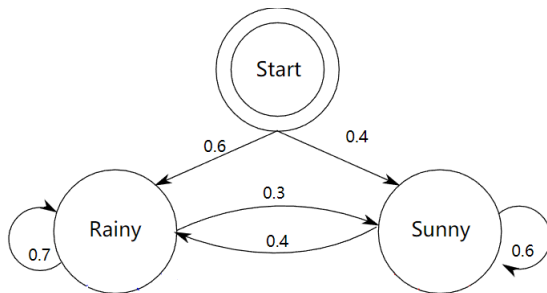
Learning higher order Markov chains is similar, but more expensive.

We only consider standard Markov chains.

# Graph Representation

picture from Wikipedia

It is intuitive to represent a Markov model as a **graph**



# Learning from examples

Now suppose we have observed  $N$  sequences of examples:

- $z_{1,1}, \dots, z_{1,T}$
- $\dots$
- $z_{n,1}, \dots, z_{n,T}$
- $\dots$
- $z_{N,1}, \dots, z_{N,T}$

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From these observations how do we *learn the model parameters*  $(\boldsymbol{\pi}, \mathbf{A})$ ?

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$$= \sum_s \mathbb{I}[z_1 = s] \ln \pi_s + \sum_{s, s'} \left( \sum_{t=2}^T \mathbb{I}[z_{t-1} = s, z_t = s'] \right) \ln a_{s, s'}$$



# Finding the MLE

So MLE is

$$\operatorname{argmax}_{\pi, A} \sum_s (\text{\#initial states with value } s) \ln \pi_s \\ + \sum_{s, s'} (\text{\#transitions from } s \text{ to } s') \ln a_{s, s'}$$

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We have seen this many times. The solution is:

$$\pi_s \propto \text{\#initial states with value } s \\ a_{s, s'} \propto \text{\#transitions from } s \text{ to } s'$$

## Example

Suppose we observed the following 2 sequences of length 5

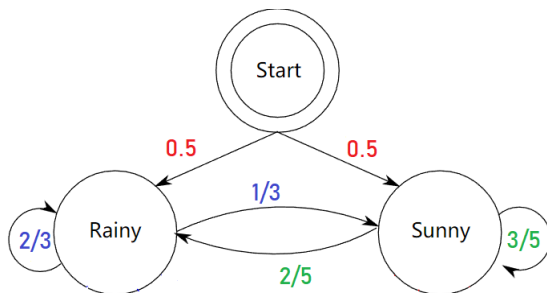
- sunny, sunny, rainy, rainy, rainy
- rainy, sunny, sunny, sunny, rainy

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- sunny, sunny, rainy, rainy, rainy
- rainy, sunny, sunny, sunny, rainy

**MLE is the following model**



## Markov Model with outcomes

Now suppose each state  $Z_t$  also “emits” some **outcome**  $X_t \in [O]$  based on the following model

$$P(X_t = o \mid Z_t = s) = b_{s,o} \quad (\text{emission probability})$$

independent of anything else.

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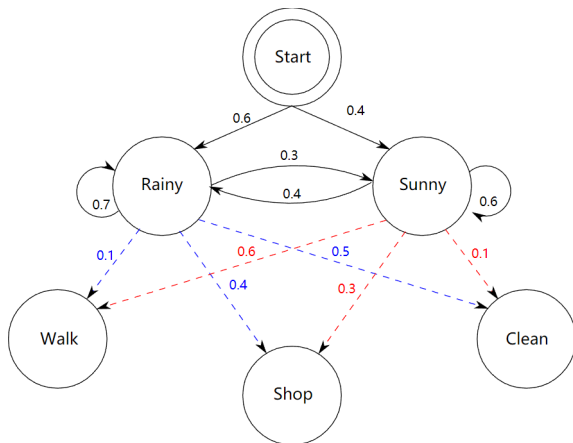
For example, in the language model,  $X_t$  is the speech signal for the underlying word  $Z_t$  (very useful for **speech recognition**).

Now the model parameters are  $(\{\pi_s\}, \{a_{s,s'}\}, \{b_{s,o}\}) = (\boldsymbol{\pi}, \mathbf{A}, \mathbf{B})$ .

## Another example

picture from Wikipedia

On each day, we also observe **Bob's activity: walk, shop, or clean**, which only depends on the weather of that day.





