

## Administration

Thank you for survey responses. Will email when digested.

Assignment 2 is out.

Remember tutorial sheets

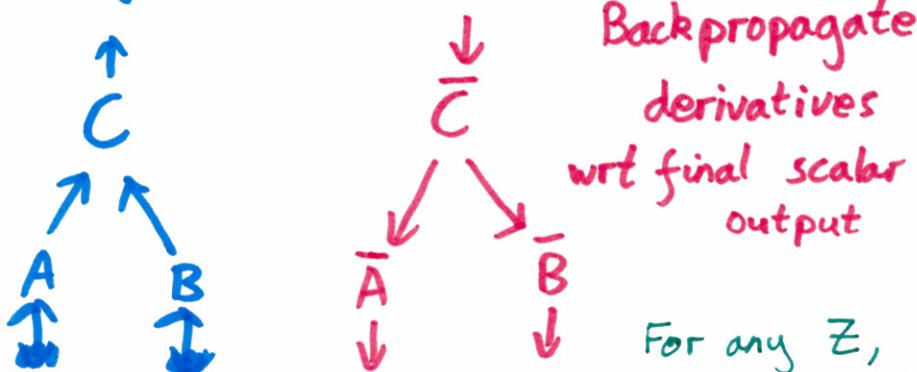
Ask — on the Hypothesis forum<sup>†</sup>  
— and you will receive \*

† Instructions on website

\* help, and answers if you have put effort in.

# Reverse mode differentiation

Piece of computation:



For any  $Z$ ,

$$\bar{Z}_{ij} = \frac{\partial \text{output}}{\partial Z_{ij}}$$

Use standard rules:

$$C = \cos A \Rightarrow \bar{A} = \bar{C} \odot \sin A$$

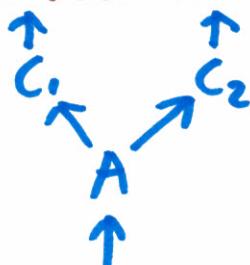
$$C = AB \Rightarrow \bar{A} = \bar{C}B^T, \bar{B} = A^T\bar{C}$$

$$C = A + B \Rightarrow \bar{A} = \bar{C}, \bar{B} = \bar{C}$$

$$C = A^T \Rightarrow \bar{A} = \bar{C}^T$$

...

Multiple children



$$\bar{A} = \bar{A}_1 + \bar{A}_2$$

$\bar{C}_1 \quad \bar{C}_2$

↓      ↓

Apply rules separately for children and add

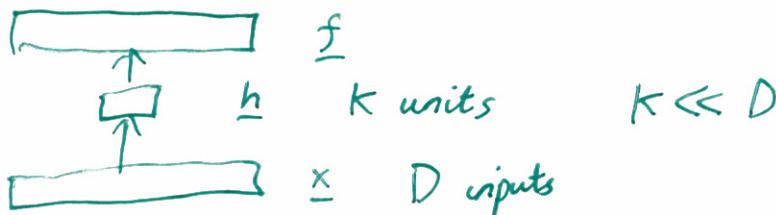
## Autoencoder



not useful

```
def autoencode(x):
    return x
    h = np.dot(I, x)
    return h
```

## Dimensionality Reduction



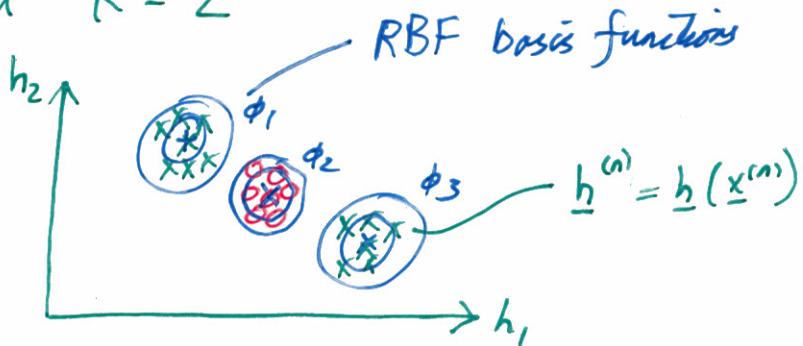
$$\underline{h} = g^{(1)}(\underline{w}^{(1)}\underline{x} + \underline{b}^{(1)})$$

$$\underline{f} = g^{(2)}(\underline{w}^{(2)}\underline{h} + \underline{b}^{(2)})$$

$\Rightarrow$  Use  $\underline{h}$  as inputs to other ML method.

