

# DIMENSIONALITY REDUCTION AND VISUALIZATION

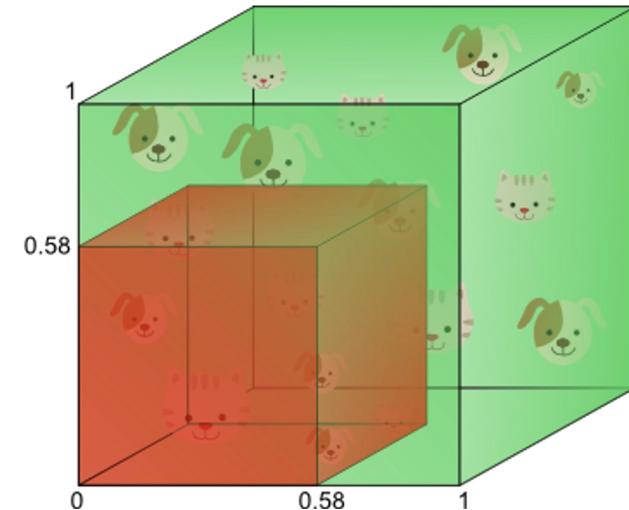
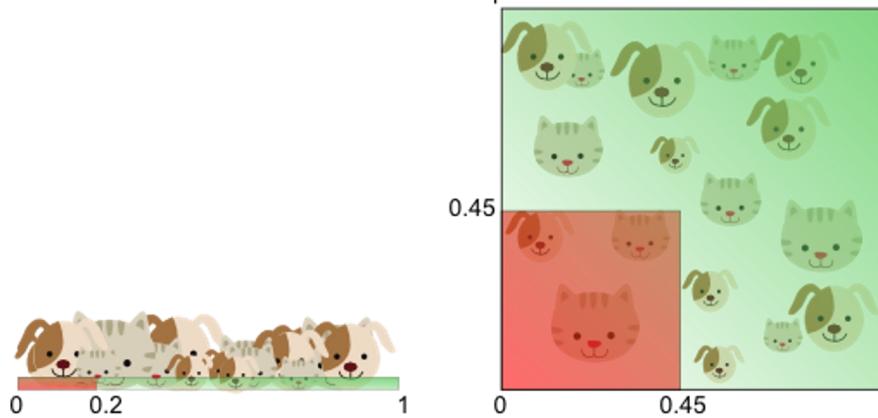
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# The curse of dimensionality



# 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



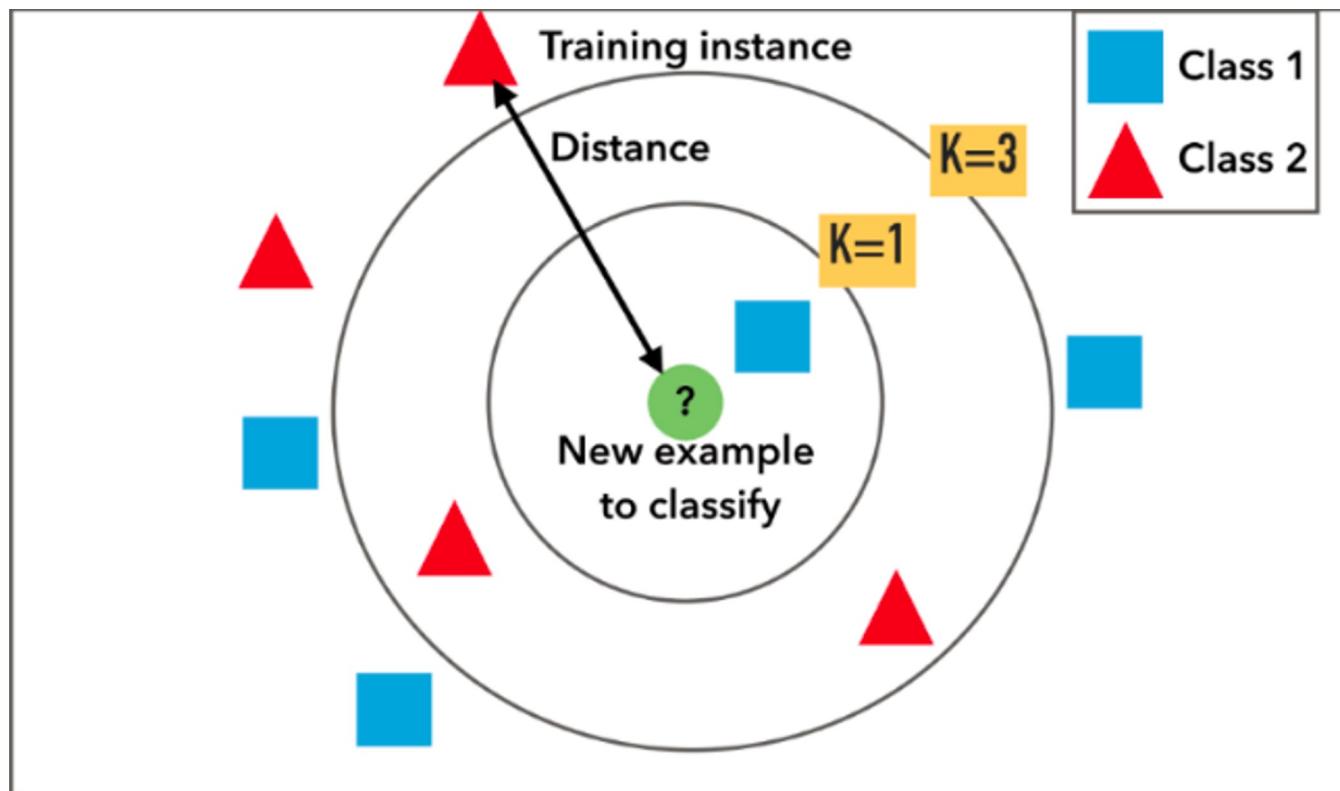
Wind in the morning       $X \in \{\text{Calm, Windy}\}$   
PM2.5 level in the afternoon     $Y \in \{\text{Low, Med, High}\}$   
PM2.5 level in the evening     $Z \in \{\text{Low, Med, High}\}$   
 $\text{argmax } P(Z | Y, X) = \text{argmax } P(Y, X | Z) P(Z)$

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

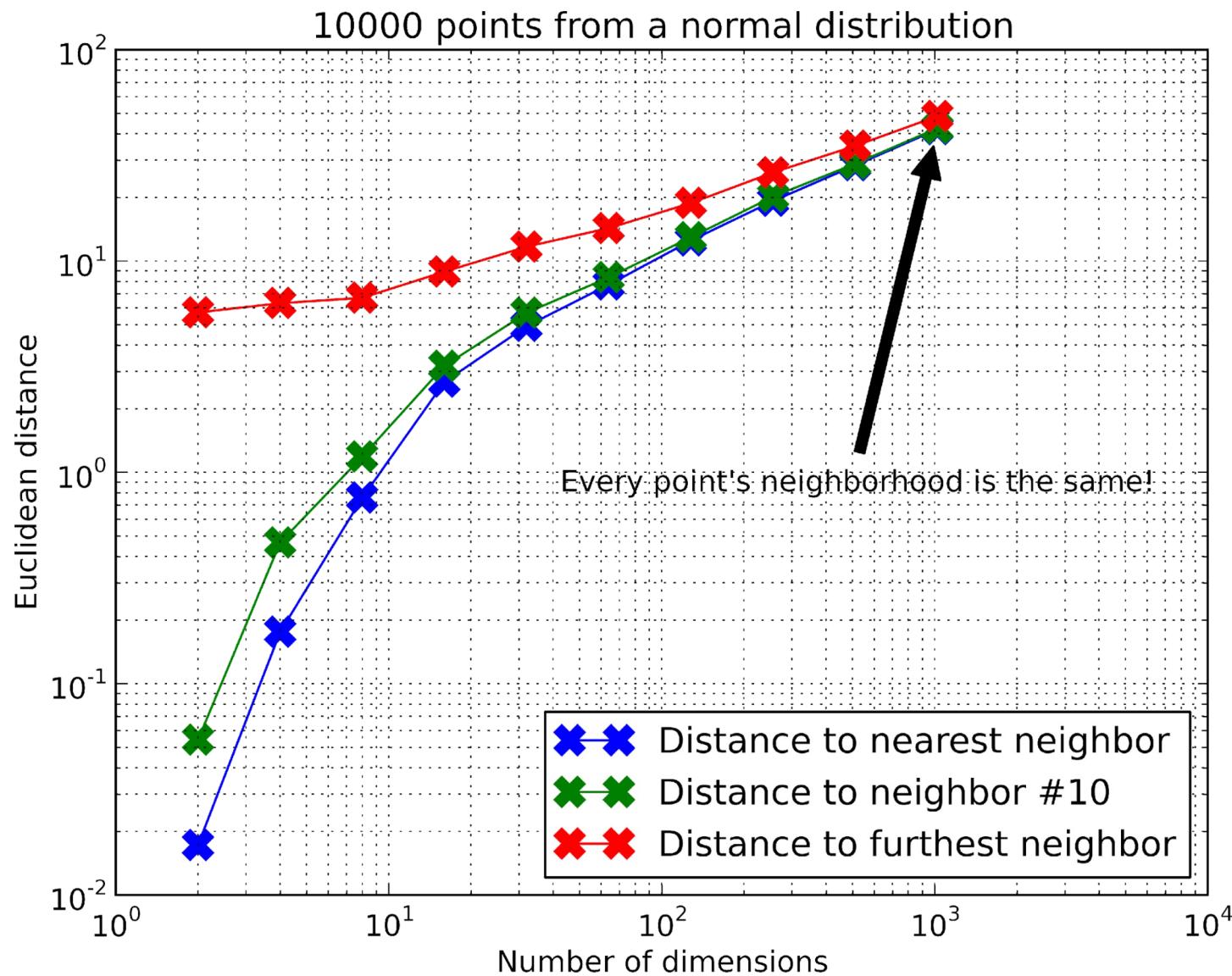
count(Z,Y,X)	Z=L	Z=M	Z=H
X=W,Y=L	0	1	0
X=W,Y=M	1	0	1
X=W,Y=H	1	1	0
X=C,Y=L	0	0	1
X=C,Y=M	1	1	0
X=C,Y=H	0	0	0

# 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

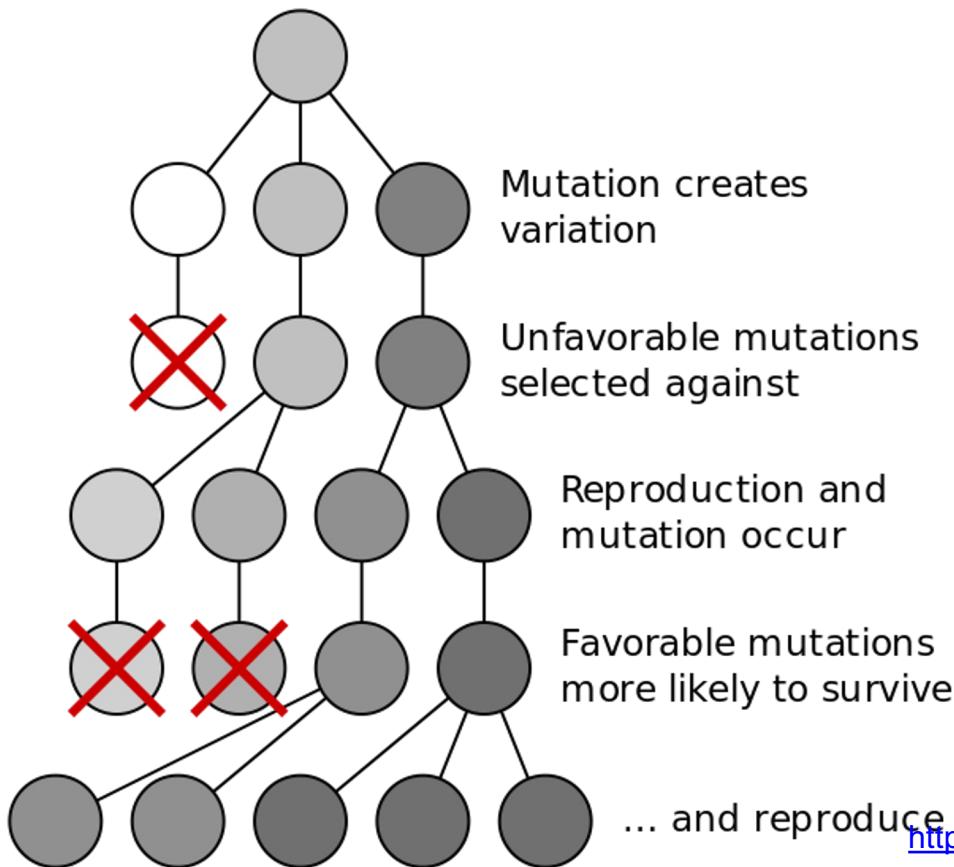
- Hackathon level (time limit days-a week)
  - Drop missing features
  - Low variance column
    - A feature that is a constant is useless. Tricky in practice
  - Forward or backward feature elimination
    - Greedy algorithm: create a simple classifier with  $n-1$  features,  $n$  times. Find which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

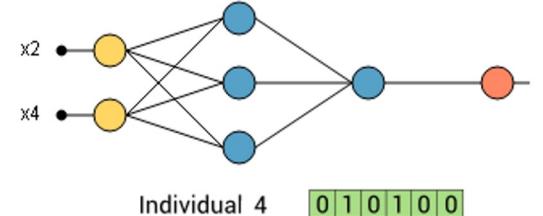
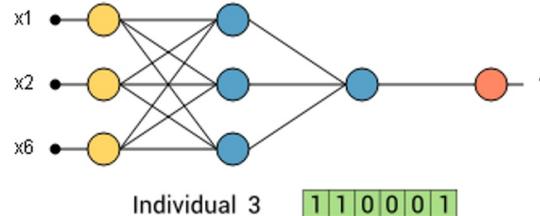
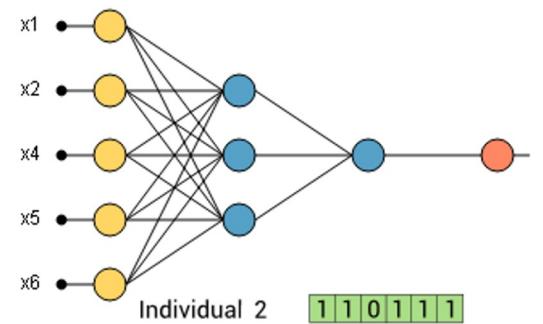
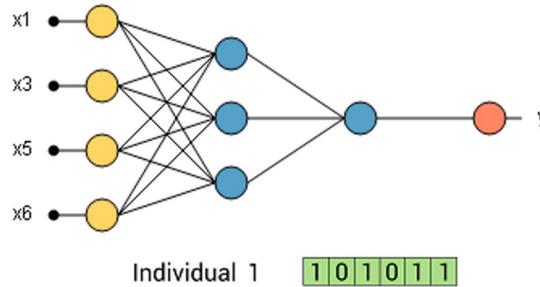


