

# Introduction to machine-learning using scikit-learn

QLSC612

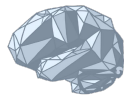
May 2025

*By*

*Mohammad Torabi & Michelle Wang*



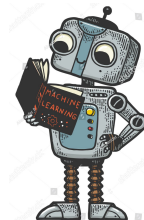
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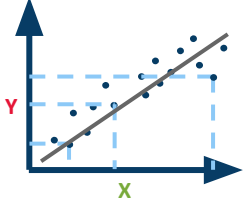
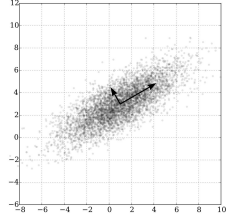
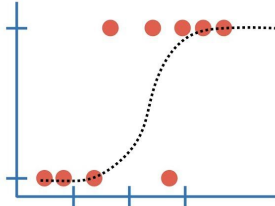
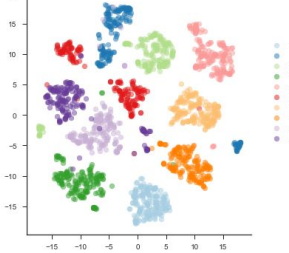
**neuro**  
Montreal Neurological  
Institute-Hospital



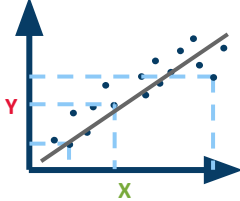
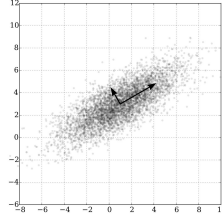
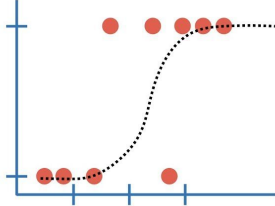
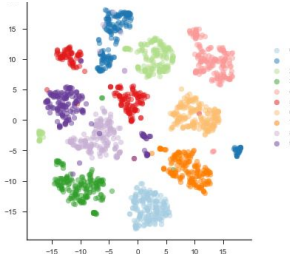
# Objectives

- Part 2: Unsupervised learning
  - Dimensionality reduction
  - Clustering
  - *Coding example: PCA, k-means*
  - *Coding example: fMRI site prediction*

# Types of ML Algorithms

Outcome	Supervised Learning	Unsupervised Learning
Continuous	<p data-bbox="604 380 797 416">Regression</p> 	<p data-bbox="1103 380 1464 416">Principal Component</p> 
Categorical	<p data-bbox="604 678 832 714">Classification</p> 	<p data-bbox="1103 678 1277 714">Clustering</p> 

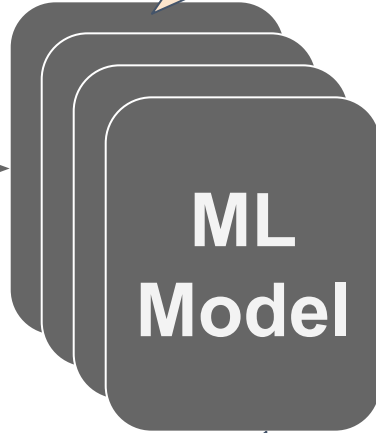
# Types of ML Algorithms

Outcome	Supervised Learning	Unsupervised Learning
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How do I validate my design choices?

Model fitting →  
**the easy part!**

**X**



**Y**

Which features?

Which model?

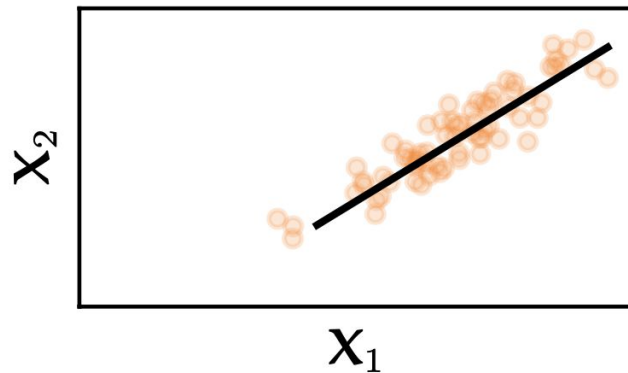
Which performance metrics?

# Unsupervised learning

- Learning without knowing the true labels
- Objectives
  - Dimensionality reduction of features through **transformation** rather than **selection**
  - Grouping of samples based on “**similarity**”
- Techniques
  - Feature Transformation/Projection
  - Clustering

# Dimensionality Reduction

Data is almost 1-dimensional  
BUT represented as  
2-dimensional



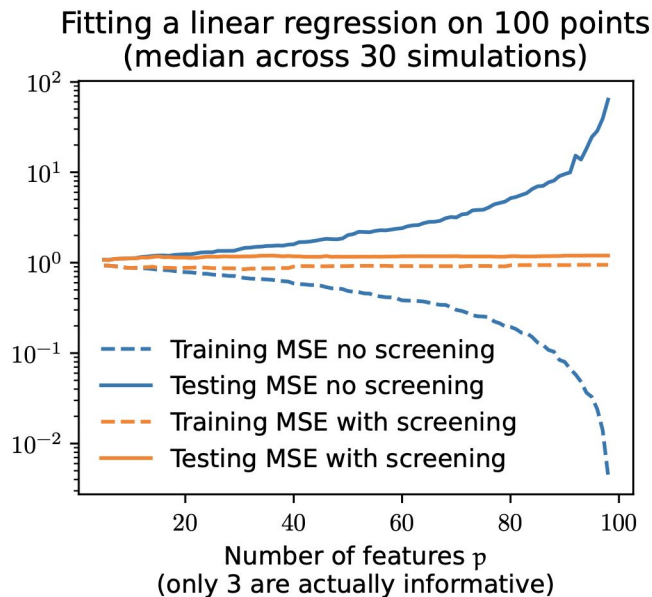
# Dimensionality Reduction

- **Curse of Dimensionality:** large number of input features can dramatically impact the performance of ML algorithms
- Techniques:
  - Feature selection (usually supervised)
  - Feature transformation (usually unsupervised)
- Feature transformation is useful for
  - Information compression
  - Data artifact clean-up
  - Visualization



