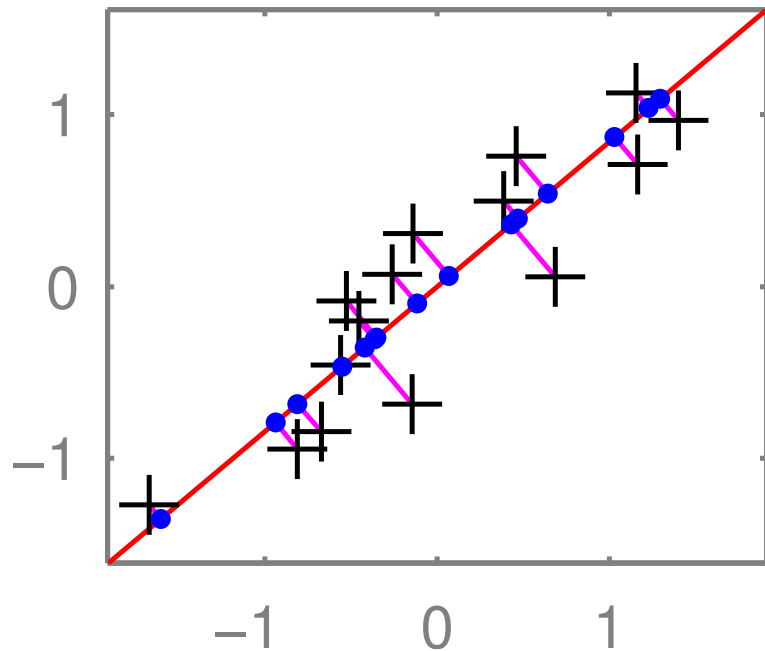


# PCA: Principal Component Analysis

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# PCA: Principal Component Analysis



$K = 1$

+ =  $X$

• =  $X_{proj}$

— =  $V(:,1)$

## 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)); % D x K
```

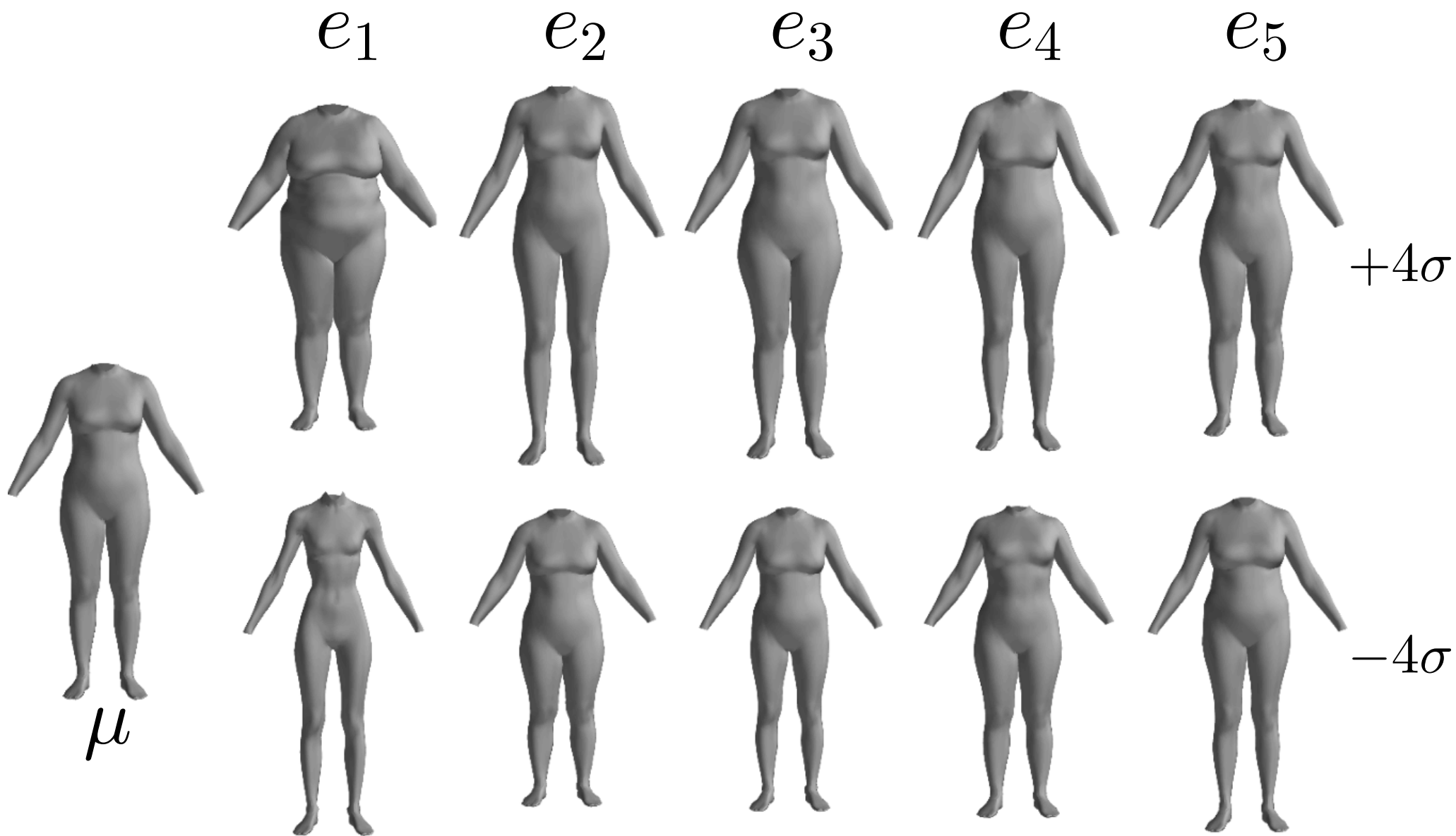
```
% Project to K-dims:
```