# Genetic Algorithm

- 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

1 | 1 | 0 | 0 | 0 | 1

Individual 4

0 | 1 | 0 | 1 | 0 | 0

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Offspring 1

0 | 1 | 0 | 1 | 0 | 1

Offspring 2

1 | 1 | 0 | 1 | 0 | 1

Offspring 3

0 | 1 | 0 | 1 | 0 | 1

Offspring 4

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      

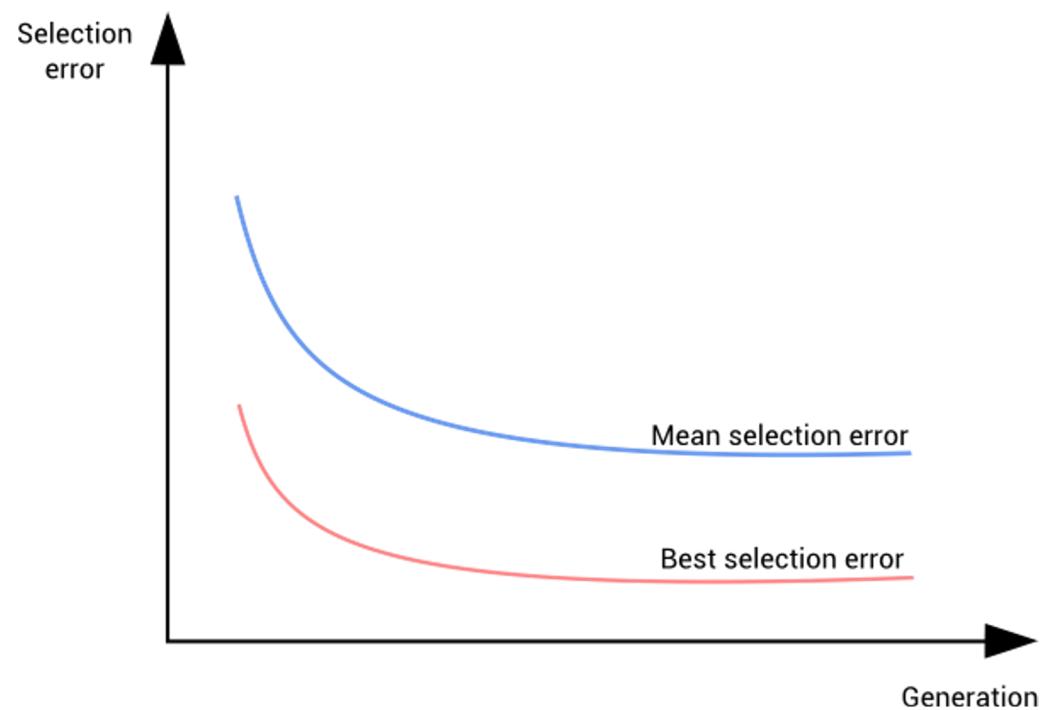
0	1	0	1	0	1
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Offspring1: Mutated      

0	1	0	0	0	0
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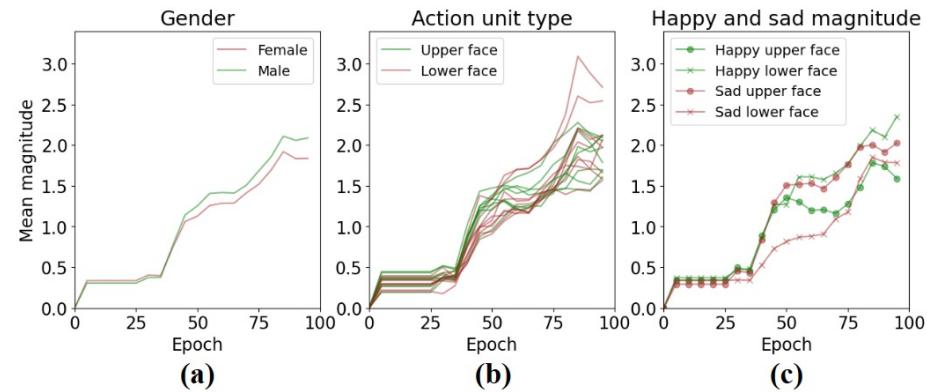
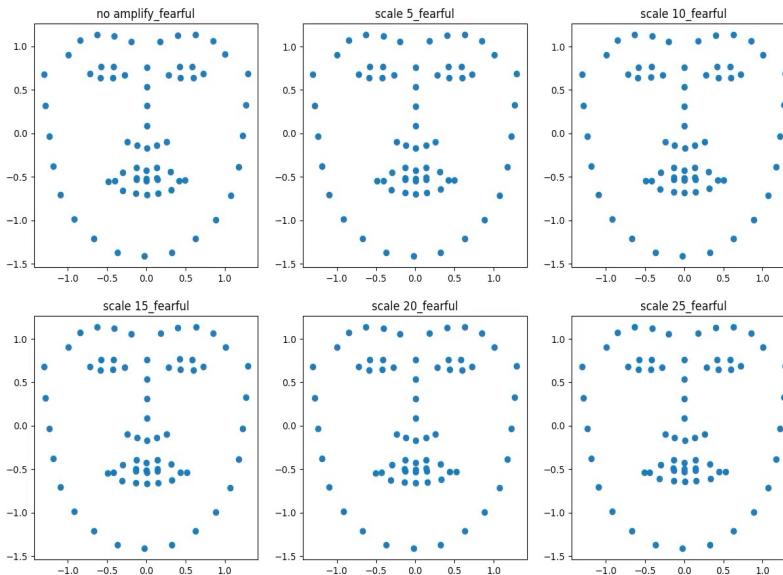
# Performance

- 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

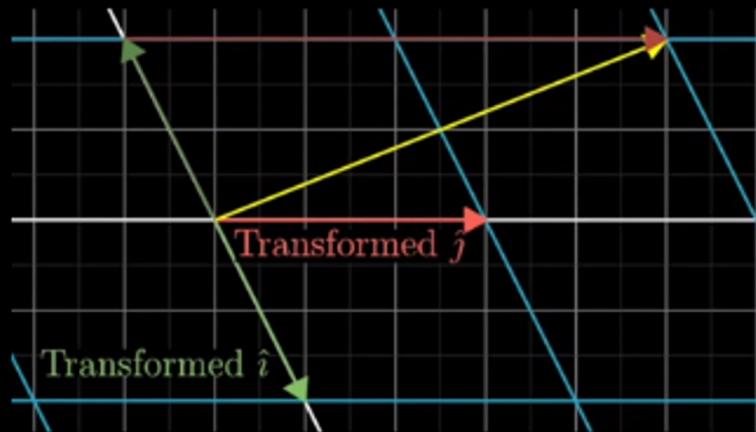
- Principal Component Analysis
- Linear Discriminant Analysis (NOT Latent Dirichlet Allocation)
- Random Projections

# Linear Algebra Review

- Matrix as a sequence of column vectors

“2x2 Matrix”

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

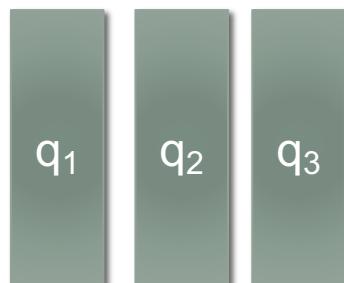


$$5 \begin{bmatrix} 3 \\ -2 \end{bmatrix} + 7 \begin{bmatrix} 2 \\ 1 \end{bmatrix}$$

# Linear Algebra Review

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

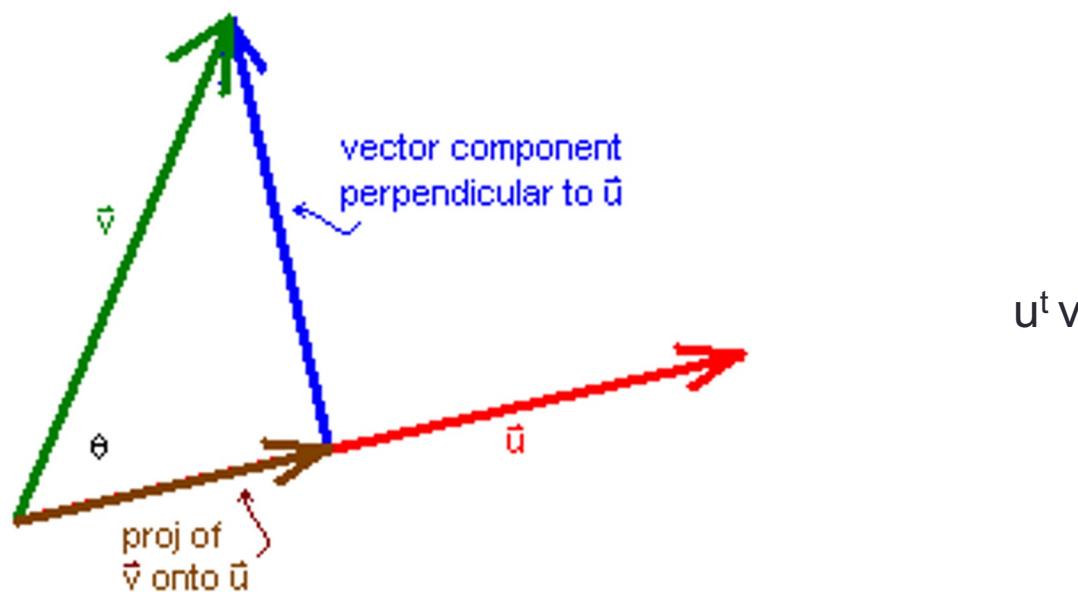
$$A = Q D Q^{-1}$$



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  $u$

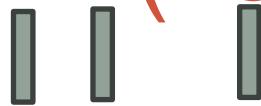


# Covariance matrix

- 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

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

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

# 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,

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

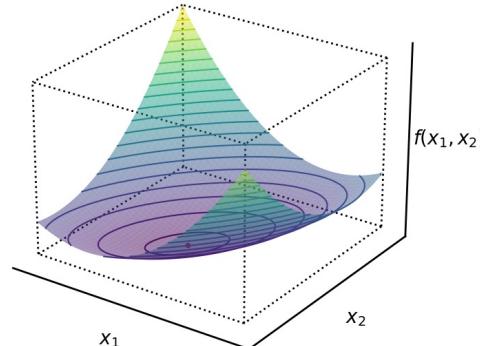
[https://en.wikipedia.org/wiki/Definite\\_matrix](https://en.wikipedia.org/wiki/Definite_matrix)

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

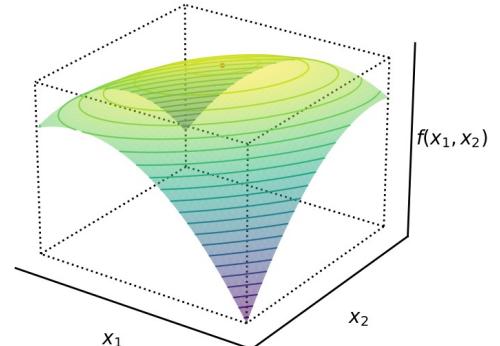
# Positive semi-definite

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

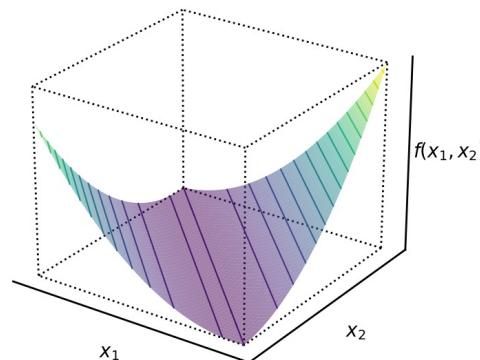
Positive definite



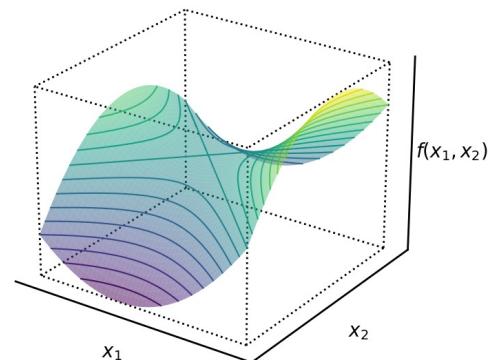
Negative definite



Singular & positive semi-definite



Indefinite



# Positive semi-definite and covariance matrixes

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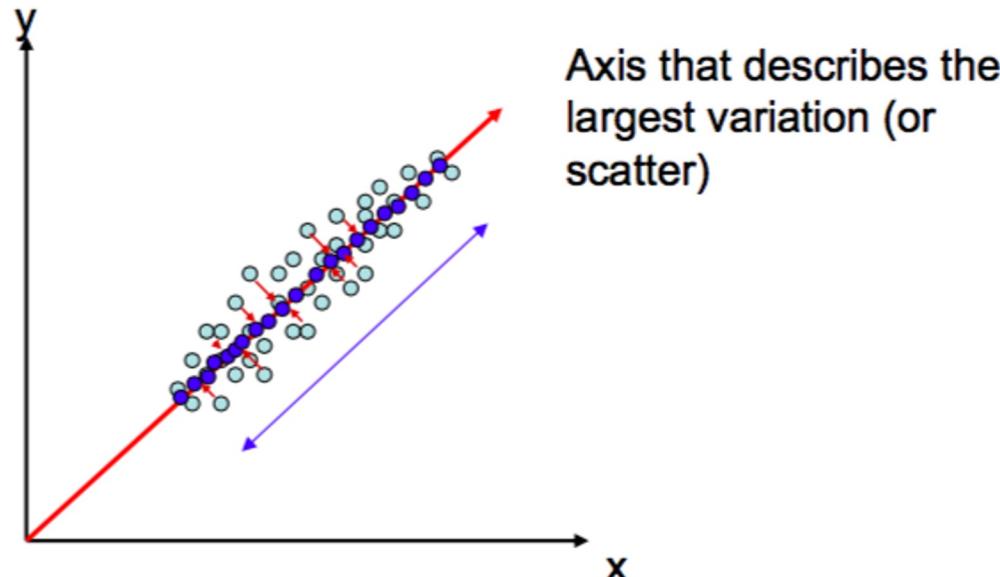
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[https://en.wikipedia.org/wiki/Definite\\_matrix](https://en.wikipedia.org/wiki/Definite_matrix)

- Covariance matrix is positive semi-definite and symmetric.
  - Symmetric -> real eigen values, eigen vectors are mutually orthogonal
    - $\mathbf{q}_i^T \mathbf{q}_j = 0$  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 describes maximum variation



# Formulation

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



# Trace properties

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

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

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

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

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

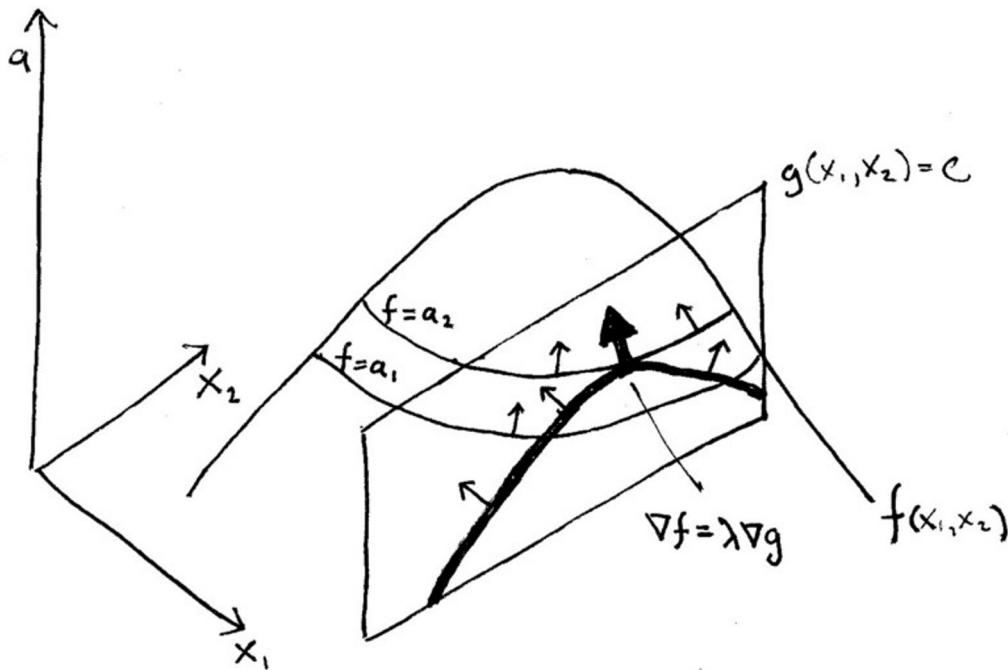
$$6 \quad \nabla_{A^T} f(A) = (\nabla_A f(A))^T$$

