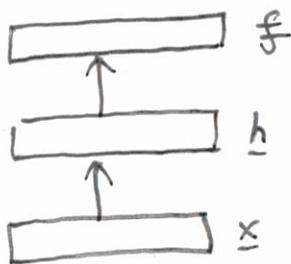


Autoencoder



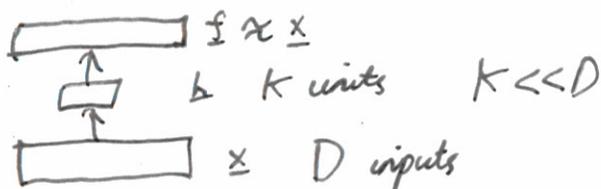
Learning task

$$f(x) \approx x$$

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

not useful!

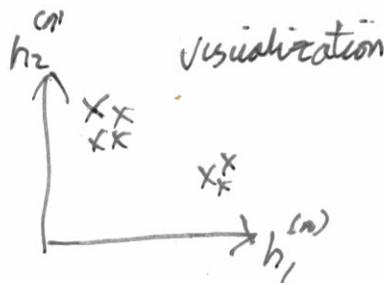
Dimensionality Reduction



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

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

\underline{h} can be used in any other ML method.



Denoising Autoencoders

h is big $k=D$ or even $k>D$

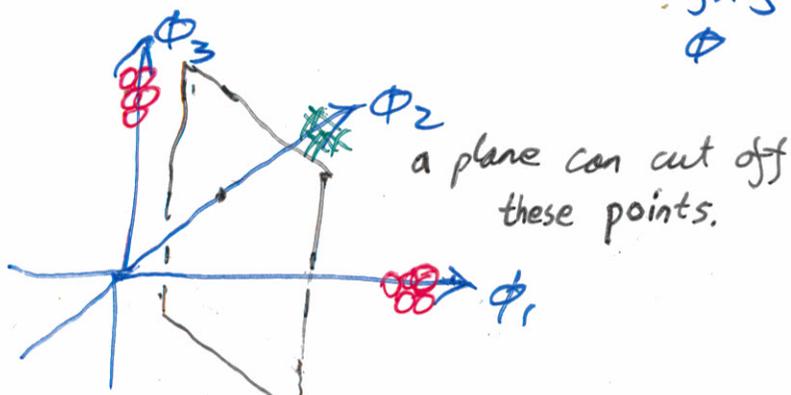
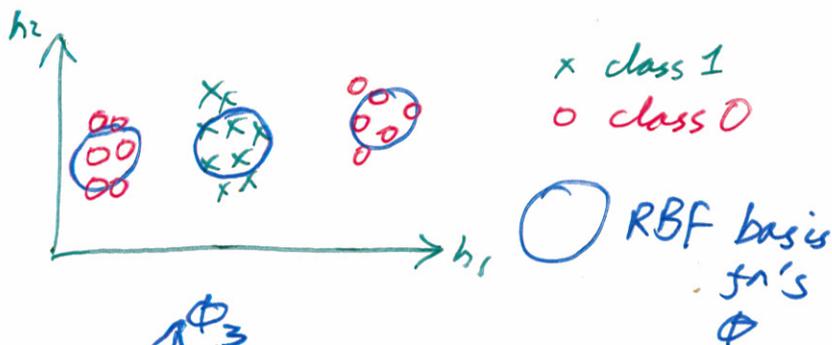
But while training we set some of the x_d inputs to zero.

Cost J^A could be $\sum_n \|f^{(n)} - \underline{x}^{(n)}\|^2$

Sparse Auto-encoders

Force most elements of h to be zero.

For high-dim features h it can be easier to fit linear classifier.



Principal Components Analysis (PCA)

It's equivalent to an auto-encoder
with no non-linearities:

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

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

And if f is matched to z by square error.

PCA advantages

- Find solⁿ with linear algebra
- Same answer every time.

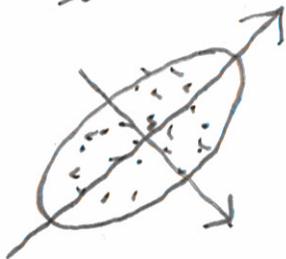
The solutions for different k

$h_1(x)$ is the same regardless of k
 $h_2(x)$ " " " " for all $k \geq 2$

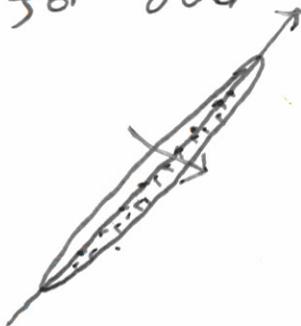
PCA first computes covariance of data

$$\Sigma = \text{cov}[X], \text{ for zero-mean data:}$$
$$= X^T X, \quad X \text{ is a } N \times D \text{ matrix}$$

