

# DIMENSIONALITY REDUCTION AND VISUALIZATION

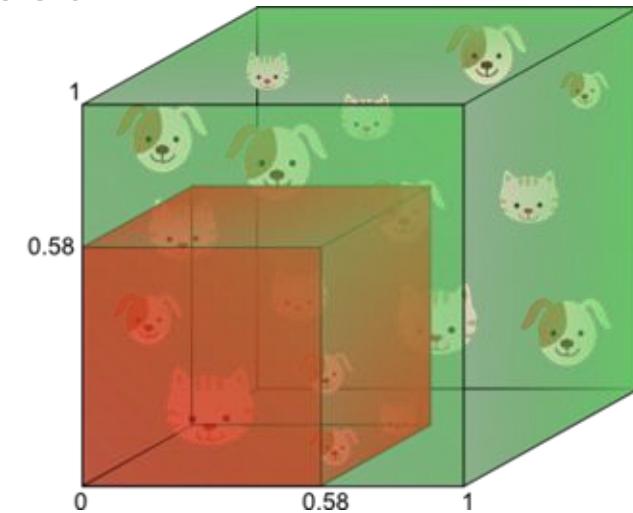
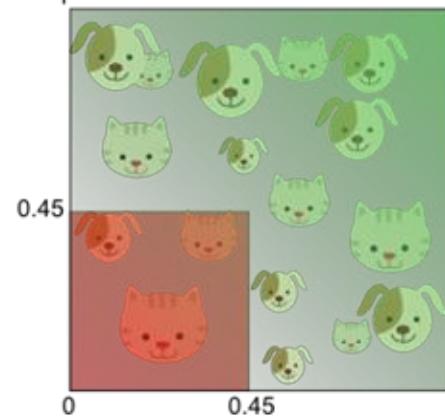
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# The curse of dimensionality



# The Curse of Dimensionality

- Harder to visualize or see structure of
  - Verifying that data come from a straight line/plane needs  $n+1$  data points
- Hard to search in high dimension – More runtime
- Need more data to get a good estimation of the data



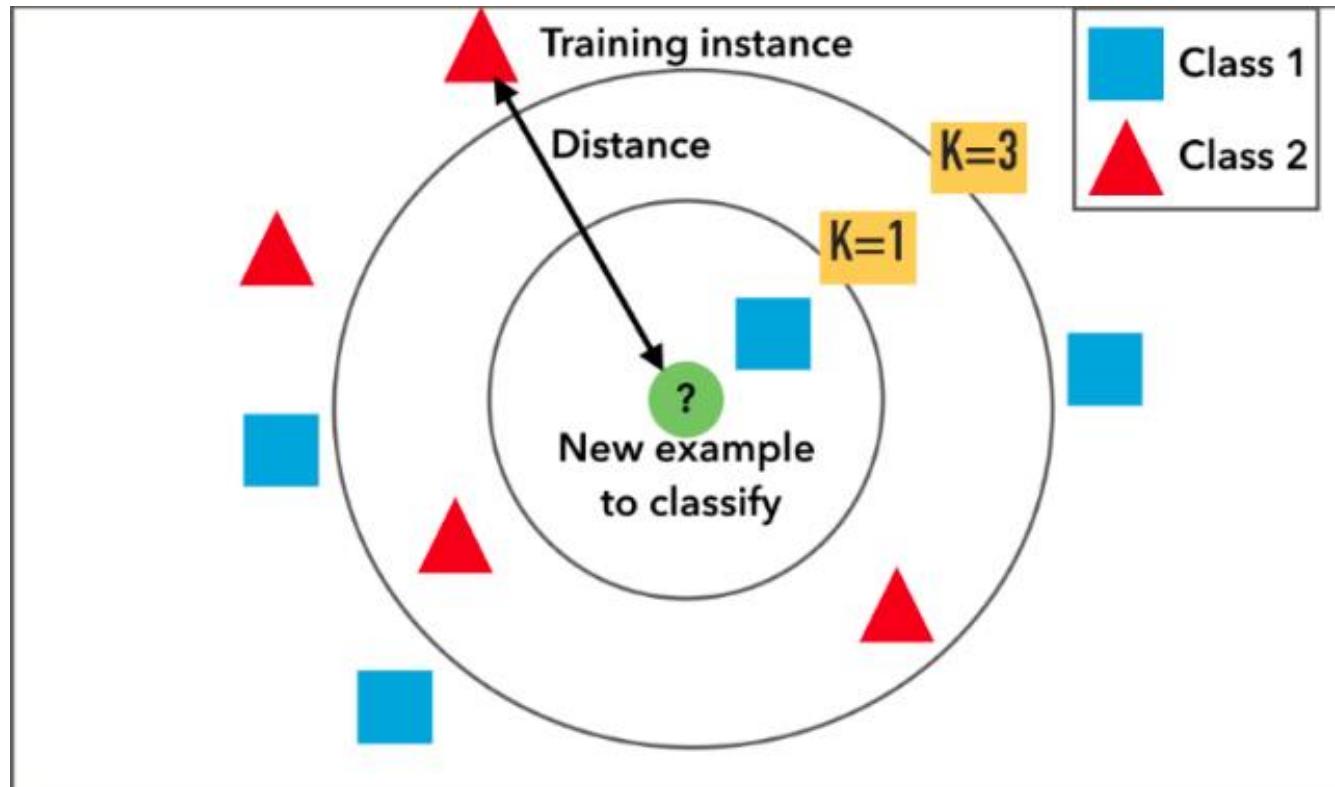
Wind in the morning       $X \in \{\text{Calm, Windy}\}$   
 PM2.5 level in the afternoon       $Y \in \{\text{Low, Med, High}\}$   
 PM2.5 level in the evening       $Z \in \{\text{Low, Med, High}\}$   
 $\text{argmax } P(Z | Y, X) = \text{argmax } P(Y, X | Z) P(Z)$

| Day | X | Y | Z |
|-----|---|---|---|
| 1   | W | L | M |
| 2   | C | M | M |
| 3   | W | H | M |
| 4   | W | M | H |
| 5   | C | M | L |
| 6   | W | M | L |
| 7   | C | L | H |
| 8   | W | H | L |

