



**SOICT**

**HUST**  
ĐẠI HỌC BÁCH KHOA HÀ NỘI  
HANOI UNIVERSITY OF SCIENCE AND TECHNOLOGY

# Dimensionality Reduction

Tran The Hung

# Contents

- Dimensionality Reduction
- Principle Component Analysis (PCA)
- PCA Applications
- PCA Shortcomings
- Autoencoders
- Independent Component Analysis

# Question 1

- 1) In the standard PCA pipeline, what is the *first* operation you should do on the data matrix  $X$ ?**
- A. Compute the SVD of  $X$  directly
  - B. Subtract the mean of each feature (center the data)
  - C. Normalize every feature to unit variance
  - D. Build the kernel matrix  $K$

# Question 2

**2) In PCA, each eigenvalue of the covariance matrix represents:**

- A. The covariance between pairs of features
- B. The variance captured along its corresponding principal component
- C. The reconstruction error of the model
- D. The correlation between the first two principal components

# Question 3

**3) Which statement best captures the relationship between SVD and PCA?**

A. PCA is done by applying SVD to the *covariance* matrix

B. PCA and SVD are unrelated

C. SVD is done by applying PCA to  $X$

D. PCA returns the left singular vectors of  $X$  as principal components

# Question 4

**4) Lloyd's  $K$ -means algorithm minimizes which objective?**

A. Sum of absolute distances to cluster medoids

B. Sum of squared distances of each point to its assigned centroid

C. Sum of pairwise distances inside each cluster

D. Negative log-likelihood under a Gaussian mixture

# Question 5

**5) In the assignment step of  $K$ -means with fixed centroids, each point is assigned to the cluster whose centroid is:**

- A. Farthest in Euclidean distance
- B. Closest in Euclidean distance
- C. Most probable under a learned density
- D. Randomly chosen to encourage exploration

# Question 6

**6) In  $K$ -means++ initialization, after choosing the first center at random, each subsequent center is chosen with probability proportional to:**

- A. Uniform probability over remaining points
- B. The (unsquared) distance to the *nearest* chosen center
- C. The **squared** distance to the nearest chosen center
- D. The inverse of the distance to the nearest chosen center

# Question 7

**7) A well-known limitation of basic  $K$ -means is that it effectively assumes clusters are:**

- A. Arbitrarily shaped with nonlinear boundaries
- B. Spherical and of roughly similar size, leading to linear decision boundaries
- C. Nested hierarchies with tree-structured boundaries
- D. Determined by a Mahalanobis metric by default

# Question 8

**8) Learning with Prototypes (LwP), using Euclidean distances for binary classes with means  $\mu_+$  and  $\mu_-$ , leads to a linear decision function  $f(x) = w^\top x + b$ . What are  $w$  and  $b$ ?**

- A.  $w = \mu_+ - \mu_-$ ,  $b = \|\mu_-\|^2 - \|\mu_+\|^2$
- B.  $w = 2(\mu_+ - \mu_-)$ ,  $b = \|\mu_-\|^2 - \|\mu_+\|^2$
- C.  $w = \mu_+ + \mu_-$ ,  $b = 0$
- D.  $w = 2(\mu_- - \mu_+)$ ,  $b = \|\mu_+\|^2 - \|\mu_-\|^2$

# Question 9

**9) In  $K$ -nearest neighbors (KNN) classification, increasing  $K$  generally tends to:**

- A. Make the decision boundary more jagged (higher variance)
- B. Make the decision boundary smoother (lower variance)
- C. Have no effect on the decision boundary
- D. Always improve accuracy regardless of data

# Question 10

**10) When pairwise distances are Euclidean, classical Multi-Dimensional Scaling (MDS) is equivalent to:**

- A. Locally Linear Embedding (LLE)
- B. Principal Component Analysis (PCA)
- C. Kernel PCA with an RBF kernel
- D. Independent Component Analysis (ICA)

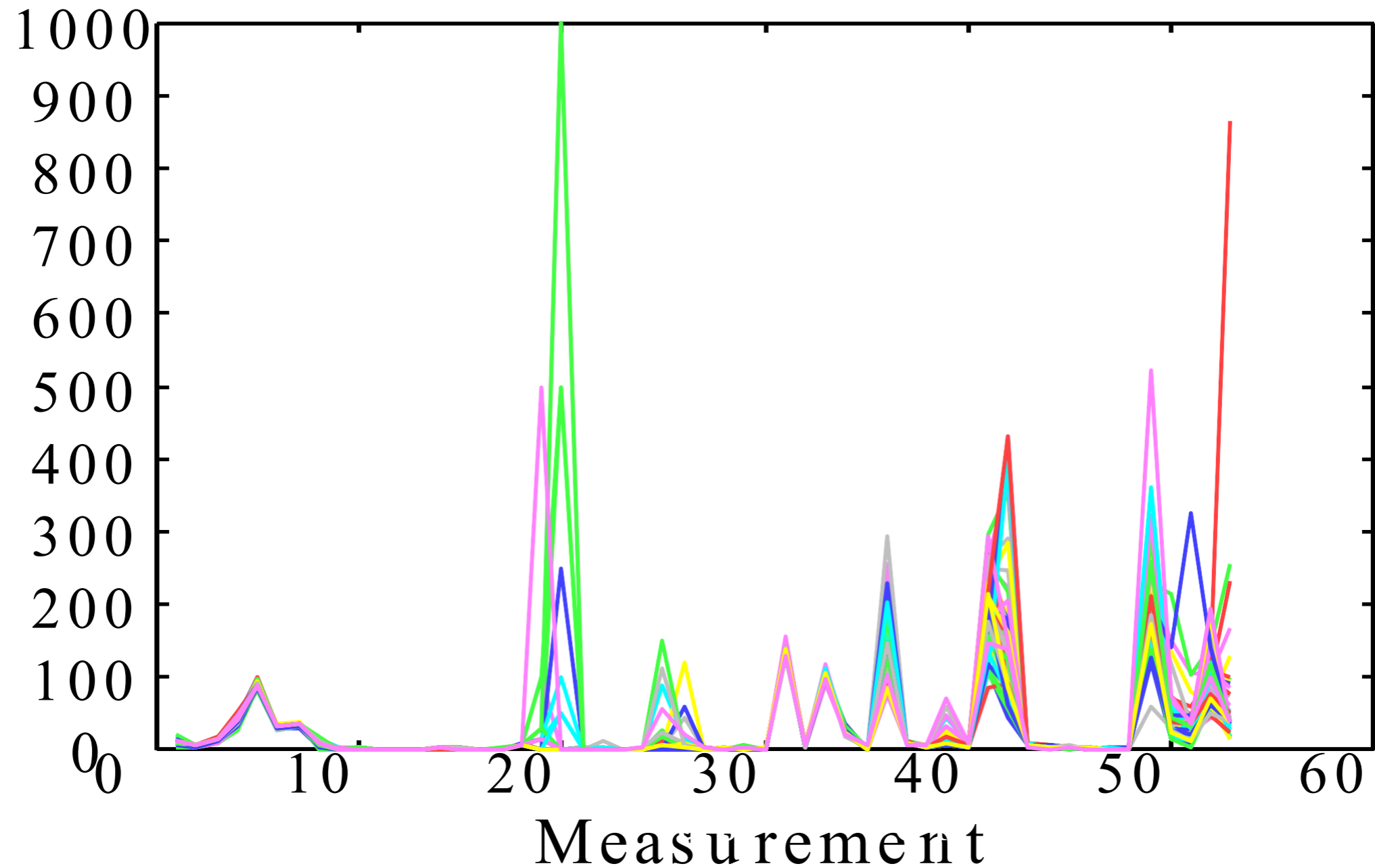
# Motivation I: Data Visualization

The diagram illustrates a data table with 9 rows and 8 columns. The first column contains instance labels A1 through A9, grouped by a vertical curly brace on the left labeled 'Instances'. The remaining seven columns contain numerical values for various blood test parameters, grouped by a horizontal curly brace at the bottom labeled 'Features'. The parameter names are in the header row, and the numerical values are in the subsequent rows.

	H-WBC	H-RBC	H-Hgb	H-Hct	H-MCV	H-MCH	H-MCHC
A1	8.0000	4.8200	14.1000	41.0000	85.0000	29.0000	34.0000
A2	7.3000	5.0200	14.7000	43.0000	86.0000	29.0000	34.0000
A3	4.3000	4.4800	14.1000	41.0000	91.0000	32.0000	35.0000
A4	7.5000	4.4700	14.9000	45.0000	101.0000	33.0000	33.0000
A5	7.3000	5.5200	15.4000	46.0000	84.0000	28.0000	33.0000
A6	6.9000	4.8600	16.0000	47.0000	97.0000	33.0000	34.0000
A7	7.8000	4.6800	14.7000	43.0000	92.0000	31.0000	34.0000
A8	8.6000	4.8200	15.8000	42.0000	88.0000	33.0000	37.0000
A9	5.1000	4.7100	14.0000	43.0000	92.0000	30.0000	32.0000

- 53 Blood and urine samples from 65 people
- Difficult to see the correlations between features

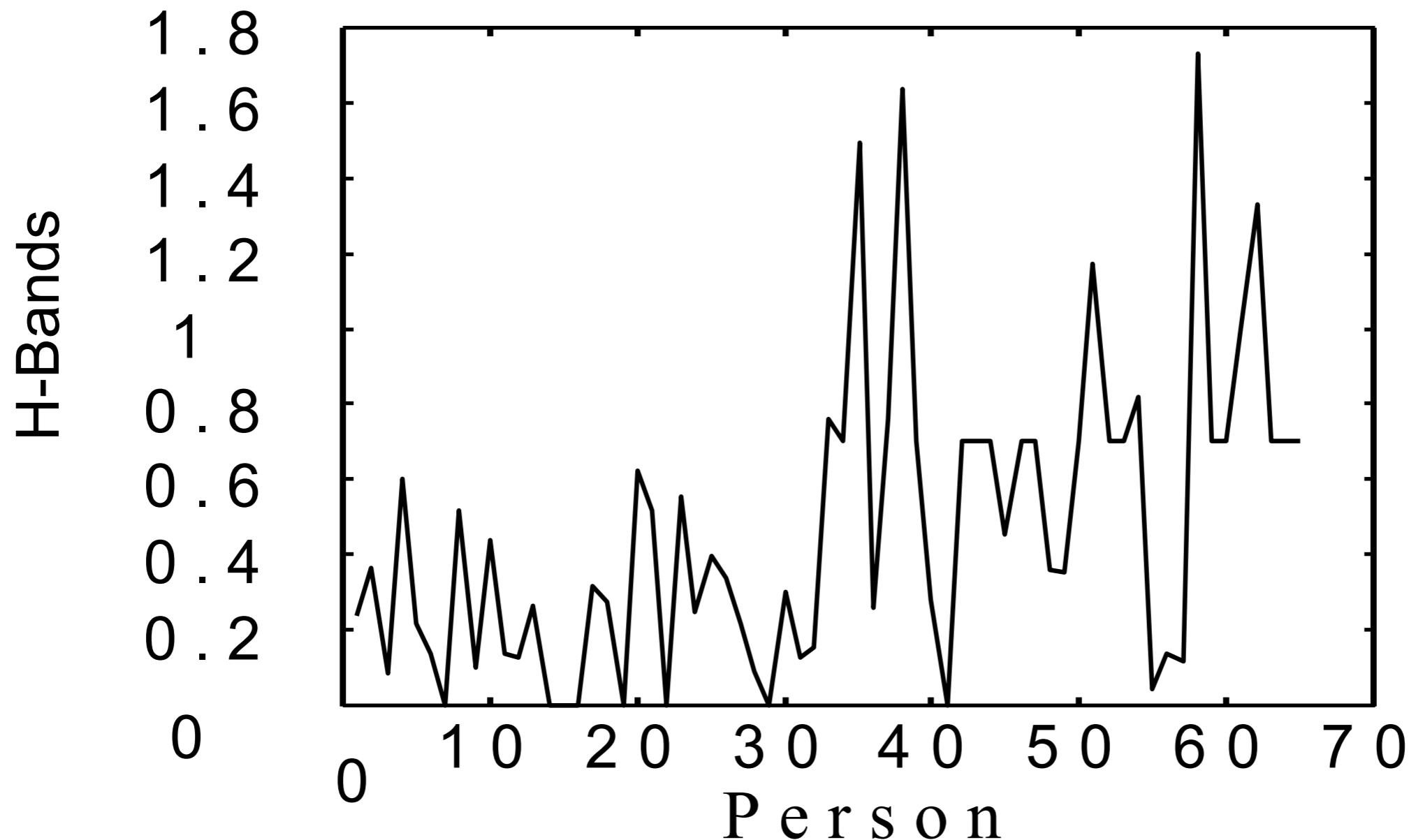
# Motivation I: Data Visualization



- Spectral format (65 curves, one for each person)
- Difficult to compare different patients

# Motivation I: Data Visualization

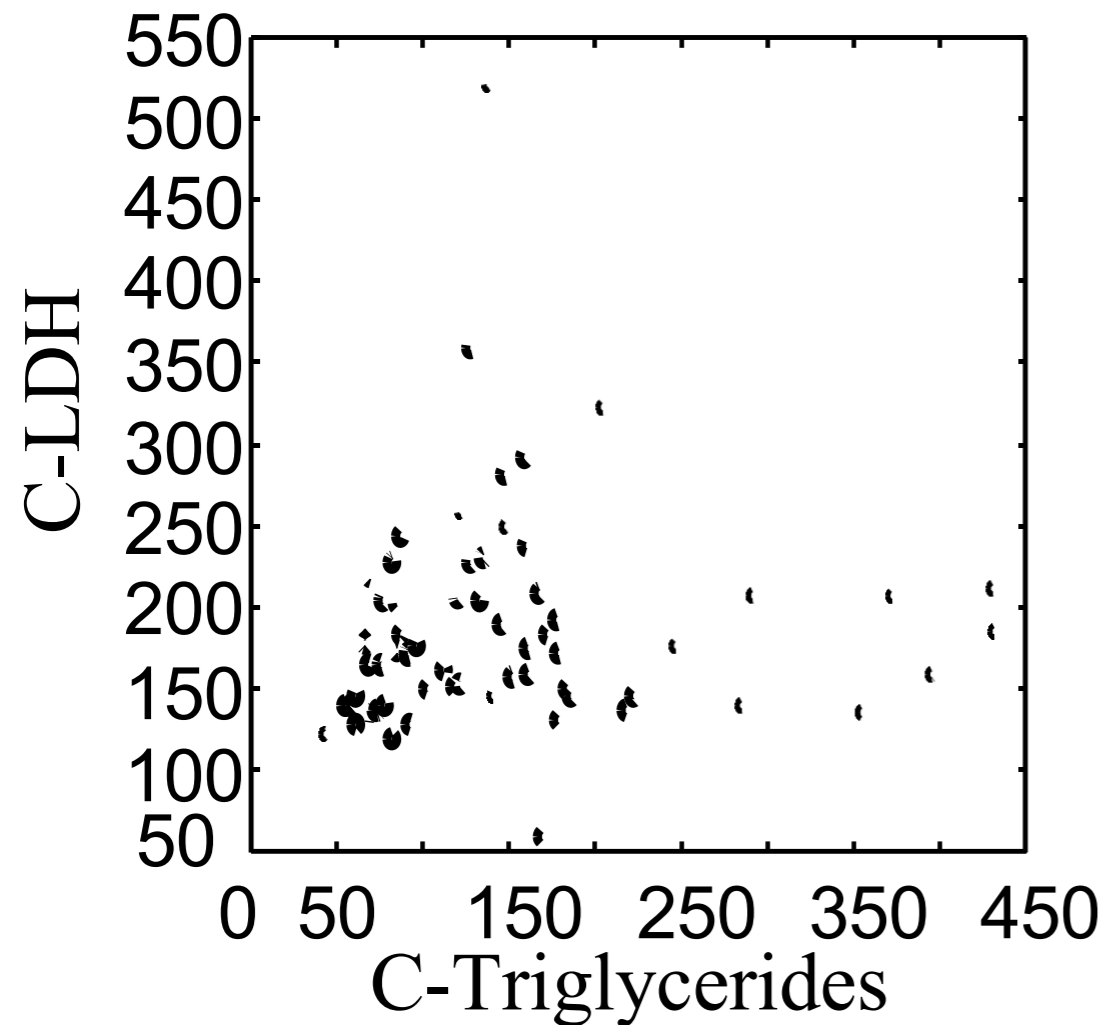
- Spectral format (53 pictures, one for each feature)