For some data



for other



MSc students

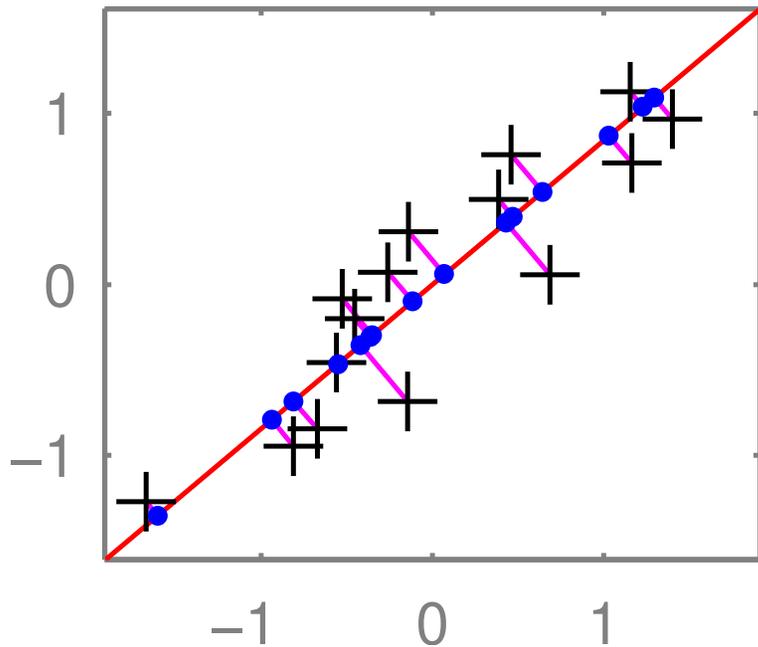
C_i course C

$$M =$$

s			

← student s

PCA: Principal Component Analysis



$K = 1$

$+ = X$

$\bullet = X_{\text{proj}}$

$\text{—} = V(:,1)$

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
```

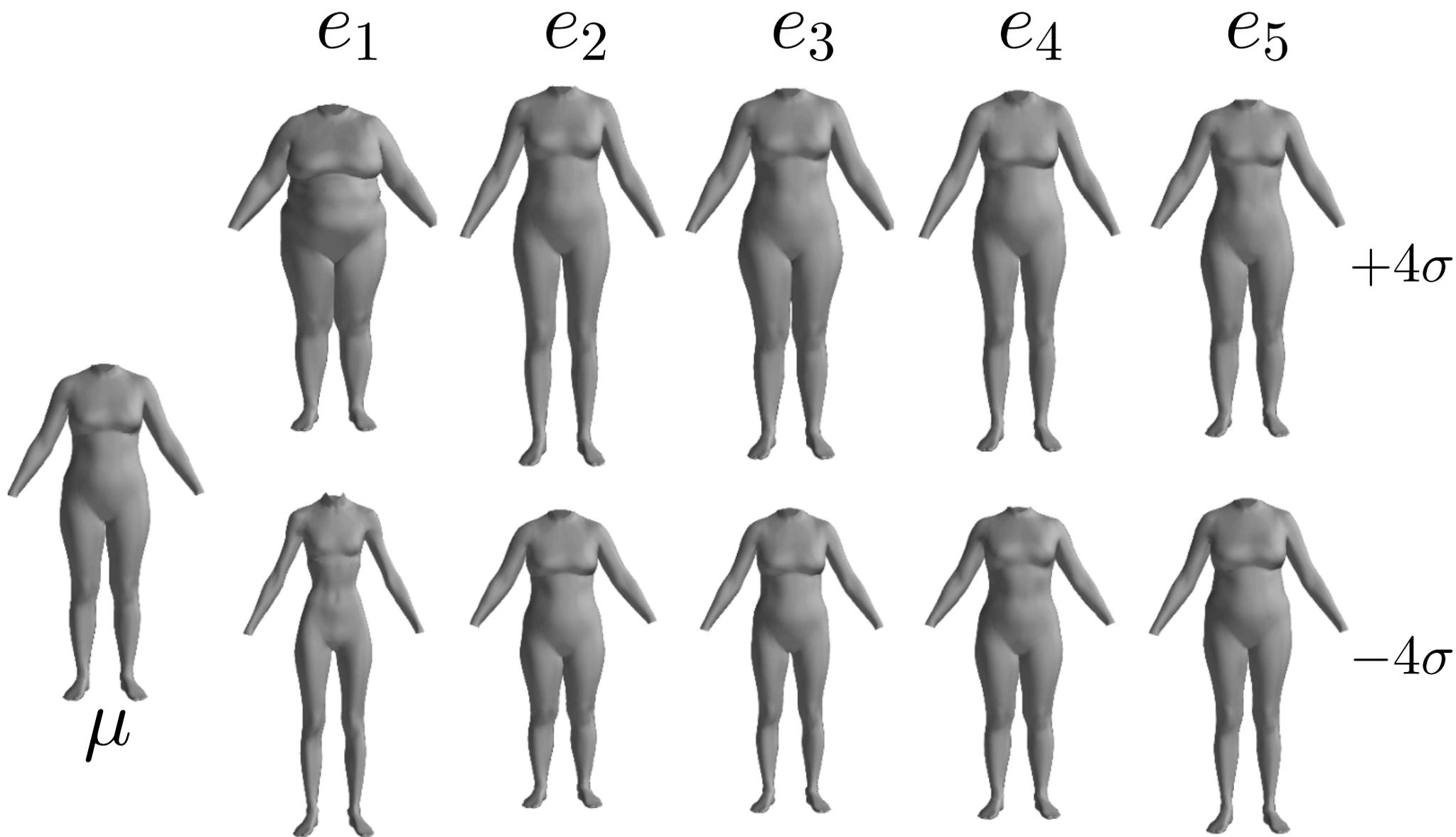
```
% Project to K-dims:
```