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

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

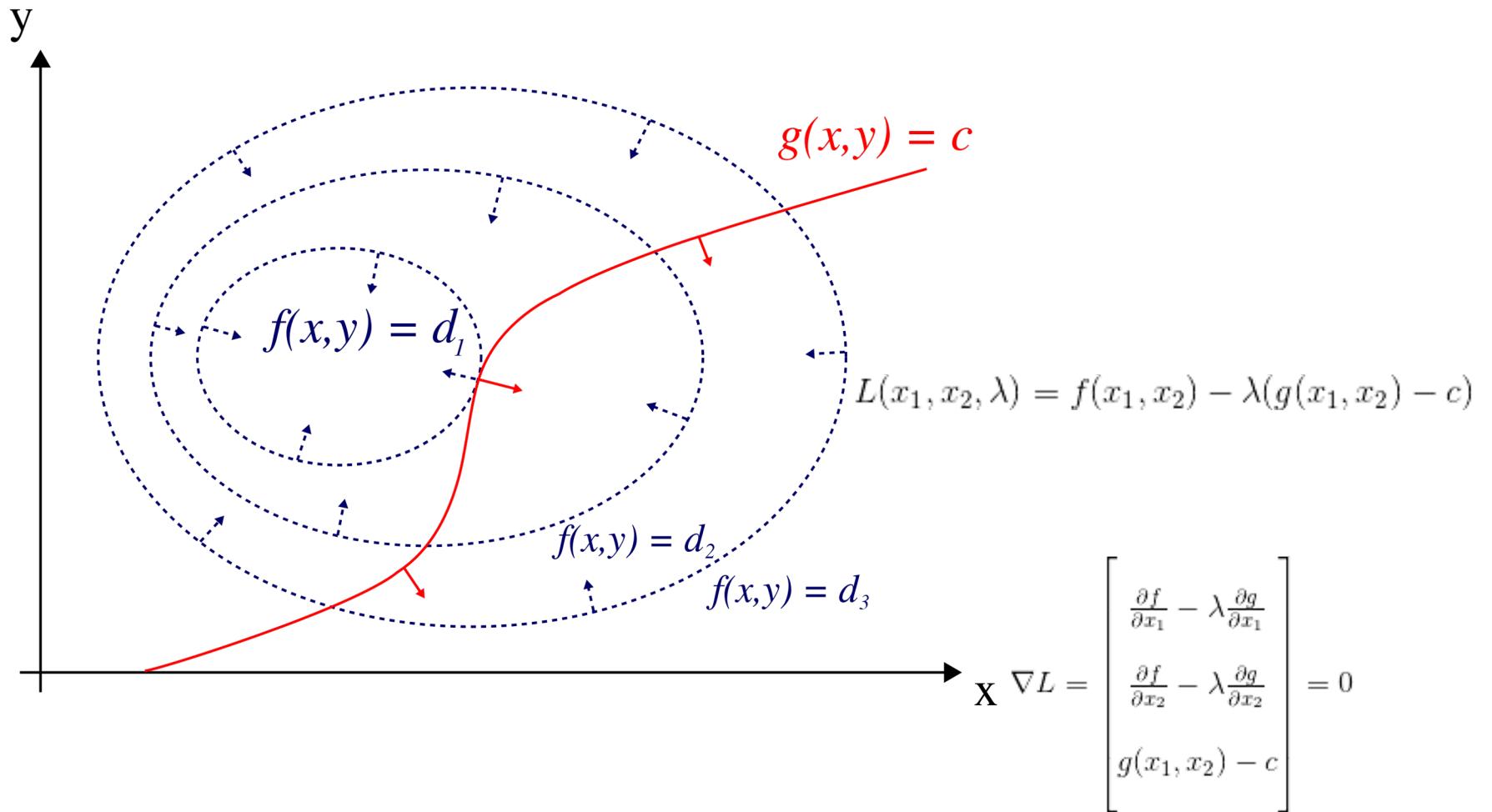
# Lagrange Multiplier

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



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

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



[https://en.wikipedia.org/wiki/Lagrange\\_multiplier#/media/File:LagrangeMultipliers2D.svg](https://en.wikipedia.org/wiki/Lagrange_multiplier#/media/File:LagrangeMultipliers2D.svg)

# 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

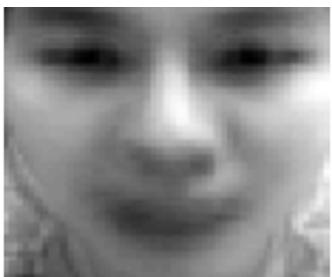
- A square  $d \times d$  matrix has full rank (e.g. rank  $d$ ) if the columns are linearly independent.
- The number of linearly independent columns is the rank of the matrix
- A covariance matrix of size  $d \times d$  will have at most  $N-1$  rank where  $N$  is the number of training samples
  - $640 \times 640$  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

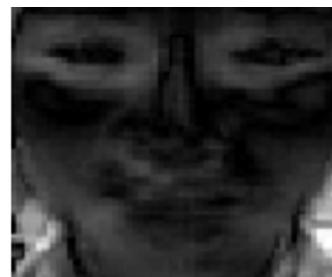
Meanface



V1



V2



V3



V4



V5



V6



V7



V8



V9



V10

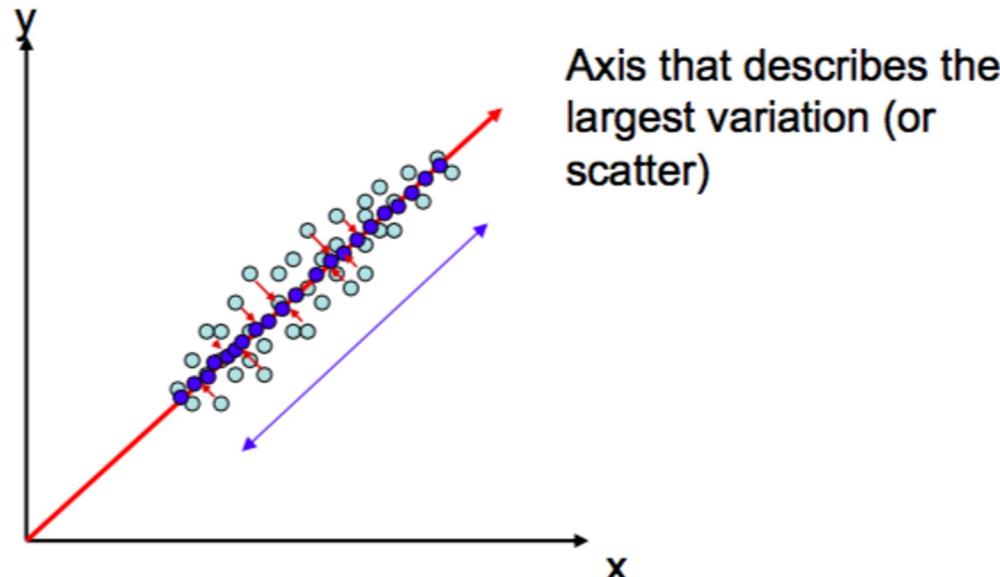


V11



# 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:

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

# Finding the weights

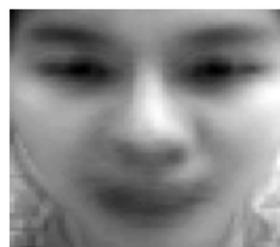
$$\mathbf{x} = \sum_{i=1}^N p_i \mathbf{v}_i = p_1 \begin{bmatrix} | \\ \mathbf{v}_1 \\ | \end{bmatrix} + p_2 \begin{bmatrix} | \\ \mathbf{v}_2 \\ | \end{bmatrix} + \dots + p_n \begin{bmatrix} | \\ \mathbf{v}_n \\ | \end{bmatrix} = \mathbf{V}\mathbf{p}$$

- 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

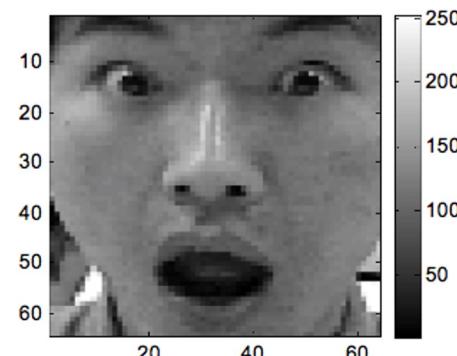


MSE=758.13

=



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?

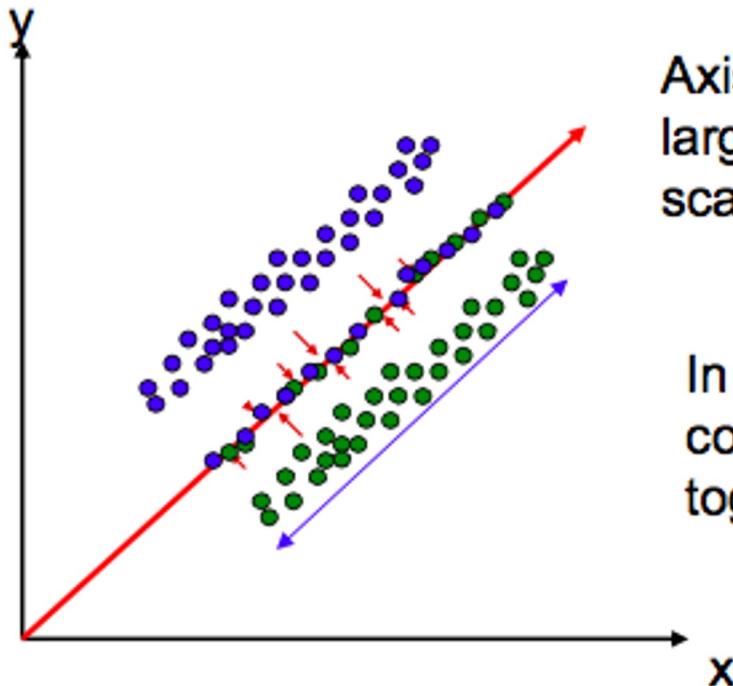
- Select based on amount of variance explained
  - Sum of eigenvalues exceeds some percent of total
- Reconstruction error

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

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

# PCA for classification

- PCA does not care about the class labels

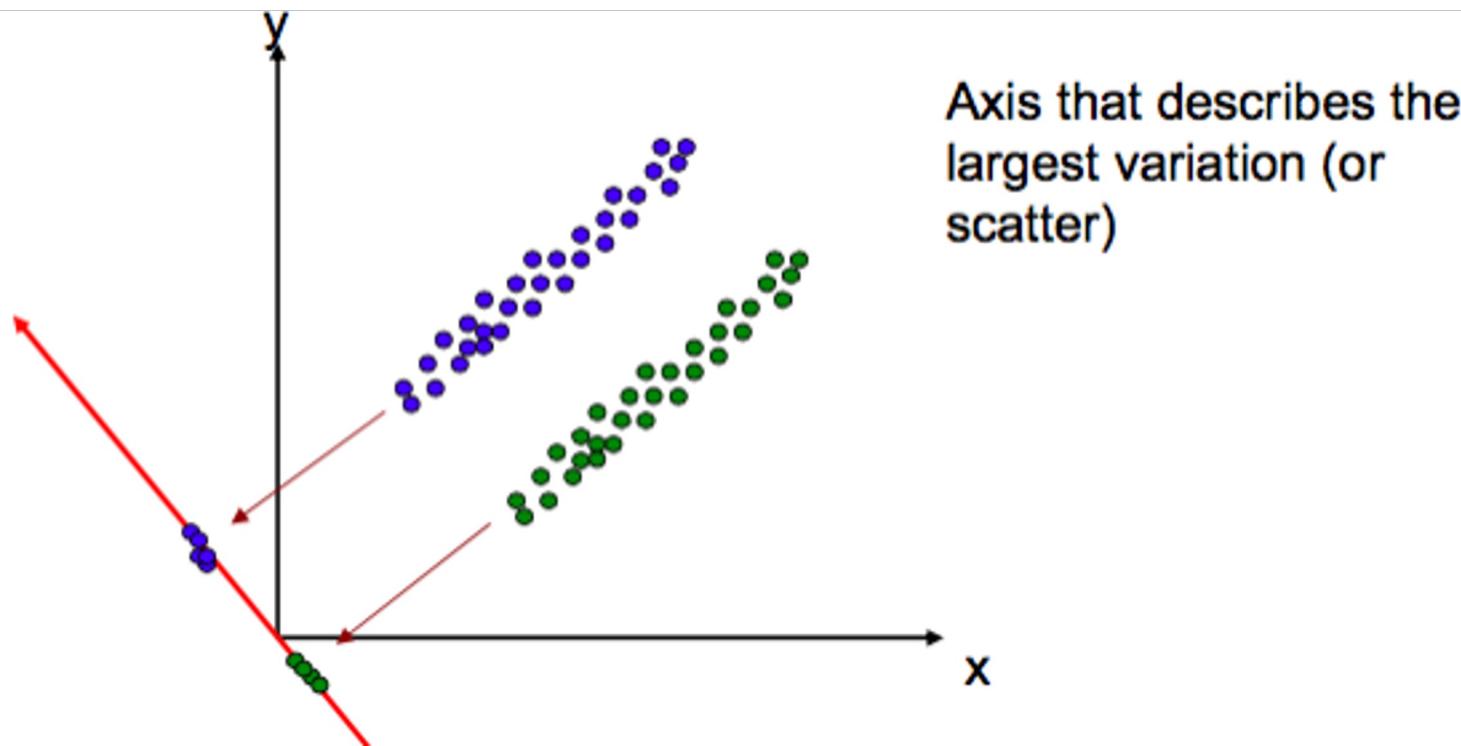


Axis that describes the largest variation (or scatter)...