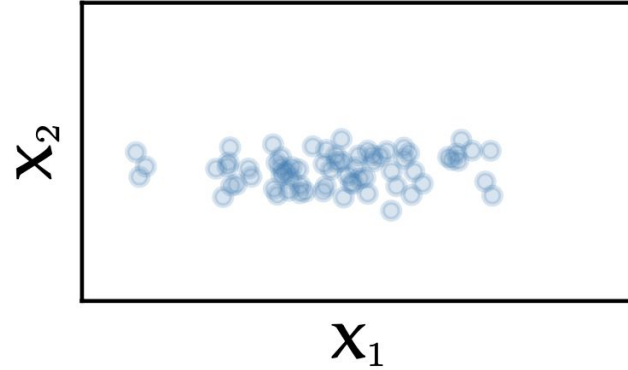
# Dimensionality Reduction

- High dimensional data:
  - Model complexity increases -> unstable solution
  - Risk of overfitting: fitting exactly training data but failing on test data

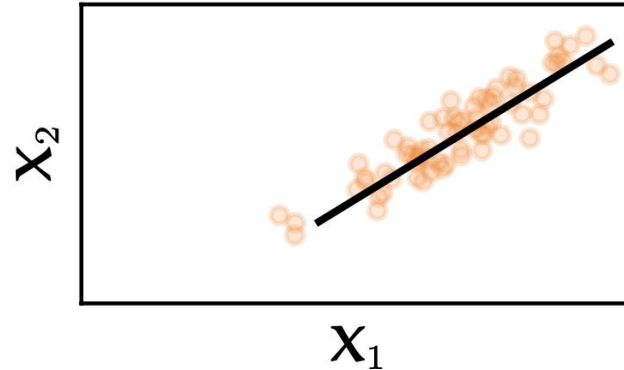


# Feature Transformation vs. Feature Selection

Maybe OK to drop  $X_2$



Data is low-dimensional BUT  
no feature can be dropped

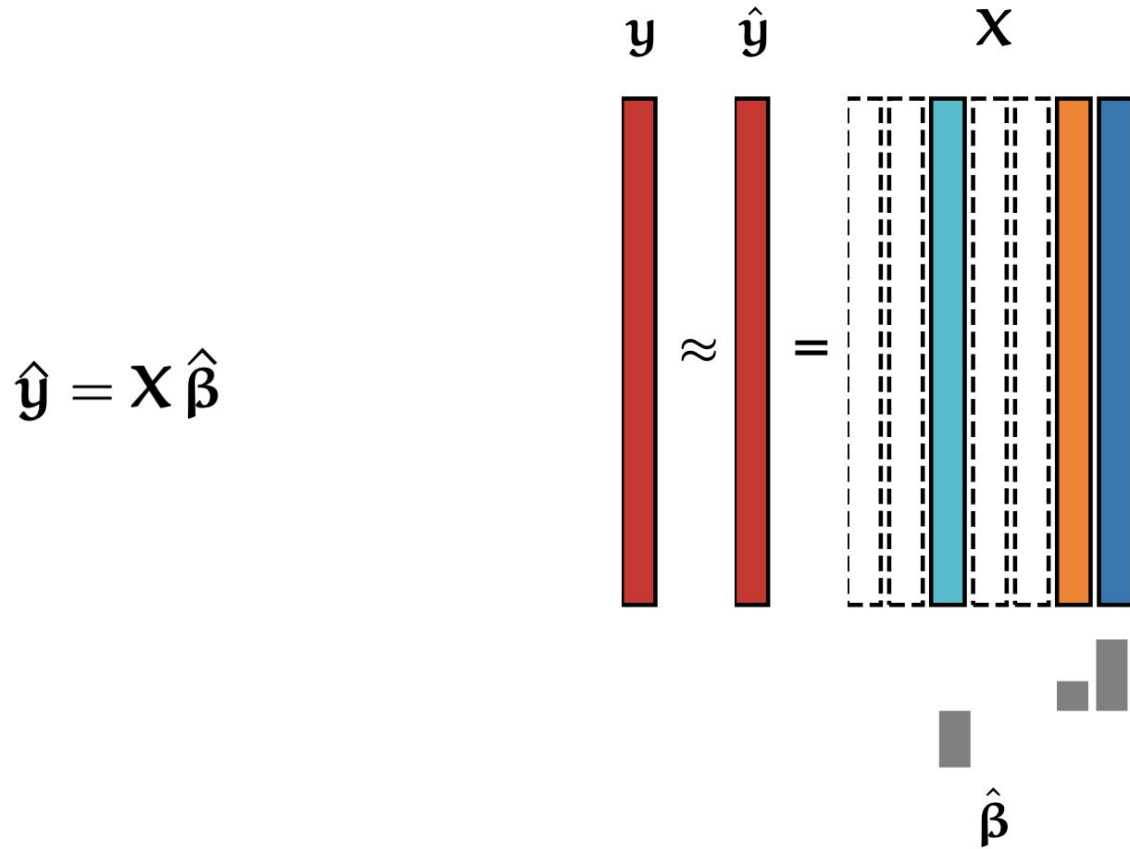


# Feature Transformation vs. Feature Selection

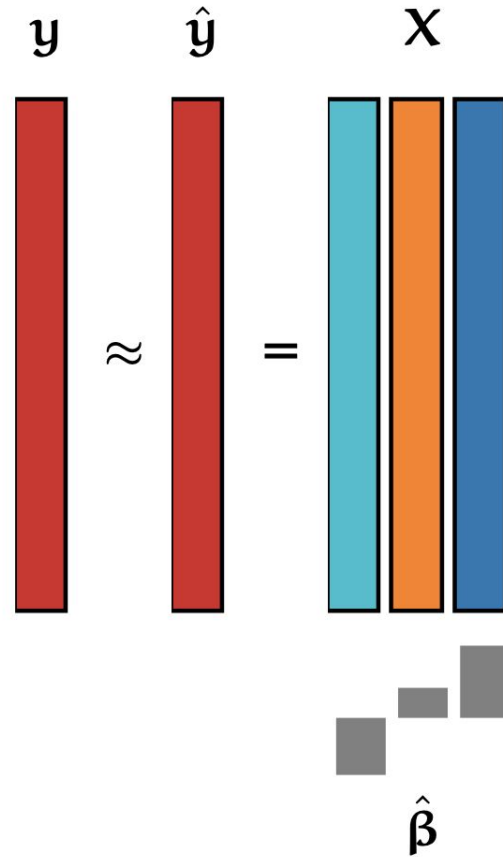
$$\hat{\mathbf{y}} = \mathbf{X} \hat{\boldsymbol{\beta}}$$

The diagram illustrates the linear regression equation  $\hat{\mathbf{y}} = \mathbf{X} \hat{\boldsymbol{\beta}}$ . It shows a red bar for  $\hat{\mathbf{y}}$ , a red bar for  $\mathbf{y}$ , a matrix  $\mathbf{X}$  with 7 colored columns, and a vector  $\hat{\boldsymbol{\beta}}$  with 7 gray squares. The equation is represented as  $\hat{\mathbf{y}} \approx \mathbf{y} = \mathbf{X} \hat{\boldsymbol{\beta}}$ .