```
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

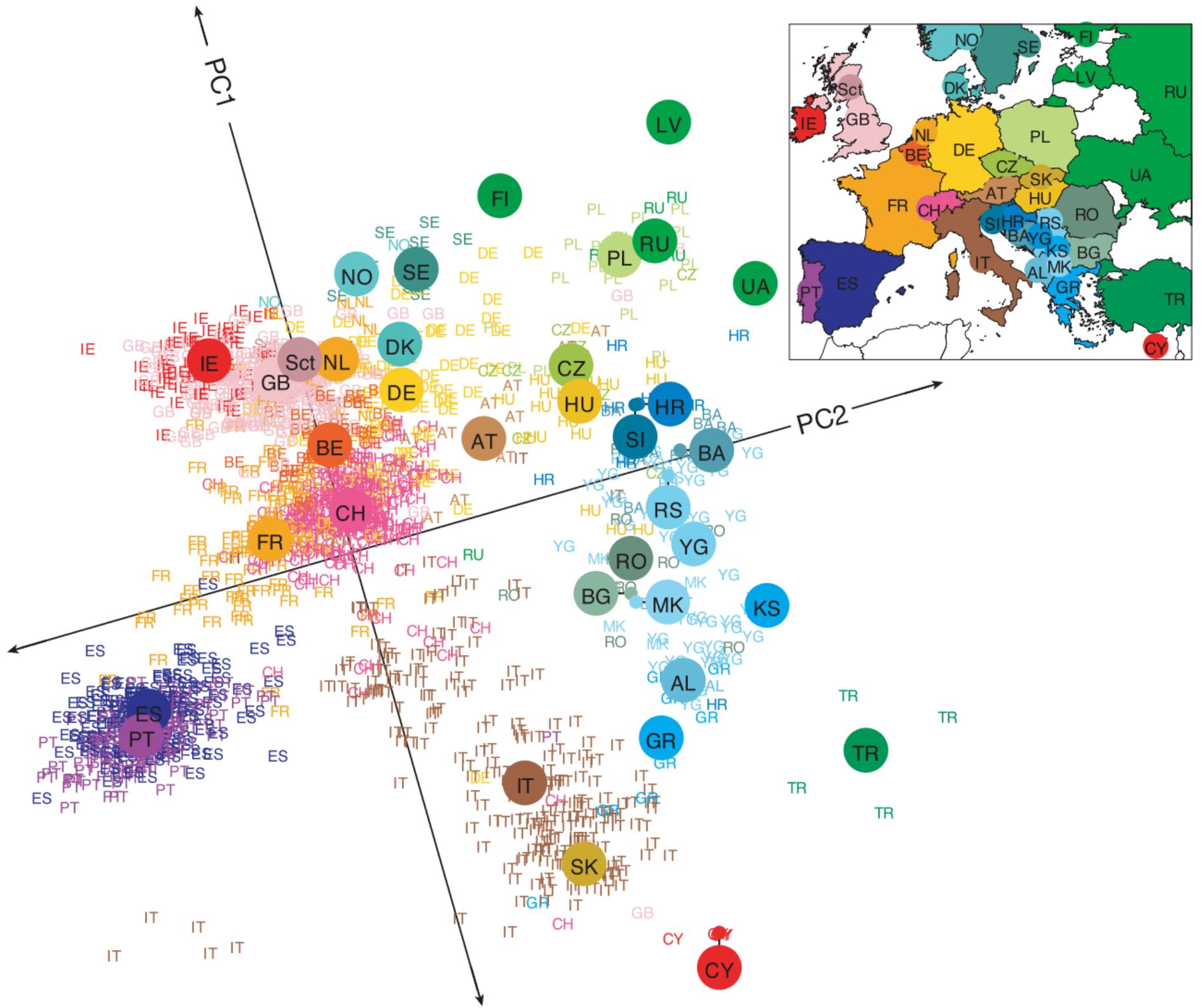
Novembre et al. (2008) — doi:10.1038/nature07331