In this case the projection vector completely smears the two classes together, making them inseparable

# What is LDA

- Find the projections that separate the classes.
- Assumes unimodal Gaussian model for each class
  - Maximize the distance between the means and minimize the variance of each class -> best classification performance



## Simple 2 class case

- We want to maximize the distance between the projected means:

e.g. maximize  $|(\tilde{\mu}_1 - \tilde{\mu}_2)|^2$

Where  $\tilde{\mu}_1$  is the projected mean  $\mu_1$  of class onto LDA direction vector  $\mathbf{w}$ , i.e.

$$\tilde{\mu}_1 = \mathbf{w}^T \mu_1$$

and for class 2:  $\tilde{\mu}_2 = \mathbf{w}^T \mu_2$  thus

$$\begin{aligned}|(\tilde{\mu}_1 - \tilde{\mu}_2)|^2 &= |(\mathbf{w}^T \mu_1 - \mathbf{w}^T \mu_2)|^2 \\&= \mathbf{w}^T (\mu_1 - \mu_2) (\mu_1 - \mu_2)^T \mathbf{w} \\&= \mathbf{w}^T \mathbf{S}_B \mathbf{w}\end{aligned}$$

# Between class scatter matrix $S_B$

$$\begin{aligned}(\tilde{\mu}_1 - \tilde{\mu}_2)^2 &= (\mathbf{w}^T \boldsymbol{\mu}_1 - \mathbf{w}^T \boldsymbol{\mu}_2)^2 \\&= \mathbf{w}^T (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2) (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)^T \mathbf{w} \\&= \mathbf{w}^T S_B \mathbf{w}\end{aligned}$$

We want to maximize  $\mathbf{w}^T S_B \mathbf{w}$  where  $S_B$  is the between class scatter matrix defined as:

$$S_B = (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)(\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)^T$$

# We also want to minimize within class scatter

- The variance or scatter of each class. We also want to minimize them.

$$\tilde{s}_1^2 = \sum_{i=1}^{N_1} (\tilde{x}_i - \tilde{\mu}_1)^2$$

Minimize the total scatter

$$\tilde{s}_1^2 + \tilde{s}_2^2$$

# Within class scatter

- Lets expand on scatter  $s_1, s_2$ .

$$\tilde{s}_1^2 = \sum_{i=1}^{N_1} (\tilde{x}_i - \tilde{\mu}_1)^2$$

$$= \sum_{i=1}^{N_1} (\mathbf{w}^T \mathbf{x}_i - \mathbf{w}^T \boldsymbol{\mu}_1)^2$$

$$= \sum_{i=1}^{N_1} \mathbf{w}^T (\mathbf{x}_i - \boldsymbol{\mu}_1)(\mathbf{x}_i - \boldsymbol{\mu}_1)^T \mathbf{w}$$

$$= \mathbf{w}^T \mathbf{S}_1 \mathbf{w}$$

# Total within class scatter

- We want to minimize

$$\tilde{s}_1^2 + \tilde{s}_2^2$$

- This is the same as  $\mathbf{w}^T \mathbf{S}_w \mathbf{w}$

$$\mathbf{S}_w = \sum_{i=1}^C \sum_{j=1}^{N_i} (\mathbf{x}_j - \boldsymbol{\mu}_i)(\mathbf{x}_j - \boldsymbol{\mu}_i)^T$$

C number of classes, Ni number of images from class i

# Fisher Linear Discriminant Criterion

- We want to maximize between class scatter
- We want to minimize within class scatter
- We have an objective function as a ratio so we can achieve both!

$$J(\mathbf{w}) = \frac{|(\tilde{\mu}_1 - \tilde{\mu}_2)|^2}{\tilde{s}_1^2 + \tilde{s}_2^2}$$

$$J(\mathbf{w}) = \frac{\mathbf{w}^T \mathbf{S}_B \mathbf{w}}{\mathbf{w}^T \mathbf{S}_W \mathbf{w}}$$

# LDA solution

- If you do calculus

$$\mathbf{S}_B \mathbf{w} = \lambda \mathbf{S}_W \mathbf{w}$$

$$\mathbf{S}_W^{-1} \mathbf{S}_B \mathbf{w} = \lambda \mathbf{w}$$

If  $\mathbf{S}_W$  is non-singular and invertible.

- Generalized eigenvalue problem. The number of solutions is  $\min(\text{rank } \mathbf{S}_B, \text{rank } \mathbf{S}_W) = C-1$  or  $N-C$
- For 2 class this simplifies to
  - Note this is only one projection direction

$$\mathbf{w} = \mathbf{S}_W^{-1} (\boldsymbol{\mu}_1 - \boldsymbol{\mu}_2)$$

# LDA+PCA

- Original features dimension L
- $S_B$   $S_W$  are LxL matrixes
- $\text{rank}S_B = C-1$ ,       $\text{rank}S_W = N-C$
- First do PCA to reduce dimension
- Then do LDA to maximize classification ability
- How many dimensions to PCA?
  - Do PCA to keep  $N-C$  eigenvectors -> Makes  $S_w$  full rank and invertible
  - Then, do LDA and compute  $C-1$  projections in this  $N-C$  subspace
- PCA+LDA = Fisher projection

# Random projection

- Original  $d$ -dimensional data is project to  $k$ -dimensional subspace
- Using a random  $k \times d$  matrix  $R$  with unit norm columns
  - Johnson-Lindenstrauss lemma: If points in a vector space are projected onto a randomly selected subspace of suitably high dimension, then the distances between the points are approximately preserved
- Elements of  $R$  are usually selected from Gaussians.
  - Generally any zero mean unit variance distribution would satisfy Johnson-Lindenstrauss lemma.

# Random projection notes

- R is not generally orthogonal.
  - But in a substantially large subspace, random vectors might be close to orthogonal.
- Looks weird but works...
- Can be used to initialized GMMs by finding good initializations in the projected space first
- Robust to outliers in the data, because it uses no data
- Faster to train than PCA if data has high dimension
  - $O(k^2 \times n + k^3)$  (covariance computation + eigen decomposition) where k - features, n – samples
- See <https://medium.com/data-science-in-your-pocket/random-projection-for-dimension-reduction-27d2ec7d40cd> for usage guides



# Workflow for dimensionality reduction in ML

1. Reduce the number of features by projecting into lower dimensions (need to pick #of dimensions via cross validation)
2. Build a model using your favorite technique
3. ???
4. Profit

**Table 1: Description of Datasets**

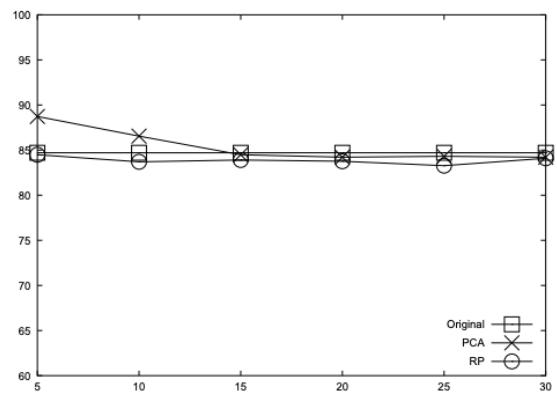
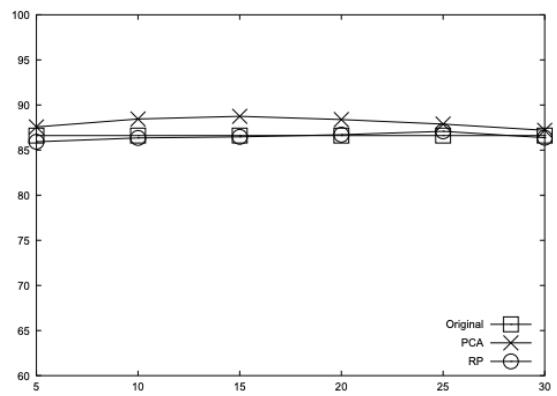
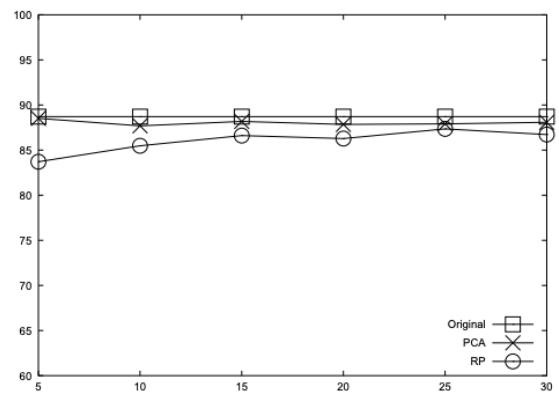
Name	# Instances	# Attributes
Ionosphere	351	34
Colon	62	2000
Leukemia	72	3571
Spam	4601	57
Ads	3279	1554

C4.5

1NN

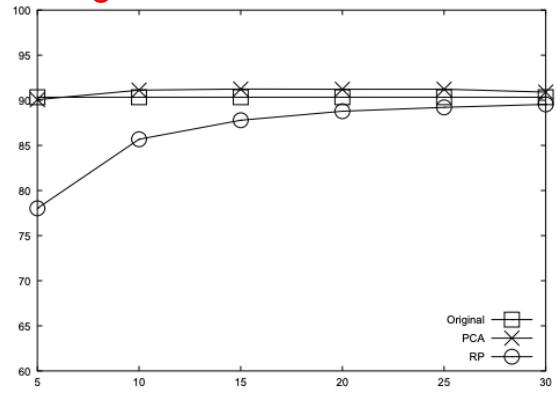
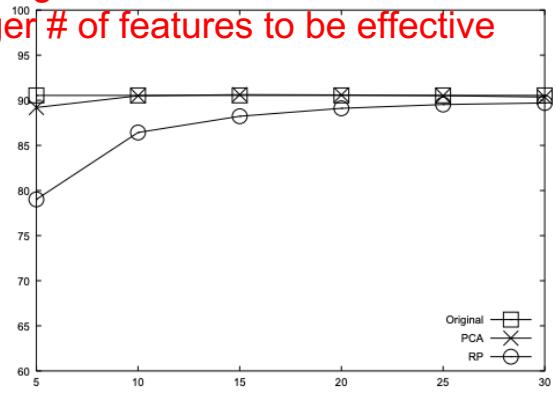
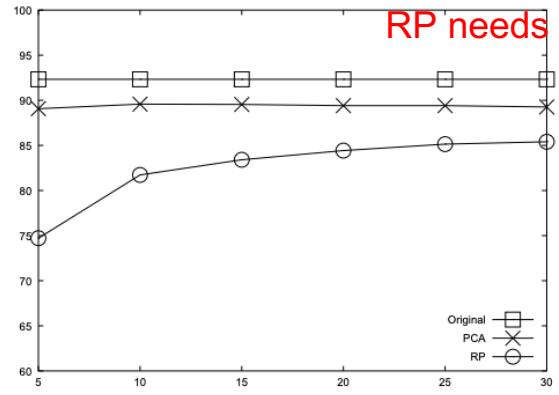
5NN

Ion

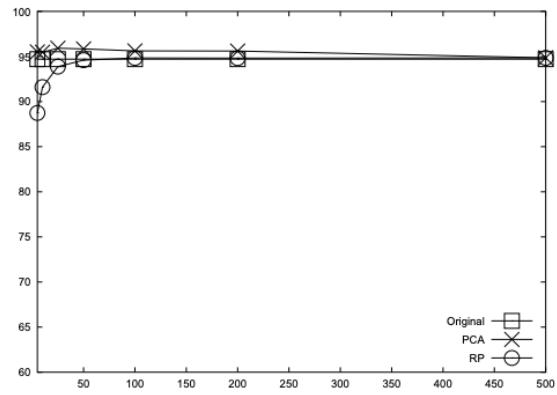
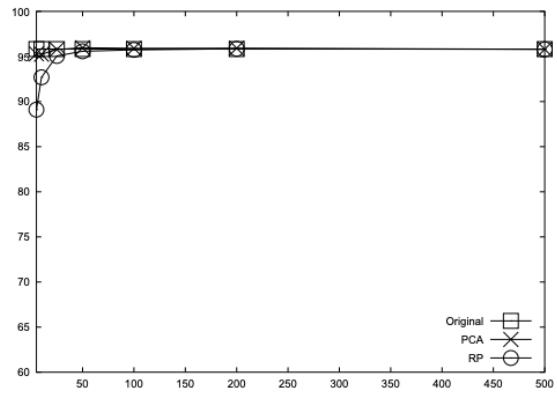
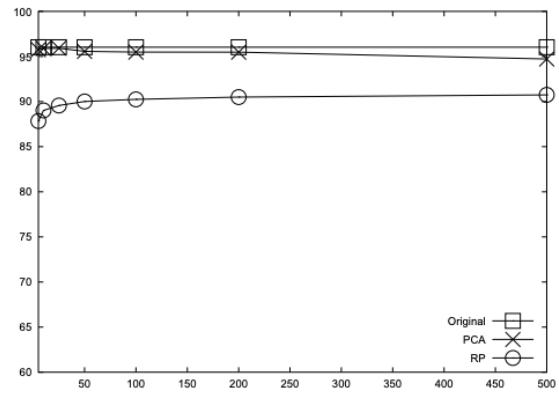


Sometimes using some of the features is better than using all of the data  
RP needs larger # of features to be effective

Spam



Ads

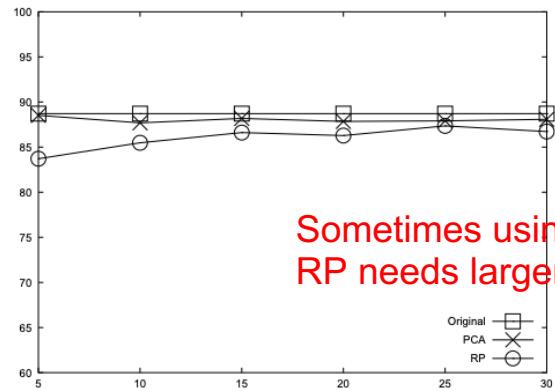


C4.5

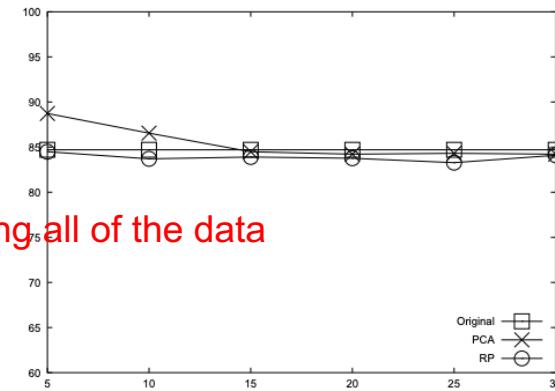
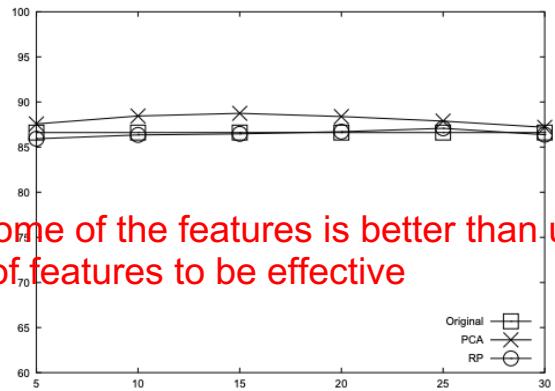
1NN