# Joint likelihood

The joint log-likelihood of a **state-outcome sequence**  $z_1, x_1, \dots, z_T, x_T$  is

$$\ln P(Z_{1:T} = z_{1:T}, X_{1:T} = x_{1:T})$$

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 & \hspace{15em} (\text{due to all the independence}) \\
 &= \ln \pi_{z_1} + \sum_{t=2}^T \ln a_{z_{t-1}, z_t} + \sum_{t=1}^T \ln b_{z_t, x_t}
 \end{aligned}$$

# Learning the model

If we observe  $N$  state-outcome sequences:  $z_{n,1}, x_{n,1}, \dots, z_{n,T}, x_{n,T}$  for  $n = 1, \dots, N$ , the MLE is again very simple (verify yourself):

$$\pi_s \propto \text{\#initial states with value } s$$

$$a_{s,s'} \propto \text{\#transitions from } s \text{ to } s'$$

$$b_{s,o} \propto \text{\#state-outcome pairs } (s, o)$$

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- first discuss how to **infer** when the model is known (key: **dynamic programming**)

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How to learn HMMs? **Roadmap:**

- first discuss how to **infer** when the model is known (key: **dynamic programming**)
- then discuss how to **learn** the model (key: **EM**)

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- **the state at some point, given an observation sequence**

$$P(Z_t = s \mid X_{1:T} = x_{1:T})$$

e.g. given Bob's activities for one week, how was the weather like on Wed?

# What can we infer for a known HMM?

Knowing the parameter of an HMM, we can infer

- **the transition at some point, given an observation sequence**

$$P(Z_t = s, Z_{t+1} = s' \mid X_{1:T} = x_{1:T})$$

e.g. given Bob's activities for one week, how was the weather like on Wed and Thu?

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Knowing the parameter of an HMM, we can infer

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$$P(Z_t = s, Z_{t+1} = s' \mid X_{1:T} = x_{1:T})$$

e.g. given Bob's activities for one week, how was the weather like on Wed and Thu?

- **most likely hidden states path, given an observation sequence**

$$\operatorname{argmax}_{z_{1:T}} P(Z_{1:T} = z_{1:T} \mid X_{1:T} = x_{1:T})$$

e.g. given Bob's activities for one week, what's the most likely weather for this week?



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- **forward messages**: for each  $s$  and  $t$

$$\alpha_s(t) = P(Z_t = s, X_{1:t} = x_{1:t})$$

- **backward messages**: for each  $s$  and  $t$

$$\beta_s(t) = P(X_{t+1:T} = x_{t+1:T} \mid Z_t = s)$$

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$$\alpha_s(t)$$

$$= P(Z_t = s, X_{1:t} = x_{1:t})$$

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 &= b_{s,x_t} \sum_{s'} a_{s',s} \alpha_{s'}(t-1) \quad (\text{recursive form!})
 \end{aligned}$$

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**Base case:**  $\alpha_s(1) = P(Z_1 = s, X_1 = x_1) = \pi_s b_{s,x_1}$

# Forward procedure

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For all  $s \in [S]$ , compute  $\alpha_s(1) = \pi_s b_{s,x_1}$ .

For  $t = 2, \dots, T$

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It takes  $O(S^2T)$  time and  $O(ST)$  space.

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**Base case:**  $\beta_s(T) = 1$

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This is true for any  $t$ ; a good way to check correctness of your code.

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Another example: the conditional probability of transition  $s$  to  $s'$  at time  $t$

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The **normalization constant** is in fact again  $P(X_{1:T} = x_{1:T})$

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Though can't use forward and backward messages directly to find the most likely path, it is **very similar to the forward procedure**.

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Though can't use forward and backward messages directly to find the most likely path, it is **very similar to the forward procedure**. Key: compute

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**the probability of the most likely path for time  $1 : t$  ending at state  $s$**

# Computing $\delta_s(t)$

Observe

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*Exactly the same as forward messages except replacing "sum" by "max"!*

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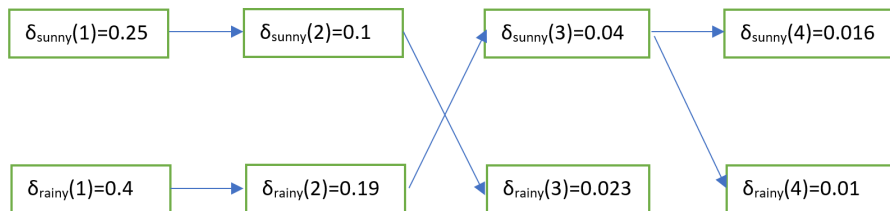
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For each  $t = T, \dots, 2$ : set  $z_{t-1}^* = \Delta_{z_t^*}(t)$ .

Output the most likely path  $z_1^*, \dots, z_T^*$ .

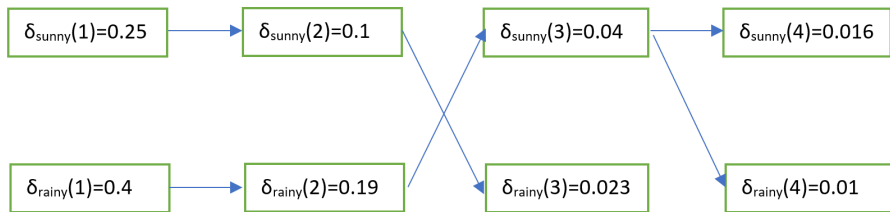
# Example

Arrows represent the “argmax”, i.e.  $\Delta_s(t)$ .