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

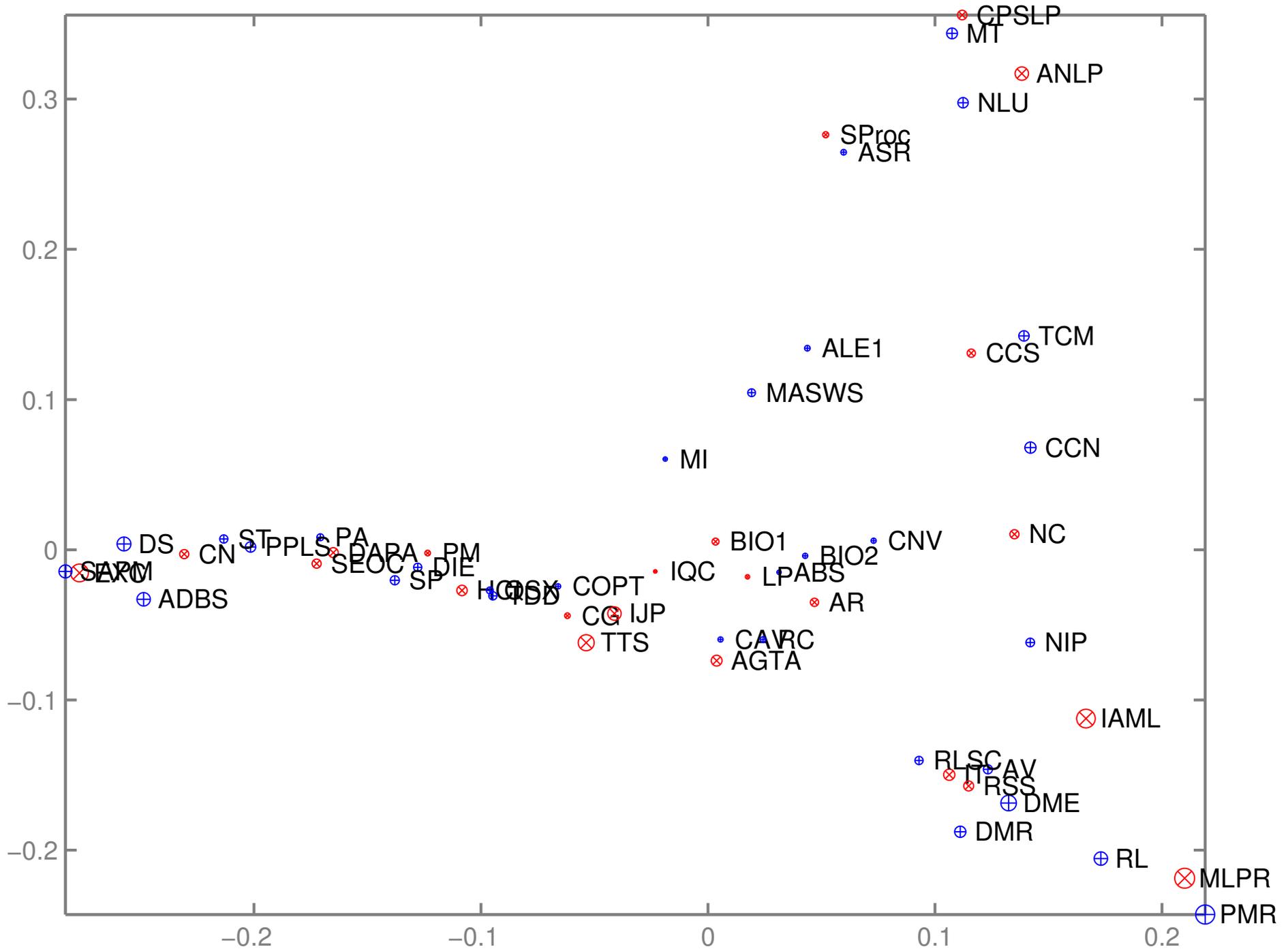
Binary $S \times C$ matrix M

$M_{sc} = 1$, 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