```
X_kdim = X*V; % N x K
```

```
% Project back:
```

```
X_proj = X_kdim * V'; % N x D
```

# PCA applied to bodies



# PCA applied to DNA

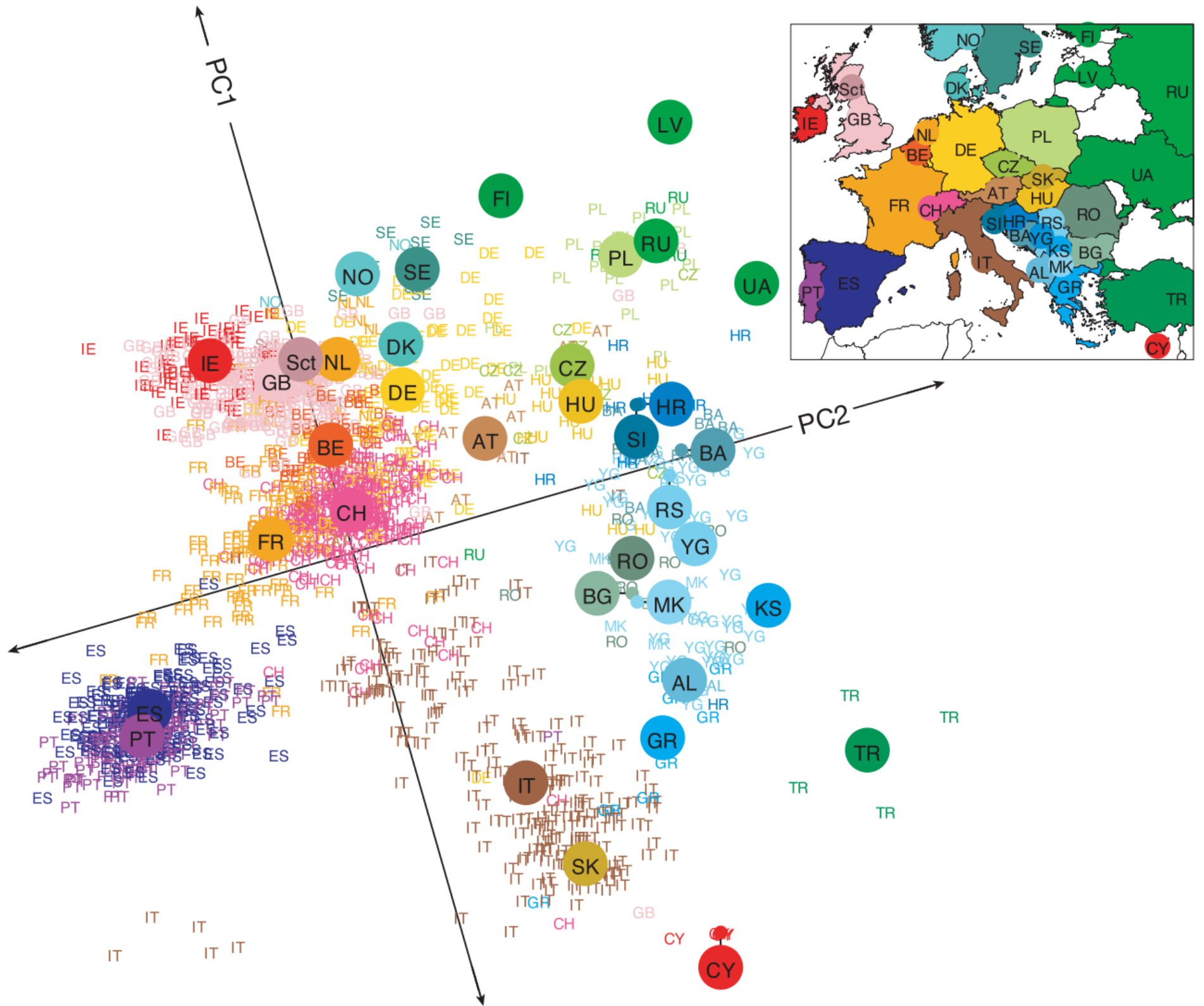
Novembre et al. (2008) — doi:10.1038/nature07331

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

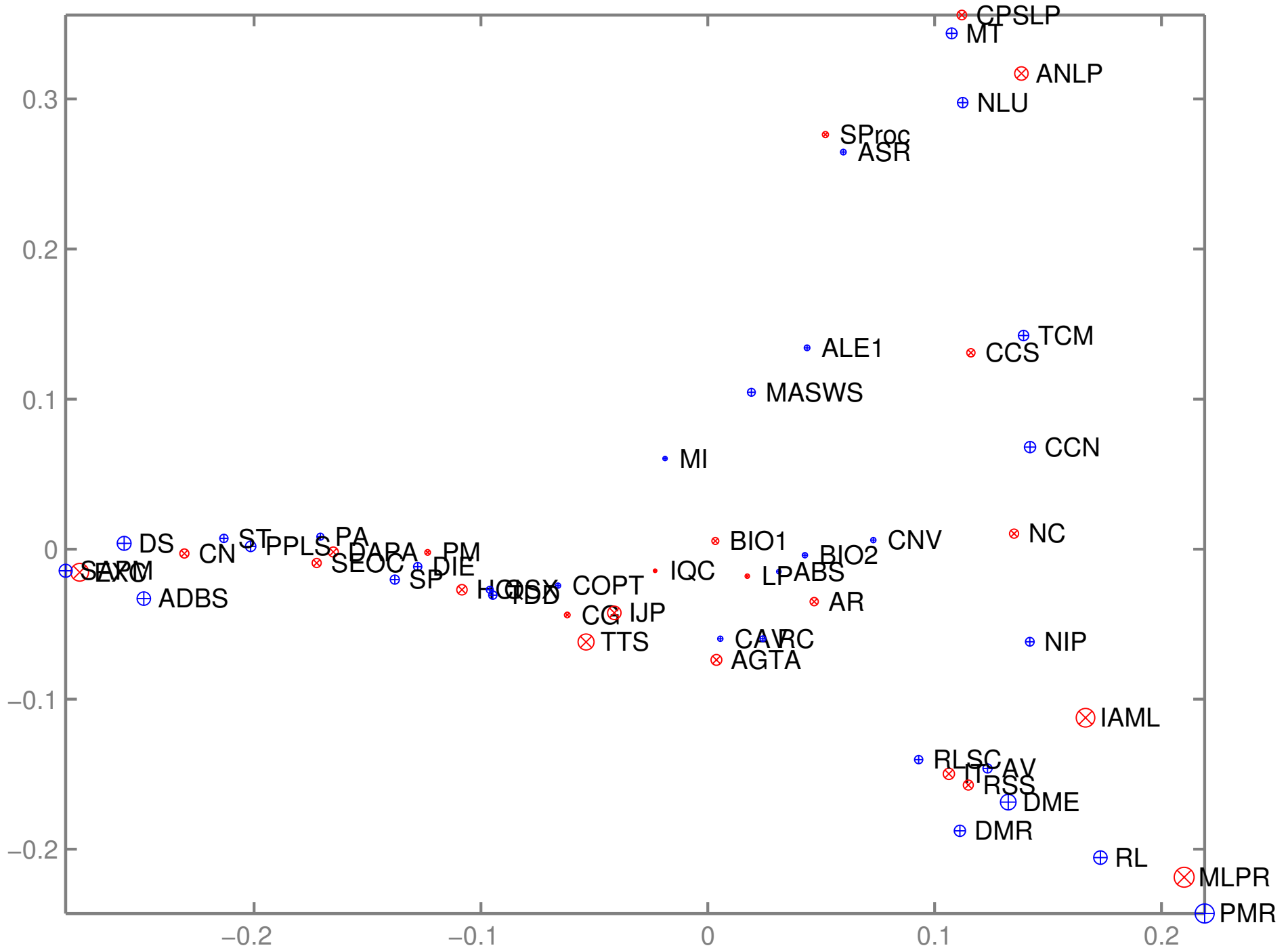
Binary  $S \times C$  matrix  $M$

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

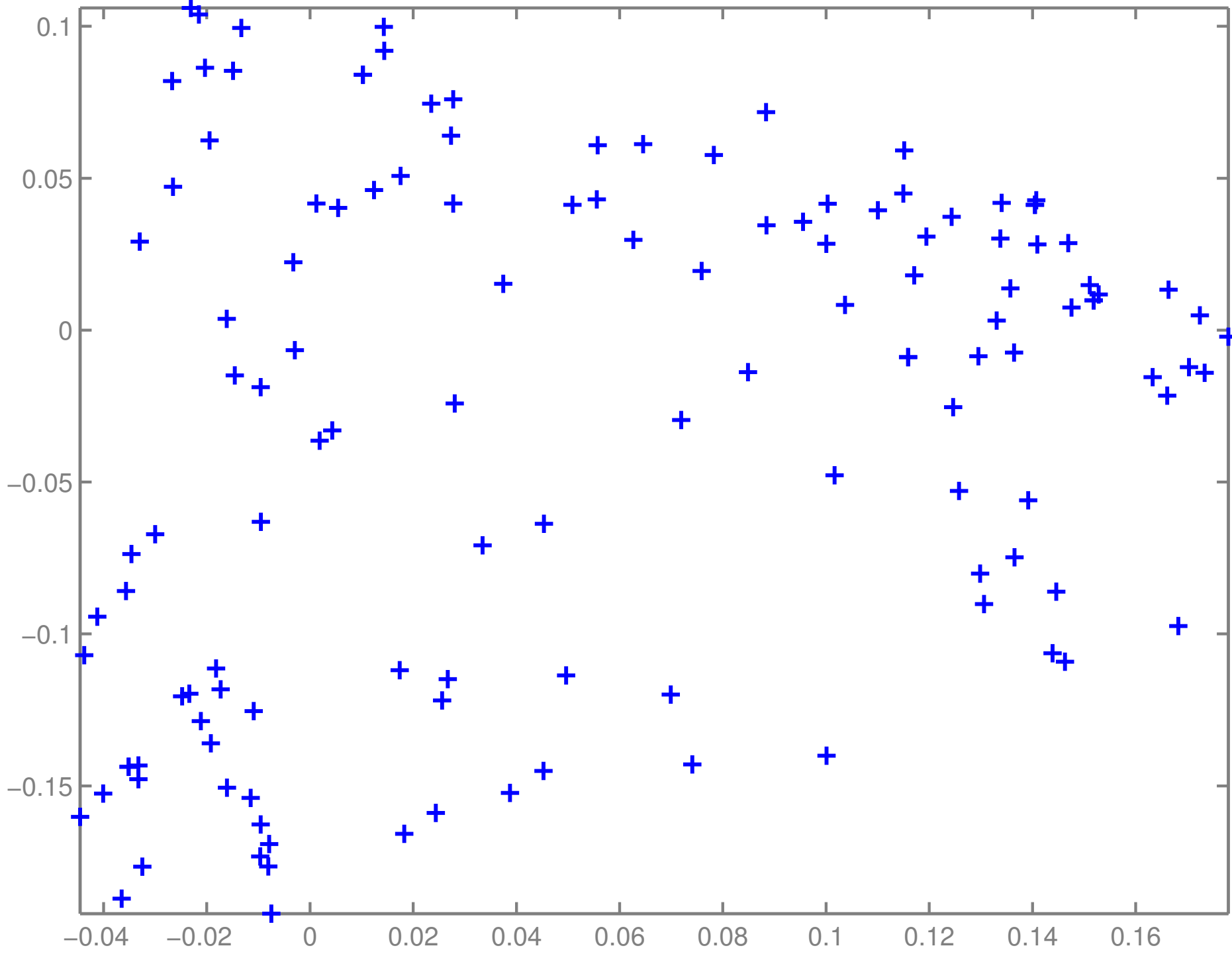