5NN

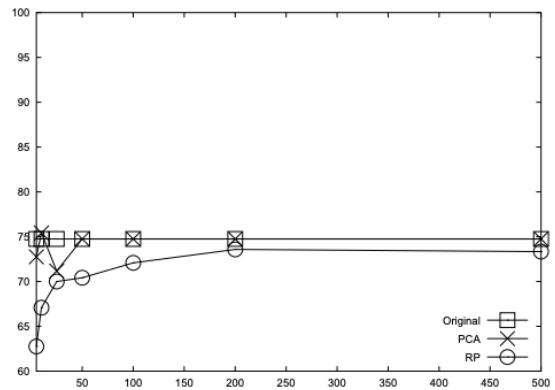
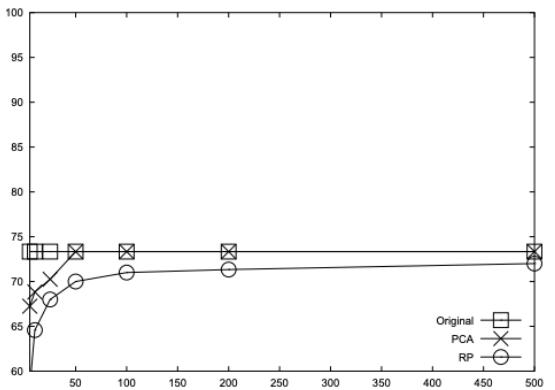
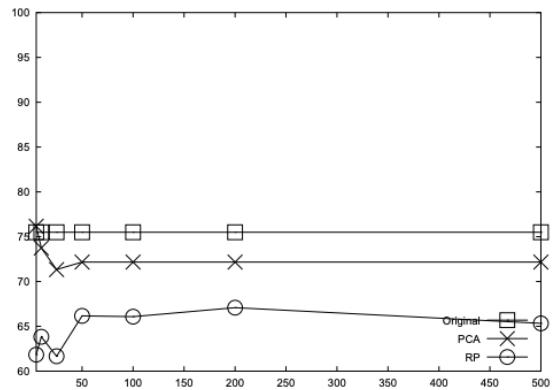
Ion



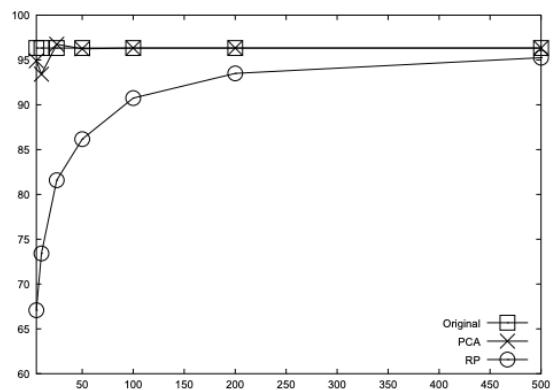
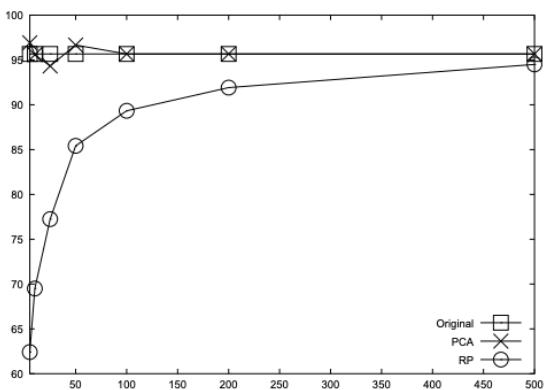
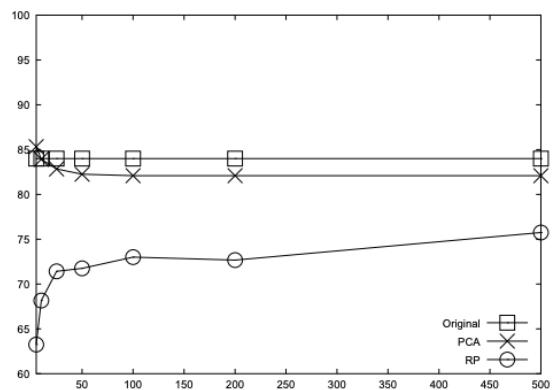
Sometimes using some of the features is better than using all of the data  
RP needs larger # of features to be effective



Colon



Leukemia



# Visualization

## Methods covered

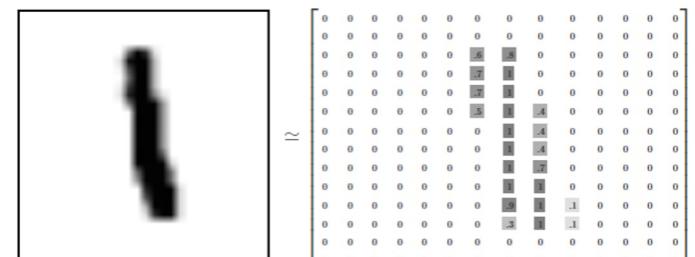
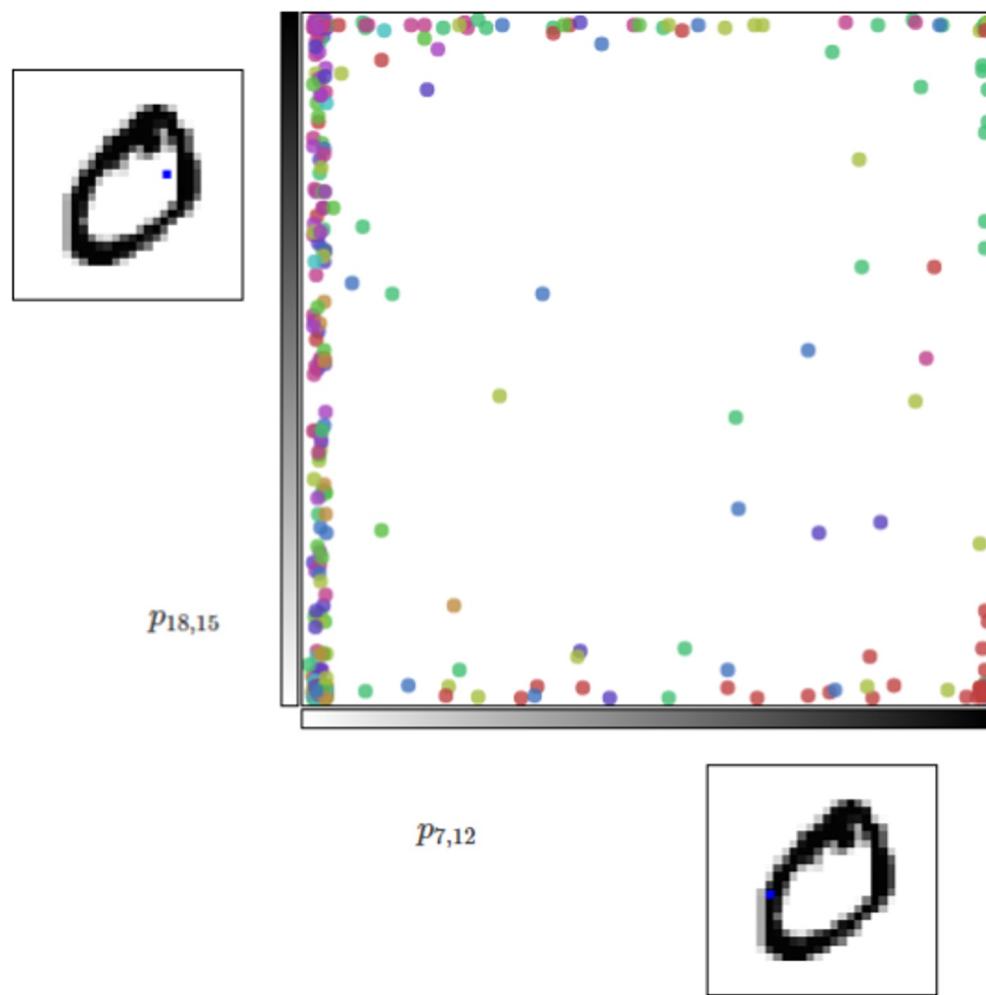
1. Reducing reconstruction error: PCA
2. Keeping direction of maximum separability: LDA
3. Preserving distance (globally): RP

These are usually useful for downstream machine learning methods. (Classification/Regression/Clustering)

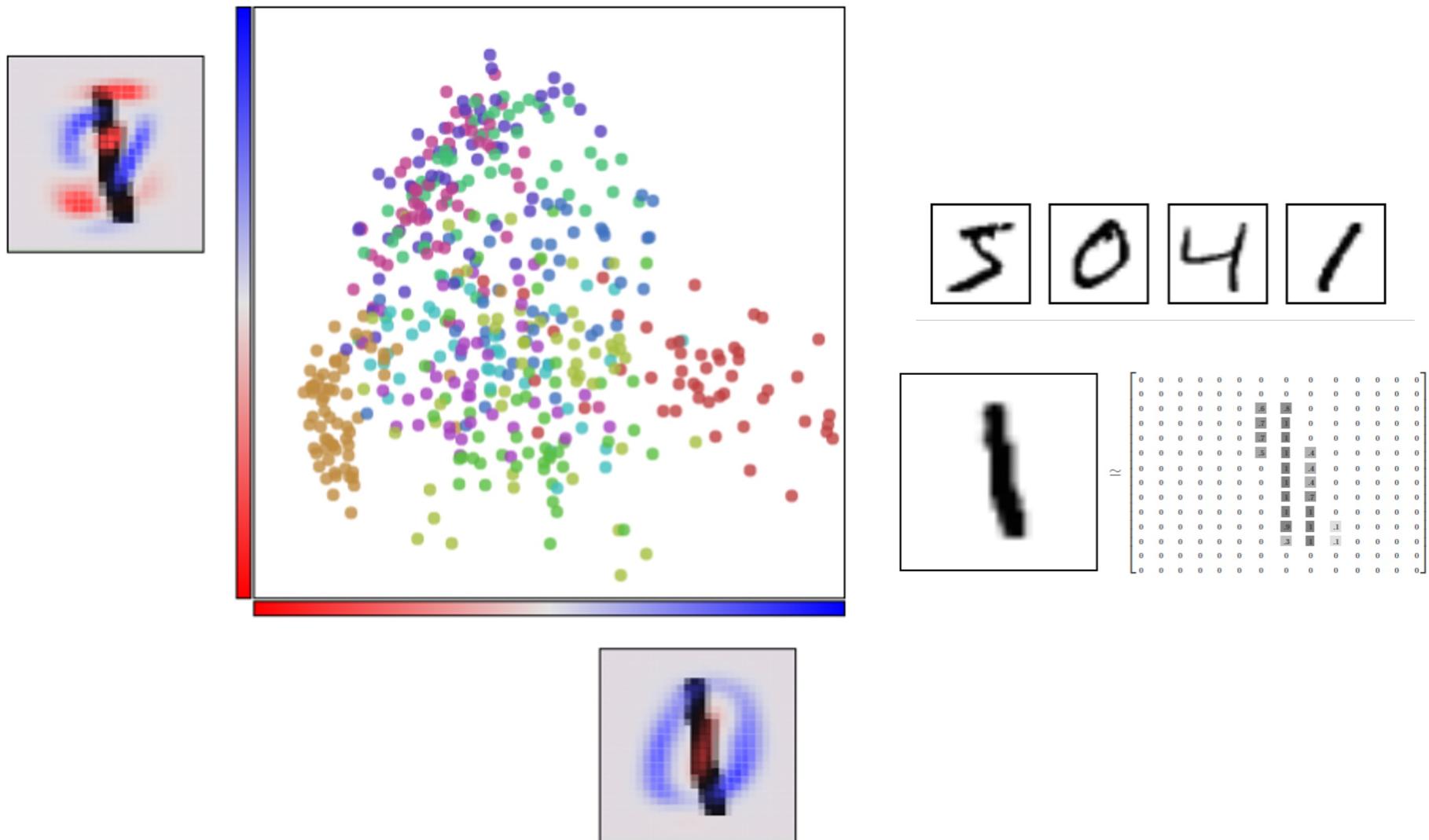
But what if we, as humans, want to get a sense of our data?

1. Interpretability (in some sense): ????
  - Check if our dimensionality reduction is good
  - Analyze clusters from k-mean, GMM, etc.

# Visualizing MNIST



# PCA with MNIST



# t-distributed Stochastic Neighbor Embedding (t-SNE)

Preserves neighbor (preserves local distance).

- Things close together should be close together in the projected space
- Prefer using few projected dimensions (2-3)

# Defining neighbors

Define  $P_{j|i}$  probability that  $i$  would pick  $j$  as its neighbor

Assume  $i$  picks proportional to Gaussian centered at  $i$

$$p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2)/2\sigma_i^2}$$

$P_{i|i} = 0$  since we don't want to have it pick itself

The variance is fixed to some value.

# Defining neighbors

Define  $p_{j|i}$  probability that  $i$  would pick  $j$  as its neighbor

Assume  $i$  picks proportional to Gaussian centered at  $i$

$$p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2)/2\sigma_i^2}$$

When projected to set of points  $\{y_i\}$ , define  $q_{j|i}$  the probability that  $i$  would pick  $j$  in embedding/latent space

$$q_{j|i} = \frac{\exp(-\|y_i - y_j\|^2)}{\sum_{k \neq i} \exp(-\|y_i - y_k\|^2)}$$

We set the variance in the  $y$  space to be  $1/\sqrt{2}$

# Defining neighbors

$$p_{j|i} = \frac{\exp(-||x_i - x_j||^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-||x_i - x_k||^2)/2\sigma_i^2}$$

$$q_{j|i} = \frac{\exp(-||y_i - y_j||^2)}{\sum_{k \neq i} \exp(-||y_i - y_k||^2)}$$

We expect p and q to be the same  $\rightarrow$  small distance

How to measure distance between probability functions?  
Kullback-Leibler (KL) divergence

# KL divergence

Distance between two distributions

$$D_{KL}(P||Q) = \sum_i P(i) \log \frac{P(i)}{Q(i)} = - \sum_i P(i) \log \frac{Q(i)}{P(i)}$$

Note  $D_{KL}(P||Q) \neq D_{KL}(Q||P)$  (Not a real distance)

Always positive. Equals 0 iff  $Q = P$  at every point.

$$P(\text{head}) = 0.5 \quad P(\text{tail}) = 0.5$$

$$Q(\text{head}) = 0.7 \quad Q(\text{tail}) = 0.3$$

$$D_{KL}(P||Q) = 0.5 * \ln 0.5/0.7 + 0.5 * \ln 0.5/0.3 = 0.087$$

$$D_{KL}(Q||P) = 0.7 * \ln 0.7/0.5 + 0.3 * \ln 0.3/0.5 = 0.082$$

# Loss function

$$p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2)/2\sigma_i^2} \quad q_{j|i} = \frac{\exp(-\|y_i - y_j\|^2)}{\sum_{k \neq i} \exp(-\|y_i - y_k\|^2)}$$

We expect p and q to be the same  $\rightarrow$  small distance

Loss function

$$\sum_i D_{KL}(p_i || q_i)$$

All points i                    KL computes over j

$$D_{KL}(P||Q) = \sum_j P(j) \log \frac{P(j)}{Q(j)}$$

Note P can be considered as the weight for the distance

Where p is large but q is small  $\rightarrow$  large penalty

p is small but q is large  $\rightarrow$  small penalty

D(p||q) focuses on local structure in p

What are we minimizing wrt?  
How to minimize loss?