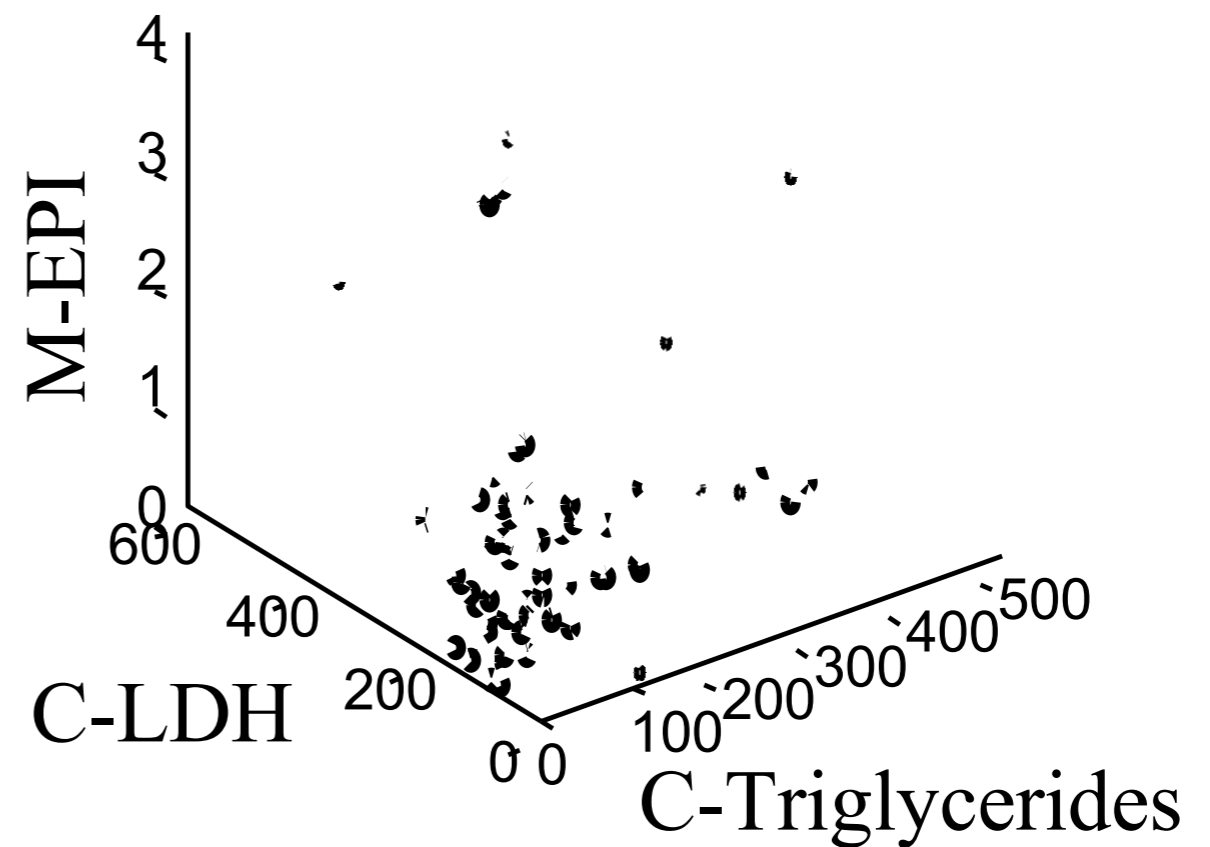
- Difficult to see the correlations between features

# Motivation I: Data Visualization

**Bi-variate**



**Tri-variate**

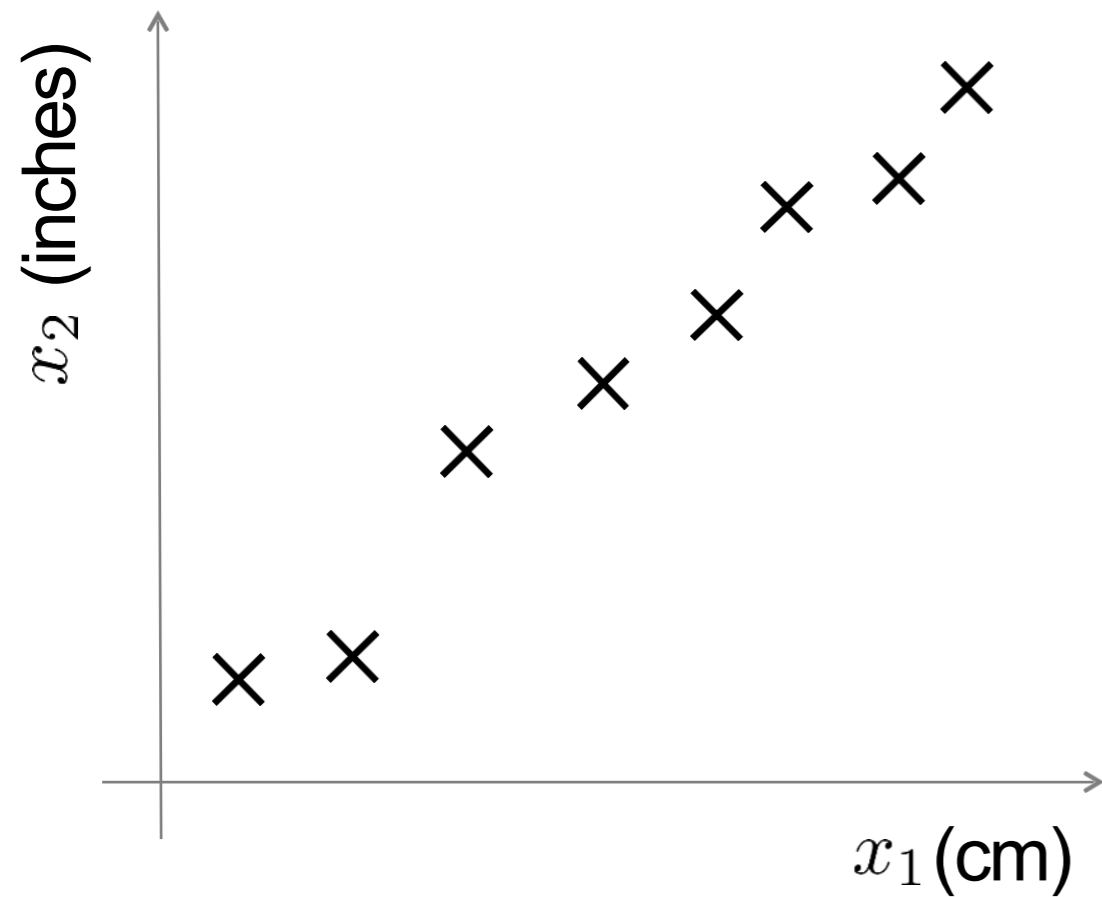


Even 3 dimensions are already difficult. How to extend this?

# Motivation I: Data Visualization

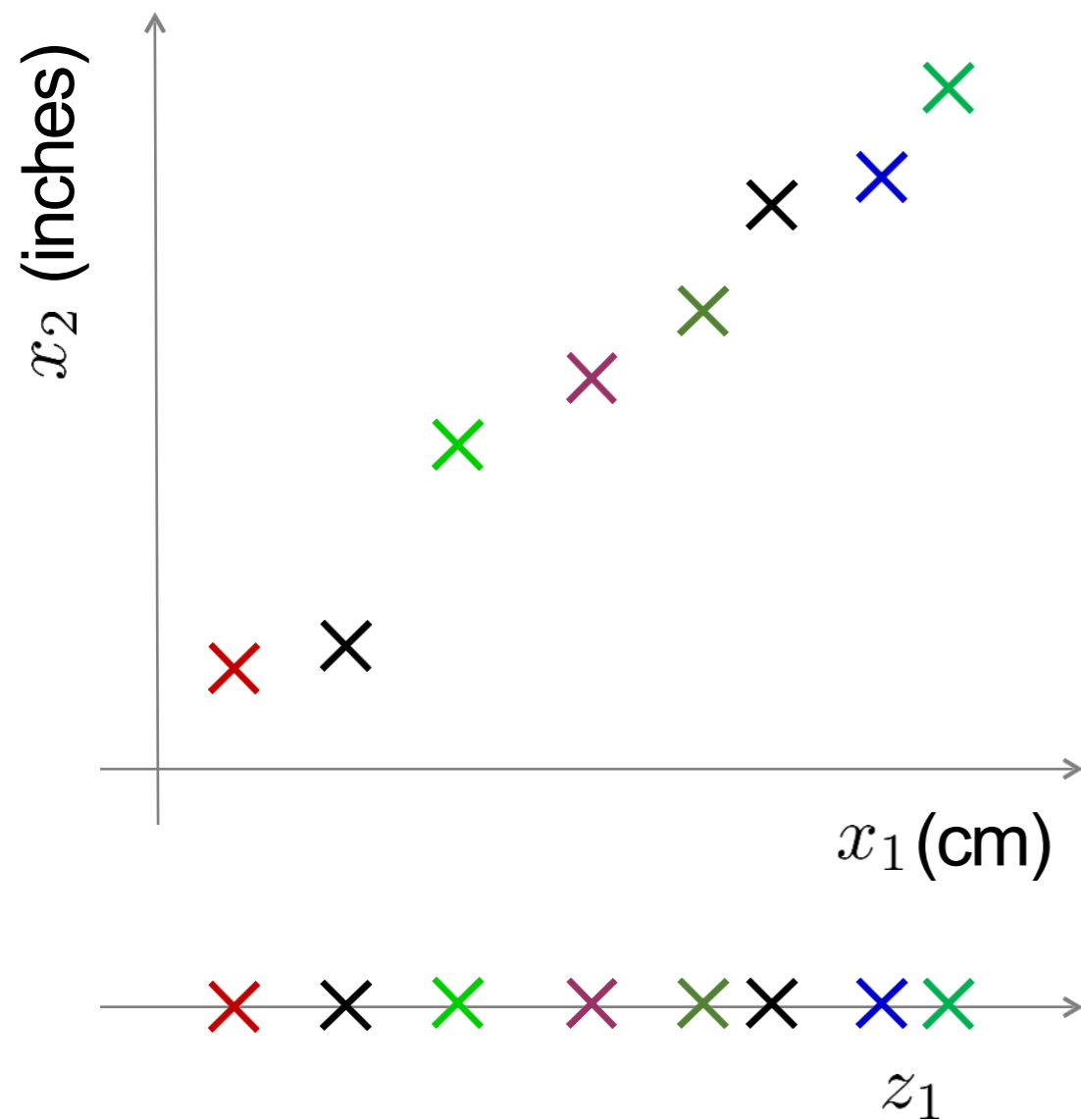
- Is there a representation better than the coordinate axes?
- Is it really necessary to show all 53 dimensions?
  - ... what if there are strong correlations between the features?
- How could we find the **smallest** subspace of the 53-D space that keeps the **most information** about the original data?

# Motivation II: Data Compression



Reduce data from 2D to 1D

# Motivation II: Data Compression

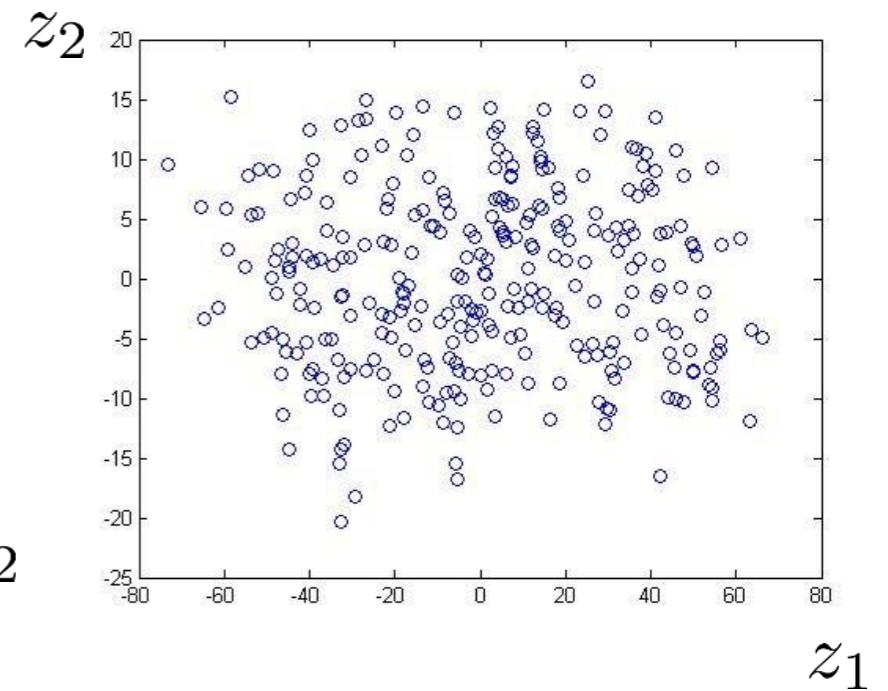
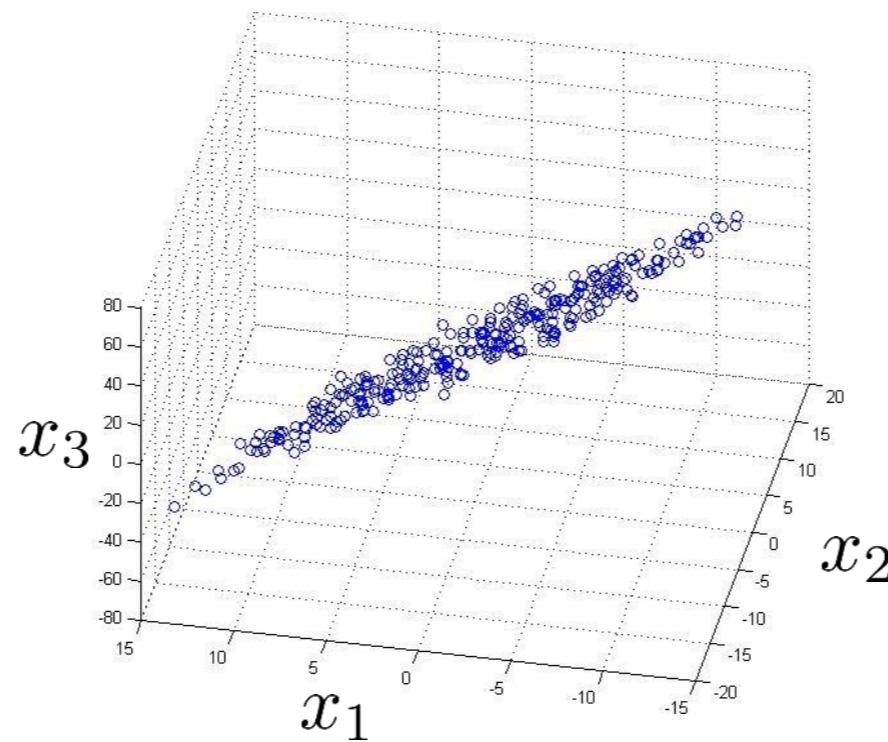
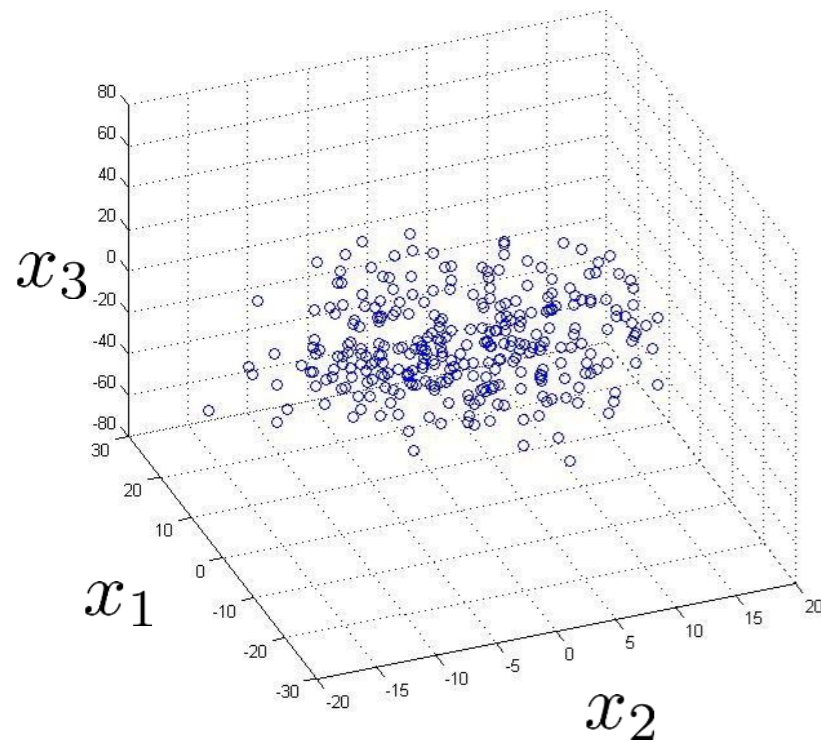


Reduce data from 2D to 1D

$$\begin{array}{ccc} x^{(1)} & \rightarrow & z^{(1)} \\ x^{(2)} & \rightarrow & z^{(2)} \\ & \vdots & \\ x^{(m)} & \rightarrow & z^{(m)} \end{array}$$