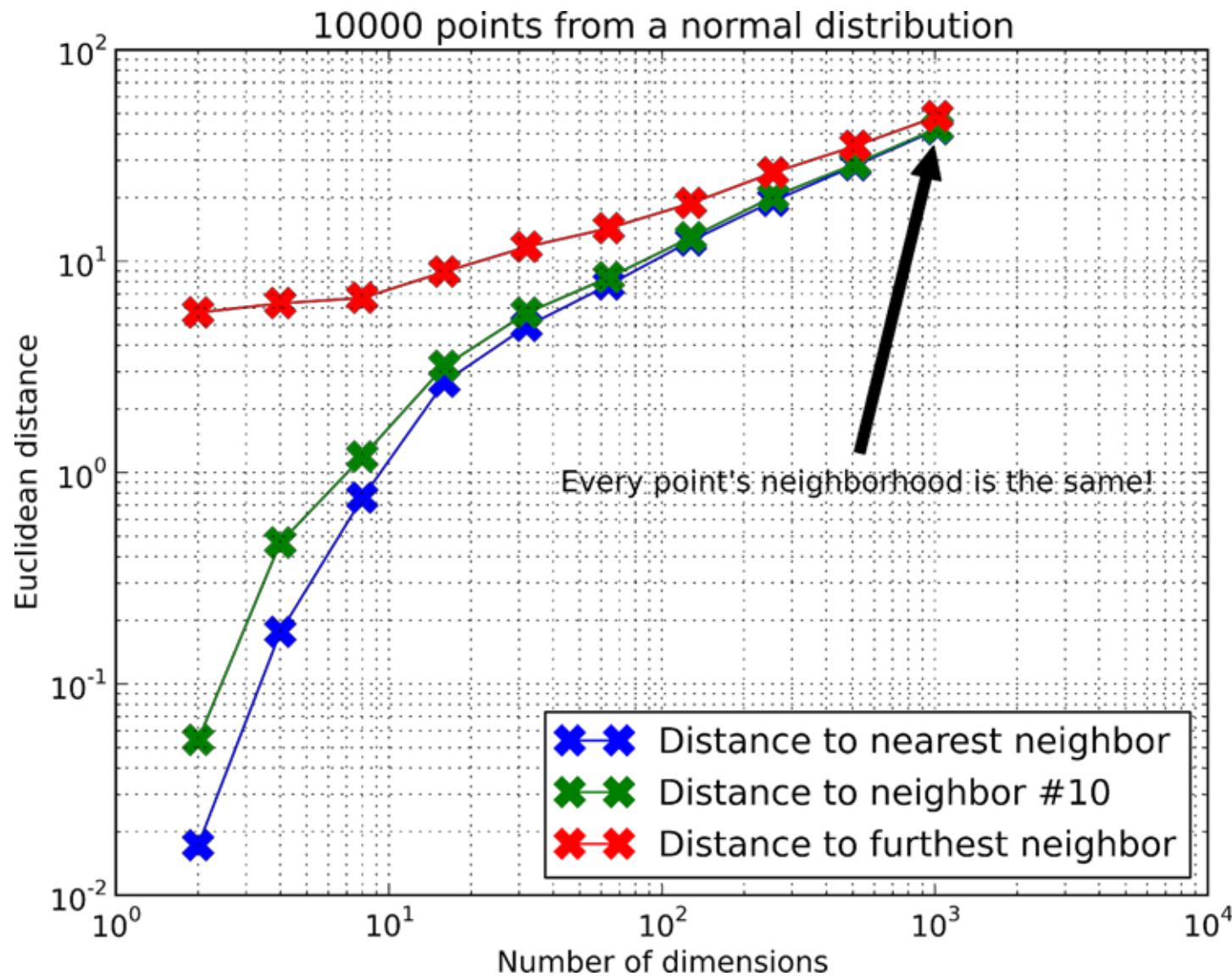
| count(Z,Y,X) | Z=L | Z=M | Z=H |
|--------------|-----|-----|-----|
| X=W,Y=L      | 0   | 1   | 0   |
| X=W,Y=M      | 1   | 0   | 1   |
| X=W,Y=H      | 1   | 1   | 0   |
| X=C,Y=L      | 0   | 0   | 1   |
| X=C,Y=M      | 1   | 1   | 0   |
| X=C,Y=H      | 0   | 0   | 0   |

# K-Nearest Neighbor Classifier

- Nearest neighbor is susceptible to label noise
- Use the k-nearest neighbors as the classification decision
  - Use majority vote



# What's wrong with knn in high dimension?



# Combating the curse of dimensionality

- Feature selection
  - Keep only “Good” features
- Feature transformation (Feature extraction)
  - Transform the original features into a smaller set of features

# Feature selection vs Feature transform

- Keep original features
  - Useful for when the user wants to know which feature matters
    - Hard to select good features automatically
- New features (a combination of old features)
  - Usually more powerful
    - Harder to interpret the model

# Feature selection

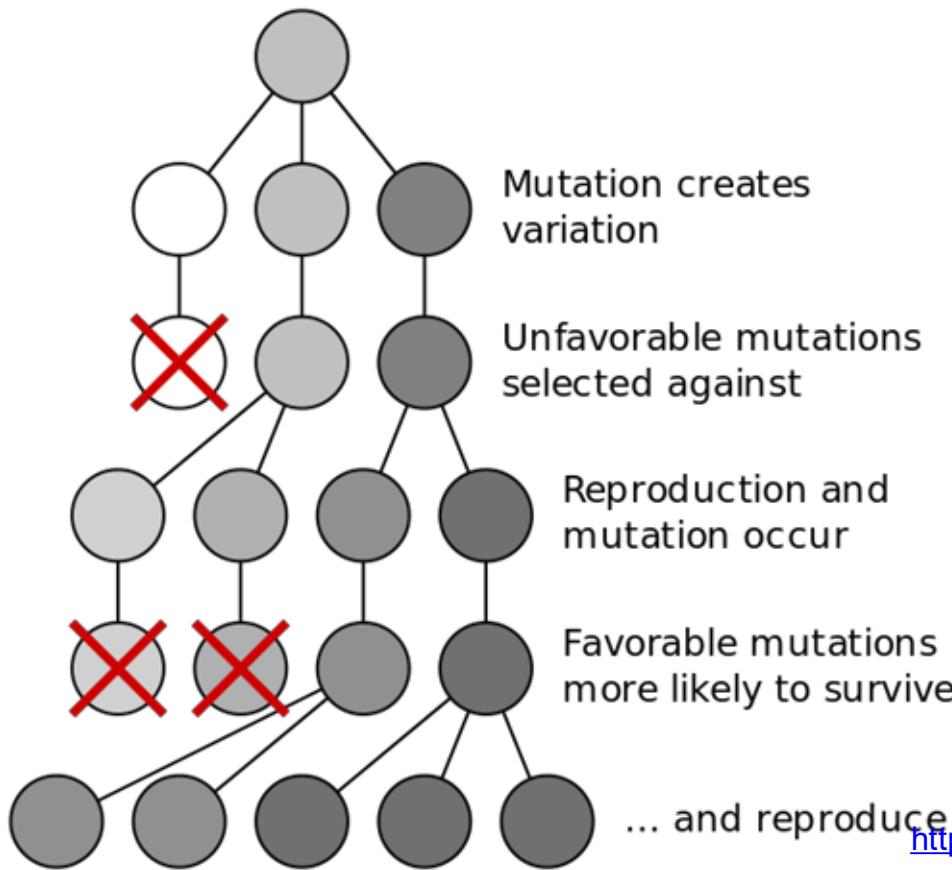
- Hackathon level (time limit days-a week)
  - Drop missing features
  - Low variance column
    - A feature that is a constant is useless. Tricky in practice
  - Forward or backward feature elimination
    - Greedy algorithm: create a simple classifier with  $n-1$  features,  $n$  times. Find which one has the best accuracy, drop that feature. Repeat.