# From SNE to t-SNE

Symmetric density  
t-distributed

# Symmetric with joint probability

$$p_{j|i} \neq p_{i|j}$$

$$D_{KL}(P||Q) = \sum_i P(i) \log \frac{P(i)}{Q(i)}$$

A point  $i$  far away from everything will have small  $p_{j|i}$

- Location of points in  $q$  no longer matter

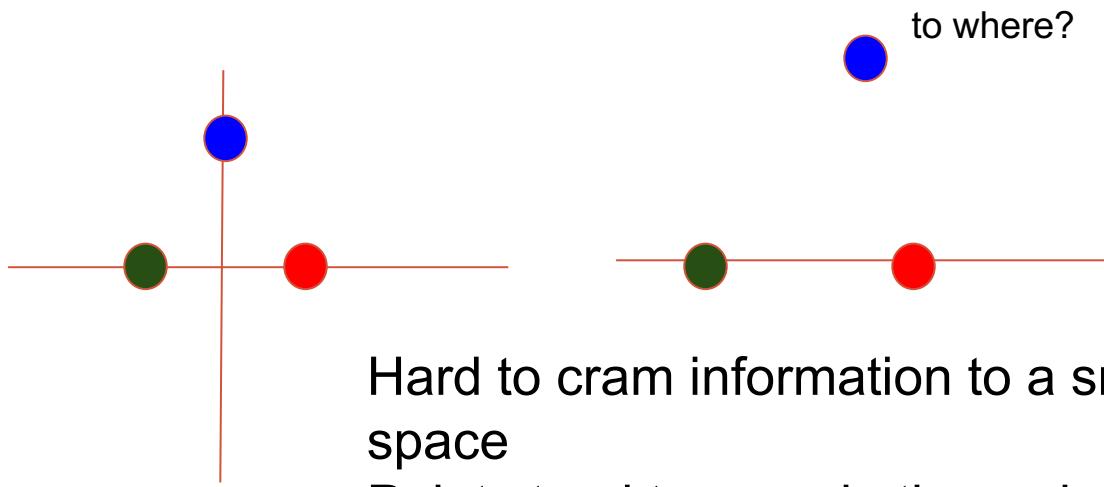
Create “joint probability”  $p_{ij} = p_{ji} = (p_{i|j} + p_{j|i})/2$

- Each data point will contribute to the loss

Use instead of conditional probability in KL divergence

# t-distributed

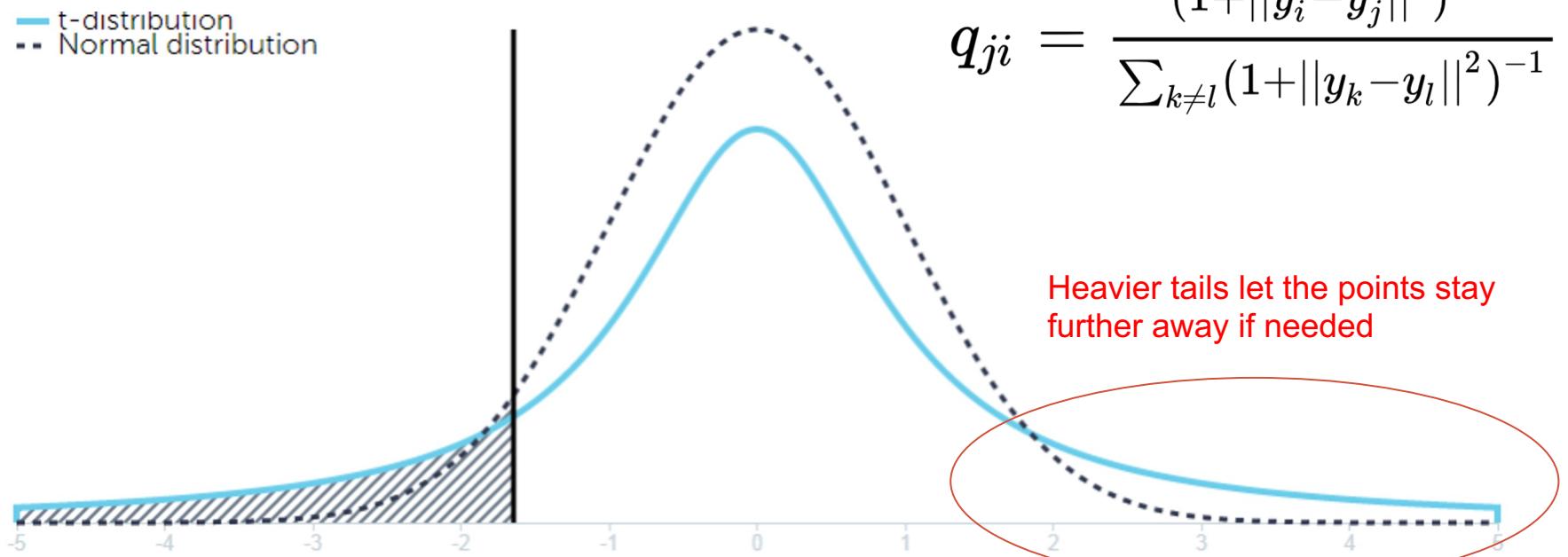
- “Crowding problem”
- In  $N$  dimension, you can have  $N+1$  points at equal distance. But you cannot model this in smaller dimension



# t-distributed

- Instead of Gaussian for  $q$  we use student's t distribution

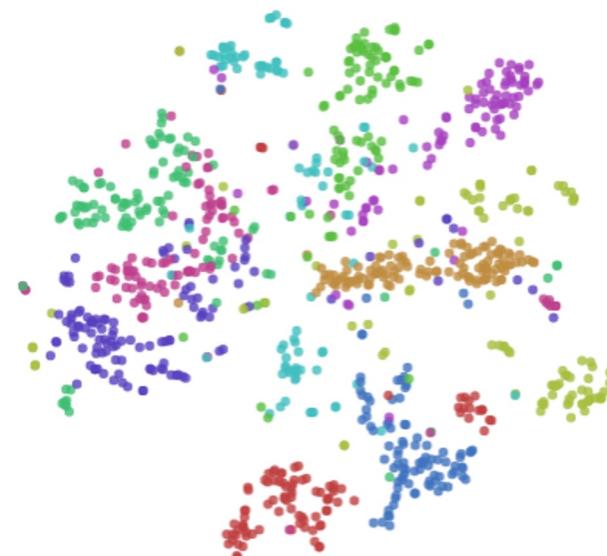
$$q_{ji} \propto (1 + \|y_i - y_j\|^2)^{-1}$$



# Crowding and t-SNE



Sammon's mapping  
(crowding problem)



t-SNE

# Variance

$$p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2)/2\sigma_i^2}$$

How to set the variance of our original space?

A single variance for all points is not ideal.

- Want small variance for dense parts
- Want big variance for sparse parts

Set variance by amount of neighbors you want!

How to quantify amount of neighbors?

# Perplexity

$$p_{j|i} = \frac{\exp(-\|x_i - x_j\|^2)/2\sigma_i^2}{\sum_{k \neq i} \exp(-\|x_i - x_k\|^2)/2\sigma_i^2}$$

$$Perp(P_i) = 2^{H(P_i)}$$

$$H(P_i) = - \sum_j p_{j|i} \log_2 p_{j|i}$$

Perplexity of  $P_i$  represents effective amount of neighbors for the point  $i$

Set  $Perp(P_i)$  then t-SNE algorithm searches for the corresponding variance

Typical values for perplexity 5 to 50

# t-SNE summary

Goal: preserves local neighbors

Gradient-based -> need multiple runs to see the best

Two parameters: #iteration, perplexity

**Does not learn a projection** (unlike PCA, LDA, RP)

- If you have a new sample, you have to re-run the whole thing
- Used for visualization only

# UMAP: Uniform Manifold Approximation and Projection

t-SNE loses structure of important feature dimension or structure (global vs local structure)

Draw upon “inspiration” from Manifold learning theory

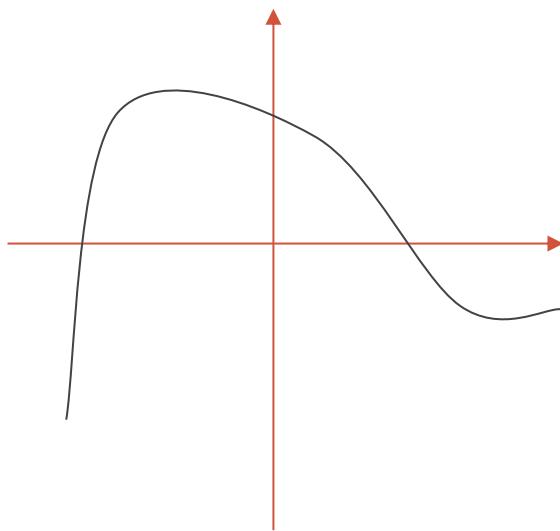
# UMAP big picture

1. Define a new kind of probability for being neighbor
  - a. Based on distance to neighbors
2. Do SGD just like t-SNE

# Manifold

Manifold: a non-linear space but locally linear

Data can be represented in 2-d but lies in 1-d manifold



UMAP defines a manifold based on  
the neighbors of points

# UMAP's distance function

Given fixed  $k$  (number of neighbors)

Let  $X_1, \dots, X_k$  be the  $k$ -nearest neighbors of  $X$

The distance between  $X_i$  and  $X_j$  is

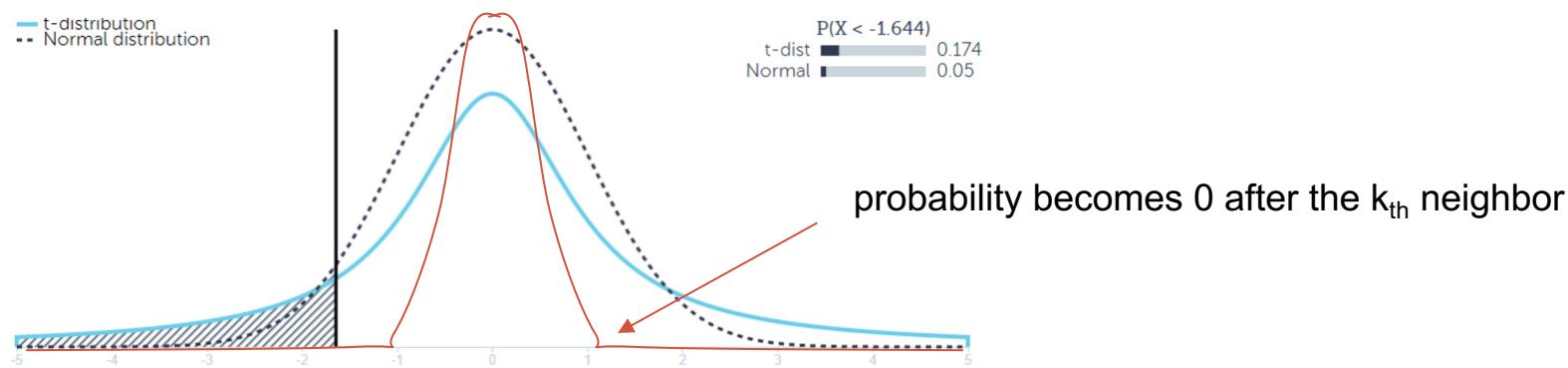
$$w_i(X_i, X_j) = \exp(-(d(X_i, X_j) - \rho_i)/\sigma_i)$$

Think of this  $w$  as giving  
“probability” that two points are  
connected

L2 distance in  
original space

distance to nearest  
neighbor so it starts  
from 0

diameter of the  
neighbors so it  
maxes at 1



# UMAP's distance function

Given fixed  $k$  (number of neighbors)

Let  $X_1, \dots, X_k$  be the  $k$ -nearest neighbors of  $X$

The distance between  $X_i$  and  $X_j$  is

$$w_i(X_i, X_j) = \exp(-(d(X_i, X_j) - \rho_i)/\sigma_i)$$

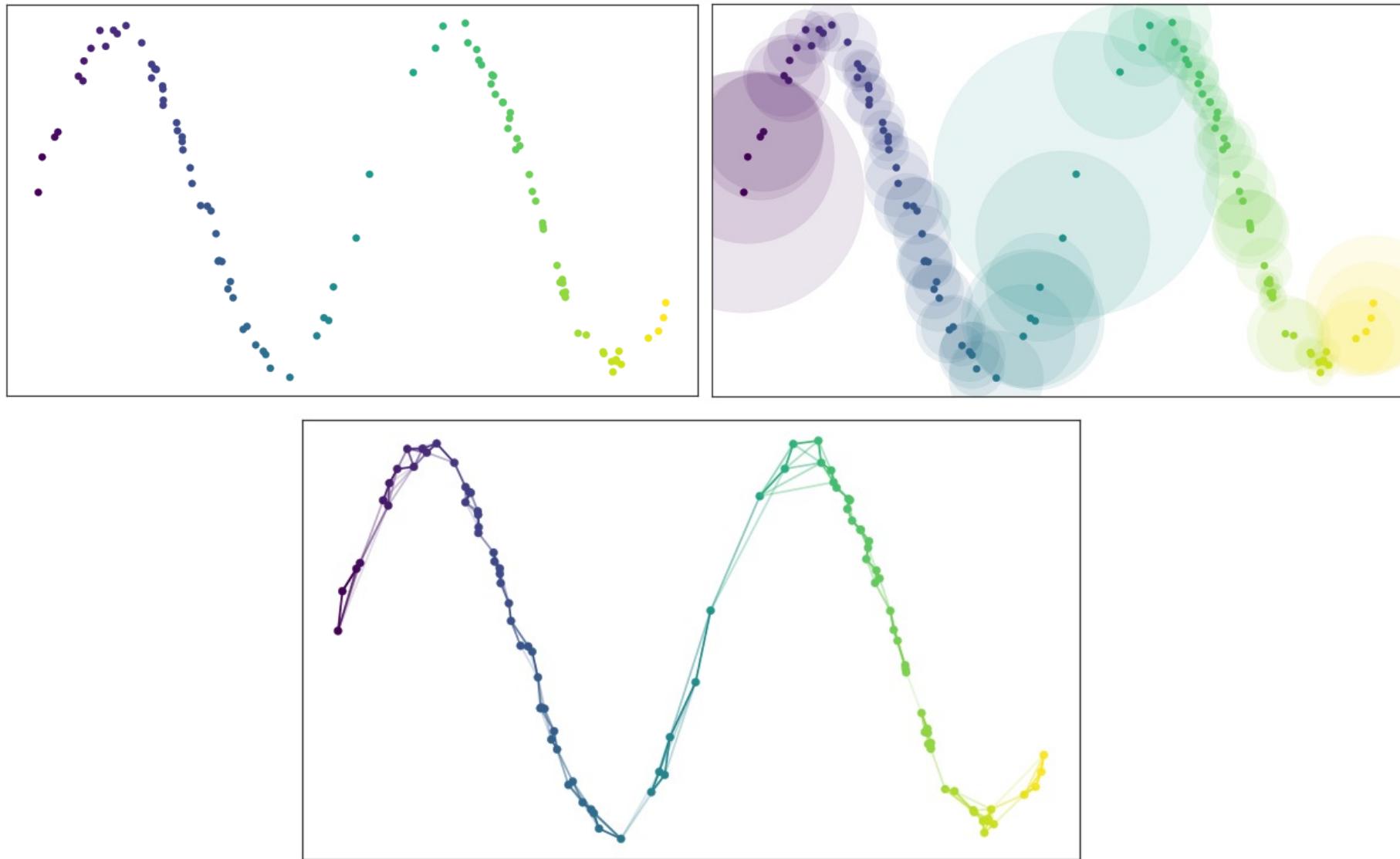
L2 distance in  
original space

distance to nearest  
neighbor so it starts  
from 0

diameter of the  
neighbors so it  
maxes at 1

Make the distance symmetric by

$$w(X_i, X_j) = w_i(X_i, X_j) + w_j(X_j, X_i) - w_i(X_i, X_j)w_j(X_j, X_i)$$



[https://umap-learn.readthedocs.io/en/latest/how\\_umap\\_works.html](https://umap-learn.readthedocs.io/en/latest/how_umap_works.html)