# Motivation II: Data Compression

Reduce data from 3D to 2D



# Dimensionality Reduction

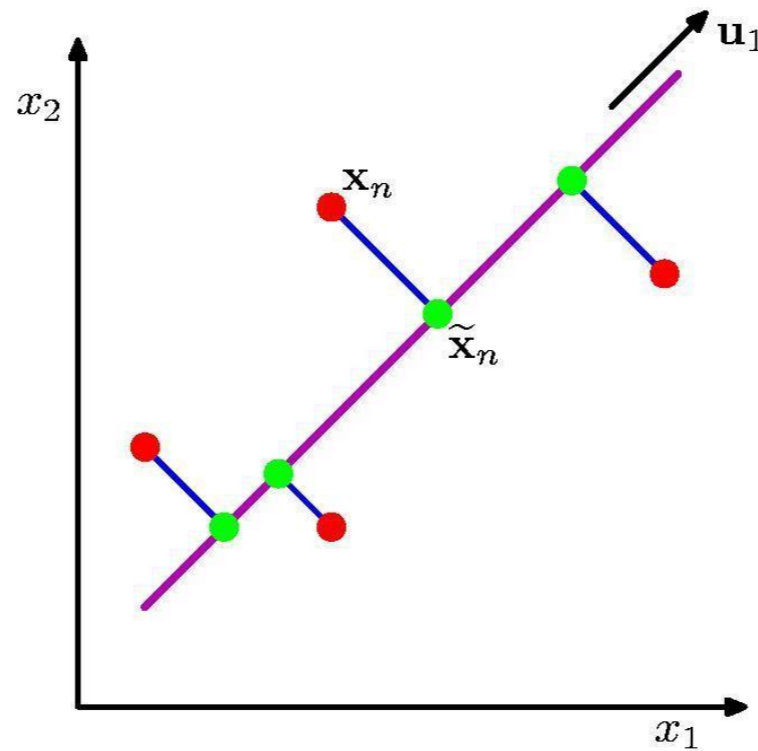
- Clustering
  - One way to summarize a complex real-valued data point with a single categorical variable
- Dimensionality reduction
  - Another way to simplify complex high-dimensional data
  - Summarize data with a lower dimensional real valued vector



- Given data points in  $d$  dimensions
- Convert them to data points in  $r < d$  dims
- With minimal loss of information

# Principal Component Analysis

# Principal Component Analysis



## PCA:

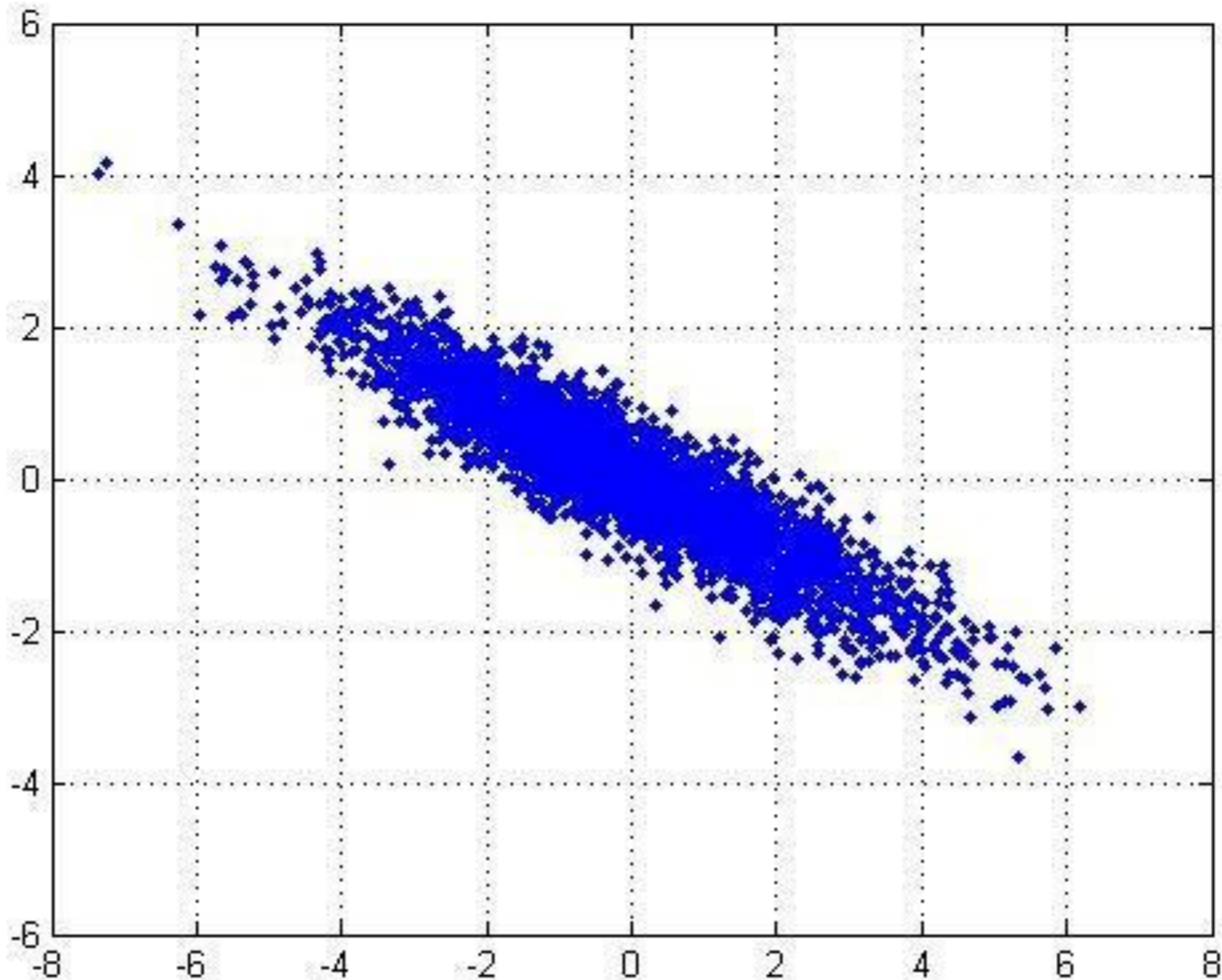
Orthogonal projection of the data onto a lower-dimension linear space that...

- maximizes variance of projected data (purple line)
- minimizes mean squared distance between
  - data point and
  - projections (sum of blue lines)

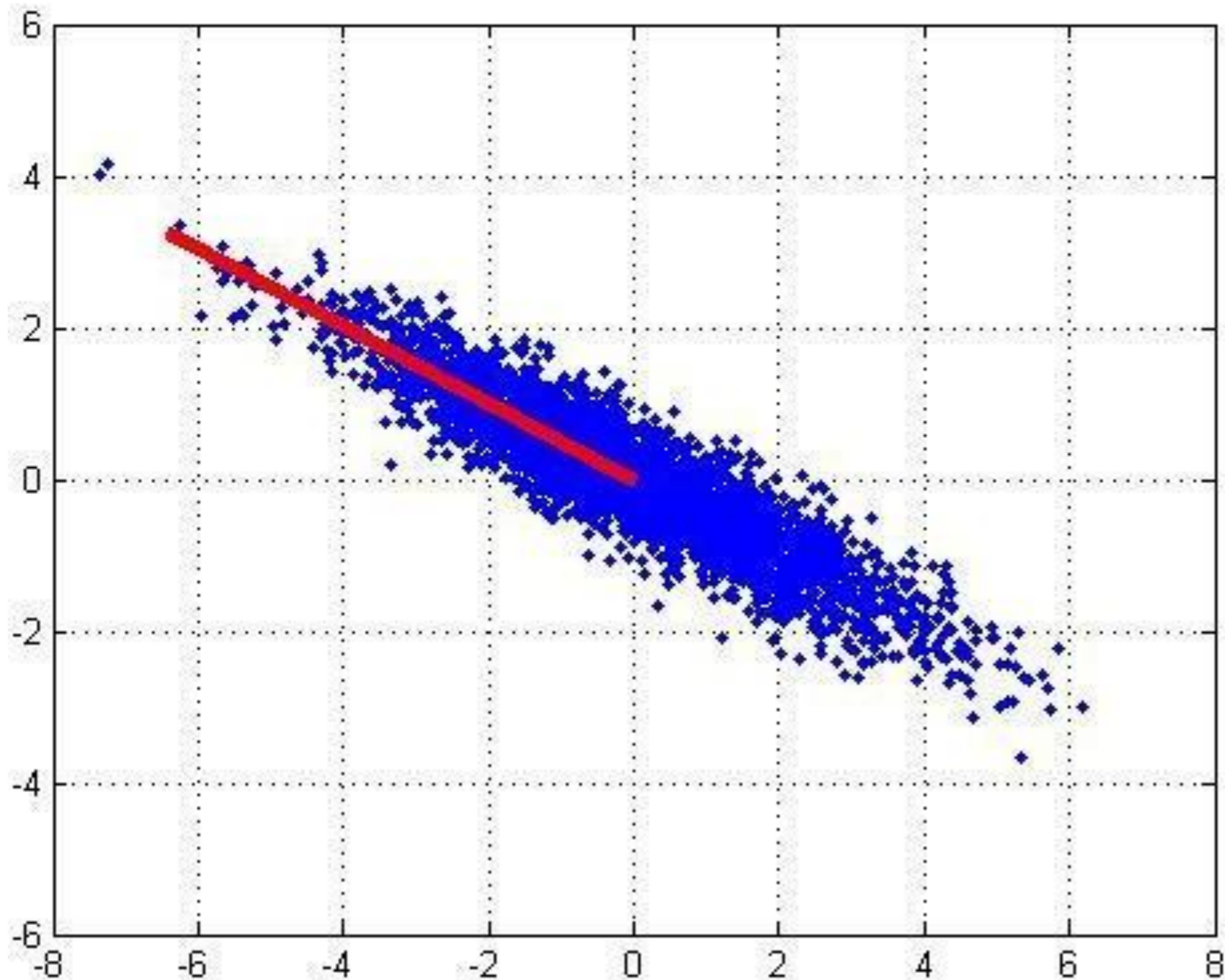
# Principal Component Analysis

- **PCA Vectors** originate from the center of mass.
- Principal component #1: points in the direction of the **largest variance**.
- Each subsequent principal component
  - is **orthogonal** to the previous ones, and
  - points in the directions of the **largest variance of the residual subspace**

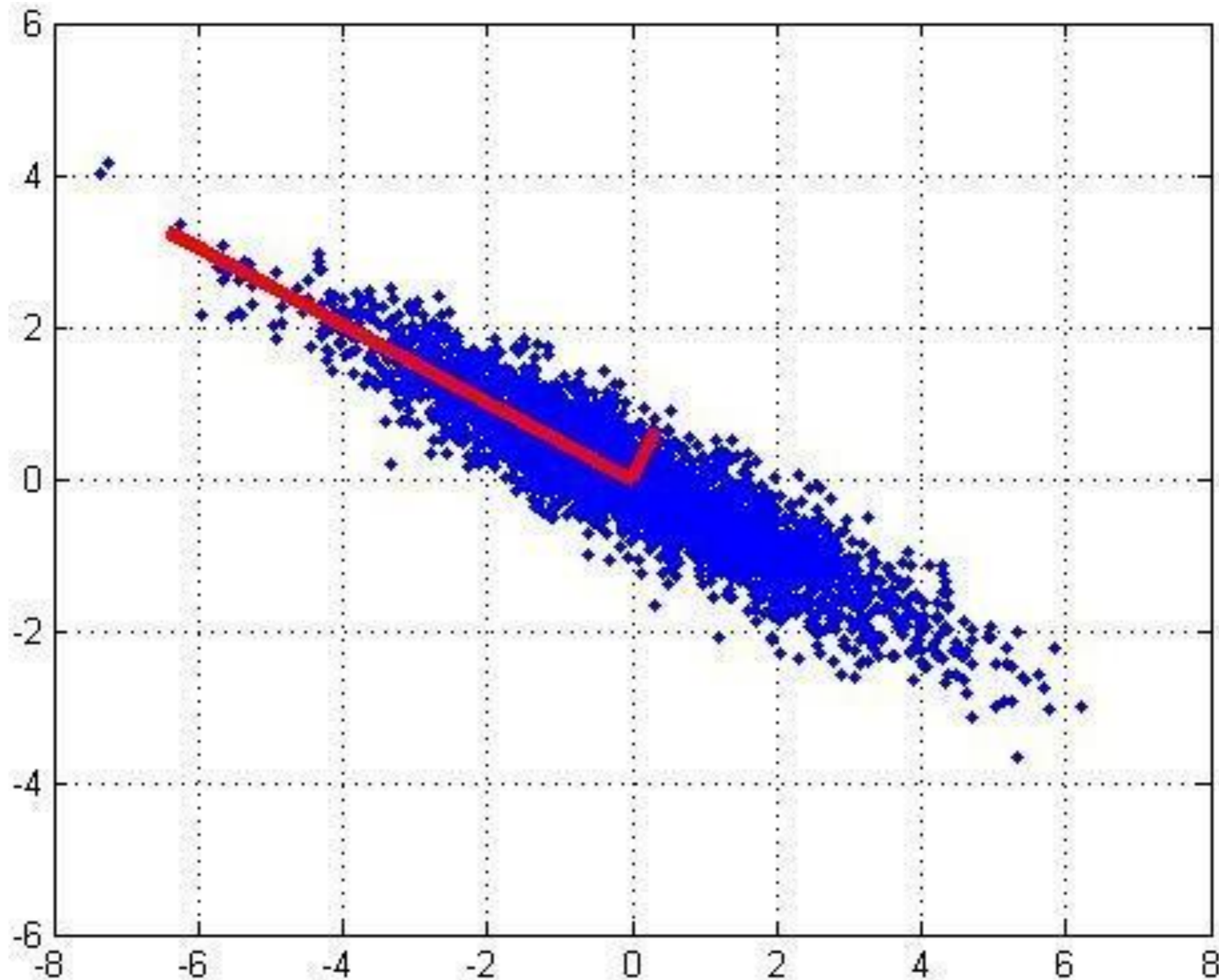
# 2D Gaussian dataset



# 1<sup>st</sup> PCA axis



# 2<sup>nd</sup> PCA axis



# PCA algorithm I (sequential)

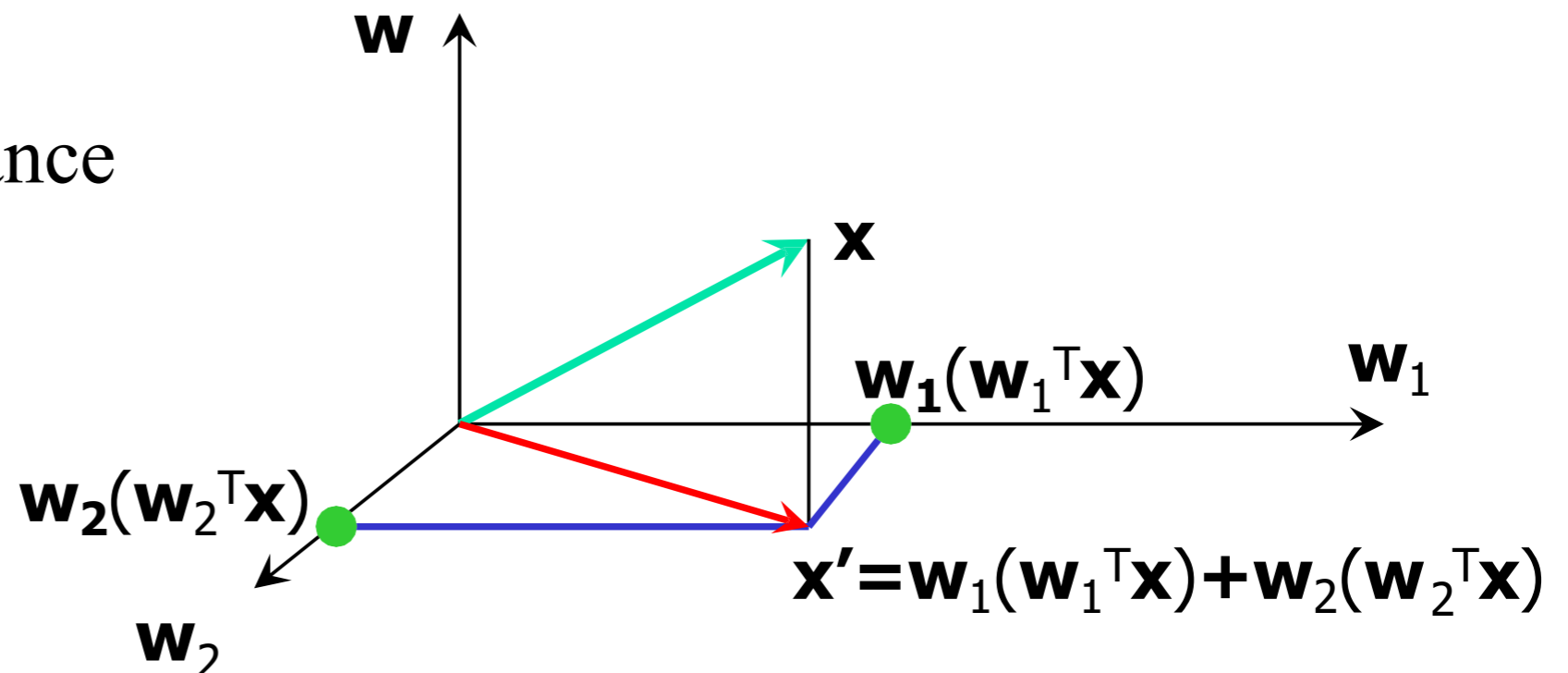
Given the **centered** data  $\{\mathbf{x}_1, \dots, \mathbf{x}_m\}$ , compute the principal vectors:

$$\mathbf{w}_1 = \arg \max_{\|\mathbf{w}\|=1} \frac{1}{m} \sum_{i=1}^m \{(\mathbf{w}^T \mathbf{x}_i)^2\} \quad \text{1st PCA vector}$$