# Feature selection

- Proper methods
  - Algorithm that handles high dimension well and do selection as a by product
    - Regression with L1 regularization
    - Tree-based classifiers: random forest, XGBoost
  - Genetic Algorithm

# Genetic Algorithm

- A method based inspired by natural selection
  - No theoretical guarantees but often work

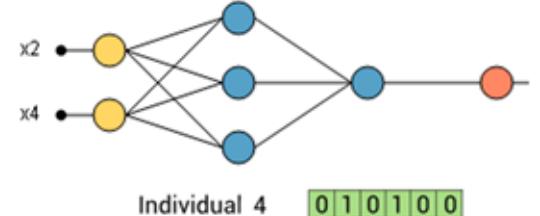
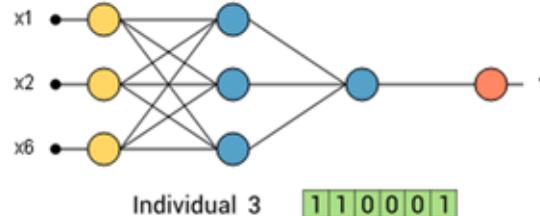
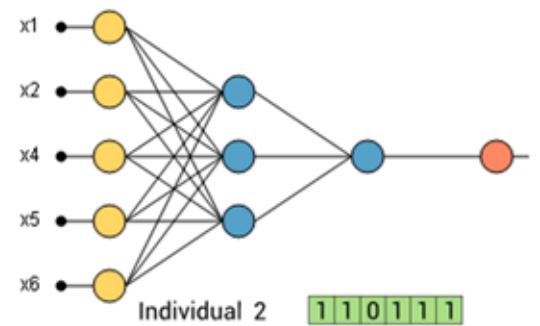
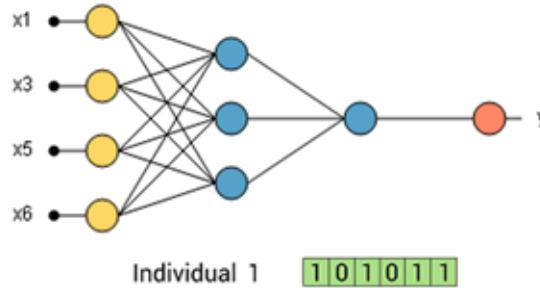


# Genetic Algorithm

- Initialization
  - Create N classifiers, each using different subset of features
- Selection process
  - Rank the N classifiers according to some criterion, kill the lower half
- Crossover
  - The remaining classifier breeds offsprings by selecting traits from the parents
- Mutation
  - The offsprings can have mutations by random in order to generate diversity
- Repeat till satisfied

# Initialization

- Create N classifiers
- Randomly select a subset of features to use



# Selection process

- Score the classifiers and kill the lower half (the amount to kill is also a parameter)

|                         | Selection error | Rank |
|-------------------------|-----------------|------|
| <del>Individual 1</del> | 0.9             | 1    |
| Individual 2            | 0.6             | 3    |
| <del>Individual 3</del> | 0.7             | 2    |
| Individual 4            | 0.5             | 4    |

# Crossover

- Breed offsprings by randomly select genes from parents

|              |   |   |   |   |   |   |   |
|--------------|---|---|---|---|---|---|---|
| Individual 3 | <table border="1"><tr><td>1</td><td>1</td><td>0</td><td>0</td><td>0</td><td>1</td></tr></table> | 1 | 1 | 0 | 0 | 0 | 1 |
| 1            | 1   | 0 | 0 | 0 | 1 |   |   |
| Individual 4 | <table border="1"><tr><td>0</td><td>1</td><td>0</td><td>1</td><td>0</td><td>0</td></tr></table> | 0 | 1 | 0 | 1 | 0 | 0 |
| 0            | 1   | 0 | 1 | 0 | 0 |   |   |
| <hr/>        |   |   |   |   |   |   |   |
| Offspring 1  | <table border="1"><tr><td>0</td><td>1</td><td>0</td><td>1</td><td>0</td><td>1</td></tr></table> | 0 | 1 | 0 | 1 | 0 | 1 |
| 0            | 1   | 0 | 1 | 0 | 1 |   |   |
| Offspring 2  | <table border="1"><tr><td>1</td><td>1</td><td>0</td><td>1</td><td>0</td><td>1</td></tr></table> | 1 | 1 | 0 | 1 | 0 | 1 |
| 1            | 1   | 0 | 1 | 0 | 1 |   |   |
| Offspring 3  | <table border="1"><tr><td>0</td><td>1</td><td>0</td><td>1</td><td>0</td><td>1</td></tr></table> | 0 | 1 | 0 | 1 | 0 | 1 |
| 0            | 1   | 0 | 1 | 0 | 1 |   |   |
| Offspring 4  | <table border="1"><tr><td>1</td><td>1</td><td>0</td><td>0</td><td>0</td><td>0</td></tr></table> | 1 | 1 | 0 | 0 | 0 | 0 |
| 1            | 1   | 0 | 0 | 0 | 0 |   |   |

# Mutation

- Offspring can mutate with some probability to introduce diversity
- Mutation rate is usually  $1/k$  where  $k$  is the number of features.
  - On average you mutate once per individual

Offspring1: Original 

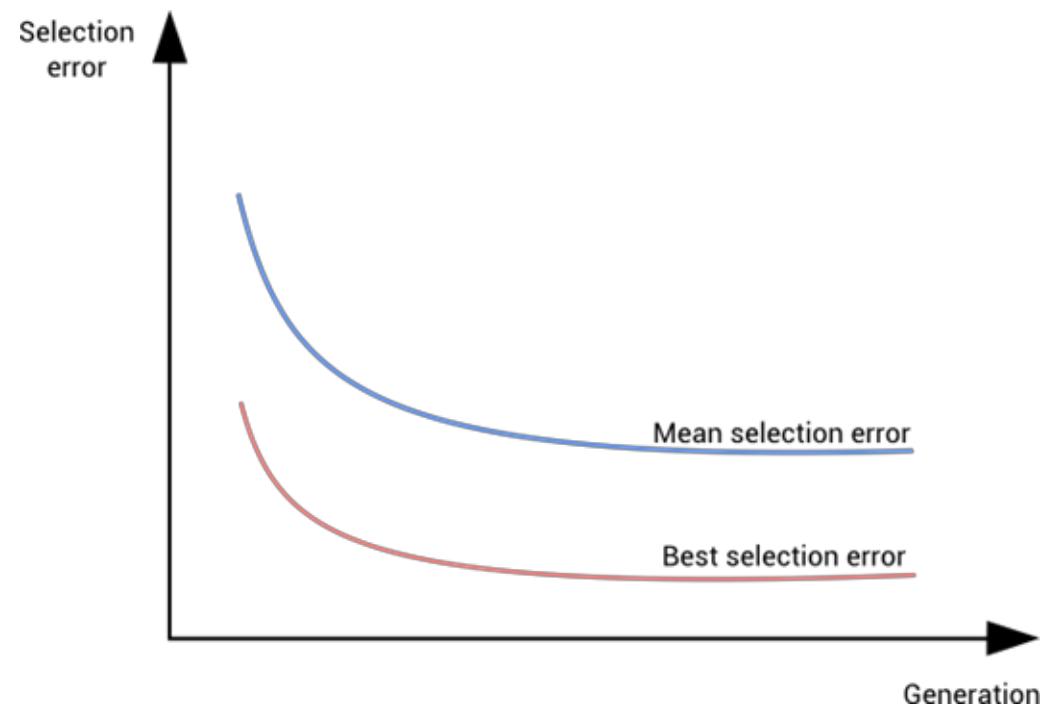
|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 0 | 1 | 0 | 1 | 0 | 1 |
|---|---|---|---|---|---|