## Visualization

Set  $K = 2$

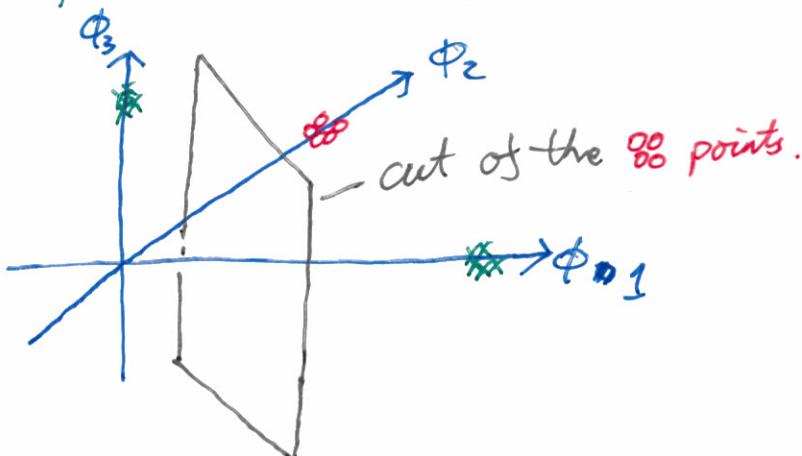


Use some labels  
to see if visualization  
makes sense..

○○ class 0

×× class 1

Or do classification in this space  
after learning mapping on unlabeled data.



## Sparse Autoencoders

Force most elements of  $h$  to be zero.

## Denoising Autoencoders

While training we mask out some of the inputs — set some  $x_d$  to zero.

$\underline{m}$  mask vector, of random 0's & 1's

Cost on one example  $\| f(\underline{x}^{(n)} \odot \underline{m}) - \underline{x}^{(n)} \| ^2$

Cost function  $\sum_{\underline{m}} p(\underline{m}) \sum_{n=1}^N \| f(\underline{x}^{(n)} \odot \underline{m}) - \underline{x}^{(n)} \| ^2$

Monte Carlo

$$\approx \| f(\underline{x}^{(n)} \odot \underline{m}) - \underline{x}^{(n)} \| ^2$$

for random  $n$  and  $\underline{m} \sim p(\underline{m})$

## Principal Components Analysis (PCA)

It fits a linear autoencoder:

$$g^{(1)}(\underline{z}) = \underline{z}$$

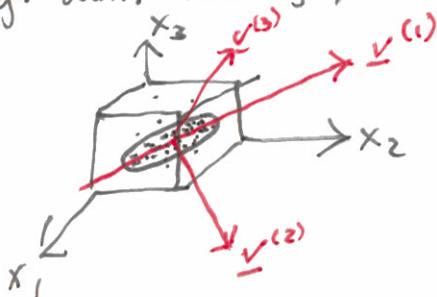
$$g^{(2)}(\underline{z}) = \underline{z}$$

PCA advantages:

- Fit with linear algebra operations
- Same answer every time
- The solutions for different  $K$  are nested  
 $h_1(\underline{x})$  is the same no matter  $K$  to be.  
 $h_2(\underline{x})$  " " " for all  $K \geq 2$

# PCA

High-dim. ball of points



— Here  $D = 3$

$v^{(k)}$   $k^{\text{th}}$  eigenvector  
of  $\text{cov}[X]$

$$V = \begin{bmatrix} | & | & | \\ v^{(1)} & v^{(2)} & \dots & v^{(k)} \\ | & | & | \end{bmatrix}$$

$V$  Pick  $k=2$  here

Reduce dim vector:

$$\underline{x} \rightarrow V^T (\underline{x} - \underline{m})$$

$D \times 1$        $K \times 1$

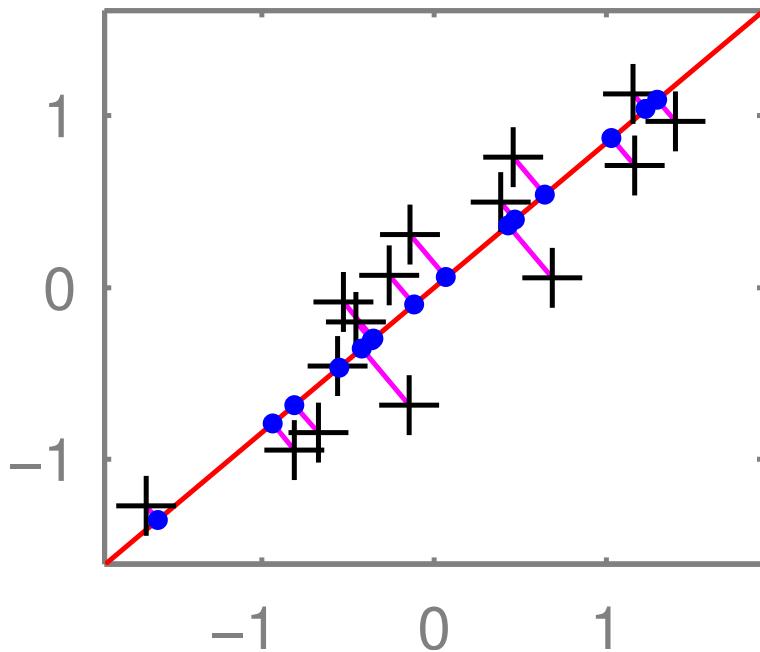
Reconstruct into 3 dimensions:

$$\hat{\underline{x}} = V \underbrace{V^T (\underline{x} - \underline{m})}_{K \times 1} + \underline{m}$$

$D \times 1$

Should have  
mentioned data  
centering.  
Next time!

# PCA: Principal Component Analysis



$K = 1$

$+$  =  $X$

$\bullet$  =  $X_{proj}$

$-$  =  $V(:,1)$

**Code assuming  $X$  is zero-mean**

```
% Find top K principal directions:  
[V, E] = eig(X'*X);  
[E,id] = sort(diag(E),1,'descend');  
V = V(:, id(1:K)); % DxK
```

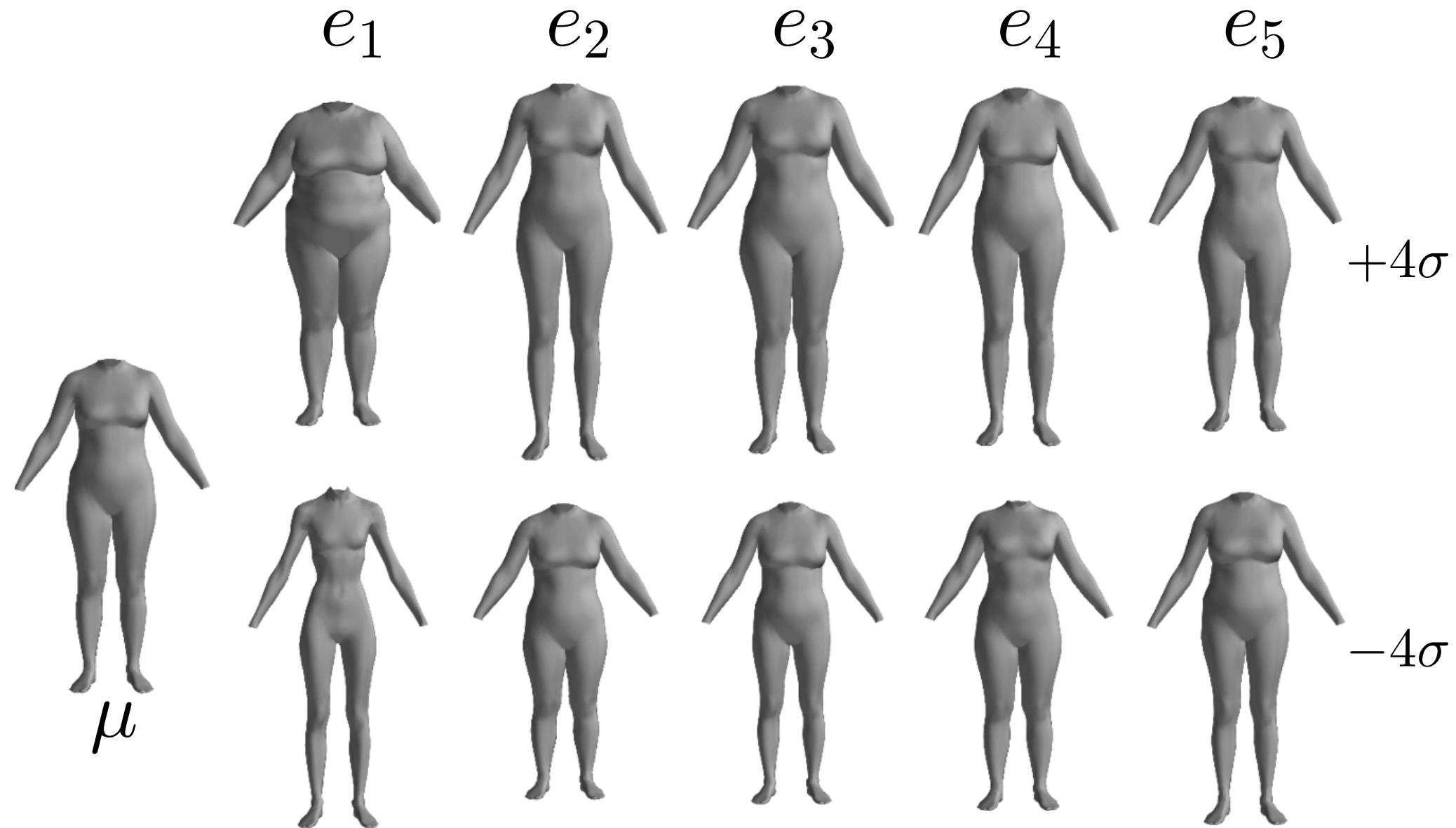
% Project to K-dims:

```
X_kdim = X*V; % NxK
```