We maximize the variance of projection of  $\mathbf{x}$

$$\mathbf{w}_k = \arg \max_{\|\mathbf{w}\|=1} \frac{1}{m} \sum_{i=1}^m \{[\mathbf{w}^T (\mathbf{x}_i - \underbrace{\sum_{j=1}^{k-1} \mathbf{w}_j \mathbf{w}_j^T \mathbf{x}_i}_{\mathbf{x}' \text{ PCA reconstruction}})]^2\} \quad k^{\text{th}} \text{ PCA vector}$$

We maximize the variance of the projection in the residual subspace



# PCA algorithm II

## (sample covariance matrix)

- Given data  $\{\mathbf{x}_1, \dots, \mathbf{x}_m\}$ , compute covariance matrix  $\Sigma$

$$\Sigma = \frac{1}{m} \sum_{i=1}^m (\mathbf{x}_i - \bar{\mathbf{x}})(\mathbf{x}_i - \bar{\mathbf{x}})^T \quad \text{where} \quad \bar{\mathbf{x}} = \frac{1}{m} \sum_{i=1}^m \mathbf{x}_i$$

- PCA** basis vectors = the eigenvectors of  $\Sigma$
- Larger eigenvalue  $\Rightarrow$  more important eigenvectors

# Reminder: Eigenvector and Eigenvalue

$$Ax = \lambda x$$

A: Square matrix

$\lambda$ : Eigenvalue or characteristic value

$x$ : Eigenvector or characteristic vector

*Show  $x = \begin{bmatrix} 2 \\ 1 \end{bmatrix}$  is an eigenvector for  $A = \begin{bmatrix} 2 & -4 \\ 3 & -6 \end{bmatrix}$*

$$\text{Solution : } Ax = \begin{bmatrix} 2 & -4 \\ 3 & -6 \end{bmatrix} \begin{bmatrix} 2 \\ 1 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

$$\text{But for } \lambda = 0, \quad \lambda x = 0 \begin{bmatrix} 2 \\ 1 \end{bmatrix} = \begin{bmatrix} 0 \\ 0 \end{bmatrix}$$

*Thus,  $x$  is an eigenvector of  $A$ , and  $\lambda = 0$  is an eigenvalue.*

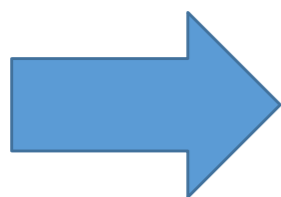
# Reminder: Eigenvector and Eigenvalue

$$\mathbf{Ax} = \lambda \mathbf{x} \quad \longrightarrow \quad \begin{aligned} \mathbf{Ax} - \lambda \mathbf{x} &= \mathbf{0} \\ (\mathbf{A} - \lambda \mathbf{I})\mathbf{x} &= \mathbf{0} \end{aligned}$$

If we define a new matrix B:  $\longrightarrow$

$$\begin{aligned} \mathbf{B} &= \mathbf{A} - \lambda \mathbf{I} \\ \mathbf{Bx} &= \mathbf{0} \end{aligned}$$

If B has an inverse:  $\longrightarrow$   $\mathbf{x} = \mathbf{B}^{-1}\mathbf{0} = \mathbf{0}$  **✗ BUT! an eigenvector cannot be zero!!**



$\mathbf{x}$  will be an eigenvector of  $\mathbf{A}$  if and only if  $\mathbf{B}$  does not have an inverse, or equivalently  $\det(\mathbf{B})=0$  :

$$\boxed{\det(\mathbf{A} - \lambda \mathbf{I}) = 0}$$

# Reminder: Eigenvector and Eigenvalue

Example 1: Find the eigenvalues of

$$A = \begin{bmatrix} 2 & -12 \\ 1 & -5 \end{bmatrix}$$

$$\begin{aligned} |\lambda I - A| &= \begin{vmatrix} \lambda - 2 & 12 \\ -1 & \lambda + 5 \end{vmatrix} = (\lambda - 2)(\lambda + 5) + 12 \\ &= \lambda^2 + 3\lambda + 2 = (\lambda + 1)(\lambda + 2) \end{aligned}$$

two eigenvalues:  $-1, -2$

*Note:* The roots of the characteristic equation can be repeated. That is,  $\lambda_1 = \lambda_2 = \dots = \lambda_k$ .  
If that happens, the eigenvalue is said to be of multiplicity  $k$ .

Example 2: Find the eigenvalues of

$$A = \begin{bmatrix} 2 & 1 & 0 \\ 0 & 2 & 0 \\ 0 & 0 & 2 \end{bmatrix}$$

$$\begin{aligned} |\lambda I - A| &= \begin{vmatrix} \lambda - 2 & -1 & 0 \\ 0 & \lambda - 2 & 0 \\ 0 & 0 & \lambda - 2 \end{vmatrix} = (\lambda - 2)^3 = 0 \end{aligned}$$

$\lambda = 2$  is an eigenvalue of multiplicity 3.

# PCA algorithm II

## (sample covariance matrix)

**Goal:** Find  $r$ -dim projection that best preserves variance

1. Compute mean vector  $\mu$  and covariance matrix  $\Sigma$  of original points
2. Compute eigenvectors and eigenvalues of  $\Sigma$
3. Select top  $r$  eigenvectors
4. Project points onto subspace spanned by them:

$$y = A(x - \mu)$$

where  $y$  is the new point,  $x$  is the old one,  
and the rows of  $A$  are the eigenvectors

# PCA algorithm III

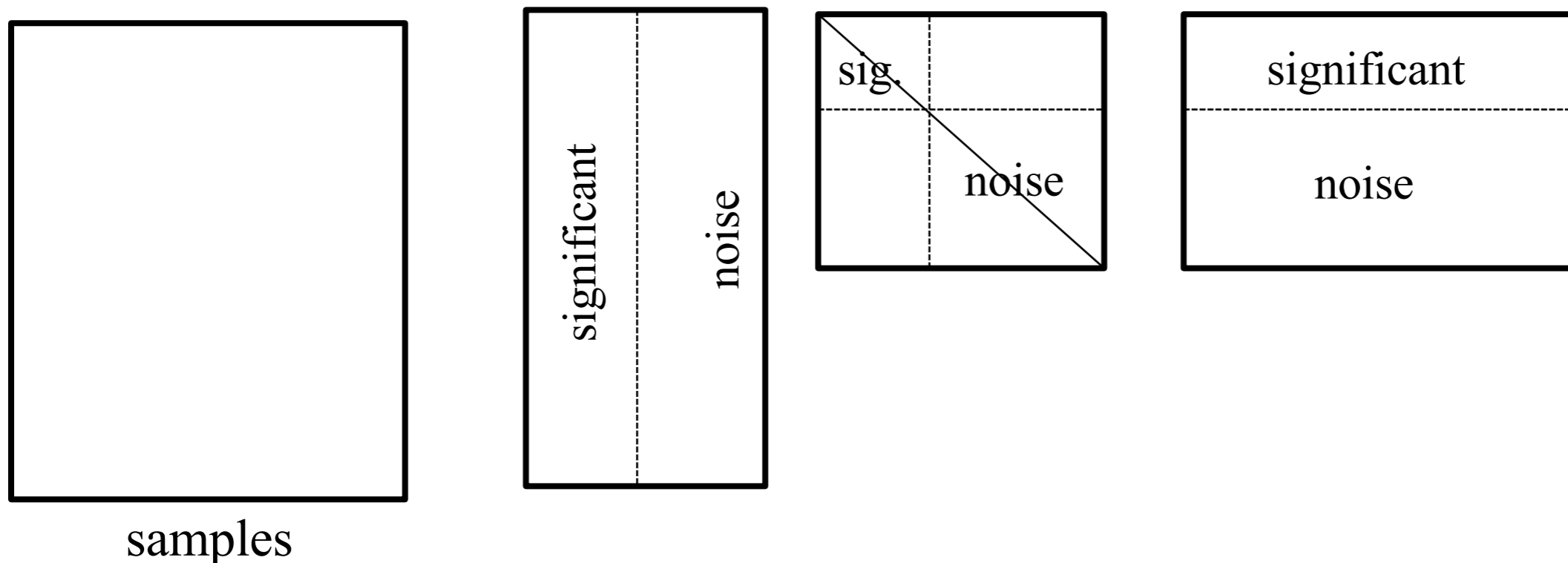
## (SVD of the data matrix)

Singular Value Decomposition of the **centered** data matrix **X**.

$$\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_m] \in \mathbb{R}^{N \times m}, \quad \begin{array}{l} m: \text{number of instances,} \\ N: \text{dimension} \end{array}$$

$$\mathbf{X}_{\text{features} \times \text{samples}} = \mathbf{U} \mathbf{S} \mathbf{V}^T$$

$$\mathbf{X} = \mathbf{U} \mathbf{S} \mathbf{V}^T$$



# PCA algorithm III

- **Columns of  $U$**

- the principal vectors,  $\{ \mathbf{u}^{(1)}, \dots, \mathbf{u}^{(k)} \}$
- orthogonal and has unit norm – so  $U^T U = I$
- Can reconstruct the data using linear combinations of  $\{ \mathbf{u}^{(1)}, \dots, \mathbf{u}^{(k)} \}$

- **Matrix  $S$**

- Diagonal
- Shows importance of each eigenvector

- **Columns of  $V^T$**

- The coefficients for reconstructing the samples

# Applications

# Face Recognition

# Face Recognition

- Want to identify specific person, based on facial image
- Robust to glasses, lighting, ...
  - Can't just use the given 256 x 256 pixels



# Applying PCA: Eigenfaces

**Method A:** Build a PCA subspace for each person and check which subspace can reconstruct the test image the best

**Method B:** Build one PCA database for the whole dataset and then classify based on the weights.



□ Example data set: Images of faces

- Famous Eigenface approach  
[Turk & Pentland], [Sirovich & Kirby]

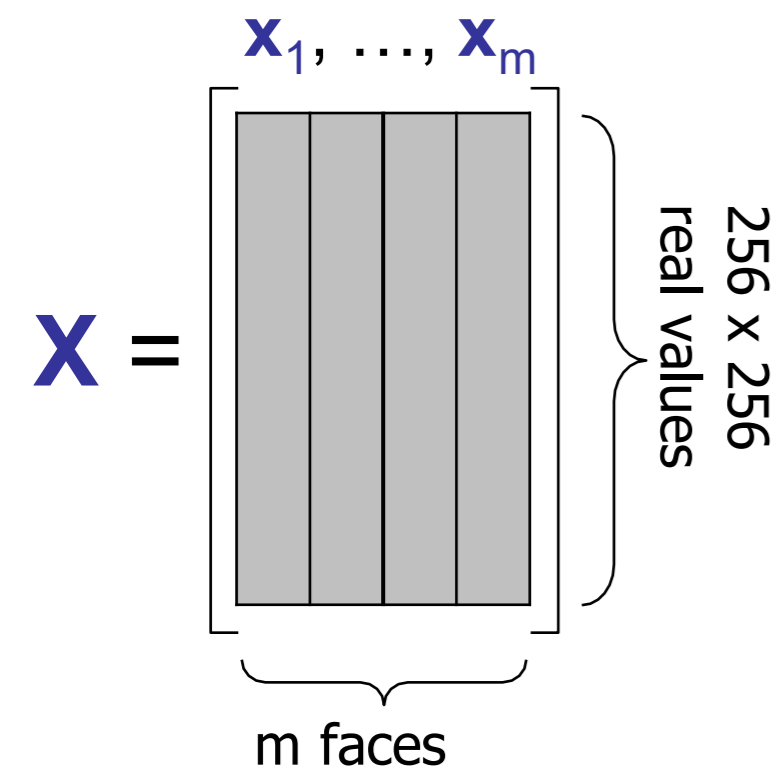
□ Each face  $\mathbf{x}$  is ...

- $256 \times 256$  values (luminance at location)
- $\mathbf{x}$  in  $\mathbb{R}^{256 \times 256}$  (view as 64K dim vector)

□ Form  $\mathbf{X} = [\mathbf{x}_1, \dots, \mathbf{x}_m]$  **centered** data mtx

□ Compute  $\mathbf{\Sigma} = \mathbf{X}\mathbf{X}^T$

□ Problem:  $\mathbf{\Sigma}$  is  $64K \times 64K$  ... HUGE!!!



# A Clever Workaround

- Note that  $m \ll 64K$
- Use  $\mathbf{L} = \mathbf{X}^T \mathbf{X}$  instead of  $\Sigma = \mathbf{X} \mathbf{X}^T$
- If  $\mathbf{v}$  is eigenvector of  $\mathbf{L}$   
then  $\mathbf{X} \mathbf{v}$  is eigenvector of  $\Sigma$

Proof:

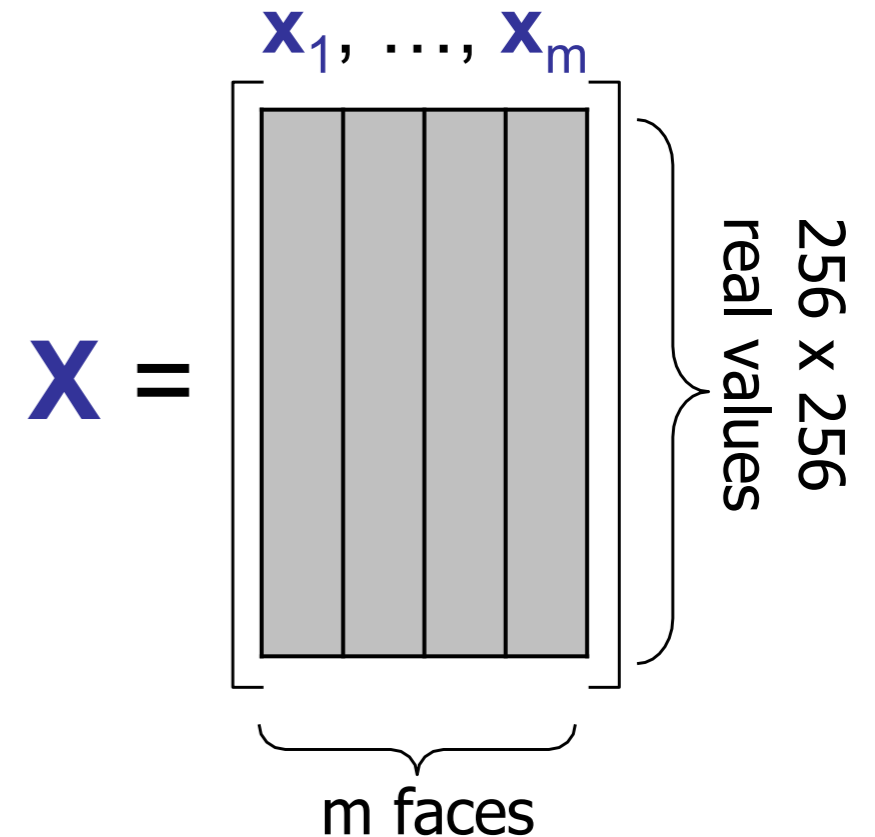
$$\mathbf{L} \mathbf{v} = \gamma \mathbf{v}$$

$$\mathbf{X}^T \mathbf{X} \mathbf{v} = \gamma \mathbf{v}$$

$$\mathbf{X} (\mathbf{X}^T \mathbf{X} \mathbf{v}) = \mathbf{X} (\gamma \mathbf{v}) = \gamma \mathbf{X} \mathbf{v}$$

$$(\mathbf{X} \mathbf{X}^T) \mathbf{X} \mathbf{v} = \gamma (\mathbf{X} \mathbf{v})$$

