04 – Unsupervised Learning

Data Science and Management

Corso di Laurea Magistrale in Ingegneria Gestionale

Marco Mamei, Natalia Hadjidimitriou, Fabio D'Andreagiovanni, Matteo Martinelli

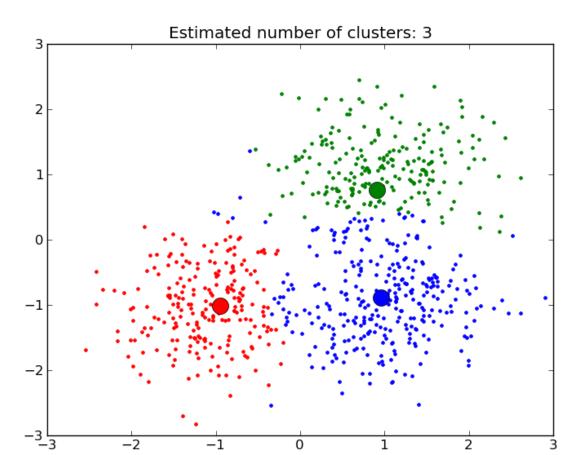
{marco.mamei, selini, fabio.dandreagiovanni, matteo.martinelli}@unimore.it

- Clustering
- Dimensionality Reduction

Clustering is a form of unsupervised learning

Supervision is costly and often hard to get

Given a set of **examples** (points in some high-dimensional space) find **groups** of similar elements



Examples

- Find Amazon users sharing similar characteristics: for the kind of objects they buy, for the budget they exploit, for the frequency of orders they make
- Group Facebook users into communities because of their friendships and the contents they like
- Given a collection of text documents, find those regarding the same topic

No supervisions implies...

- No target to be computed
- No straightforward performance measure to evaluate the success of our algorithm
- Heuristic approaches to assess validity of results
- Partial lack of theoretical grounds

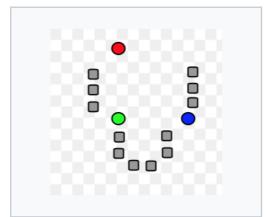
Main idea of clustering algorithms

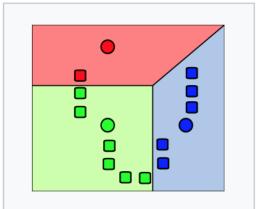
- Partition data samples into K sets (named clusters)
 - All examples belong to one and only one cluster
- High intra-cluster similarity
- High inter-cluster dissimilarity
- Based on a distance/metric between examples

The most famous clustering algorithm is **K-Means**:

- Choose a number of clusters K (in advance!!!)
- Start with K random cluster centroids
- Assign each point to the closest centroid
- Compute new cluster centroids
- Iterate until convergence (?)

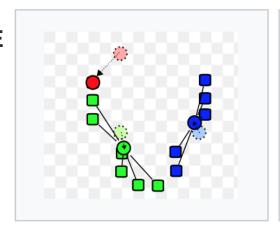
1. INIT

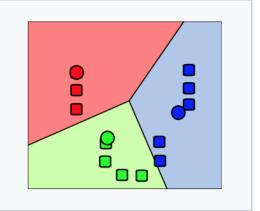




2. ASSIGN

3. COMPUTE





4. CONVERGE

Image from Wikipedia
2024 – Marco Mamei, Full Professor (marco.mamei@unimore.it)

K-Means algorithm

- 1. init centroids (K random points)
- 2. repeat

$$s(x) = \arg\min_{c_i \in C} d(c_i, x)$$

$$s(x) = \arg\min_{c_i \in C} d(c_i, x)$$
$$c_i = \frac{1}{|x, s(x) = c_i|} \sum_{x, s(x) = c_i} x$$

3. until stopping criterion

Pros

Straightforward and intuitive algorithm

Cons

- Depends on random initialization
- Choose K in advance
- Clustering only by linear separations

Clustering indices:

INTERNAL: LABELS NOT NEED TO BE KNOWN

• Dunn Index, Silhouette, ...

Homogeneity, Completeness, V-Measure, ...