Offspring1: Mutated 

|   |   |   |   |   |   |
|---|---|---|---|---|---|
| 0 | 1 | 0 | 0 | 0 | 0 |
|---|---|---|---|---|---|

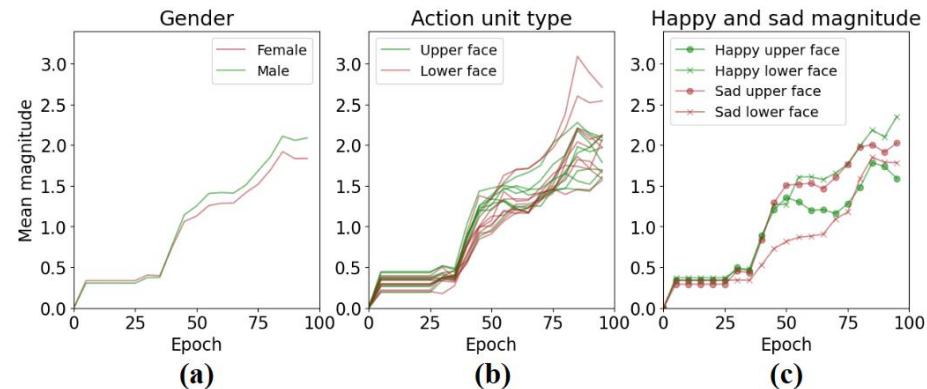
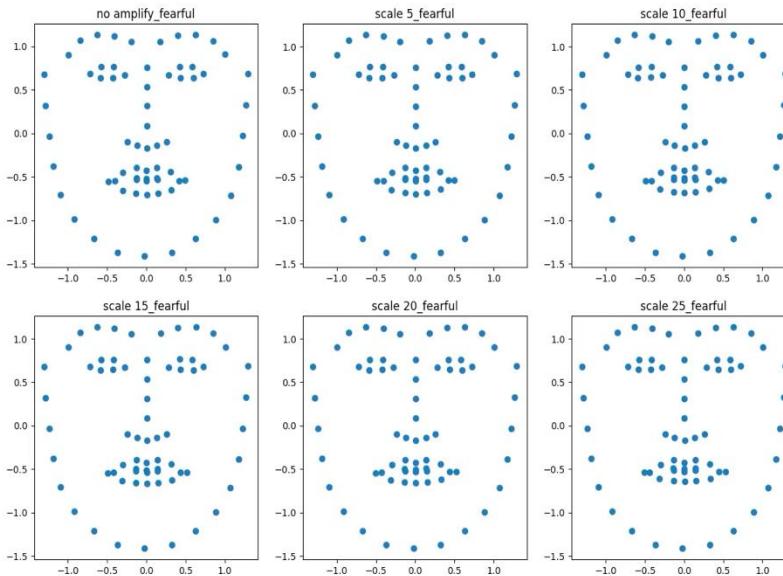
# Performance

- Usually performs well. The general population usually gets better (mean). The best performing (individual) also gets better after each generation



# Other examples of genetic algorithm

- Tuning hyperparameters in a neural network
  - <https://blog.coast.ai/lets-evolve-a-neural-network-with-a-genetic-algorithm-code-included-8809bece164>
- Tune augmentation algorithms



Generation ->

# Feature transformation

- Principal Component Analysis
- Linear Discriminant Analysis (NOT Latent Dirichlet Allocation)
- Random Projections

# Linear Algebra Review

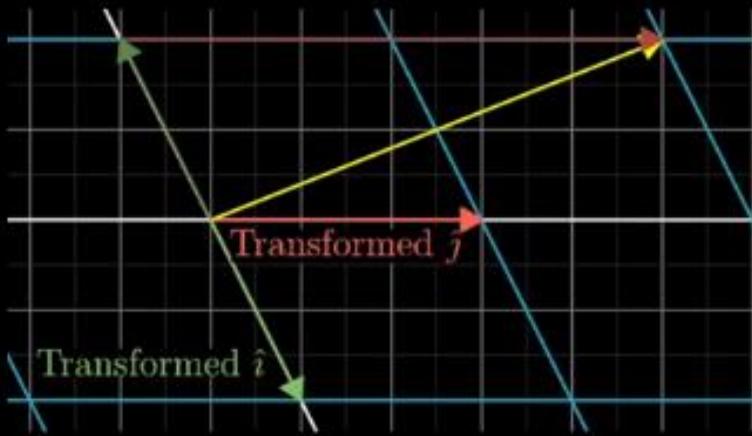
- Matrix as a sequence of column vectors

“2x2 Matrix”

$$\begin{bmatrix} 3 & 2 \\ -2 & 1 \end{bmatrix}$$

$$\begin{bmatrix} 5 \\ 7 \end{bmatrix}$$

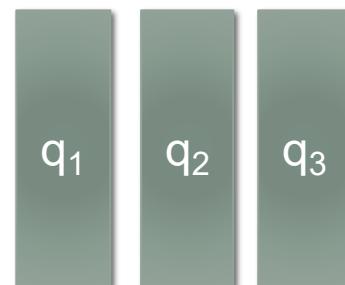
$$5 \begin{bmatrix} 3 \\ -2 \end{bmatrix} + 7 \begin{bmatrix} 2 \\ 1 \end{bmatrix}$$



# Linear Algebra Review

- View Eigendecomposition (ED) and Singular Value Decomposition (SVD) as rotations and stretches