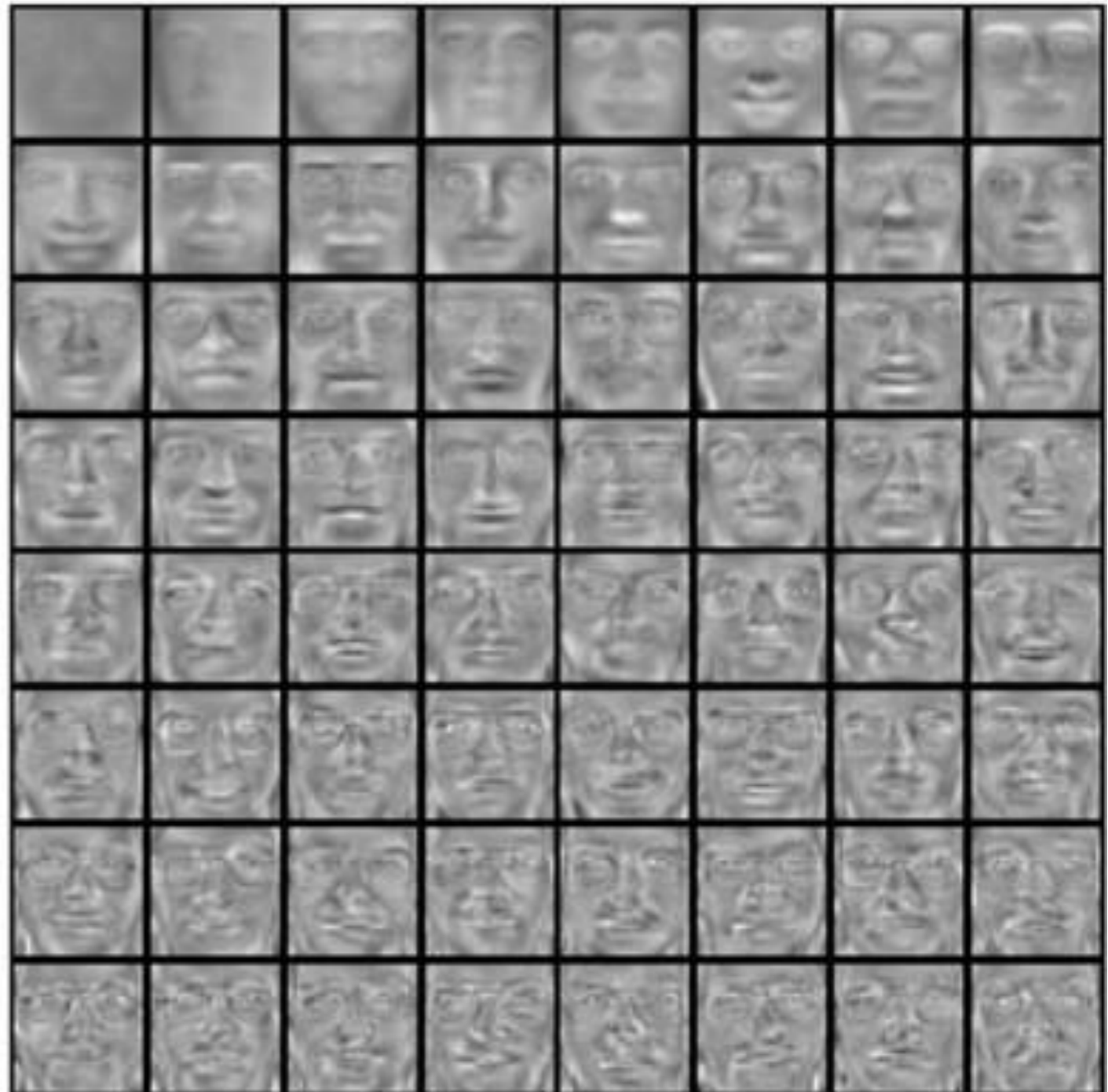
$$\Sigma (\mathbf{X} \mathbf{v}) = \gamma (\mathbf{X} \mathbf{v})$$



# Eigenfaces Example

Top eigenvectors:  $u_1, \dots, u_k$

Mean:  $\mu$



# Representation and Reconstruction

- Face  $\mathbf{x}$  in “face space” coordinates:



$$\mathbf{x} \rightarrow [\mathbf{u}_1^T (\mathbf{x} - \mu), \dots, \mathbf{u}_k^T (\mathbf{x} - \mu)]$$

$$= w_1, \dots, w_k$$

- Reconstruction:



=



+



$\hat{\mathbf{x}}$

=

$\mu$

+

$w_1 u_1 + w_2 u_2 + w_3 u_3 + w_4 u_4 + \dots$

# Principle Components (Method B)



# Principle Components (Method B)



- ... faster if train with ...
  - only people w/out glasses
  - same lighting conditions

# When projecting strange data

- Original images
- Reconstruction doesn't look like the original



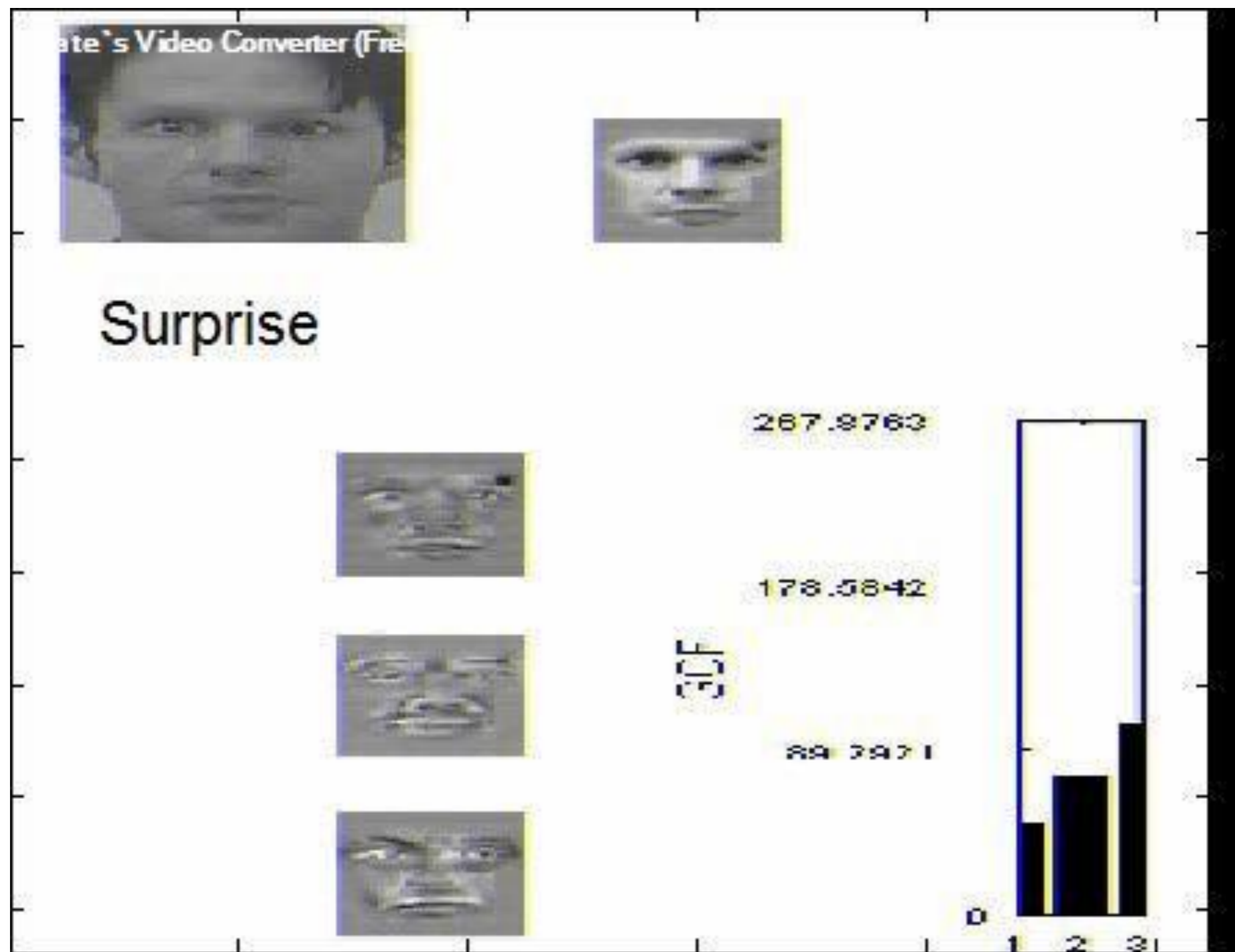
# Happiness subspace (method A)



# Disgust subspace (method A)



# Facial Expression Recognition Movies

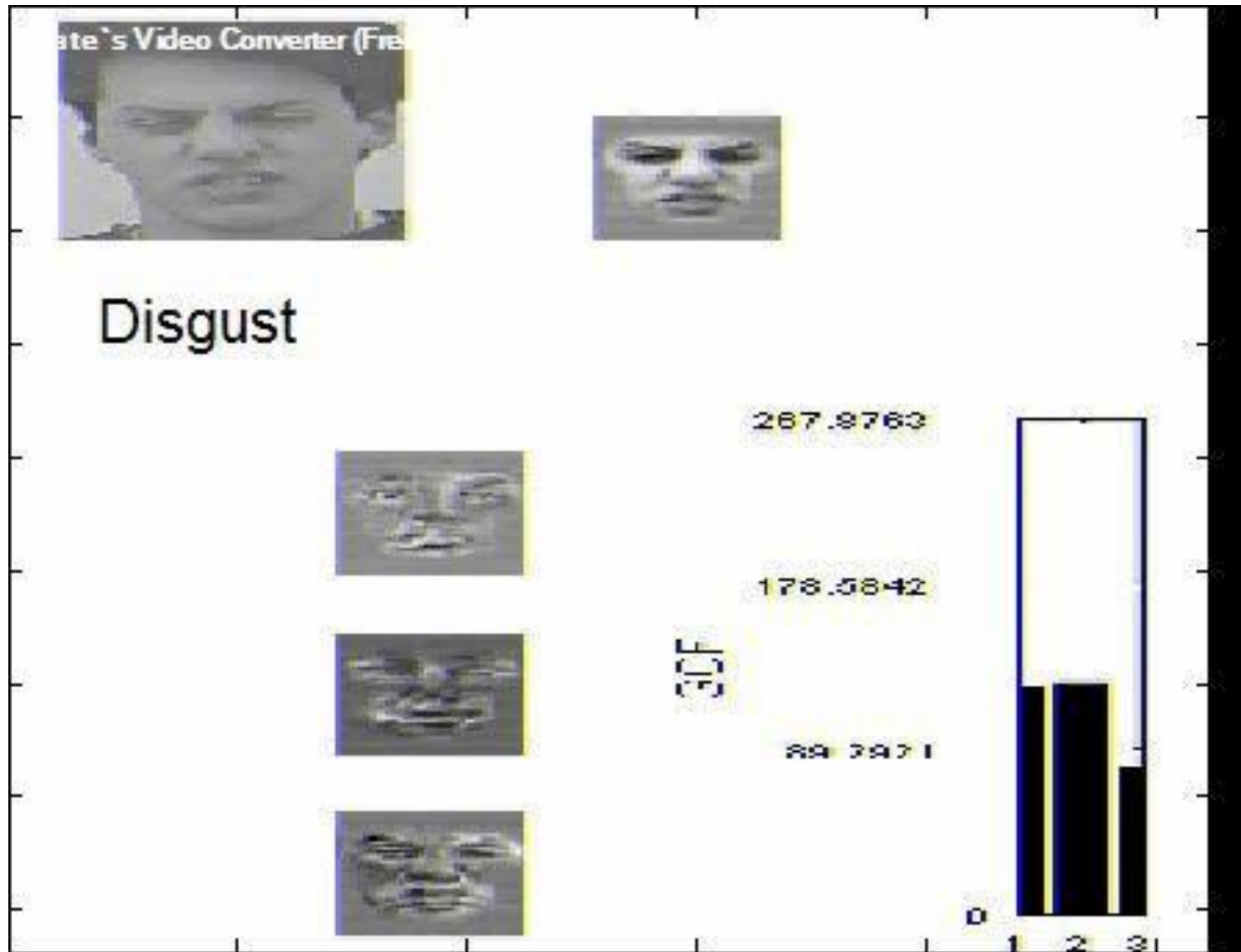


# Facial Expression Recognition

## Movies



# Facial Expression Recognition Movies



# Shortcomings

- Requires carefully controlled data:
  - All faces centered in frame
  - Same size
  - Some sensitivity to angle
- Method is completely knowledge free
  - (sometimes this is good!)
  - Doesn't know that faces are wrapped around 3D objects (heads)
  - Makes no effort to preserve class distinctions

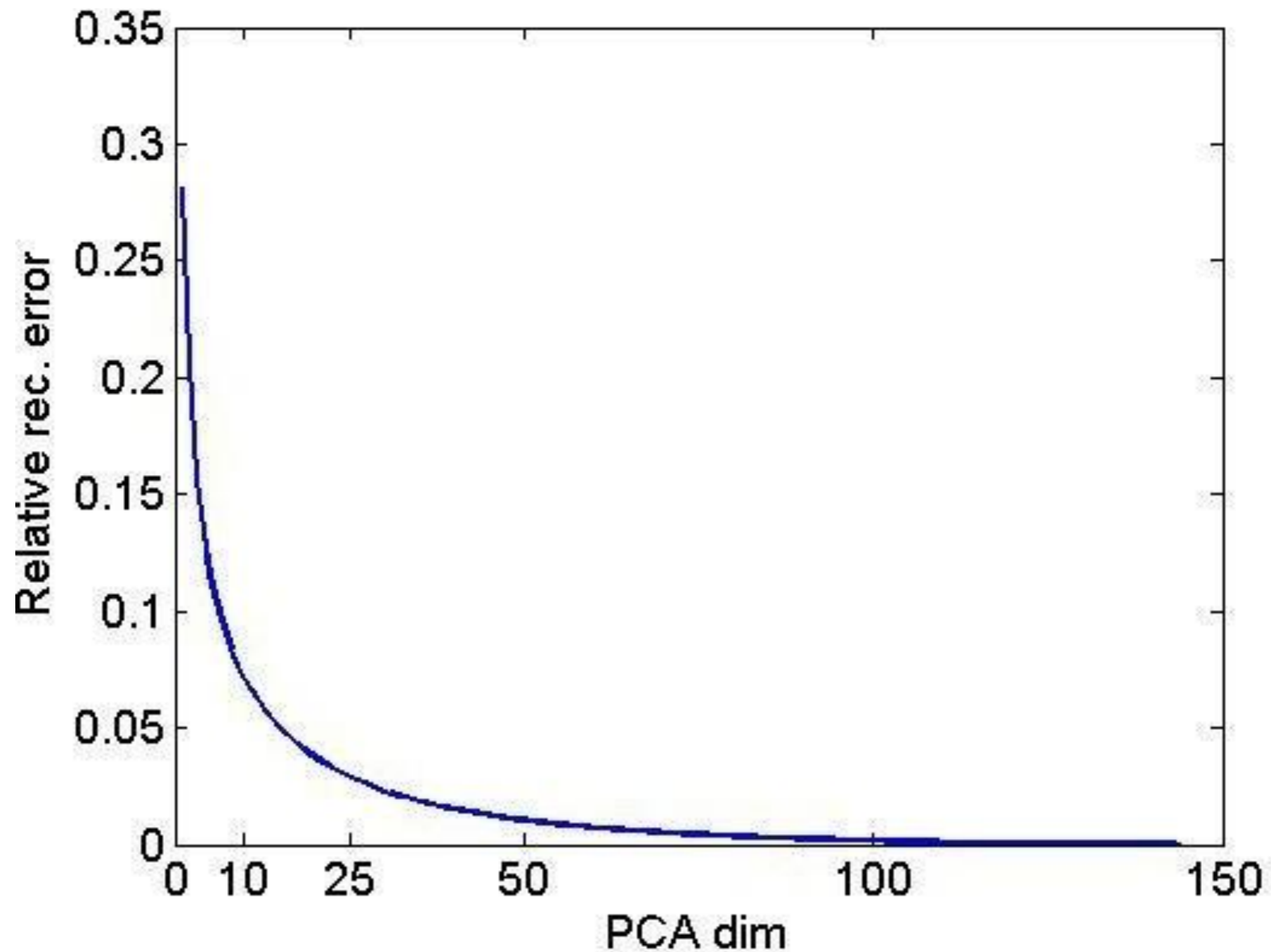
# Image Compression

# Original Image



- Divide the original 372x492 image into patches:
  - Each patch is an instance
- View each as a 144-D vector