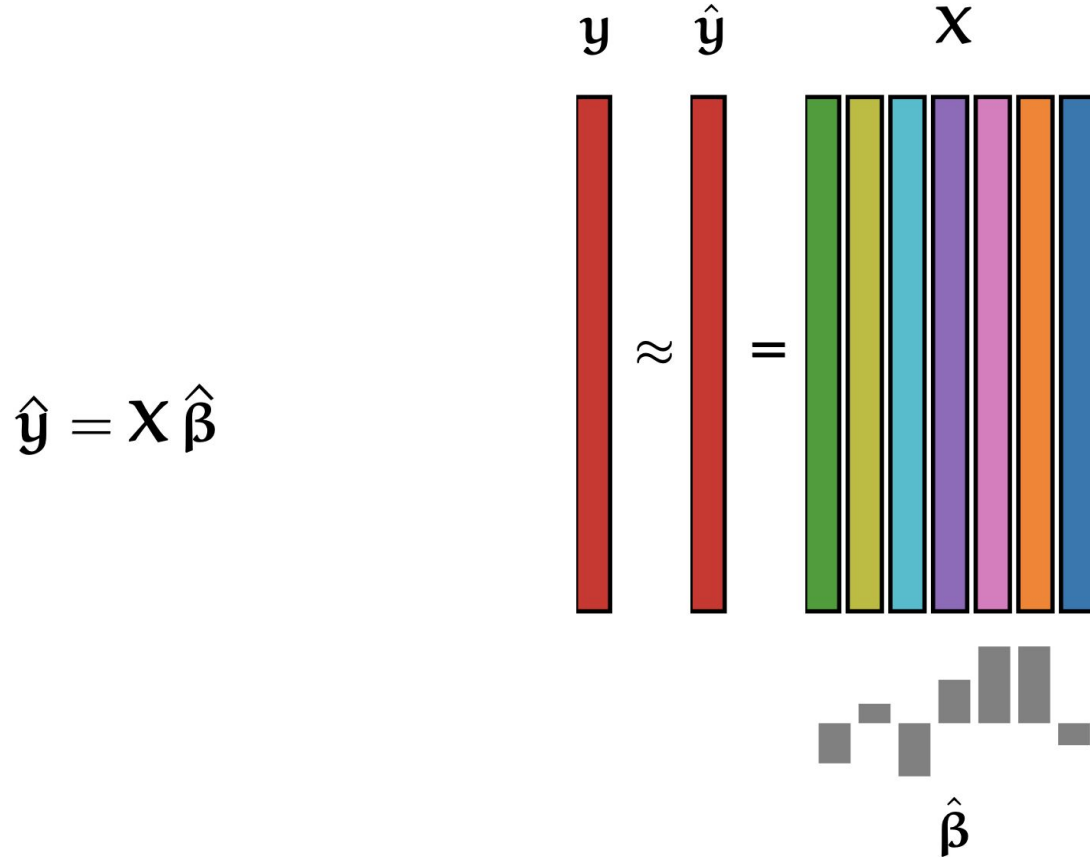
# Feature Transformation vs. Feature Selection



# Feature Transformation vs. Feature Selection



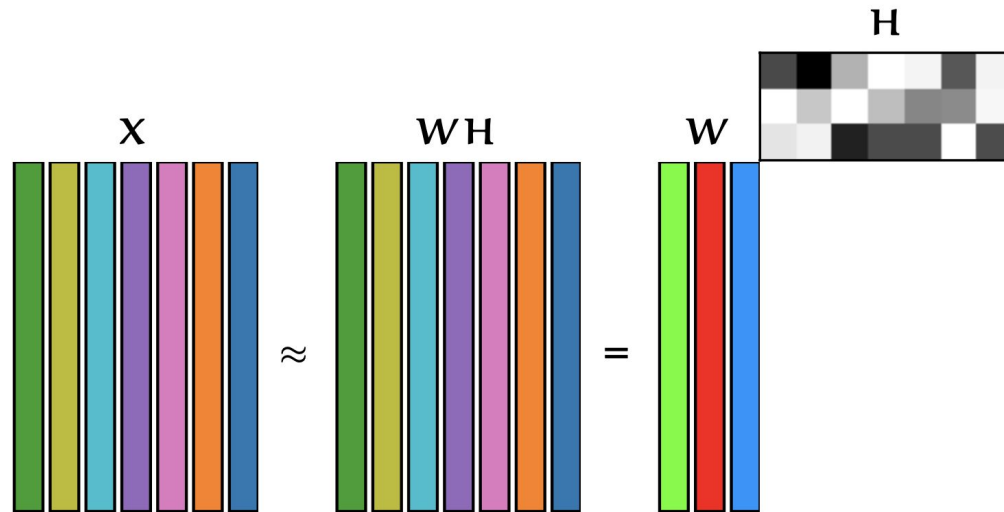
# Feature Transformation vs. Feature Selection



# Feature Transformation vs. Feature Selection

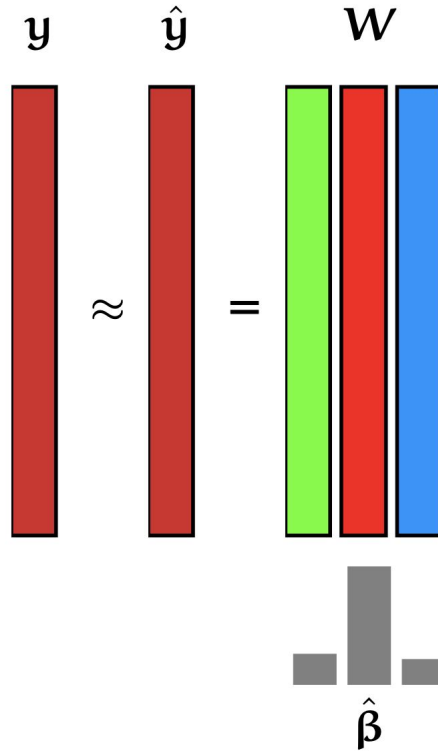
Minimize

$$\|\mathbf{X} - \mathbf{W}\mathbf{H}\|_F^2 = \sum_{i,j} (\mathbf{X}_{i,j} - (\mathbf{W}\mathbf{H})_{i,j})^2$$