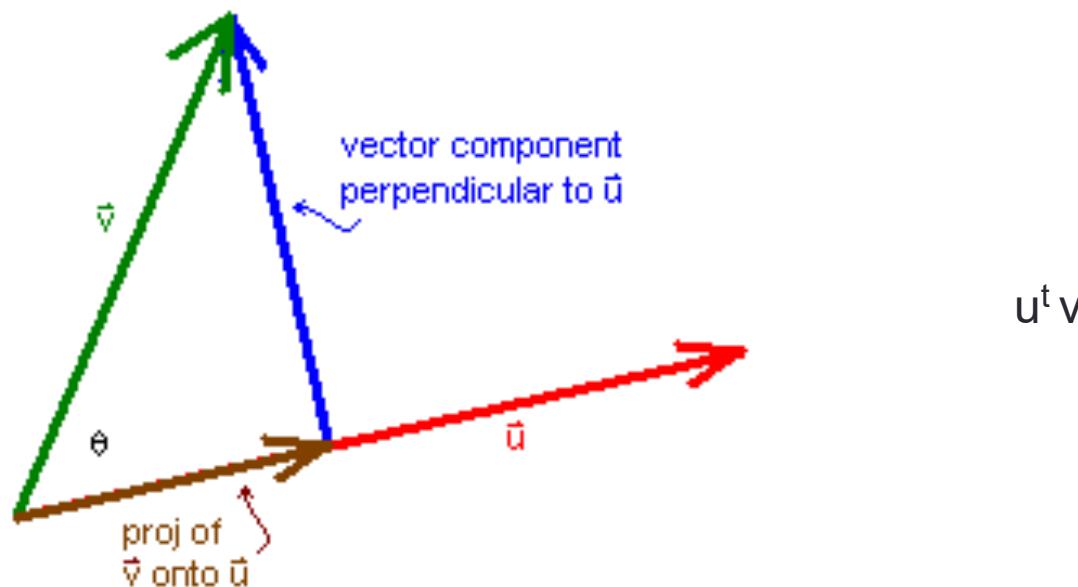
$$A = Q D Q^{-1}$$



D has eigenvalues on the diagonal  
Q is a matrix where  $i^{\text{th}}$  column is the  $q^{\text{th}}$  eigenvector

# Linear Algebra Review

- Projection as a change of basis
- Change basis from x,y coordinates to be on  $u$

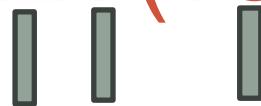


# Covariance matrix

- Given a set of RVs,  $X_1 X_2 \dots X_n$
- The covariance matrix is a matrix which has the covariance of the  $i$  and  $j$  RV in position  $(i,j)$

$$\Sigma = \begin{bmatrix} E[(X_1 - \mu_1)(X_1 - \mu_1)] & E[(X_1 - \mu_1)(X_2 - \mu_2)] & \cdots & E[(X_1 - \mu_1)(X_n - \mu_n)] \\ E[(X_2 - \mu_2)(X_1 - \mu_1)] & E[(X_2 - \mu_2)(X_2 - \mu_2)] & \cdots & E[(X_2 - \mu_2)(X_n - \mu_n)] \\ \vdots & \vdots & \ddots & \vdots \\ E[(X_n - \mu_n)(X_1 - \mu_1)] & E[(X_n - \mu_n)(X_2 - \mu_2)] & \cdots & E[(X_n - \mu_n)(X_n - \mu_n)] \end{bmatrix}.$$

# Covariance matrix (vector view)



- Given a set of datapoints  $x_1 x_2 \dots x_n$
- The covariance matrix based on the data can be written as

$$E[ \underline{x} \underline{x}^T ] = [ \underline{\underline{x}} + \underline{\underline{x}} + \dots + \underline{\underline{x}} ] / n$$

$$\Sigma = \begin{bmatrix} E[(X_1 - \mu_1)(X_1 - \mu_1)] & E[(X_1 - \mu_1)(X_2 - \mu_2)] & \dots & E[(X_1 - \mu_1)(X_n - \mu_n)] \\ E[(X_2 - \mu_2)(X_1 - \mu_1)] & E[(X_2 - \mu_2)(X_2 - \mu_2)] & \dots & E[(X_2 - \mu_2)(X_n - \mu_n)] \\ \vdots & \vdots & \ddots & \vdots \\ E[(X_n - \mu_n)(X_1 - \mu_1)] & E[(X_n - \mu_n)(X_2 - \mu_2)] & \dots & E[(X_n - \mu_n)(X_n - \mu_n)] \end{bmatrix}.$$

# Positive semi-definite and covariance matrixes

## Definitions for real matrices edit

An  $n \times n$  symmetric real matrix  $M$  is said to be **positive-definite** if  $\mathbf{x}^T M \mathbf{x} > 0$  for all non-zero  $\mathbf{x}$  in  $\mathbb{R}^n$ . Formally,

$$M \text{ positive-definite} \iff \mathbf{x}^T M \mathbf{x} > 0 \text{ for all } \mathbf{x} \in \mathbb{R}^n \setminus \{\mathbf{0}\}$$

An  $n \times n$  symmetric real matrix  $M$  is said to be **positive-semidefinite** or **non-negative-definite** if  $\mathbf{x}^T M \mathbf{x} \geq 0$  for all  $\mathbf{x}$  in  $\mathbb{R}^n$ . Formally,

$$M \text{ positive semi-definite} \iff \mathbf{x}^T M \mathbf{x} \geq 0 \text{ for all } \mathbf{x} \in \mathbb{R}^n$$

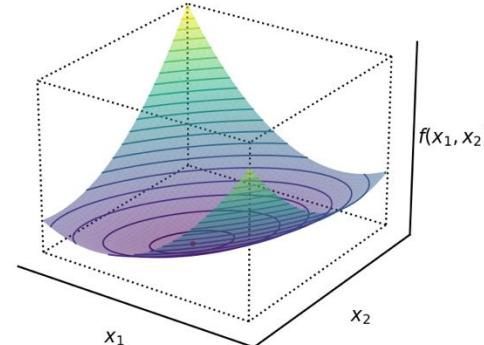
[https://en.wikipedia.org/wiki/Definite\\_matrix](https://en.wikipedia.org/wiki/Definite_matrix)

- Covariance matrix is positive semi-definite and symmetric.
  - Semi-definite because the variance can be zero

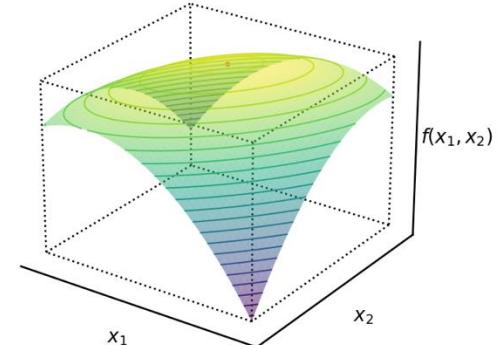
# Positive semi-definite

$$f(x_1, x_2) = \frac{1}{2} \begin{bmatrix} x_1 & x_2 \end{bmatrix} \mathbf{A} \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} - \mathbf{b}^\top \begin{bmatrix} x_1 \\ x_2 \end{bmatrix} + c$$