# $L_2$ error and PCA dim



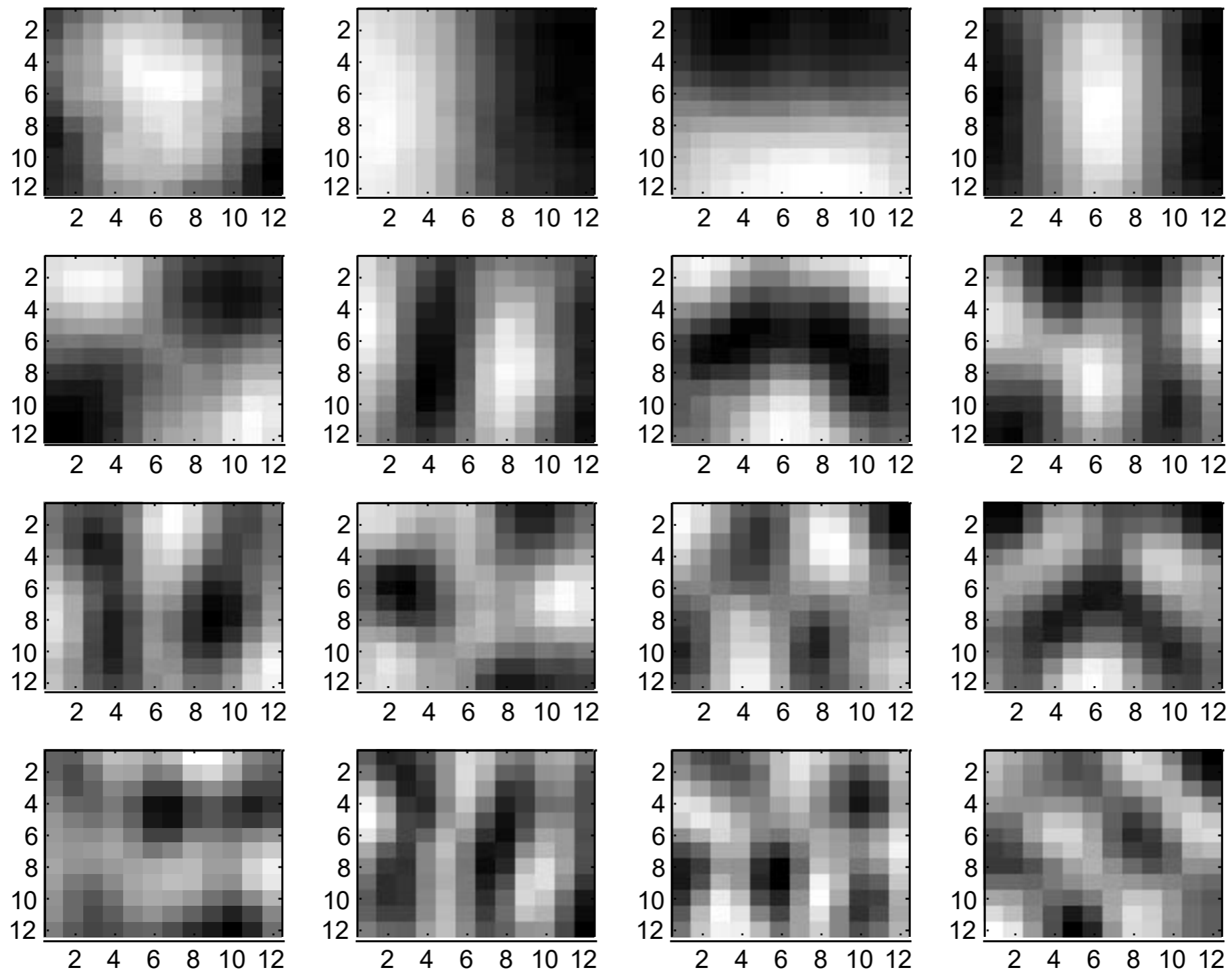
PCA compression: 144D => 60D



PCA compression: 144D => 16D



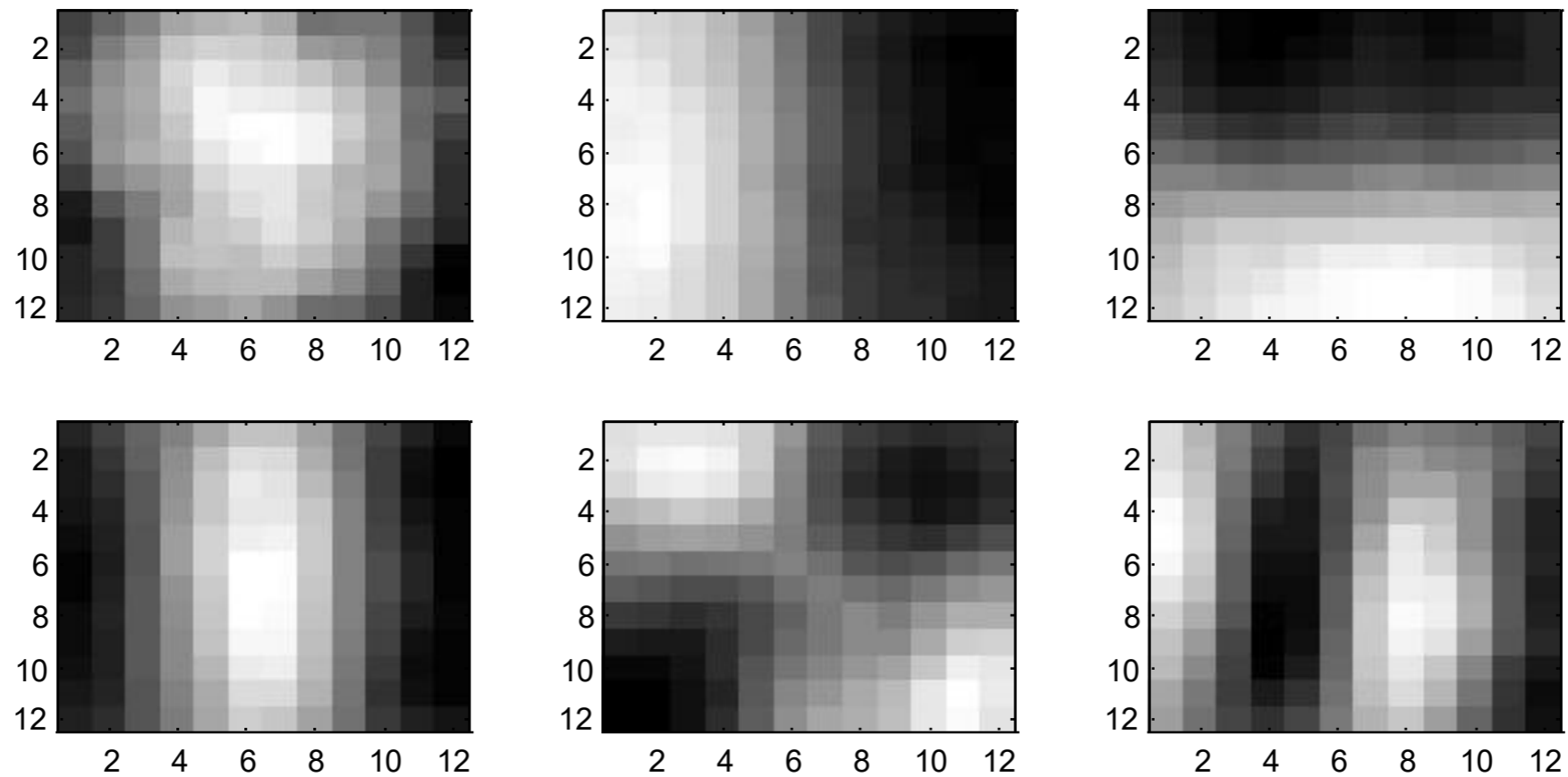
# 16 most important eigenvectors



PCA compression: 144D  $\Rightarrow$  6D



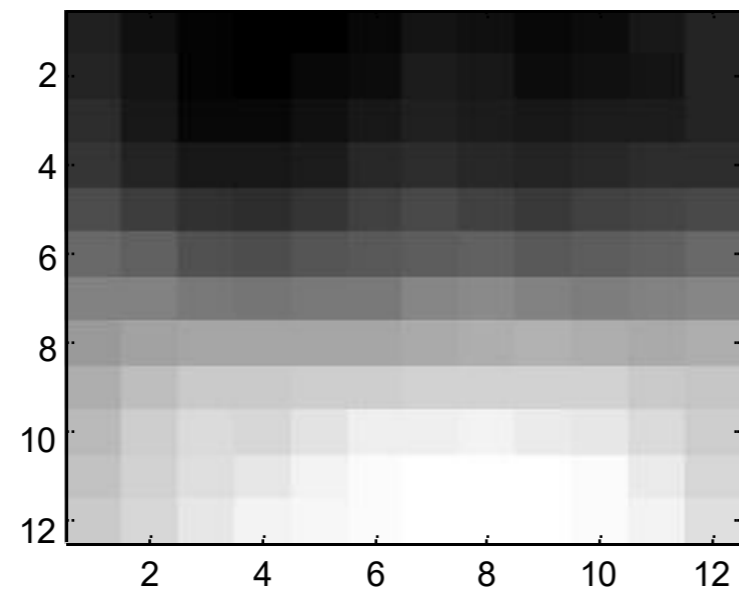
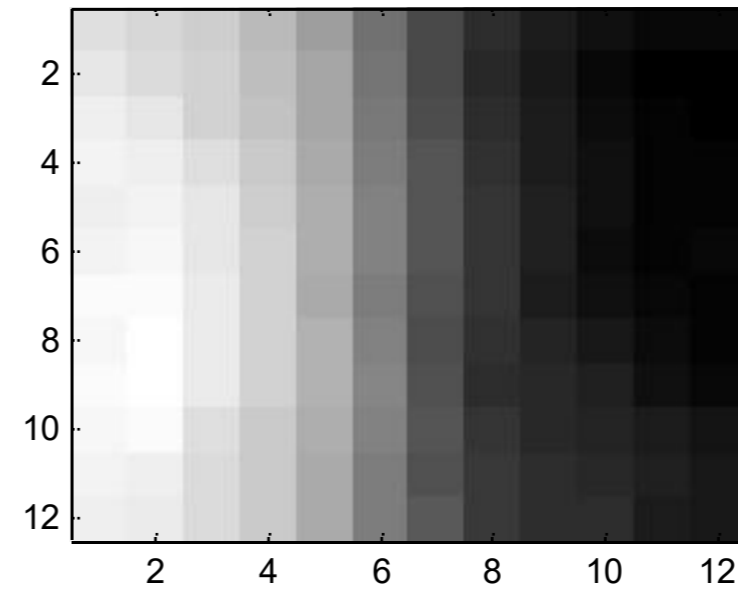
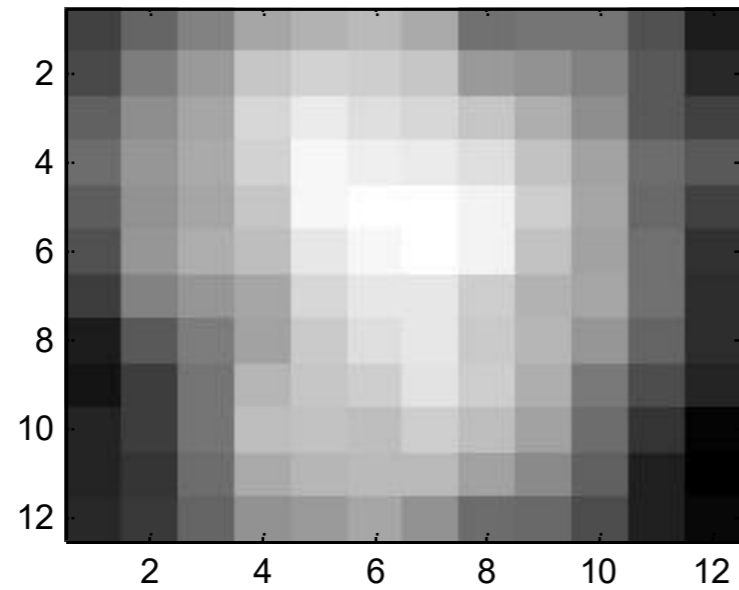
# 6 most important eigenvectors