# Feature Transformation vs. Feature Selection

$$\hat{y} = W \hat{\beta}$$



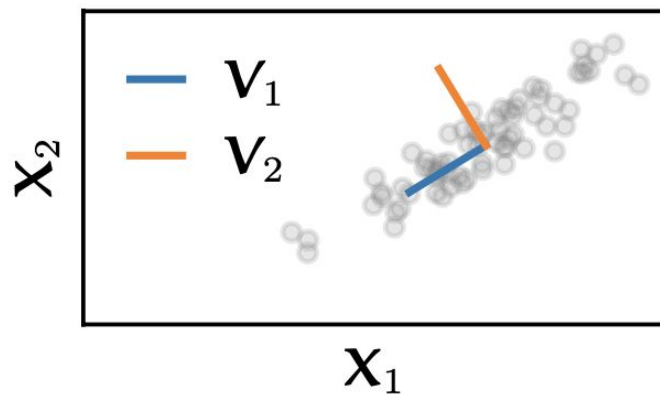


# Feature Transformation

- Change of basis (i.e. “perspective”) for data representation
- Priors on data generation process
  - Singular Value Decomposition (SVD)
  - Principal Component Analysis (PCA)
  - Independent Component Analysis (ICA)
  - Non-negative Matrix Factorization (NMF)

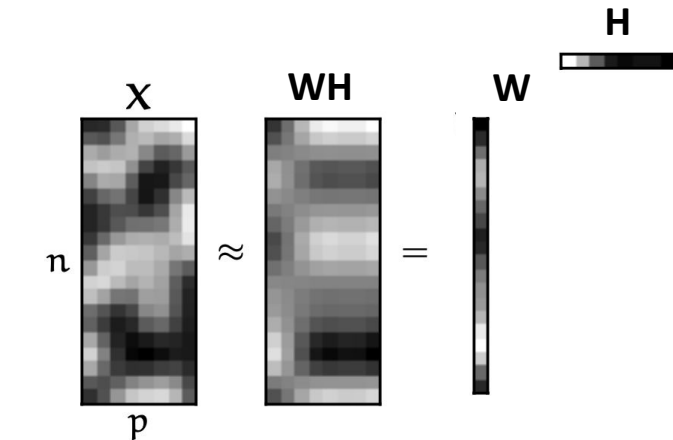
# Principal Component Analysis (PCA)

- PCA finds the components (eigenvectors) that are orthogonal and capture the maximum variance in data.
- These components form the basis of the new space that the data will be transformed to
- Truncating the components to keep only the first  $k$  components gives the best rank- $k$  approximation of  $X$  and transforms  $X$  to  $k$ -dim space



# Principal Component Analysis (PCA)

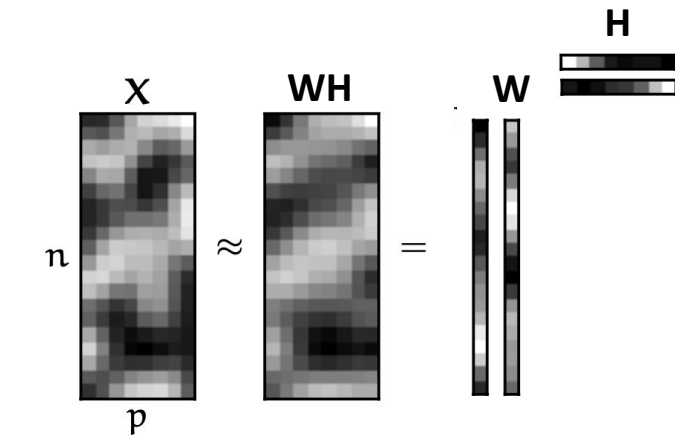
**Reconstructing with 1 principal component:**



Explained variance: 0.53

# Principal Component Analysis (PCA)

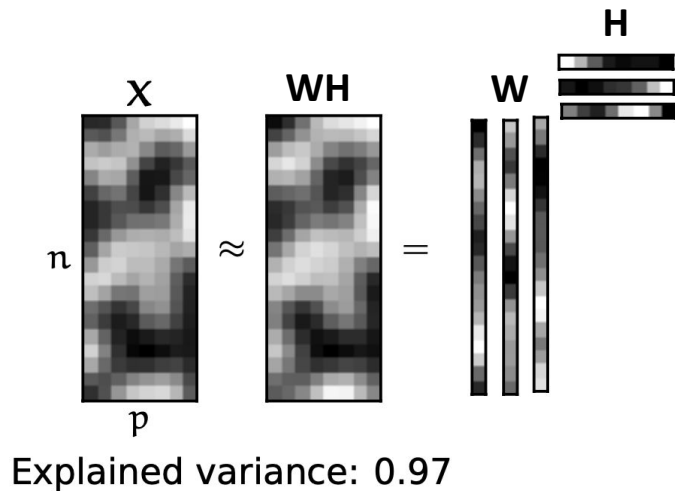
**Reconstructing with 2 principal components:**