% Project back:

```
X_proj = X_kdim * V'; % NxD
```

# PCA applied to bodies



# PCA applied to DNA

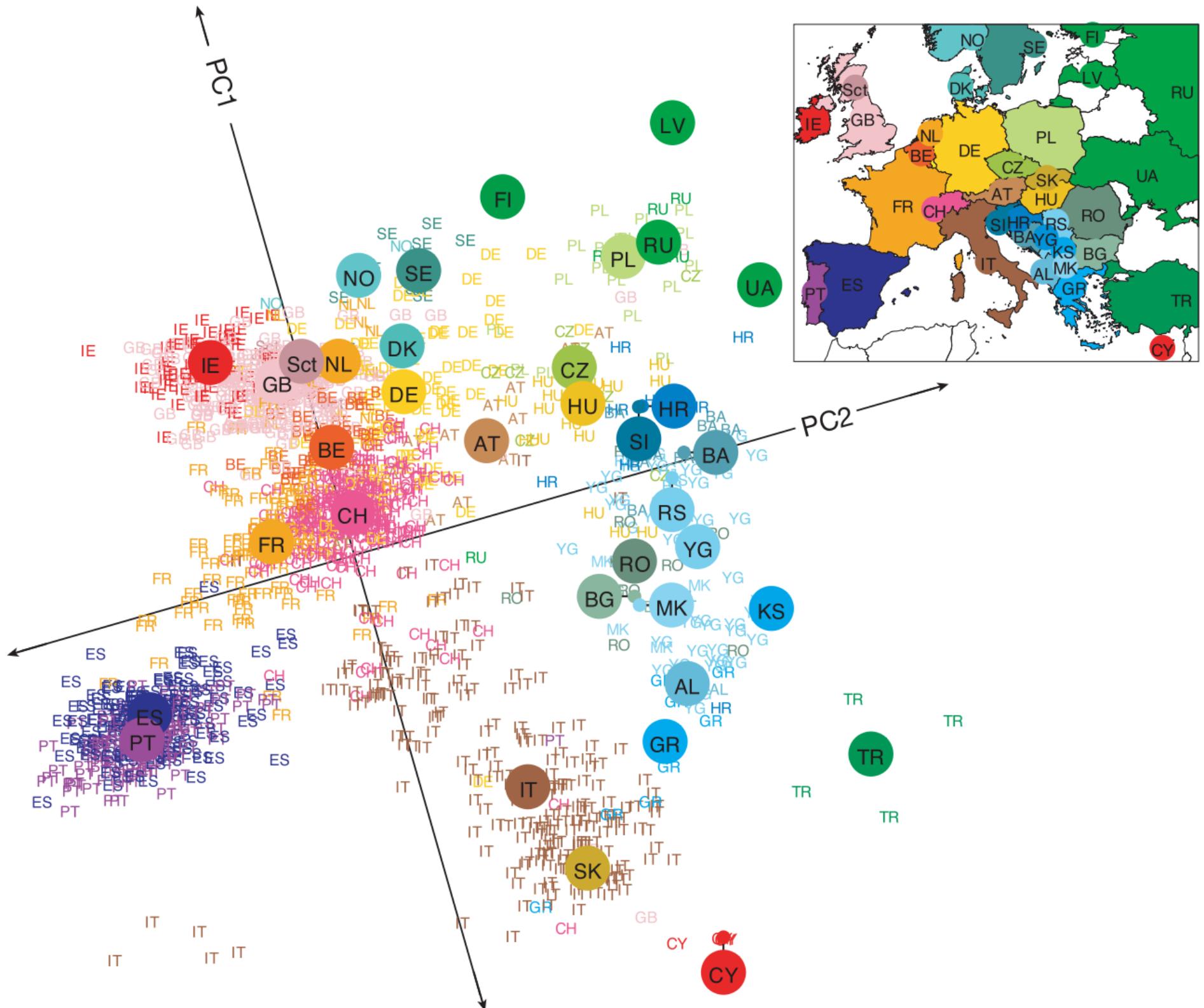
Novembre et al. (2008) — doi:10.1038/nature07331