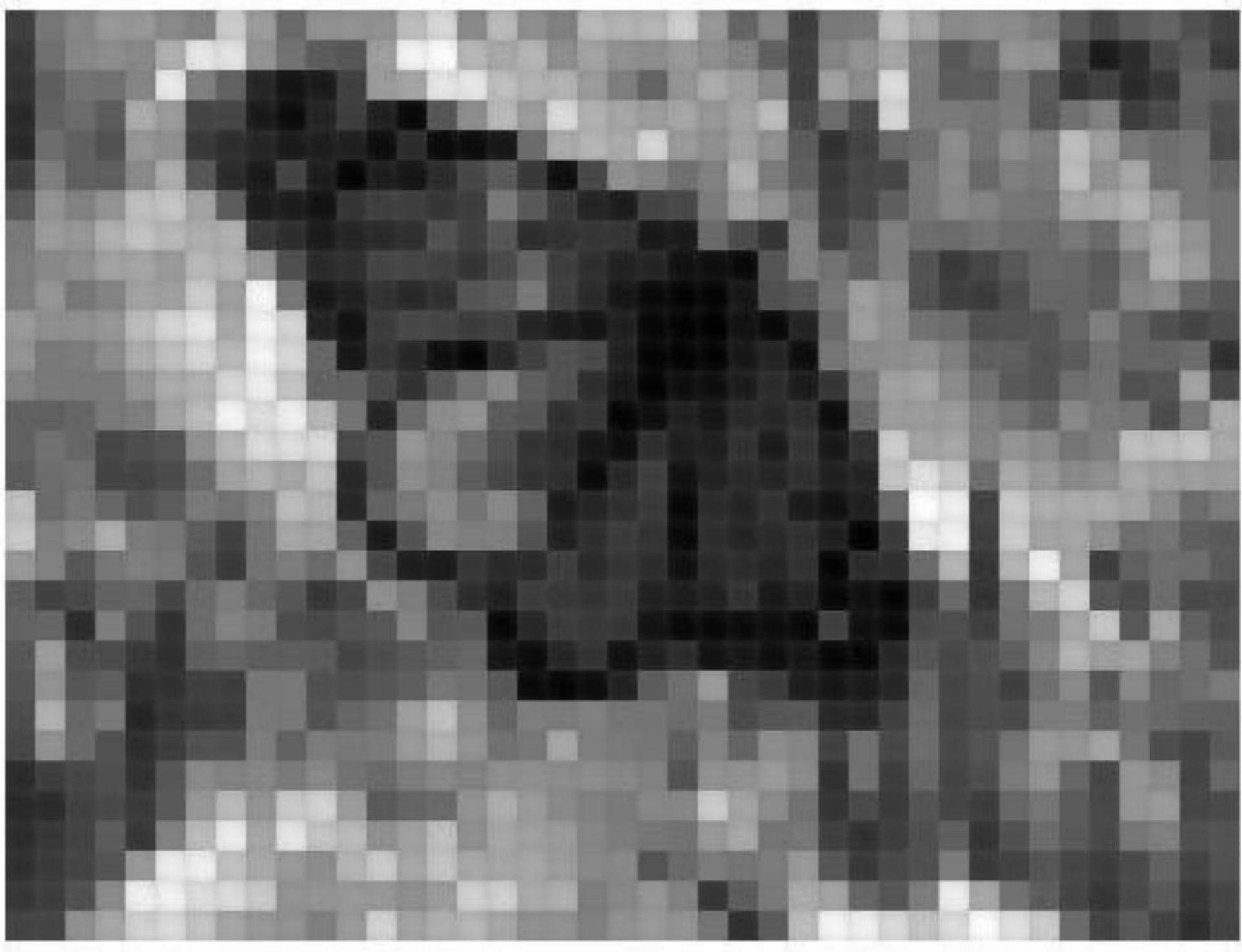
# PCA compression: 144D => 3D



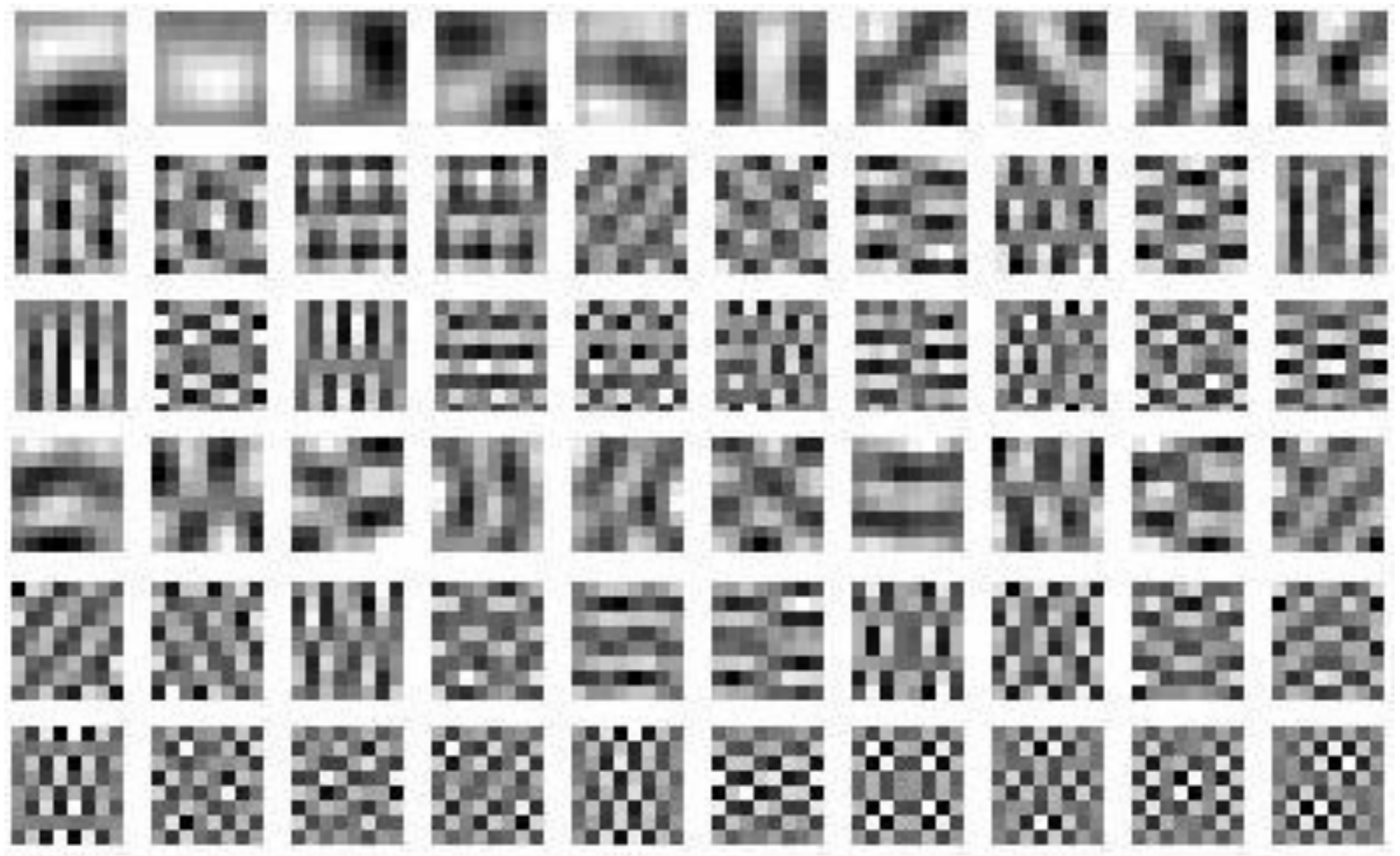
# 3 most important eigenvectors



PCA compression: 144D  $\Rightarrow$  1D

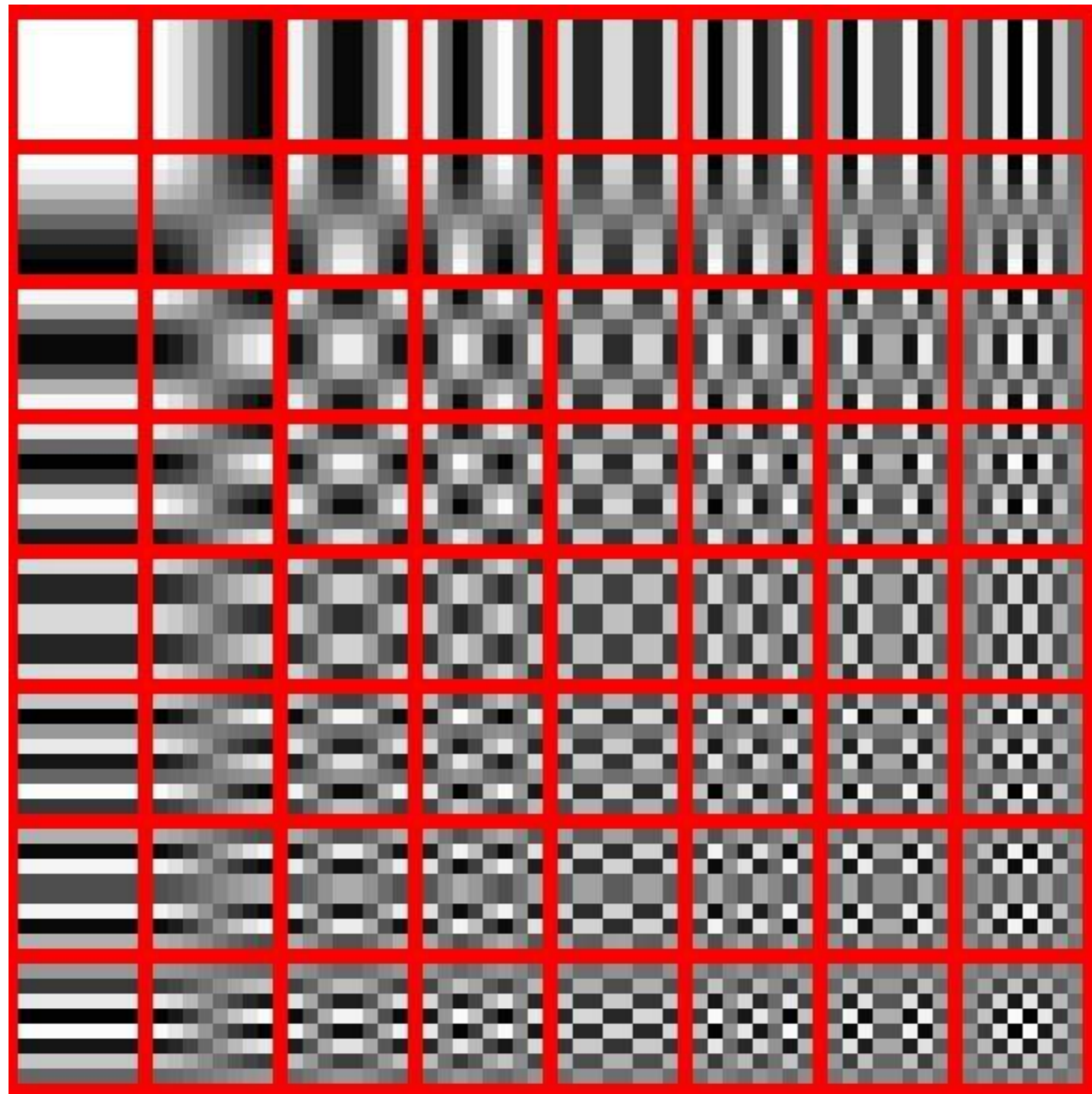


# 60 most important eigenvectors



- Looks like the discrete cosine bases of JPEG!...

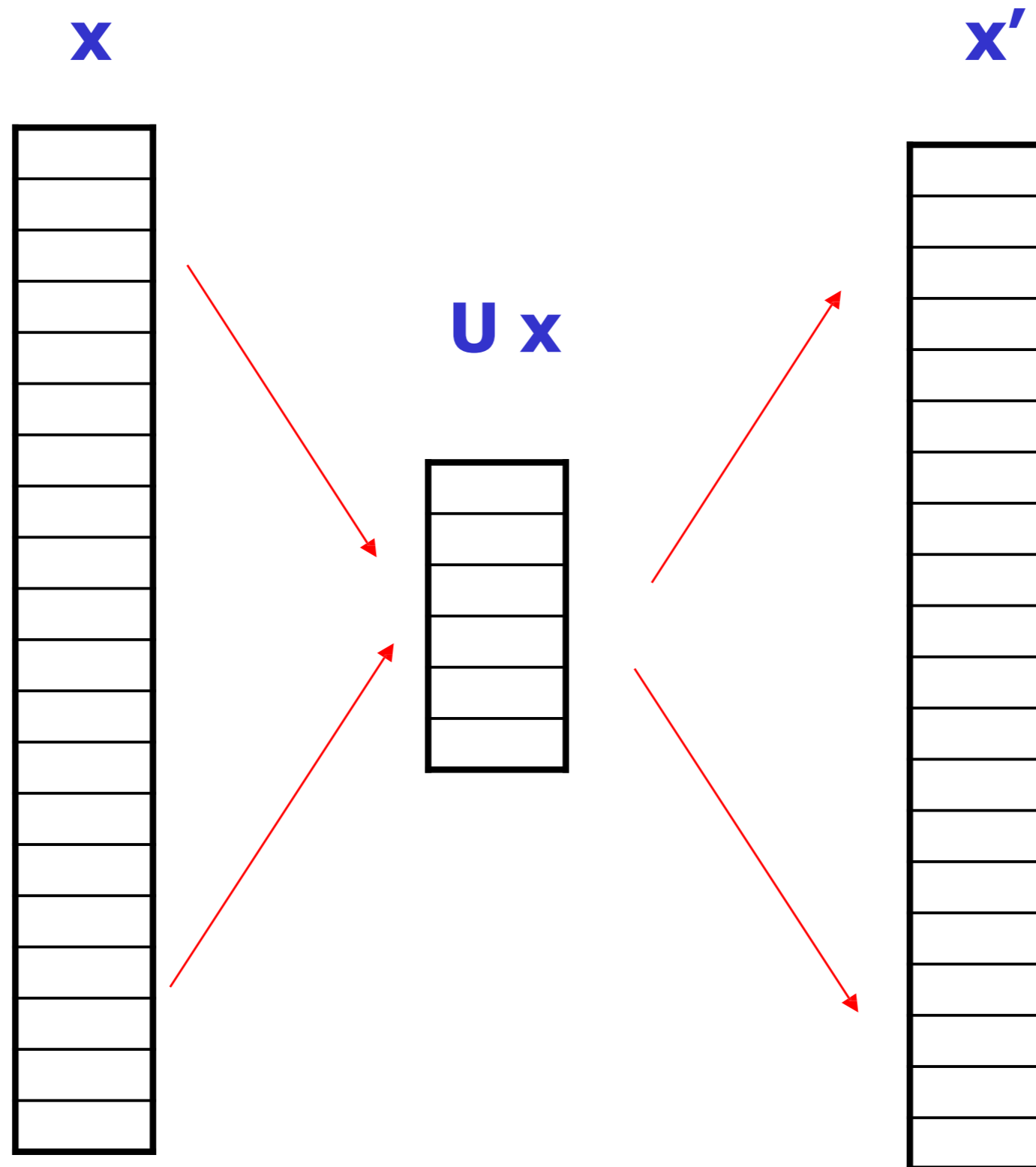
# 2D Discrete Cosine Basis



[http://en.wikipedia.org/wiki/Discrete cosine transform](http://en.wikipedia.org/wiki/Discrete_cosine_transform)

# Noise Filtering

# Noise Filtering



# Noisy image



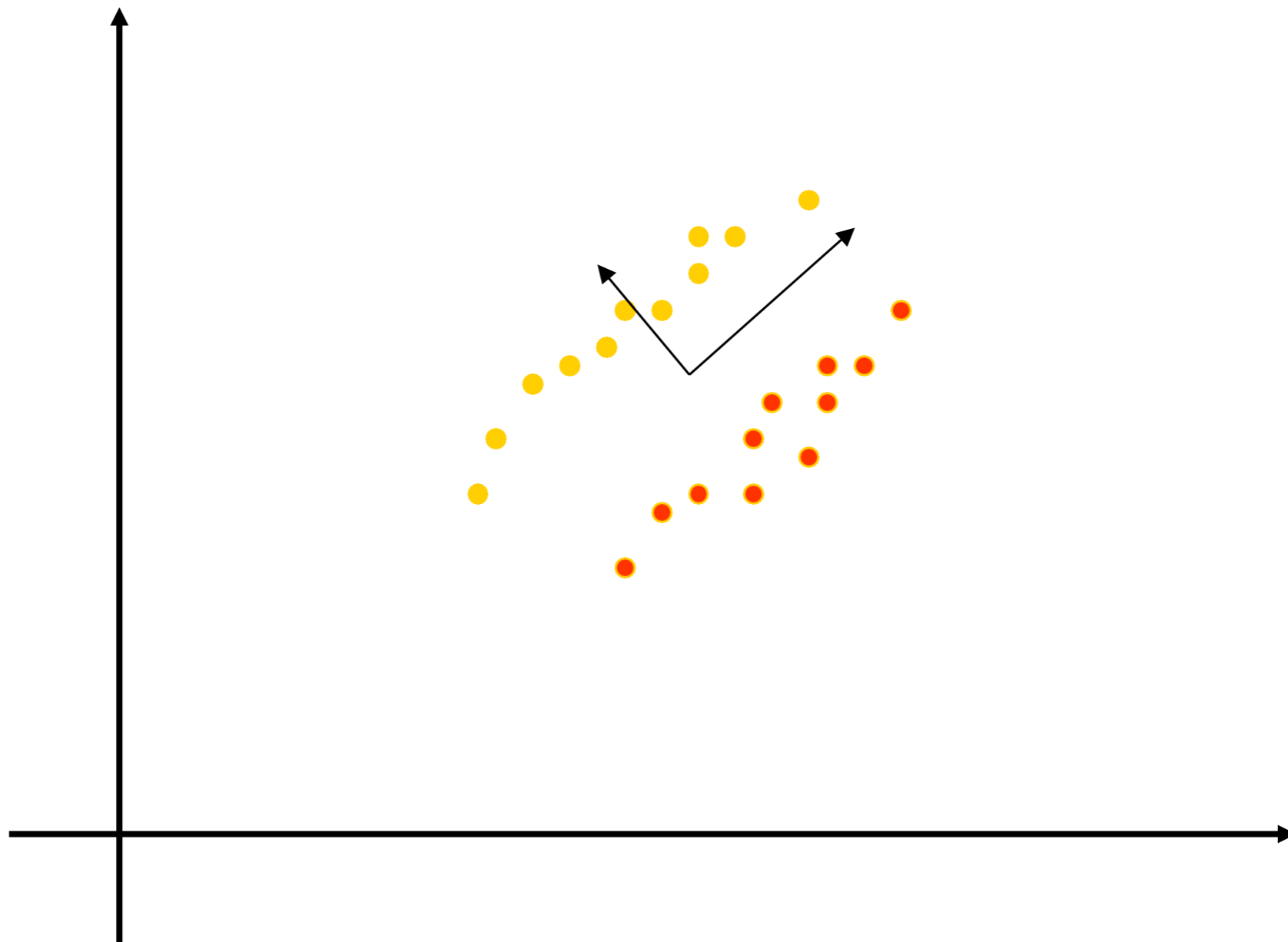
# Denoised image using 15 PCA components



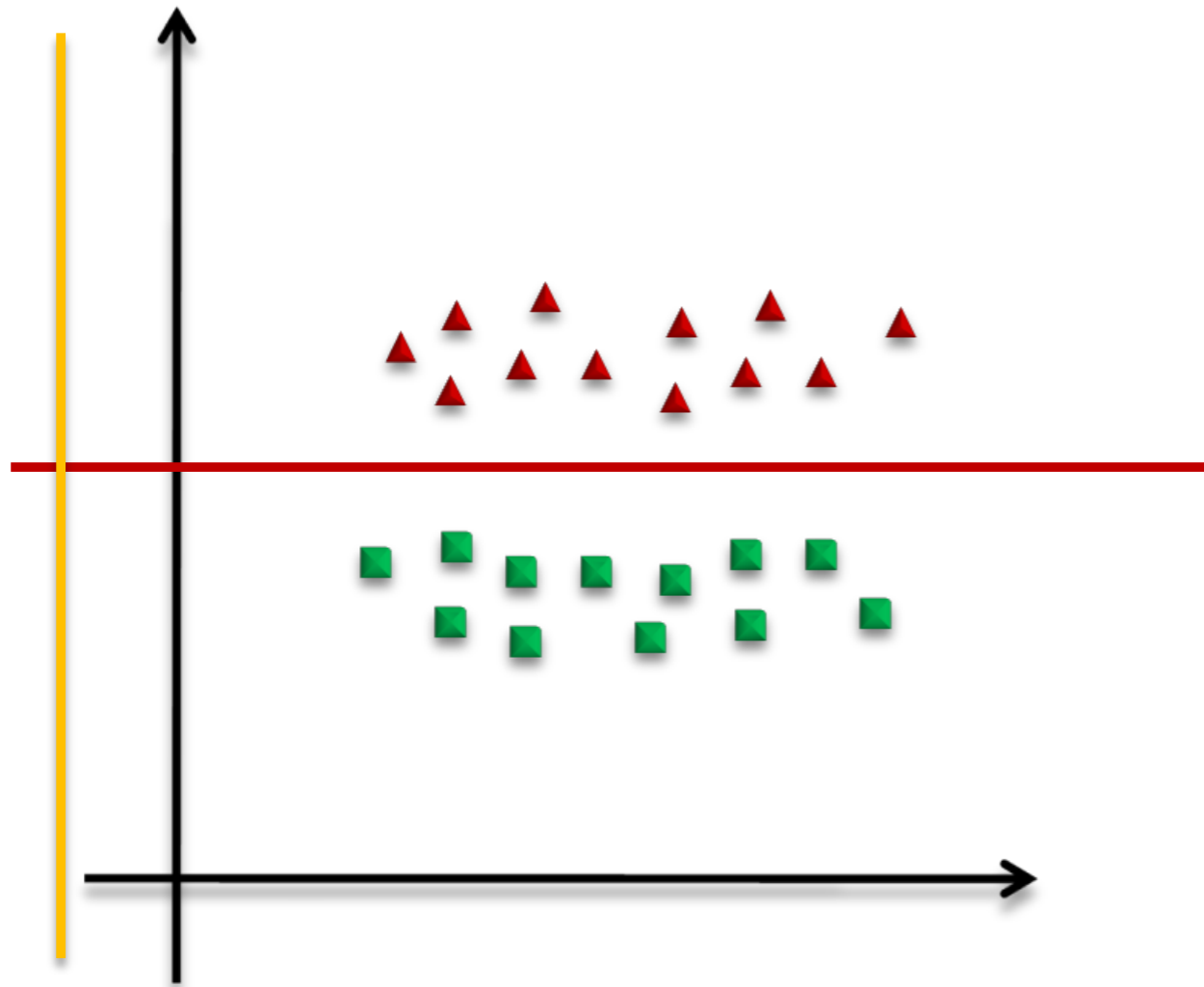
# PCA Shortcomings

# Problematic Data Set for PCA

- PCA doesn't know labels!