Explained variance: 0.84

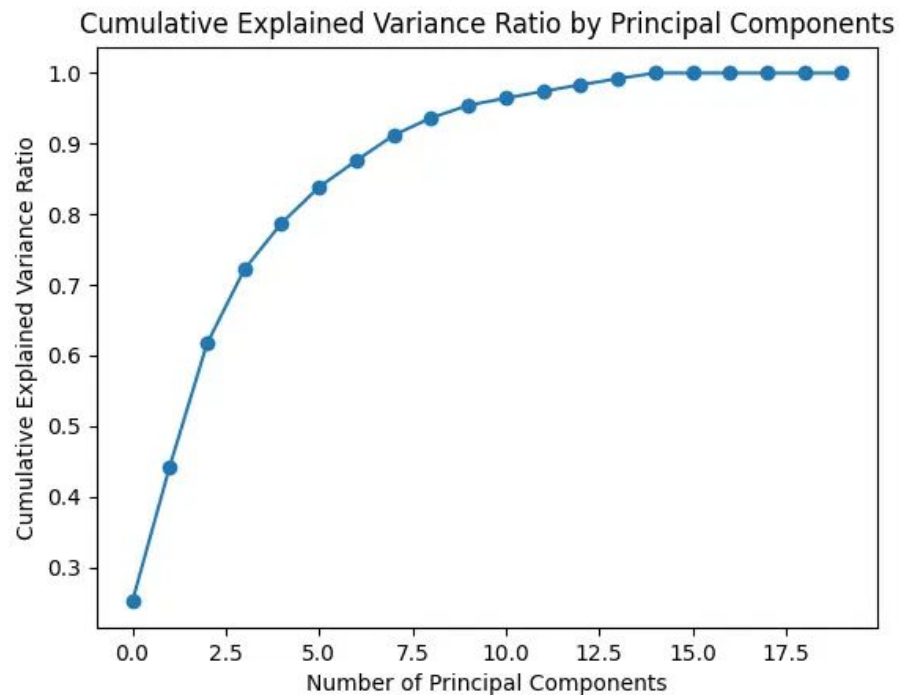
# Principal Component Analysis (PCA)

**Reconstructing with 3 principal components:**

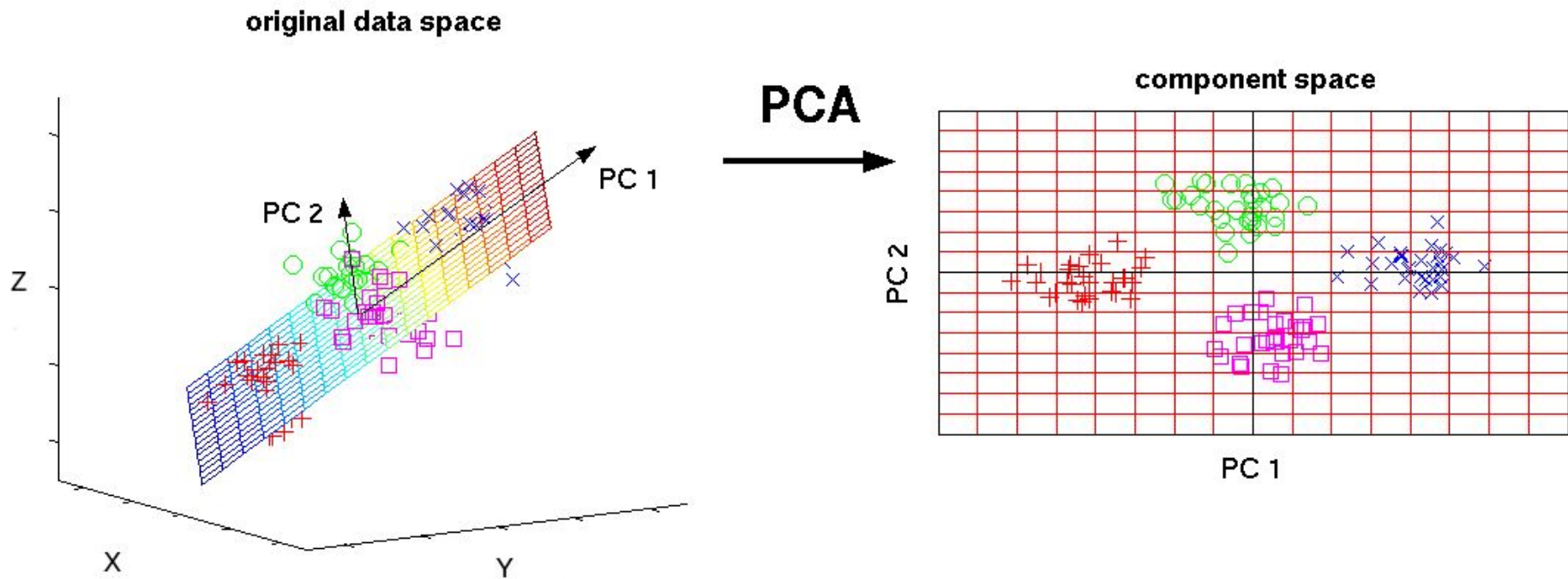


# Principal Component Analysis

- Variance explained

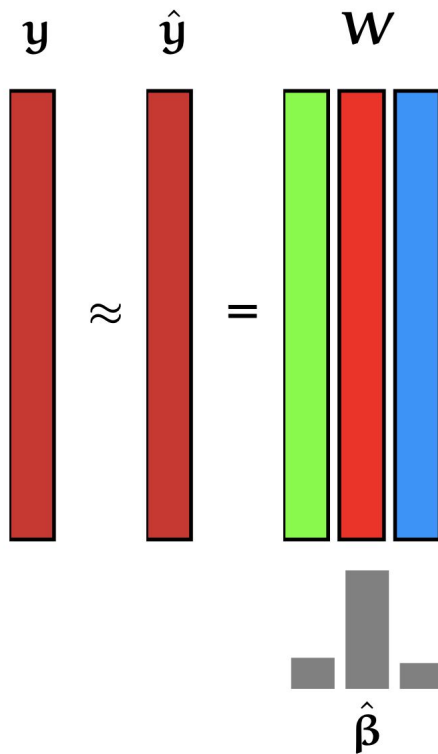


# Principal Component Analysis (PCA)



# Principal Component Analysis (PCA)

$$\hat{\mathbf{y}} = \mathbf{W} \hat{\boldsymbol{\beta}}$$





# Principal Component Analysis

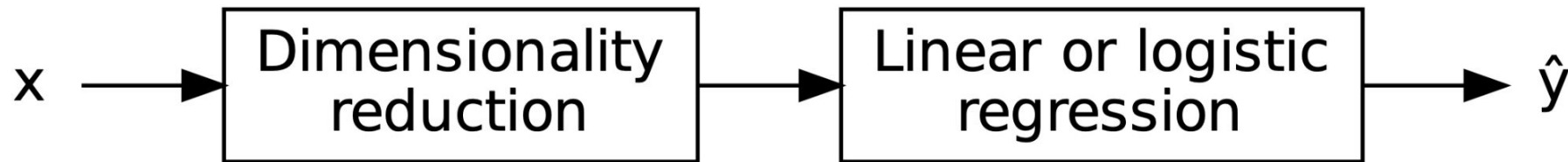
- sklearn

```
transformer = PCA(n_components=N)
transformer.fit(X)
transformed_X = transformer.transform(X)
print(transformed_X.shape) #(n_samples, n_components)
```

```
transformer = PCA(n_components=N)
transformed_X = transformer.fit_transform(X)
```