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The most likely path is **“rainy, rainy, sunny, sunny”**.

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Need to apply **EM** again! Known as the **Baum–Welch algorithm**.

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$$\begin{aligned} & \mathbb{E}_{z_{1:T} \sim q} [\ln(Z_{1:T} = z_{1:T}, X_{1:T} = x_{1:T})] \\ &= \mathbb{E}_{z_{1:T} \sim q} \left[ \ln \pi_{z_1} + \sum_{t=1}^{T-1} \ln a_{z_t, z_{t+1}} + \sum_{t=1}^T \ln b_{z_t, x_t} \right] \end{aligned}$$

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 &= \sum_s \gamma_s(1) \ln \pi_s + \sum_{t=1}^{T-1} \sum_{s, s'} \xi_{s, s'}(t) \ln a_{s, s'} + \sum_{t=1}^T \sum_s \gamma_s(t) \ln b_{s, x_t}
 \end{aligned}$$

We have discussed how to compute

$$\begin{aligned}
 \gamma_s(t) &= P(Z_t = s \mid X_{1:T} = x_{1:T}) \\
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The maximizer of complete log-likelihood is simply doing **weighted counting** (compared to the unweighted counting on Slide 20):

$$\pi_s \propto \sum_n \gamma_s^{(n)}(1) = \mathbb{E}_q [ \text{\#initial states with value } s ]$$

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**Step 3** Return to Step 1 if not converged

# Summary

Very important models: **Markov chains**, **hidden Markov models**

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Several algorithms:

- forward and backward procedures
- inferring HMMs based on forward and backward messages
- Viterbi algorithm
- Baum–Welch algorithm

# Outline

- 1 Review of last lecture
- 2 (Hidden) Markov models
- 3 Principal Component Analysis (PCA)
  - PCA
  - Kernel PCA

# Dimensionality reduction

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

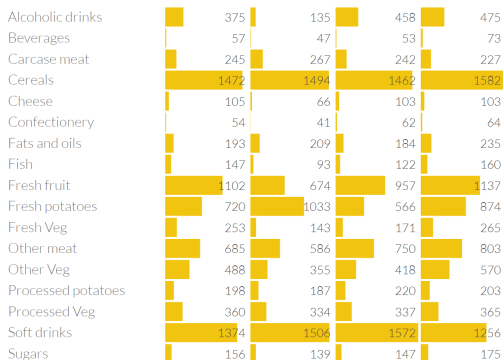
**Principal Component Analysis (PCA)**

# Example

picture from here

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



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Consider the following dataset:

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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	102	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
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Hard to say anything looking at all these 17 features.

# Example

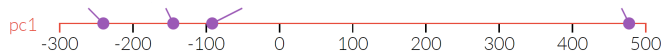
picture from here

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picture from here

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

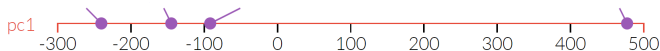


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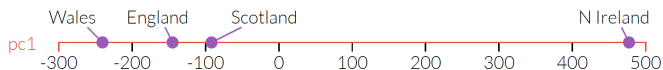
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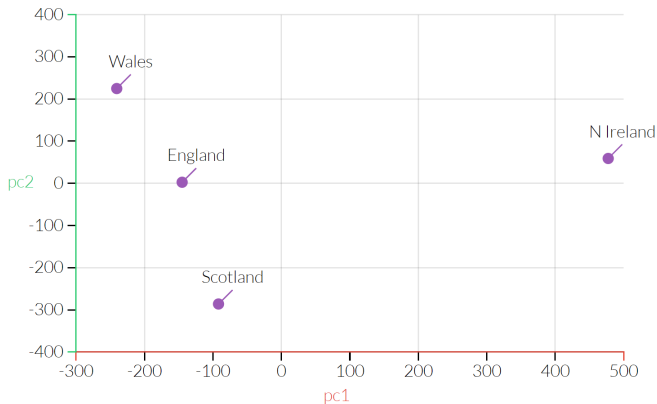
**Now one data point is clearly different from the rest!**

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

# Example

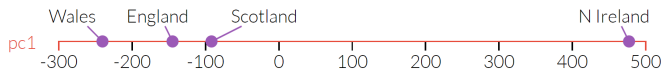
picture from here

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



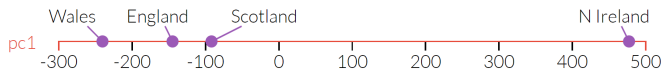
# High level idea

*How does PCA find these principal components (PC)?*



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This 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