# PCA vs. Fisher Linear Discriminant



## Principal Component Analysis

- higher variance
- bad for discriminability



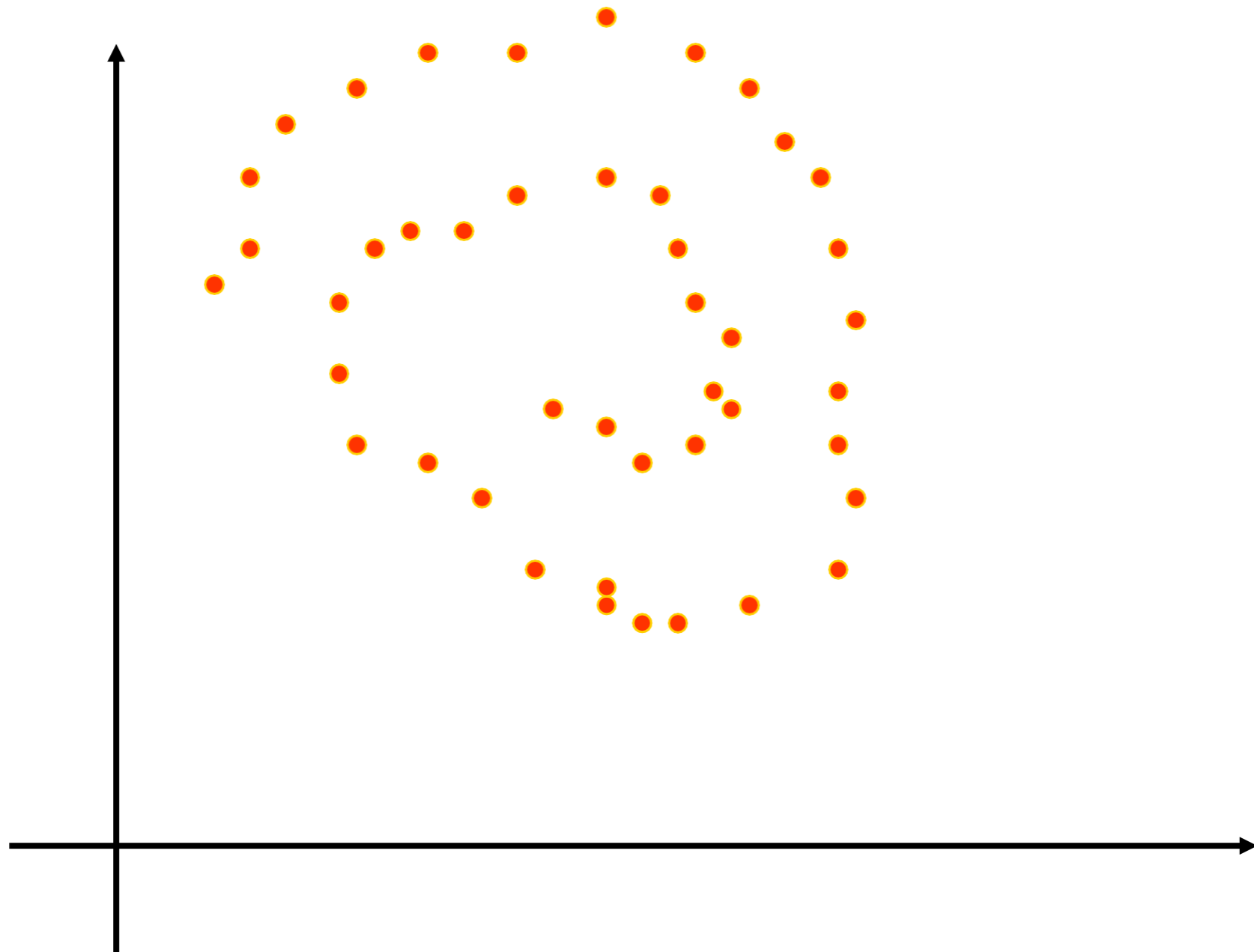
## Fisher Linear Discriminant

- smaller variance
- good discriminability



# Problematic Data Set for PCA

- PCA cannot capture NON-LINEAR structure!



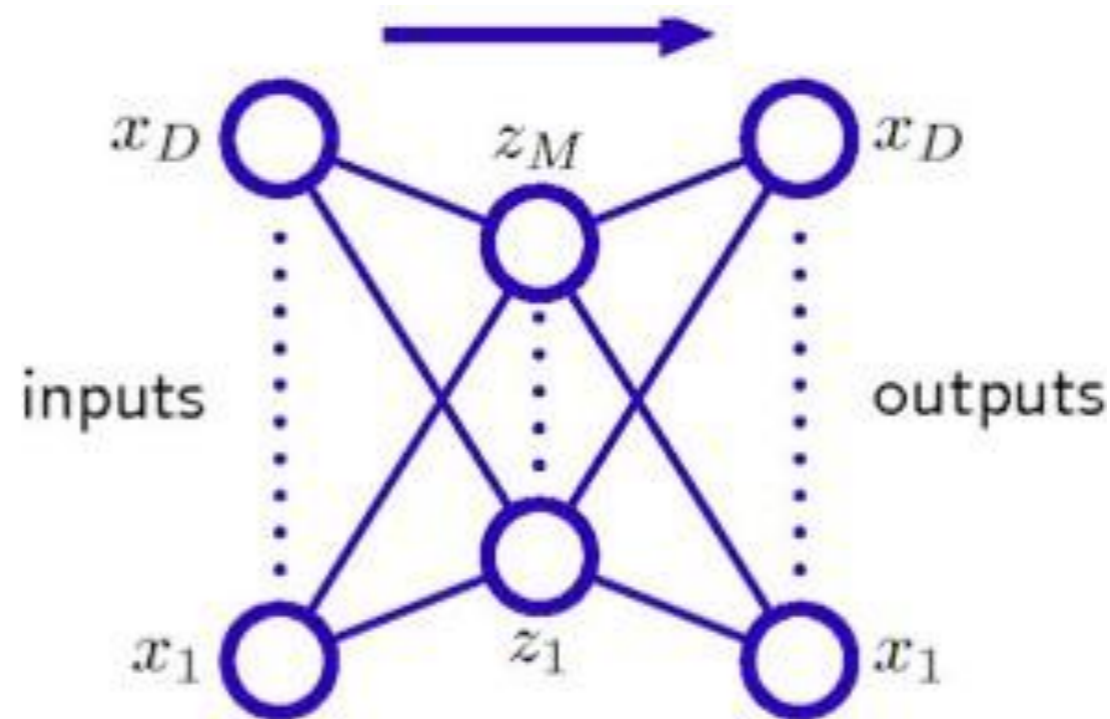
# PCA Conclusions

- PCA
  - Finds orthonormal basis for data
  - Sorts dimensions in order of “importance”
  - Discard low significance dimensions
- Uses:
  - Get compact description
  - Ignore noise
  - Improve classification (hopefully)
- Not magic:
  - Doesn't know class labels
  - Can only capture linear variations
- One of many tricks to reduce dimensionality!

# Autoencoders

# Relation to Neural Networks

- PCA is closely related to a particular form of neural network
- An **autoencoder** is a neural network whose outputs are its own inputs



- The goal is to minimize **reconstruction error**

# Auto encoders

- Define

$$\mathbf{z} = f(W\mathbf{x}); \quad \hat{\mathbf{x}} = g(V\mathbf{z})$$

- Goal:

$$\min_{W,V} \frac{1}{2N} \sum_{n=1}^N \|\mathbf{x}^{(n)} - \hat{\mathbf{x}}^{(n)}\|^2$$

- If  $g$  and  $f$  are linear

$$\min_{W,V} \frac{1}{2N} \sum_{n=1}^N \|\mathbf{x}^{(n)} - VW\mathbf{x}^{(n)}\|^2$$

# Auto encoders

- Define

$$\mathbf{z} = f(W\mathbf{x}); \quad \hat{\mathbf{x}} = g(V\mathbf{z})$$

- Goal:

$$\min_{W,V} \frac{1}{2N} \sum_{n=1}^N \|\mathbf{x}^{(n)} - \hat{\mathbf{x}}^{(n)}\|^2$$

- If  $g$  and  $f$  are linear

$$\min_{W,V} \frac{1}{2N} \sum_{n=1}^N \|\mathbf{x}^{(n)} - VW\mathbf{x}^{(n)}\|^2$$

- In other words, the optimal solution is PCA

# Auto encoders: Nonlinear PCA

- What if  $g(\cdot)$  is not linear?
- Then we are basically doing nonlinear PCA

# Comparing Reconstructions



Real data

30-d deep autoencoder

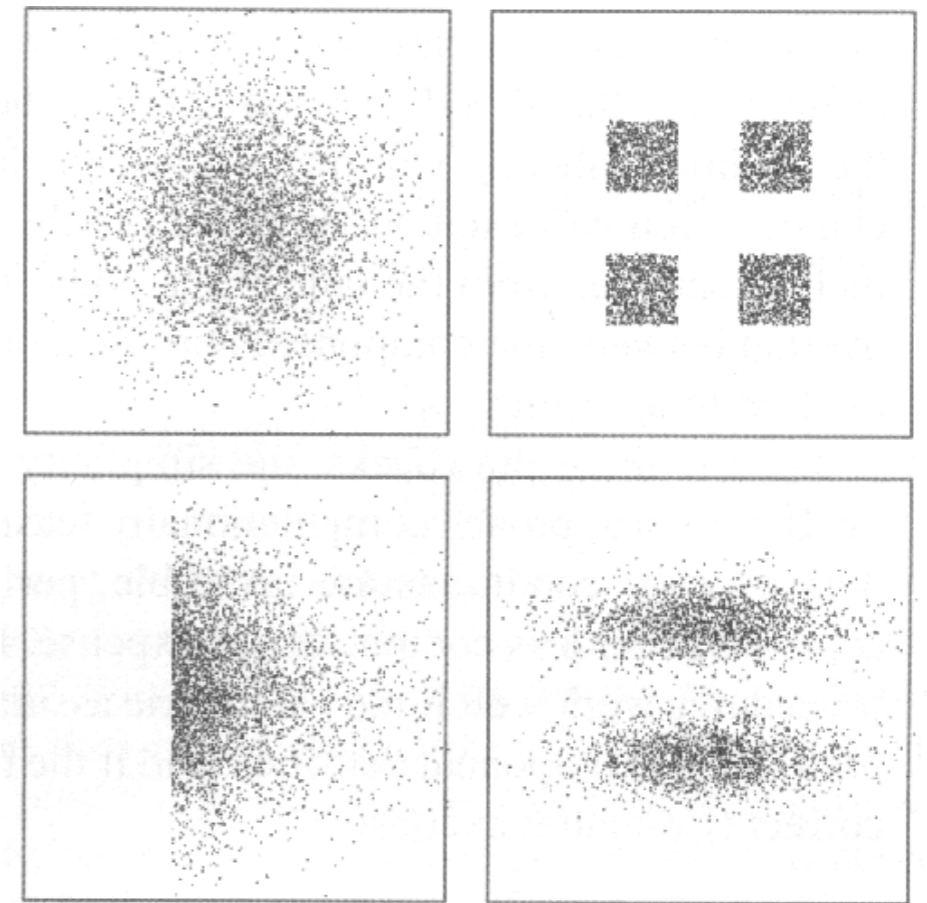
30-d logistic PCA

30-d PCA

# Independent Component Analysis (ICA)

# A Serious Limitation of PCA

- Recall that PCA looks at the covariance matrix only. What if the data is not well described by the covariance matrix?



- The only distribution which is uniquely specified by its covariance (with the subtracted mean) is the Gaussian distribution. Distributions which deviate from the Gaussian are poorly described by their covariances.

# Faithful vs Meaningful Representations

- Even with non-Gaussian data, variance maximization leads to the most faithful representation in a reconstruction error sense (recall that we trained our autoencoder network using a mean-square error in an input reconstruction layer).
- The mean-square error measure implicitly assumes Gaussianity, since it penalizes datapoints close to the mean less than those that are far away.
- But it does not in general lead to the most meaningful representation.
- We need to perform gradient descent in some function other than the reconstruction error.

# A Criterion Stronger than Decorrelation

- The way to circumvent these problems is to look for components which are **statistically independent**, rather than just uncorrelated.

- For statistical independence, we require that

$$p(\xi_1, \xi_2, \dots, \xi_N) = \prod_{i=1}^N p(\xi_i)$$

- For uncorrelatedness, all we required was that

$$\langle \xi_i \xi_j \rangle - \langle \xi_i \rangle \langle \xi_j \rangle = 0, \quad i \neq j$$

- Independence is a stronger requirement; under independence,

$$\langle g_1(\xi_i) g_2(\xi_j) \rangle - \langle g_1(\xi_i) \rangle \langle g_2(\xi_j) \rangle = 0, \quad i \neq j$$

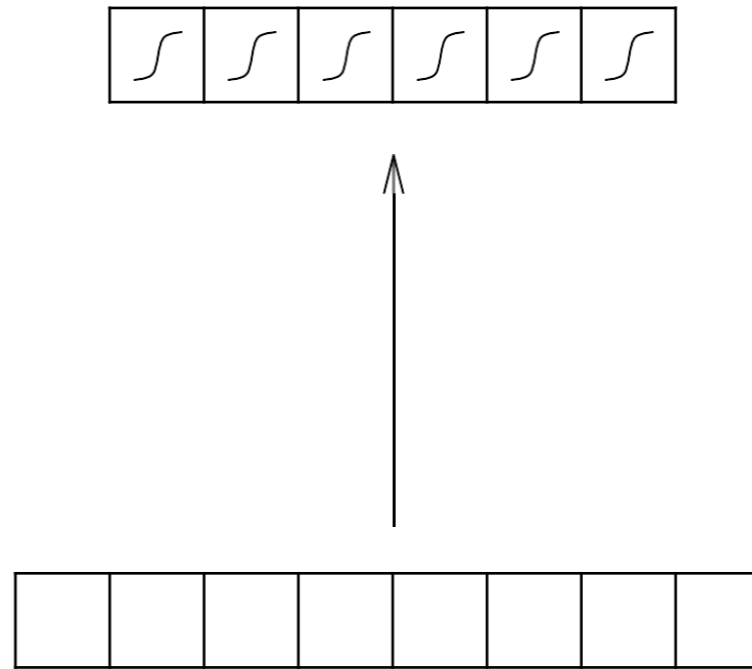
for any functions  $g_1$  and  $g_2$ .

# Independent Component Analysis (ICA)

- Like PCA, except that we're looking for a transformation subject to the stronger requirement of independence, rather than uncorrelatedness.
- In general, no analytic solution (like eigenvalue decomposition for PCA) exists, so ICA is implemented using neural network models.
- To do this, we need an architecture and an objective function to descend/climb in.
- Leads to  $N$  independent (or as independent as possible) components in  $N$ -dimensional space; they need not be orthogonal.
- When are independent components identical to uncorrelated (principal) components? When the generative distribution is uniquely determined by its first and second moments. This is true of only the Gaussian distribution.

# Neural Network for ICA

- Single layer network:

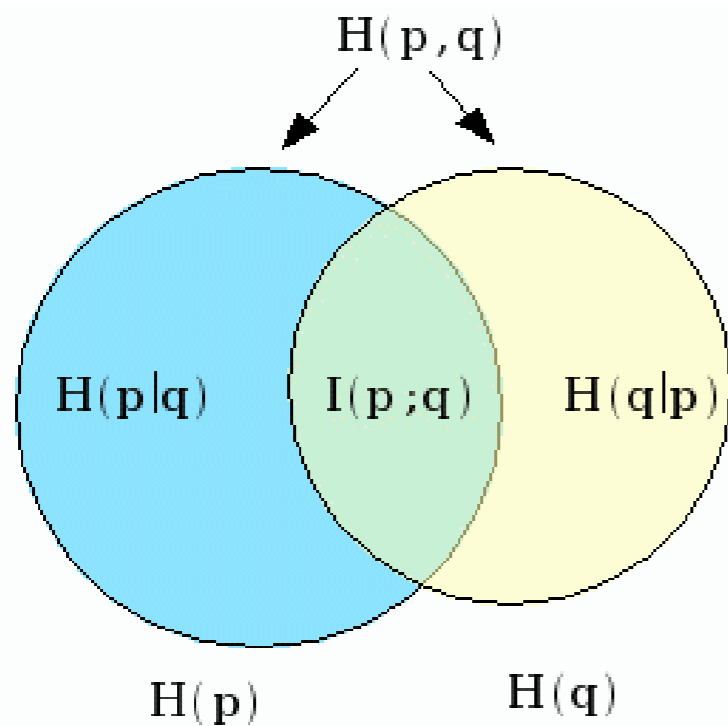


- Patterns  $\{\xi\}$  are fed into the input layer.
- Inputs multiplied by weights in matrix  $\mathbf{W}$ .
- Output logistic (vector notation here):

$$\bar{y} = \frac{1}{1 + e^{\mathbf{W}^T \bar{\xi}}}$$

# Objective Function for ICA

- Want to ensure that the outputs  $y_i$  are maximally independent.
- This is identical to requiring that the mutual information be small. Or alternately that the joint entropy be large.



$H(p)$  = entropy of distribution  $p$  of first neuron's output

$H(p|q)$  = conditional entropy

$I(p; q)$  =  $H(p) - H(q|p)$   
=  $H(q) - H(p|q)$   
= mutual information

- Gradient ascent in this objective function is called infomax (we're trying to maximize the enclosed area representing information quantities).

# Blind Source Separation (BSS)

- The most famous application of ICA.
- Have  $K$  sources  $\{s_k[t]\}$ , and  $K$  signals  $\{x_k[t]\}$ . Both  $\{s_k[t]\}$  and  $\{x_k[t]\}$  are time series ( $t$  is a discrete time index).

- Each signal is a linear mixture of the sources

$$x_k[t] = \mathbf{A}s_k[t] + n_k[t]$$

where  $n_k[t]$  is the noise contribution in the  $k$ th signal  $x_k[t]$ , and  $\mathbf{A}$  is a mixture matrix.

- The problem: given  $x_k[n]$ , determine  $\mathbf{A}$  and  $s_k[n]$ .

# The Cocktail Party