Carefully selected both individuals and features

1,387 individuals

197,146 single nucleotide polymorphisms (SNPs)

Each person reduced to two(!) numbers with PCA



# MSc course enrollment data

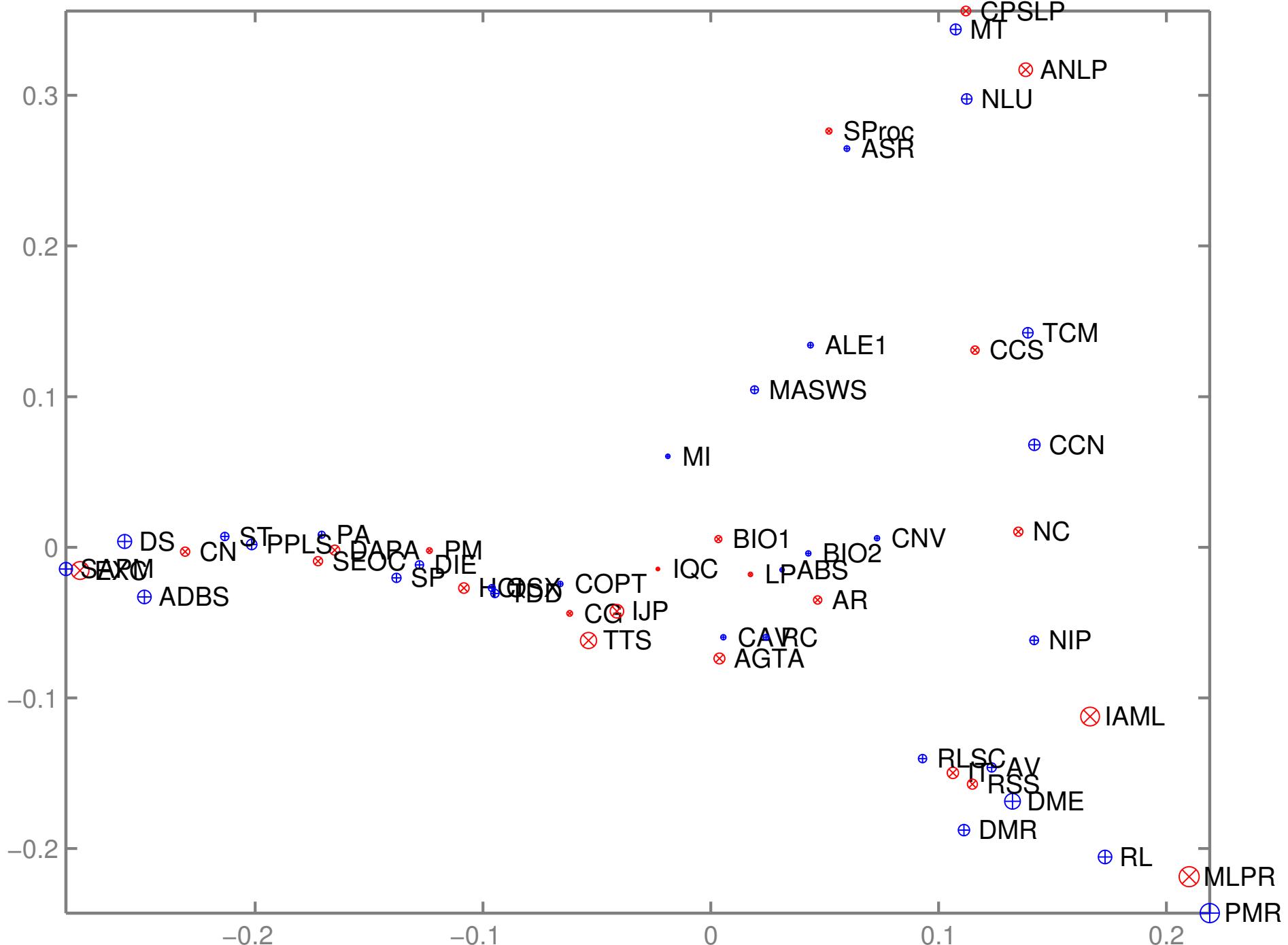
Binary  $S \times C$  matrix  $M$

$M_{sc} = 1$ , if student  $s$  taking course  $c$

Each course is a length  $S$  vector

... OR each student is a length  $C$  vector

# PCA applied to MSc courses



# PCA applied to MSc students