# UMAP optimization

From the weights minimize the cross-entropy between original and projected points (in terms of w)

$$\sum_{e \in E} w_h(e) \log\left(\frac{w_h(e)}{w_l(e)}\right) + (1 - w_h(e)) \log\left(\frac{1 - w_h(e)}{1 - w_l(e)}\right)$$

All neighbors

Distance in original space

Distance in new space

Similar to KL metric in t-SNE

Loss function

$$D_{KL}(P || Q) = \sum_j P(j) \log \frac{P(j)}{Q(j)}$$

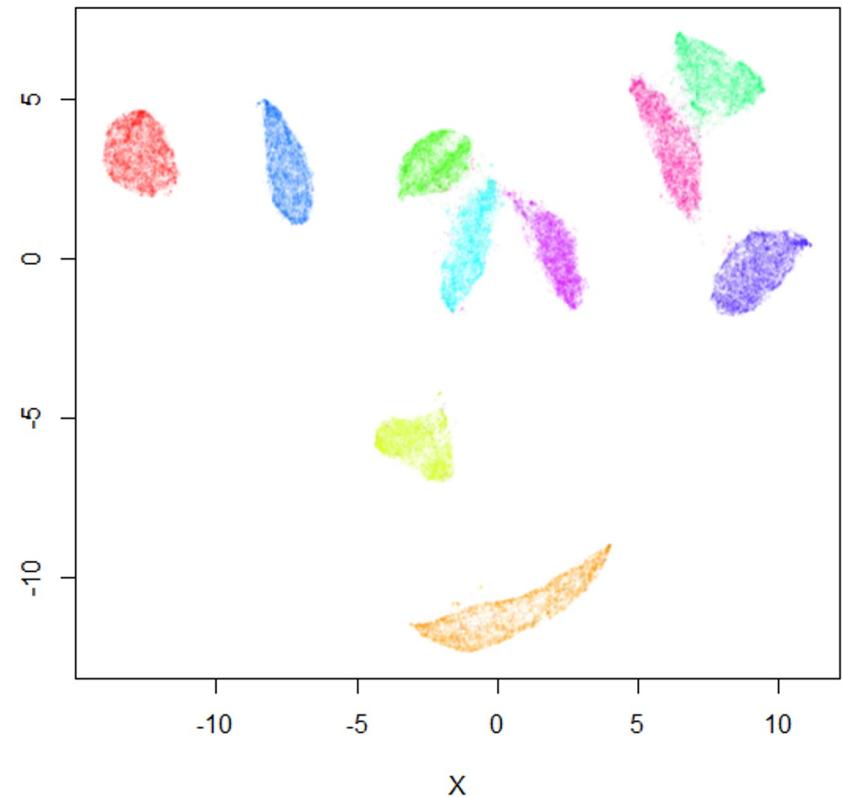
All points i

KL computes over j

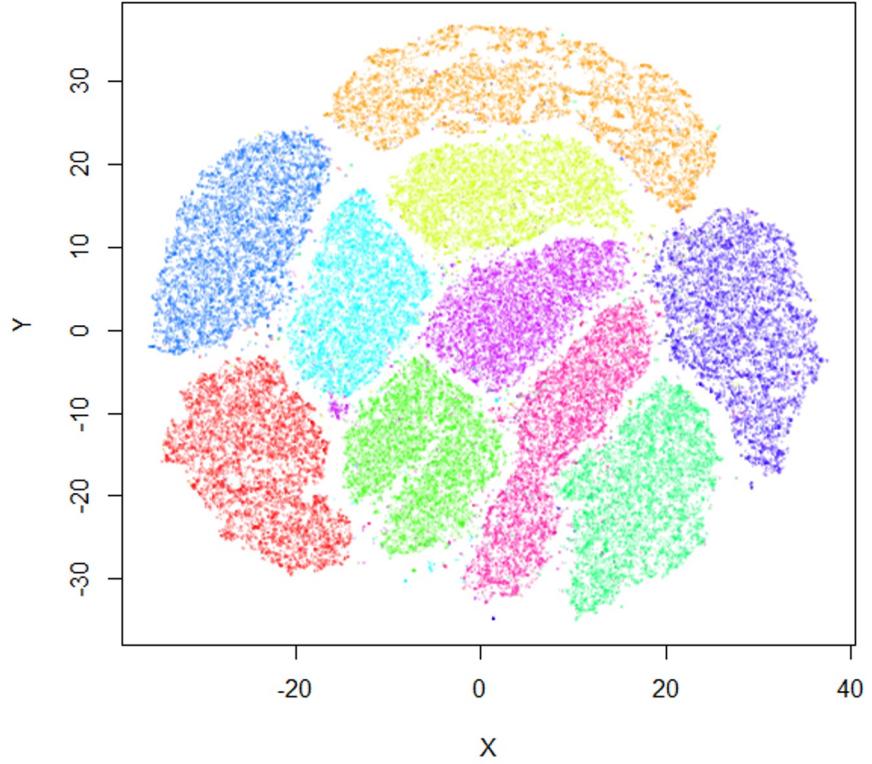
Use gradient descent to optimize

# MNIST

**MNIST UMAP**



**MNIST t-SNE**

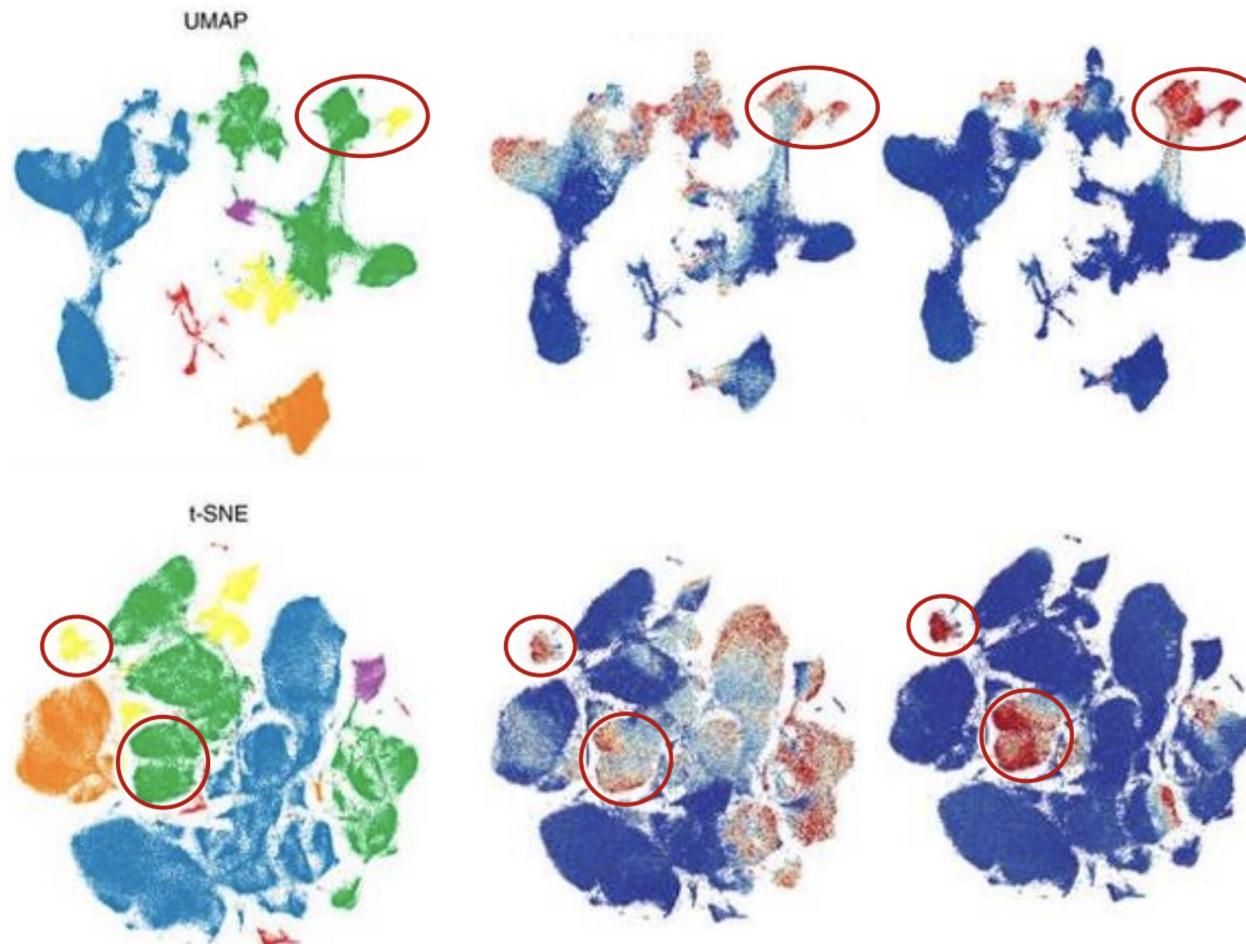


<https://jlmelville.github.io/uwot/umap-examples.html>

# Dimensionality reduction for visualizing single-cell data using UMAP

Analysis | Published: 03 December 2018

nature  
biotechnology



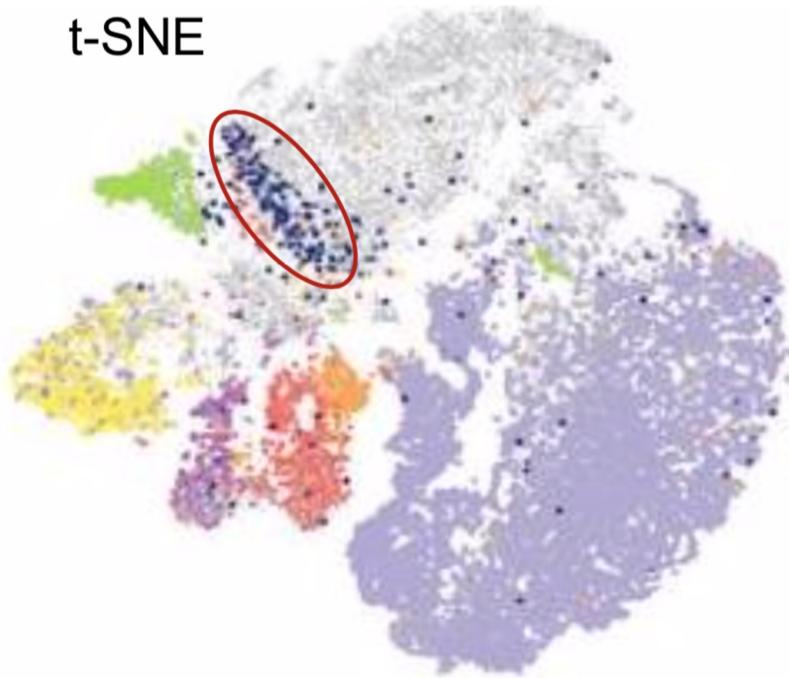
- UMAP can capture cross-class relationship

# UMAP vs t-SNE on continuous classes

UMAP



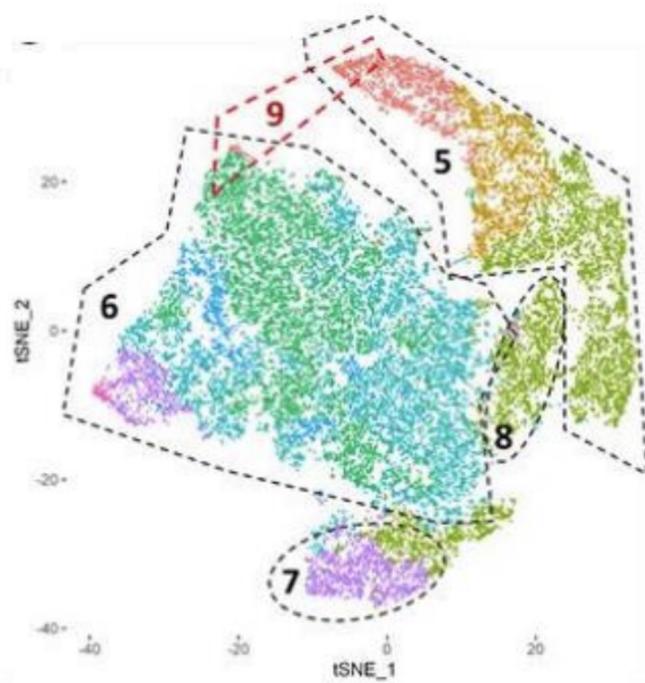
t-SNE



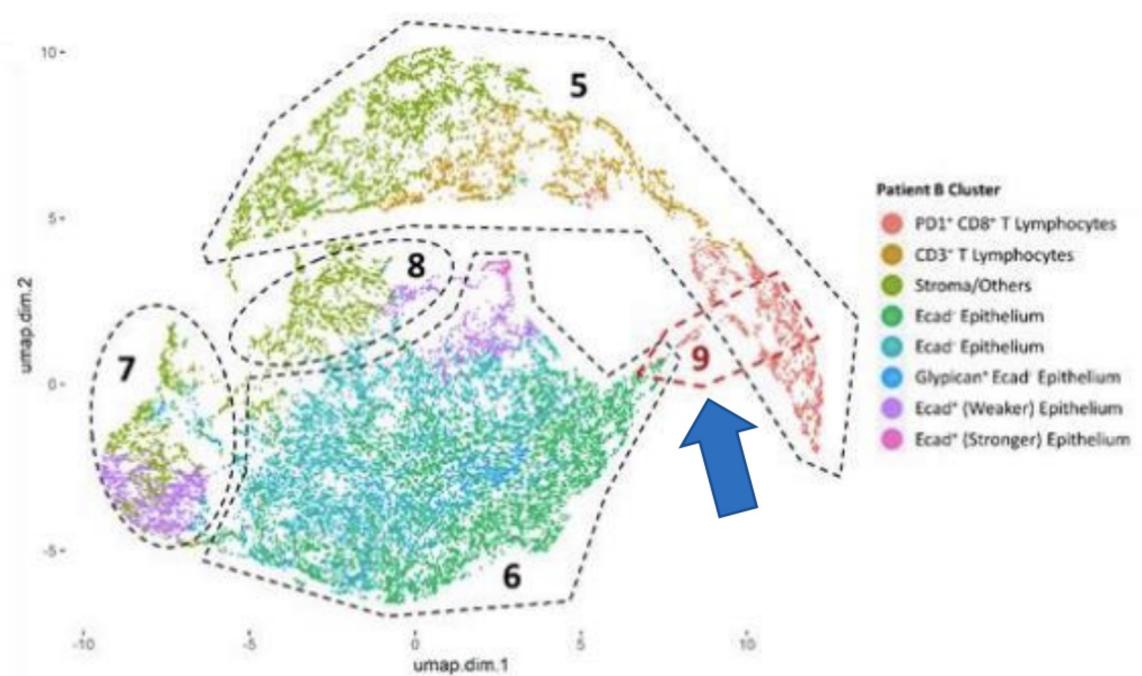
- MPP
- Macrophage
- Neutrophil
- Erythrocyte
- B cell
- T cell
- NK cell