## Finding the other PCs

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

## Another visualization example

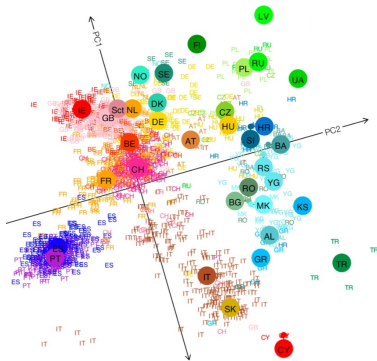
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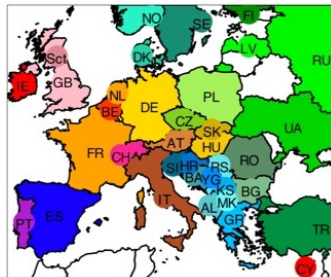
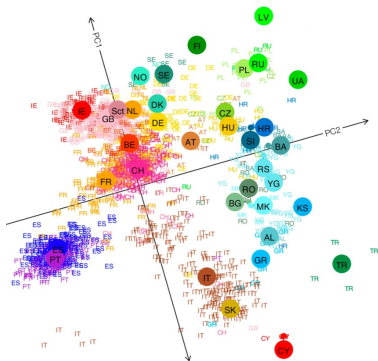
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## Another visualization example

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?

picture from Wikipedia

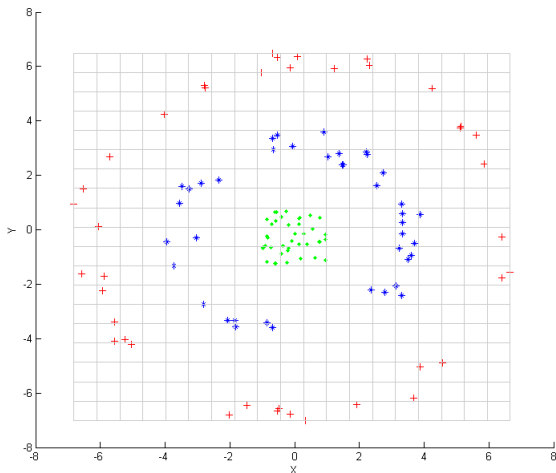
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PCA is a **linear method** (recall the new dataset is  $XV$ ), it does not do much when **every direction has similar variance**.



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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  $\alpha$  so that its L2 norm is  $1/\sqrt{\lambda}$** , where  $\lambda$  it's the corresponding eigenvalue.

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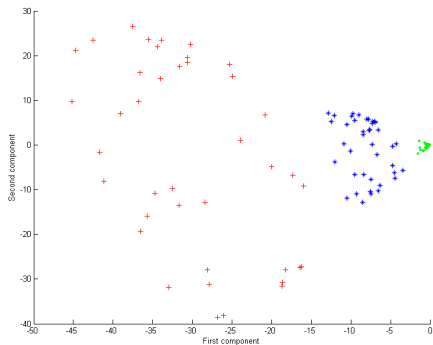
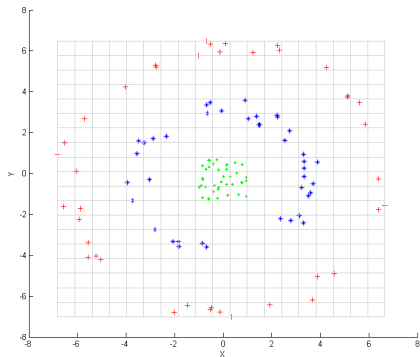
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**Step 3** Construct the new dataset  $(\Phi - \mathbf{E}\Phi)(\Phi - \mathbf{E}\Phi)^T \mathbf{A} = \bar{\mathbf{K}} \mathbf{A}$

# Example

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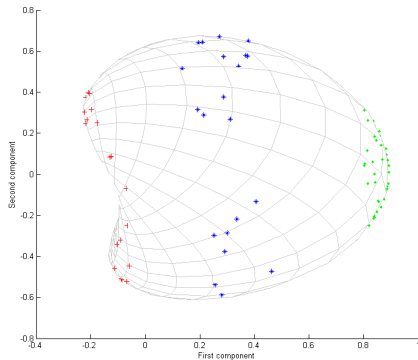
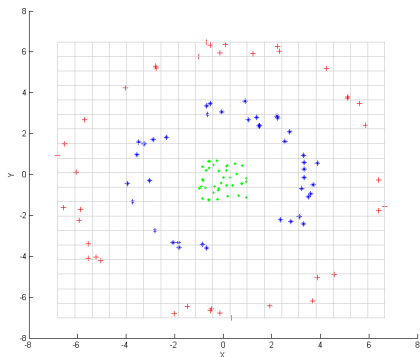
Applying kernel  $k(\mathbf{x}, \mathbf{x}') = (\mathbf{x}^T \mathbf{x}' + 1)^2$ :



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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