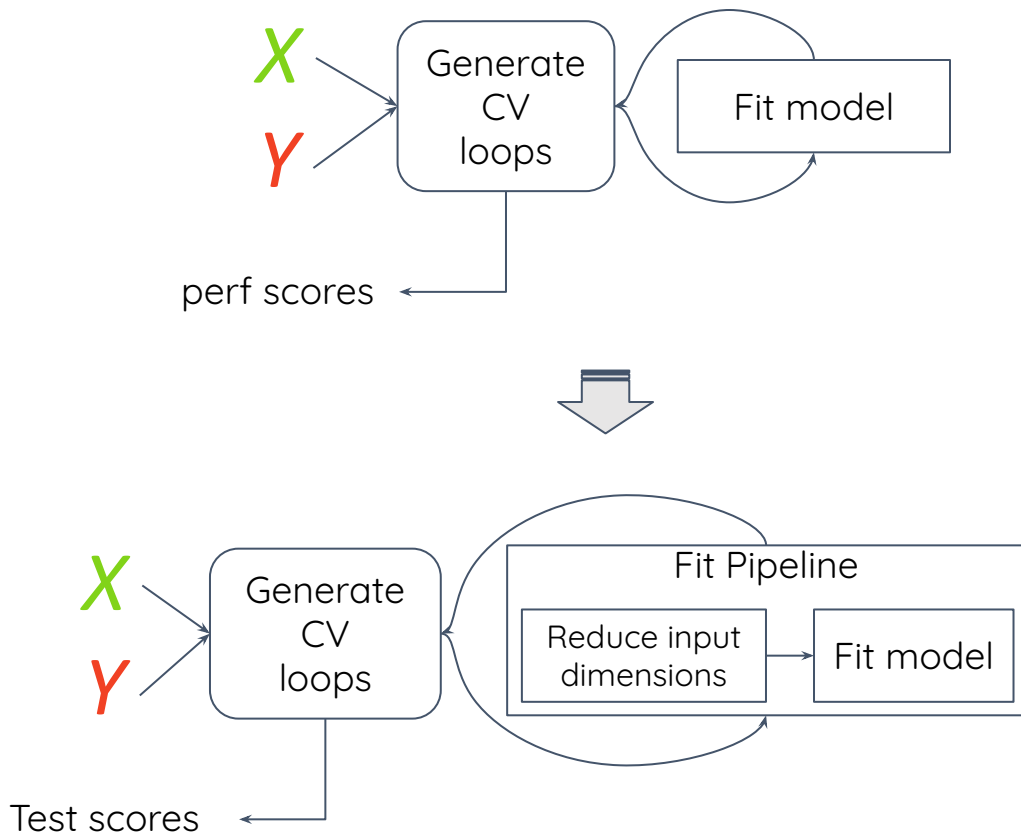
# Dimensionality Reduction

- A preprocessing step



# Pipelines

- Chain various “preprocessing” tasks in your analysis
  - Feature scaling
  - Dimensionality reduction
- Avoids mistakes e.g. double dipping
- Simplifies changes to your analysis



# Pipelines

- Feature selection / transformation only on the training data!

```
transformer = PCA(n_components=N)
transformed_train = transformer.fit_transform(X_train)
Transformed_test = transformer.transform(X_test)
```

# Pipelines

```
pipeline = make_pipeline(PCA(n_components=N), LinearRegression())  
pipeline.fit(X_train, y_train)  
y_test_predicted = pipeline.predict(X_test)
```

# Clustering

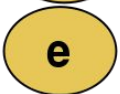
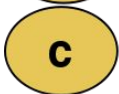
- Grouping observations together without knowing their true labels
- Use distance (i.e. similarity) between samples (often in a high-dimensional space!)
- Things to consider
  - Priors on parameters (e.g. `n_clusters`)
  - Scalability

# Clustering

Method name	Parameters	Scalability	Usecase	Geometry (metric used)
K-Means	number of clusters	Very large <code>n_samples</code> , medium <code>n_clusters</code> with <a href="#">MiniBatch code</a>	General-purpose, even cluster size, flat geometry, not too many clusters, inductive	Distances between points
Agglomerative clustering	number of clusters or distance threshold, linkage type, distance	Large <code>n_samples</code> and <code>n_clusters</code>	Many clusters, possibly connectivity constraints, non Euclidean distances, transductive	Any pairwise distance
Gaussian mixtures	many	Not scalable	Flat geometry, good for density estimation, inductive	Mahalanobis distances to centers

# Clustering

- Which samples will cluster together?

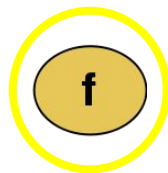
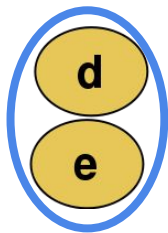
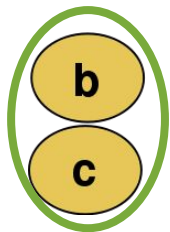
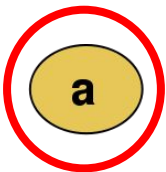


Sample space



# Clustering

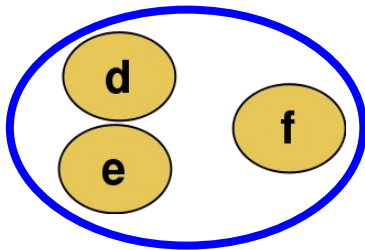
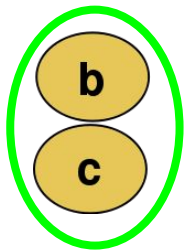
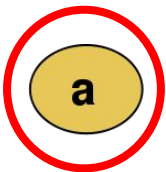
- Which samples will cluster together if  $n\_clusters=4$ ?