Each course is a length  $S$  vector

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

# PCA applied to MSc courses



# PCA applied to MSc students





# Truncated SVD

$$\begin{bmatrix} X_{11} & X_{12} & \cdots & X_{1D} \\ X_{21} & X_{22} & \cdots & X_{2D} \\ X_{31} & X_{32} & \cdots & X_{3D} \\ X_{41} & X_{42} & \cdots & X_{4D} \\ X_{51} & X_{52} & \cdots & X_{5D} \\ \vdots & \vdots & \ddots & \vdots \\ X_{N1} & X_{N2} & \cdots & X_{ND} \end{bmatrix} \approx$$

$$\begin{bmatrix} U_{11} & \cdots & U_{1K} \\ U_{21} & \cdots & U_{2K} \\ U_{31} & \cdots & U_{3K} \\ U_{41} & \cdots & U_{4K} \\ U_{51} & \cdots & U_{5K} \\ \vdots & \ddots & \vdots \\ U_{N1} & \cdots & U_{NK} \end{bmatrix} \begin{bmatrix} S_{11} & 0 & 0 \\ 0 & \cdots & 0 \\ 0 & 0 & S_{KK} \end{bmatrix} \begin{bmatrix} V_{11} & V_{21} & \cdots & V_{D1} \\ \vdots & \vdots & \ddots & \vdots \\ V_{1K} & V_{2K} & \cdots & V_{DK} \end{bmatrix}$$

$$X \approx U S V^T$$