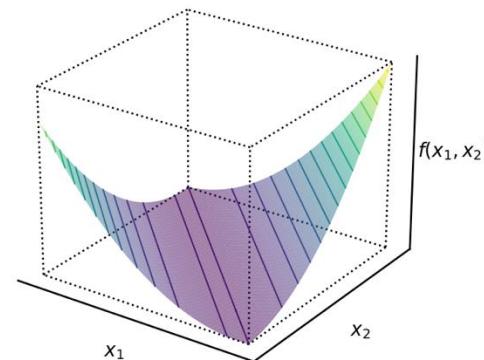
Positive definite



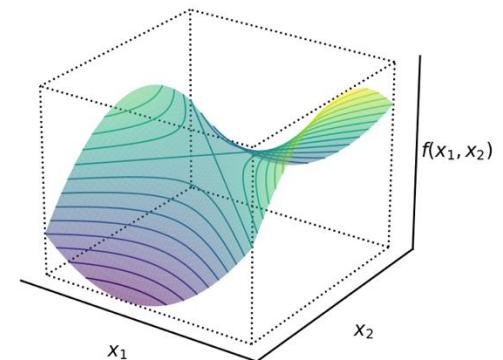
Negative definite



Singular &amp; positive semi-definite



Indefinite



# Positive semi-definite and covariance matrixes

## Definitions for real matrices edit

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An  $n \times n$  symmetric real matrix  $M$  is said to be **positive-semidefinite** or **non-negative-definite** if  $\mathbf{x}^T M \mathbf{x} \geq 0$  for all  $\mathbf{x}$  in  $\mathbb{R}^n$ . Formally,

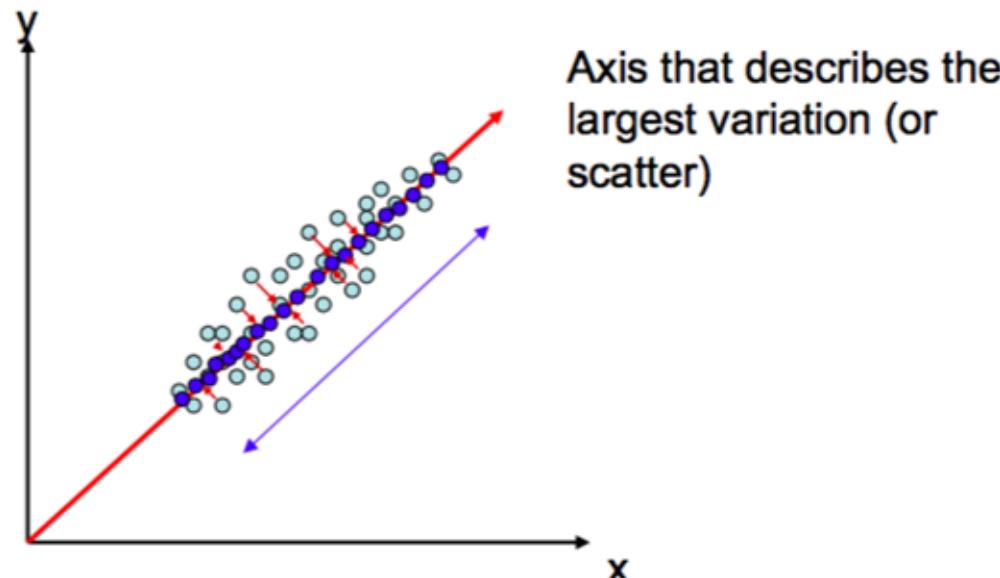
$$M \text{ positive semi-definite} \iff \mathbf{x}^T M \mathbf{x} \geq 0 \text{ for all } \mathbf{x} \in \mathbb{R}^n$$

[https://en.wikipedia.org/wiki/Definite\\_matrix](https://en.wikipedia.org/wiki/Definite_matrix)

- Covariance matrix is positive semi-definite and symmetric.
  - Symmetric -> real eigen values, eigen vectors are mutually orthogonal
    - $q_i^T q_j = 0$  for  $i \neq j$
  - Positive semi-definite -> eigen values are nonnegative
  - Positive definite -> eigen values are positive -> invertible

# What is PCA?

- We want to reduce the dimensionality but keep useful information
  - What is useful information? Variation
- We want to find a projection (a transformation) that describe maximum variation



# Formulation

- Maximize the variance after projection ie
  - $\operatorname{argmax} \operatorname{Var}(\mathbf{w}^t \mathbf{x})$
  - Subject to  $\mathbf{w}$  is a unit vector
- $\Sigma \mathbf{w} = \lambda \mathbf{w} \leftarrow \text{eigenvector}$



# Trace properties

$$1 \cdot \text{tr}(a) = a$$

$$2 \cdot \text{tr}A = \text{tr}A^T$$

$$3 \cdot \text{tr}(A+B) = \text{tr}A + \text{tr}B$$

$$4 \cdot \text{tr}(aA) = a\text{tr}(A)$$

$$5 \quad \nabla_A \text{tr}AB = B^T$$

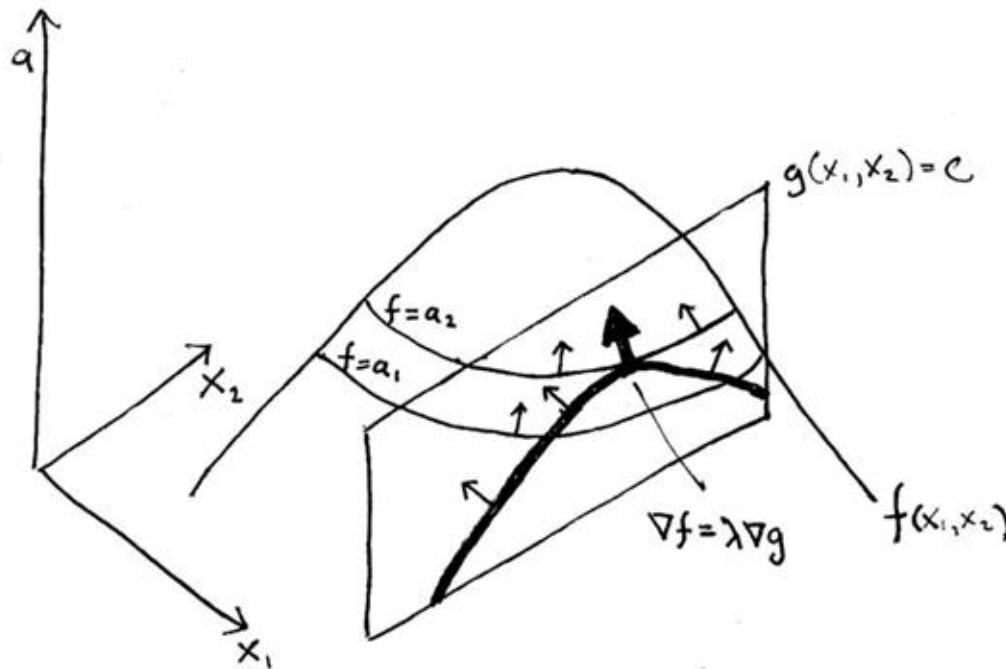
$$6 \quad \nabla_{A^T} f(A) = (\nabla_A f(A))^T$$