Sample space

# Clustering

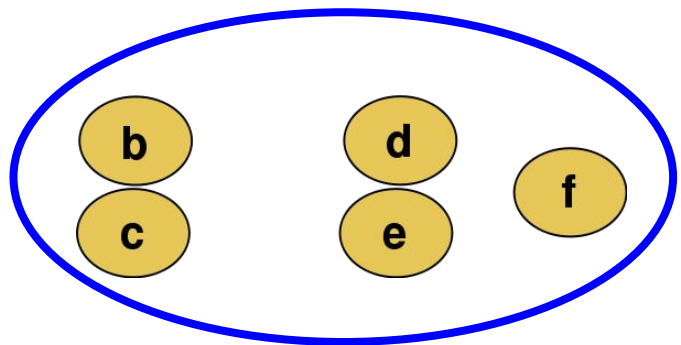
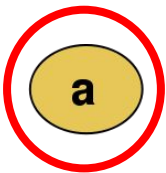
- Which samples will cluster together if  $n\_clusters=3$ ?



Sample space

# Clustering

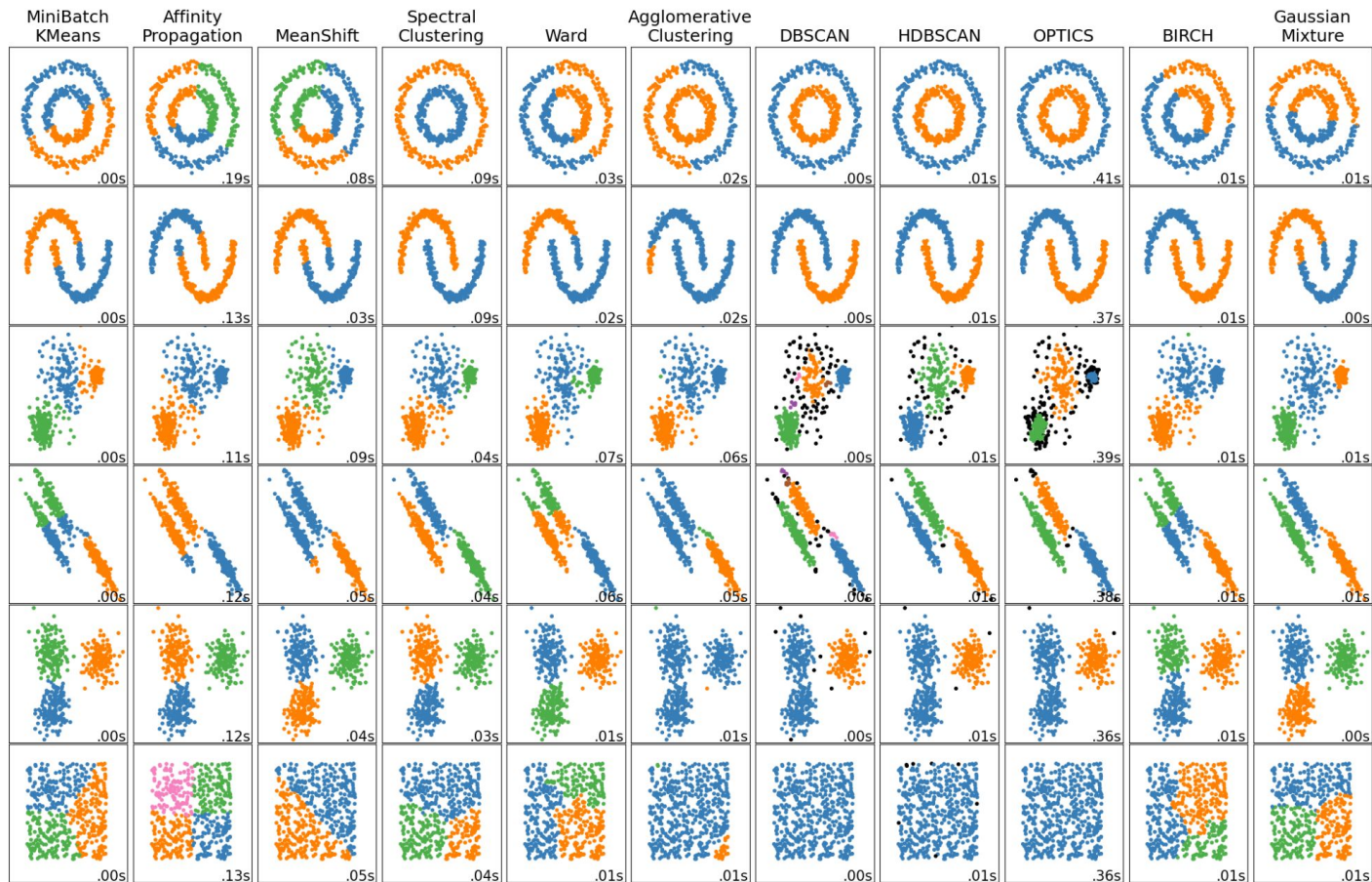
- Which samples will cluster together if  $n\_clusters=2$ ?