# UMAP find continuous transition across classes

t-SNE

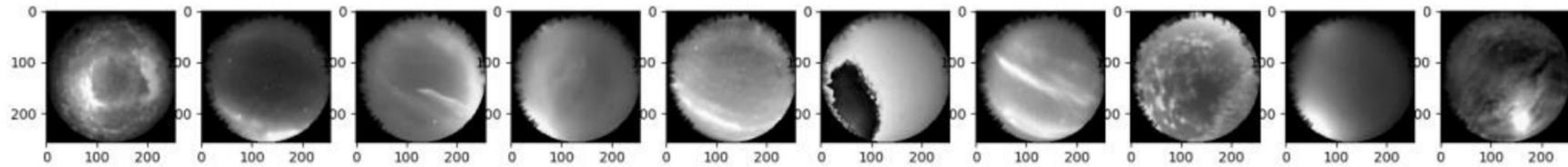


UMAP

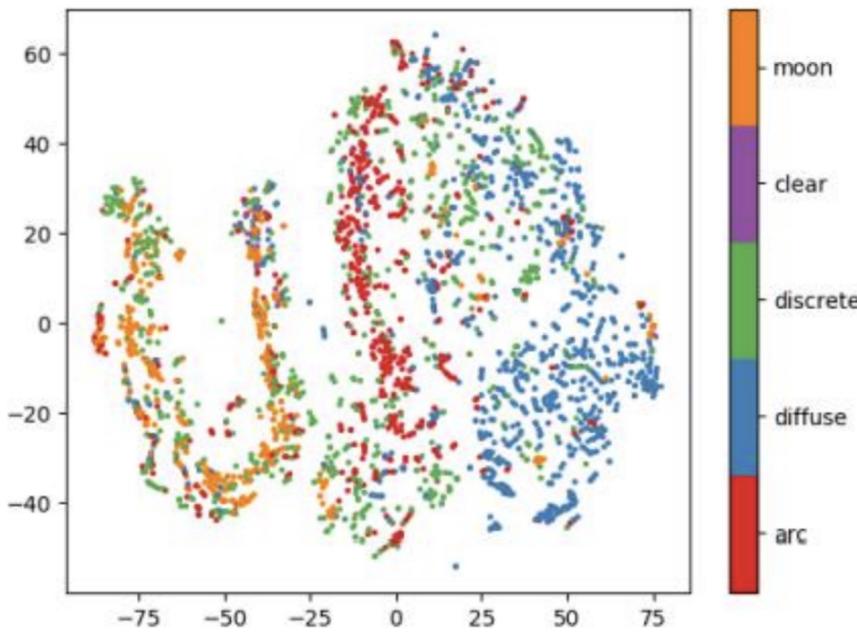


# Correlation of Auroral Dynamics and GNSS Scintillation with an Autoencoder

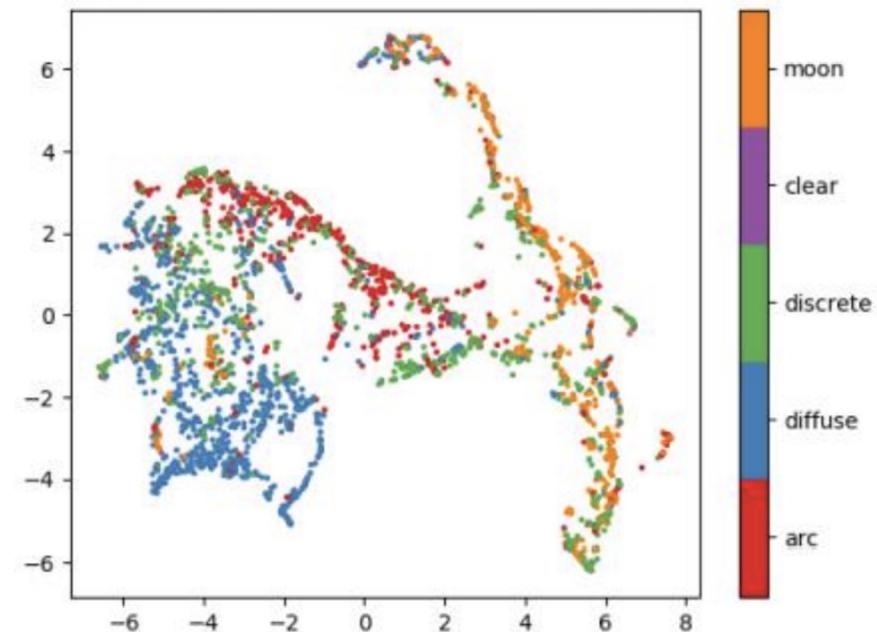
33rd Conference on Neural Information Processing Systems (NeurIPS 2019), Vancouver, Canada.



t-SNE

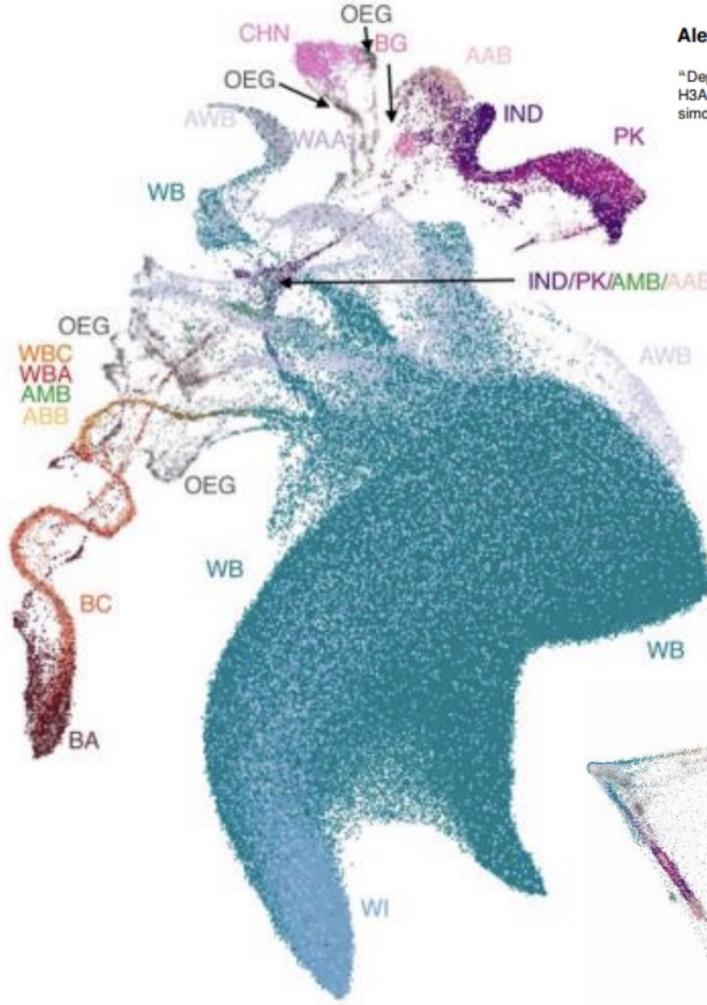


UMAP



# UMAP vs t-SNE on population genomics

UMAP

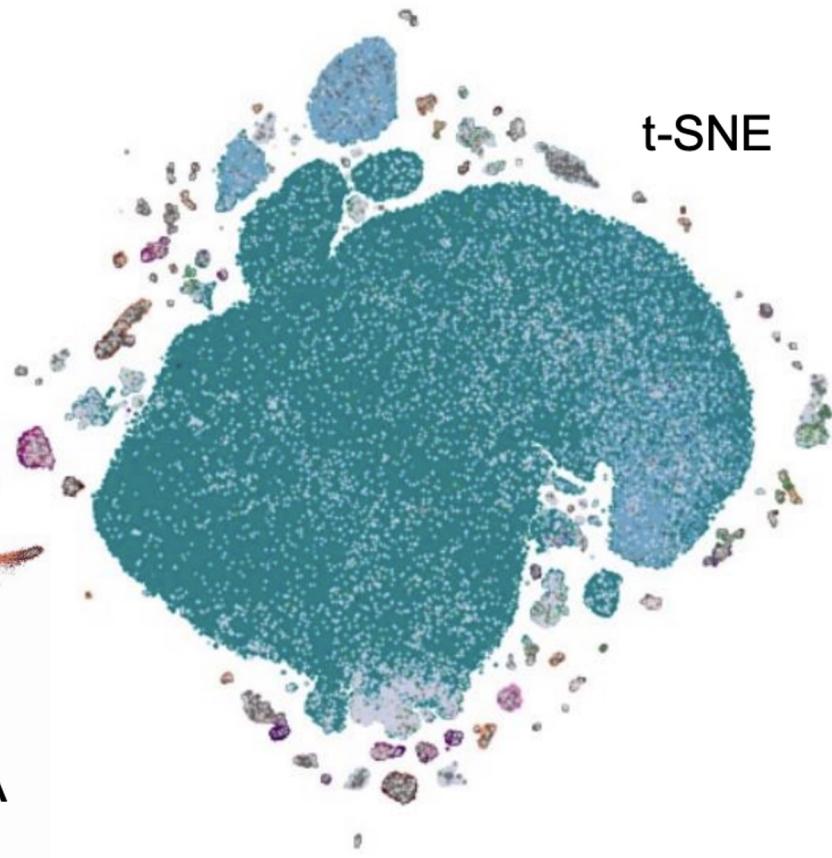


Revealing multi-scale population structure in large cohorts

Alex Diaz-Papkovich<sup>a,b</sup>, Luke Anderson-Trocme<sup>b,c</sup>, and Simon Gravel<sup>b,c,1</sup>

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t-SNE



PCA

# Embedding Projector

## DATA

5 tensors found

Word2Vec 10K

Label by

word

Color by

No color map

Edit by

word

Tag selection as

Load

Publish

Download

Label

Sphereize data 

Checkpoint: Demo datasets

Metadata: oss\_data/word2vec\_10000\_200d

UMAP

T-SNE

PCA

CUSTOM

Dimension

2D



3D

Neighbors 



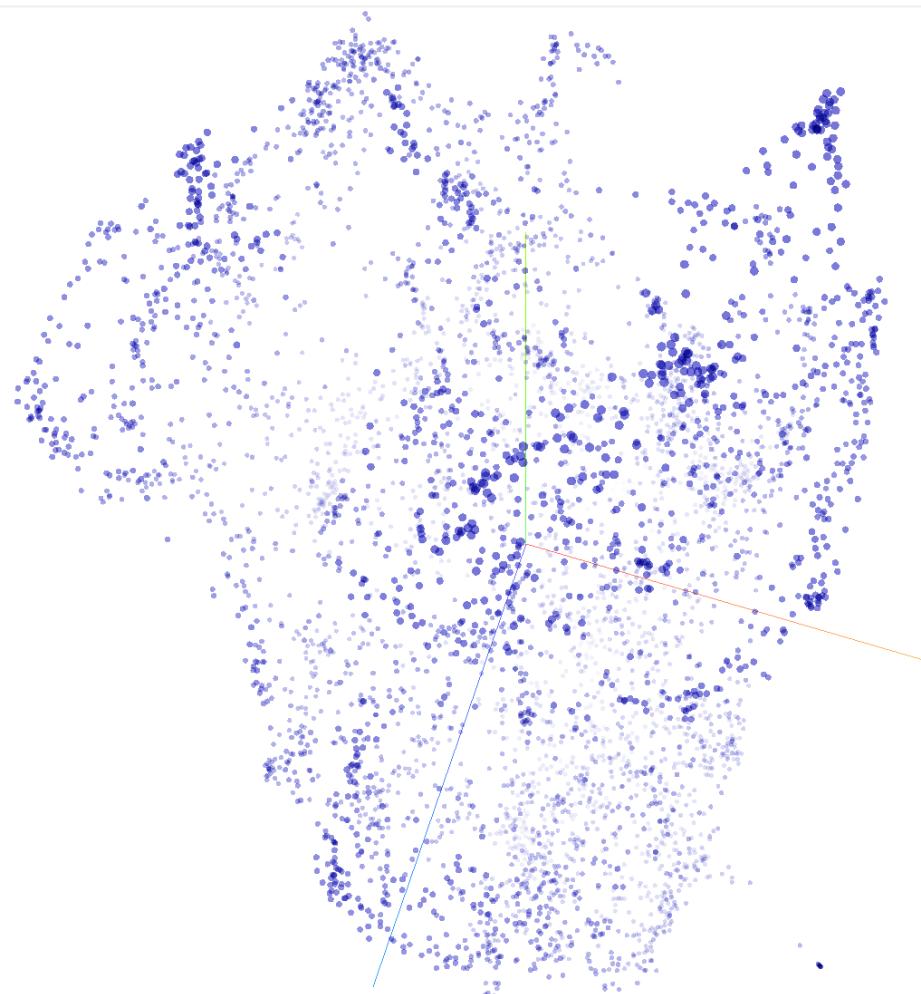
15

Run

For faster results, the data will be sampled down to 5,000 points.

 [Learn more about UMAP.](#)

    | Points: 10000 | Dimension: 200

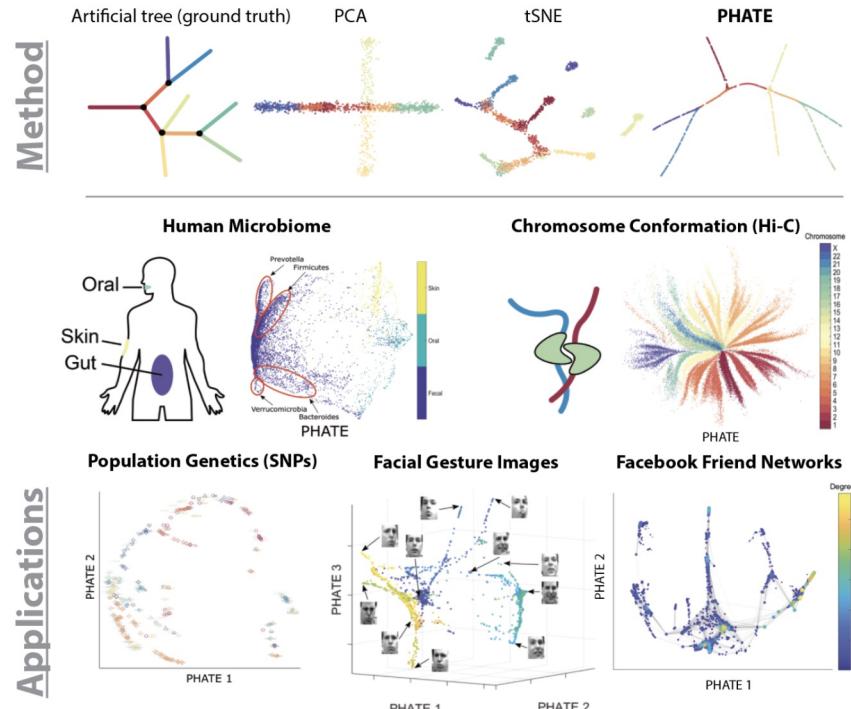


<https://projector.tensorflow.org/>

# Other improvements

PHATE (<https://www.krishnaswamylab.org/projects/phate>)

Learn local structure/distance (just like UMAP) and global structures (using diffusion maps to traverse the graph). Probably better, but not popular yet.



# Summary

- Curse of dimensionality
- PCA
- LDA
  - PCA+LDA
- Random projection
- tSNE
- Homework