$$7 \quad \nabla_A \text{tr}ABA^TC = CAB + C^T AB^T$$

$$8 \quad \nabla_{A^T} \text{tr}ABA^TC = B^T A^T C^T + BA^T C$$

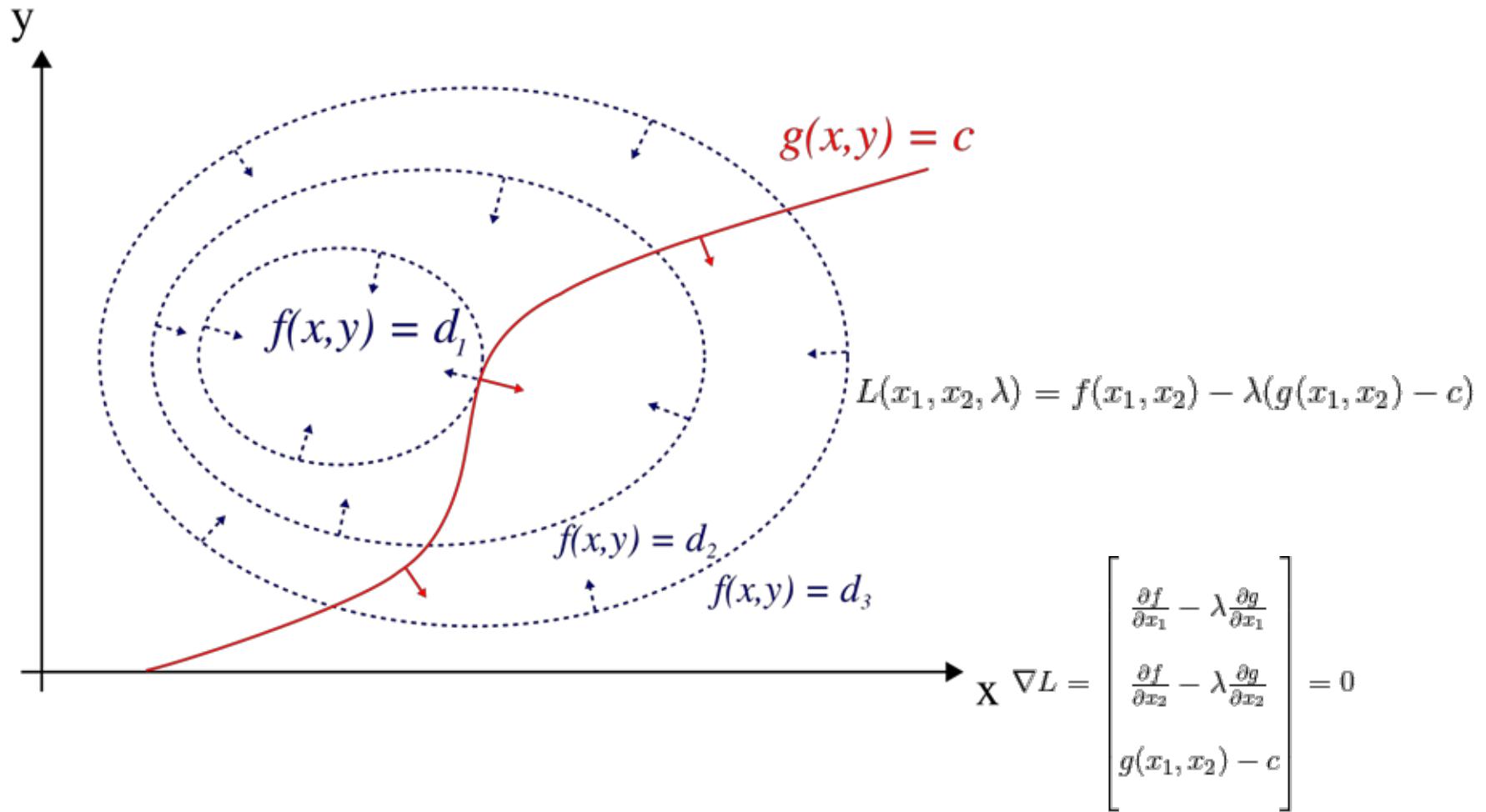
# Lagrange Multiplier

<https://medium.com/@andrew.chamberlain/a-simple-explanation-of-why-lagrange-multipliers-works-253e2cdcbf74>



$$L(x_1, x_2, \lambda) = f(x_1, x_2) - \lambda(g(x_1, x_2) - c)$$

$$\nabla L = \begin{bmatrix} \frac{\partial f}{\partial x_1} - \lambda \frac{\partial g}{\partial x_1} \\ \frac{\partial f}{\partial x_2} - \lambda \frac{\partial g}{\partial x_2} \\ g(x_1, x_2) - c \end{bmatrix} = 0$$



# So we got to eigenvectors

- A  $d \times d$  covariance matrix has  $d$  eigenvectors/values pair.  
Do we use all of them?
- Which pair to use?

# Selecting eigenvectors

- Remember the variance of projected data is

$$\omega^T \Sigma \omega. \quad (1)$$

- And our solution yielded

$$\Sigma \omega = \lambda \omega \quad (2)$$

- Plug (2) in (1) and we get

$$\begin{aligned}\text{projected variance} &= \omega^T \Sigma \omega = \omega^T \lambda \omega \\ &= \lambda \omega^T \omega \quad (\text{remember } \|\omega\|=1) \\ &= \lambda\end{aligned}$$

# PCA

- The direction vector captures the variance corresponding to the eigenvalue
- So we want the higher eigenvalues
  - How many?

# Matrix rank

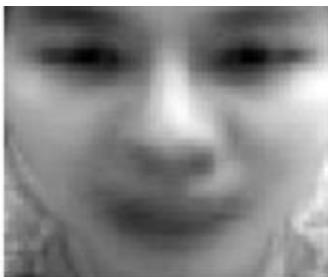
- A square  $d \times d$  matrix has full rank (e.g. rank  $d$ ) if the columns are linearly independent.
- The number of linearly independent columns is the rank of the matrix
- A covariance matrix of size  $d \times d$  will have have at most  $N-1$  rank where  $N$  is the number of training samples
  - $640 \times 640$  images =  $\sim 400000$  dimensions
  - 1000 training images
  - The covariance matrix will be at most rank 999. The missing rank is because of the mean.

# PCA

- The direction vector captures the variance corresponding to the eigenvalue
- So we want the higher eigenvalues
- Take the eigenvalues with non-zero eigenvalues (at most  $N-1$  non-zero eigenvalues)