Sample space

# Clustering

*... is in the  
eyes of the  
beholder*



# K-means Clustering

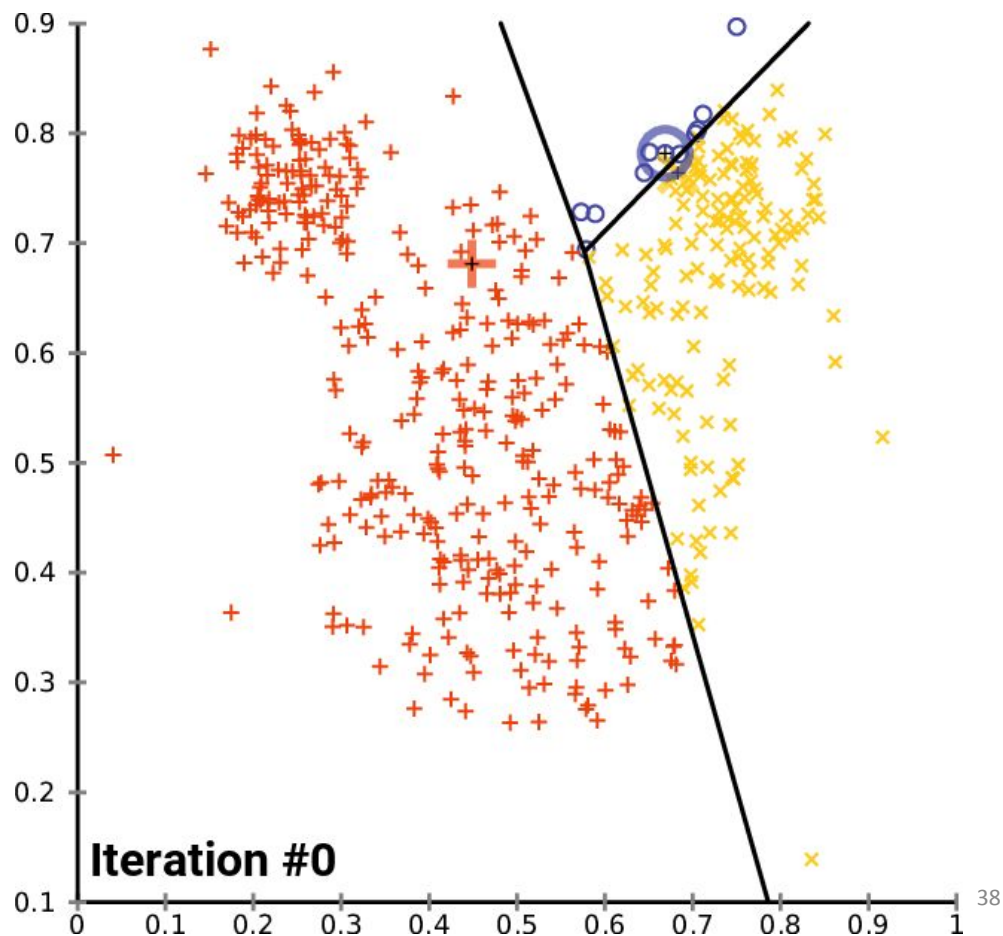
- The K-means algorithm aims to choose centroids that minimise the inertia, or within-cluster sum-of-squares criterion
- Each centroid represents a cluster
- This algorithm requires the number of clusters to be specified
- Very high-dimensional spaces result in inflated Euclidean distances (an instance of curse of dimensionality)
  - Run a dimensionality reduction algorithm (e.g. PCA) prior to k-means clustering

$$\sum_{i=0}^n \min_{\mu_j \in C} (||x_i - \mu_j||^2)$$

# K-means Clustering

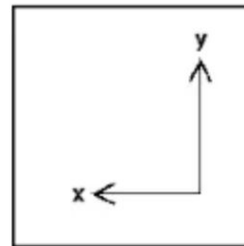
## Steps:

1. **Initialization:** Choose  $k$  random centroids
2. **Assignment step:** Assign each observation to the cluster with the nearest mean.
3. **Update step:** Recalculate means (centroids) for observations assigned to each cluster.

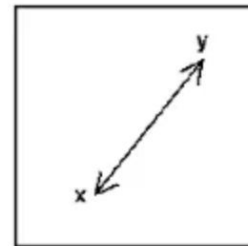


# Distance Metrics

- Euclidean distance
- Manhattan distance
- Hamming distance
- Correlation ( $1 - \text{corr}$ )



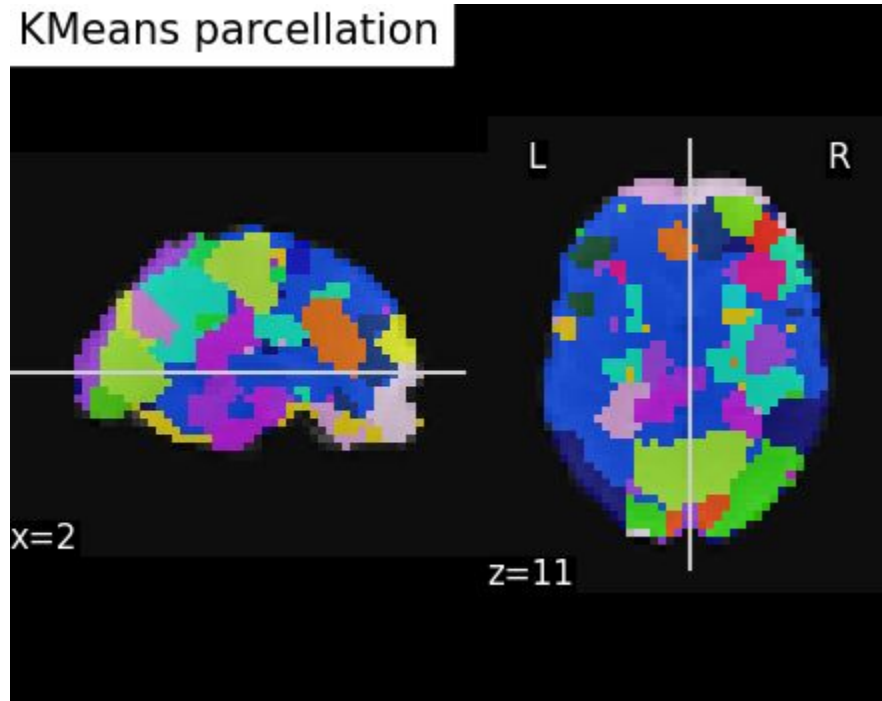
**Manhattan**



**Euclidean**

# Biological Example

- Parcellate brain voxels based on their fMRI signals
- How do we know if the clustering is done well?
- What metrics do we have?





# Evaluation of clusters

- Internal validation (without true labels):

- Silhouette Coefficient

$$s = \frac{b - a}{\max(a, b)}$$

- external validation

- With true labels:

- Rand Index (RI) and Adjusted Rand Index (ARI)

$$\text{RI} = \frac{a + b}{C_2^{n_{\text{samples}}}}$$

- Mutual Information

$$\text{ARI} = \frac{\text{RI} - E[\text{RI}]}{\max(\text{RI}) - E[\text{RI}]}$$

# Project

- **Data:** X: connectivity features derived from fMRI data, y: fMRI site label for each participant.
- **Visualize the data:** you have to apply dimensionality reduction first
- **Classification (supervised learning):** Use different models to classify and predict the fMRI site using the connectivity features and compare their performance. We will use scikit-learn pipeline for this purpose, which chains different transformations. Then we will fit the whole pipeline on our data using cross-validation.
- **Clustering (unsupervised learning):** use K-means clustering to cluster the participants. Find the best number of clusters and evaluate the clustering performance.