```
% PCA via SVD,  
% for zero-mean X:  
[U, S, V] = svd(X, 0);  
U = U(:, 1:K);  
S = S(1:K, 1:K);  
V = V(:, 1:K);  
X_kdim = U*S;  
X_proj = U*S*V';
```

# PCA summary

Project data onto major axes of covariance

$X^T X$  is covariance if make data zero mean

Low-dim coordinates can be useful:

- visualization
- if can't cope with high-dim data

Can project back into original space:

- detail is lost: still in  $K$ -dim subspace
- PCA minimizes the square error

# PPCA: Probabilistic PCA

**Gaussian model:**  $\Sigma = WW^\top + \sigma^2 I$

$W$  is  $D \times K$ ,  $\sigma^2$  small  $\Rightarrow$  nearly low-rank

$W$  is also orthogonal

As  $\sigma^2 \rightarrow 0$ , recover PCA.

Need  $\sigma^2 > 0$  to explain data

Special case of factor analysis:  $\Sigma = WW^\top + \Phi$ , with  $\Phi$  diagonal

# Dim reduction in other models

Can replace  $\mathbf{x}$  with  $A\mathbf{x}$  in any model

$A$  is a  $K \times D$  matrix of projection params

Large  $D$ : a lot of extra parameters

NB: Neural nets already have such projections

# Practical tip

## Scale features to have unit variance

Equivalently: find eigenvectors of correlation rather than covariance

Avoids issues with (arbitrary?) scaling.

If multiply feature by  $10^9$ , PC points along that feature

E.g., if change unit of feature from metres to nanometres