# Eigenfaces

Meanface



V1



V2



V3



V4



V5



V6



V7



V8



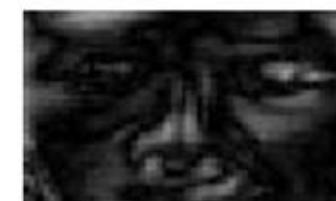
V9



V10

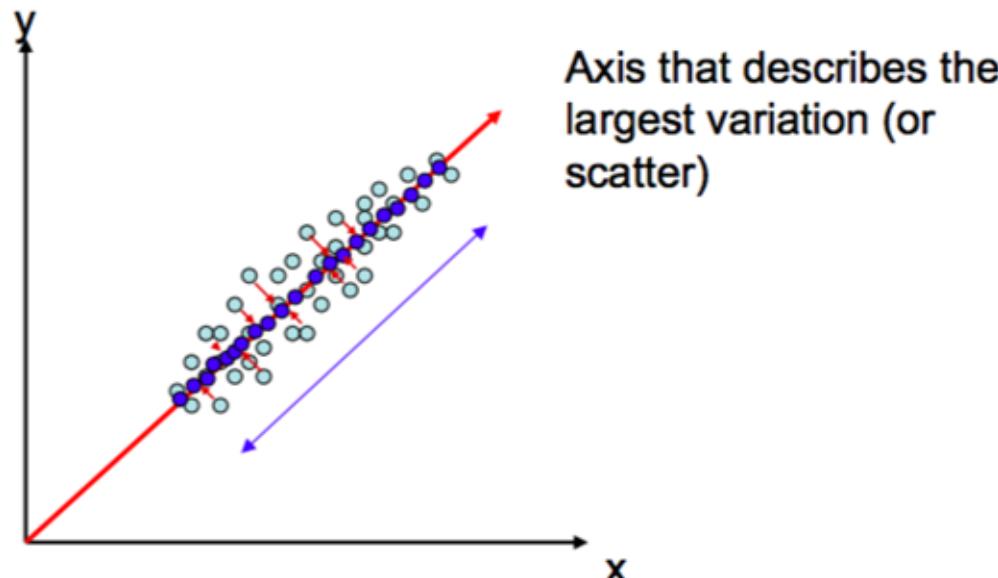


V11



# What is PCA?

- We want to reduce the dimensionality but keep useful information
  - What is useful information? Variation
- We want to find a projection (a transformation) that describe maximum variation



# Means

- In PCA, we model variance. (Variation around the mean)
- In our projection we need to remove the mean

$$\mathbf{p} = \mathbf{V}^T (\mathbf{x} - \mathbf{m})$$

- The mean is the mean of all your training data
- If we want to reconstruct the data we need to add back the mean

$$\mathbf{x} = \sum_{i=1}^N p_i \mathbf{v}_i + \mathbf{m} = p_1 \begin{bmatrix} | \\ \mathbf{v}_1 \\ | \end{bmatrix} + p_2 \begin{bmatrix} | \\ \mathbf{v}_2 \\ | \end{bmatrix} + \dots + p_n \begin{bmatrix} | \\ \mathbf{v}_n \\ | \end{bmatrix} + \mathbf{m} = \mathbf{V}\mathbf{p} + \mathbf{m}$$

# Basis decomposition

- Let's consider our projection  $w_i$  which is the eigenvectors to be a **basis vector**  $v_i$
- We can represent any vector as a sum of basis vectors as follows:

$$\mathbf{x} = \sum_{i=1}^N p_i \mathbf{v}_i = p_1 \begin{bmatrix} | \\ \mathbf{v}_1 \\ | \end{bmatrix} + p_2 \begin{bmatrix} | \\ \mathbf{v}_2 \\ | \end{bmatrix} + \dots + p_n \begin{bmatrix} | \\ \mathbf{v}_n \\ | \end{bmatrix} = \mathbf{Vp}$$

# Finding the weights

$$\mathbf{x} = \sum_{i=1}^N p_i \mathbf{v}_i = p_1 \begin{bmatrix} | \\ \mathbf{v}_1 \\ | \end{bmatrix} + p_2 \begin{bmatrix} | \\ \mathbf{v}_2 \\ | \end{bmatrix} + \dots + p_n \begin{bmatrix} | \\ \mathbf{v}_n \\ | \end{bmatrix} = \mathbf{V}\mathbf{p}$$

- If  $\mathbf{v}_i$  are orthogonal, the projection of  $\mathbf{x}$  onto  $\mathbf{v}_i$  gives  $p_i$

$$\mathbf{V}^T \mathbf{x} = \begin{bmatrix} - & \mathbf{v}_1 & - \\ - & \mathbf{v}_2 & - \\ - & \mathbf{v}_3 & - \end{bmatrix} \begin{bmatrix} | \\ \mathbf{x} \\ | \end{bmatrix} = \begin{bmatrix} p_1 \\ p_2 \\ p_3 \end{bmatrix}$$

# Reconstruction with eigenfaces

Mean



+ 230

v1



- 917

v2



+ 1050

v3

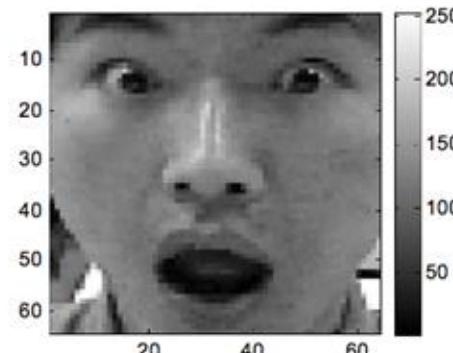


MSE=758.13

=



reconstructed  
 $\tilde{\mathbf{x}}$



Original  
 $\mathbf{x}$

# Practical issues

- If your data has different magnitudes in different dimensions, normalize each dimension before PCA
- If we have 640x640 images = ~400000 dimensions.
- What is the size of the covariance matrix?
- $400000 \times 400000$



# Practical issues

- You have  $N$  training examples.
- For the case where  $N \ll 400000$ , we only have  $N-1$  eigenvalues we care about anyway

# Gram Matrix

$$\Sigma = E(x - \mu)(x - \mu)^T = XX^T$$

Covariance matrix  
is the **outer-product**  
of the input matrix

Must solve  $\Sigma v = \lambda v$

$$XX^T v = \lambda v \quad (\text{pre-mult by } X^T) \quad (1)$$

$$X^T XX^T v = \lambda X^T v \quad (v' = X^T v) \quad (2)$$

Solve eigenvalue problem  $X^T X v' = \lambda v'$

- $X^T X$  is a gram of **inner-product** matrix. Its size is  $N \times N$  where  $N$  is the number of data samples.

# But how to get $v$ from $v'$ ?

- From previous slide, equation (1) and (2)
  - $XX^T v = \lambda v$  (1)
  - $v' = X^T v$  (2)
- Substitute (2) into (1)
  - $Xv' = \lambda v$
- Thus,  $v = Xv'$ . We don't care about the scaling term because we will always scale the eigenvector so that it is orthonormal i.e.  $\|v\| = 1$ .

# How many eigenvectors?

- Select based on amount of variance explained
  - Sum of eigenvalues exceeds some percent of total
- Reconstruction error

$$\mathbf{x} = \sum_{i=1}^N p_i \mathbf{v}_i = p_1 \begin{bmatrix} | \\ \mathbf{v}_1 \\ | \end{bmatrix} + p_2 \begin{bmatrix} | \\ \mathbf{v}_2 \\ | \end{bmatrix} + \dots + p_n \begin{bmatrix} | \\ \mathbf{v}_n \\ | \end{bmatrix} = \mathbf{Vp}$$

- Select enough  $\mathbf{v}$  so that the difference between original  $\mathbf{x}$  and reconstructed  $\mathbf{x}$  is small

# Summary

- Feature selection and dimensionality reduction techniques help combats curse of dimensionality.
- PCA tries to maximize reconstruction of the data while using the least amount of dimension.