EXTERNAL: LABELS NEED TO BE KNOWN

Dunn Index

Minimum intra-cluster similarity

Maximum inter-cluster similarity

$$DI = \frac{\min_{i,j|C(i)=C(j)} s(x_i, x_j)}{\max_{i,j|C(i)\neq C(j)} s(x_i, x_j)}$$

Silhouette

-1 <= s <= 1

 $s = \frac{1}{n} \sum_{I=1}^{n} \frac{b(i) - a(i)}{\max\{a(i) \ b(i)\}}$

Average dissimilarity

of i with points in
the same cluster

Minimum average dissimilarity
of i with points of
other clusters

Homogeneity (H)

Each cluster contains only points of a single label

Completeness (C)

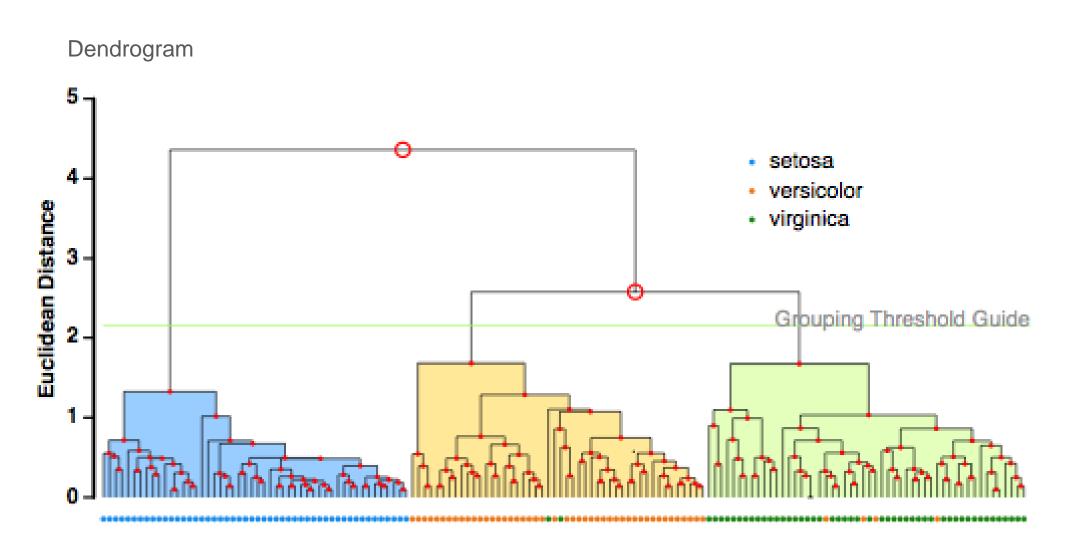
•All points of a label are assigned to the same cluster

V-Measure

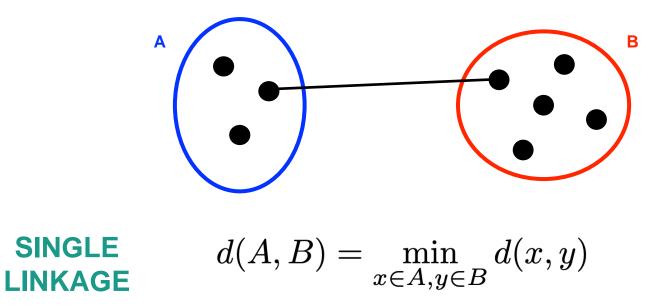
Harmonic mean between H and C

Hierarchical clustering

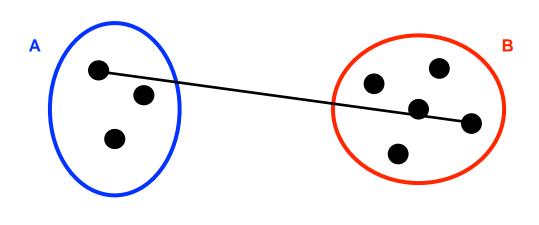
- Start with pairwise distances between data points
- Iteratively agglomerate clusters
- Need to define a distance between groups
- At the end we obtain a tree, named dendrogram



Distances between groups of points:



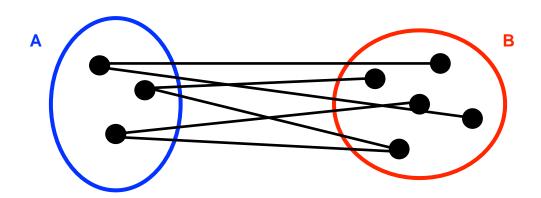
Distances between groups of points



COMPLETE LINKAGE

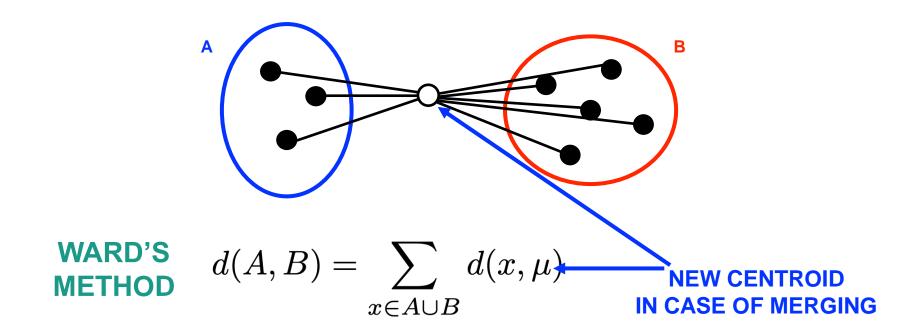
$$d(A,B) = \max_{x \in A, y \in B} d(x,y)$$

Distances between groups of points



AVERAGE
$$d(A,B) = \frac{1}{|A||B|} \sum_{x \in A, y \in B} d(x,y)$$

Improvement in total distance in case of merging



Many other algorithms...

- Spectral clustering
- Affinity propagation
- •DBScan (it also estimates K)

•...

Iris dataset

- A very famous dataset in machine learning
- Measurements in cm of sepal/petal width/length for 50 flowers from each of 3 species of iris
- 150 examples, 4 features, 3 classes

```
from sklearn import datasets
from sklearn.cluster import KMeans
from sklearn.metrics import homogeneity_completeness_v_measure

X, y = datasets.load_iris(return_X_y=True)

kmeans = KMeans(n_clusters=3)
kmeans.fit(X)
print(kmeans.inertia_)
print(kmeans.cluster_centers_)
print(kmeans.labels_)
print(homogeneity_completeness_v_measure(y, kmeans.labels_))
```

```
from sklearn import datasets
from sklearn.cluster import AgglomerativeClustering
import matplotlib.pyplot as plt
import numpy as np

X, y = datasets.make_moons(n_samples=1000, noise=0.05)

clusters = AgglomerativeClustering(n_clusters=2, linkage='single').fit(X)
predictions = clusters.labels_
colors = np.array(['red', 'blue'])
plt.scatter(X[:, 0], X[:, 1], color=colors[predictions])
plt.show()
```

Dimensionality Reduction

Unsupervised

- Principal Component Analysis (PCA)
- •...

Supervised

- Linear Discriminant Analysis (LDA)
- •...

Principal Component Analysis (PCA) is a technique for **mapping** a set of examples, represented by **many** features, to a **lower-dimensional** space, where the main data characteristics are **preserved** It is particularly useful for **exploratory data analysis**, for example to **visualize** data with many features

Suppose to have N examples with P features

How to **project** the P-dimensional space into a **two-dimensional**space, preserving distances between data points, so that we can **plot**the examples?

We look for principal components of data

PCA is an orthogonal **linear** transformation that maps the original matrix X of data from the original feature space into a lower-dimensional space

$$T = XW$$

$$X \in \mathbb{R}^{N \times P}, \quad W \in \mathbb{R}^{P \times Q}, \quad T \in \mathbb{R}^{N \times Q}$$

In particular, we search for the projection W that maximizes the **variance** within data (in order to better **discriminate** among data)

There are several ways to derive PCA...

One of the most general algorithms is based on the computation of the **covariance matrix**

$$C_{ij} = \text{cov}(X_i, X_j) = E[(X_i - \mu_i)(X_j - \mu_j)]$$

Then, the eigenvectors of matrix C are computed and ordered by descending eigenvalues

The largest eigenvectors correspond to the principal components of the original data

```
from sklearn import datasets
from sklearn.decomposition import PCA
import matplotlib.pyplot as plt
import numpy as np

X, y = datasets.load_iris(return_X_y=True)

pca = PCA(n_components=2)
T = pca.fit_transform(X)
colors = np.array(['red', 'blue', 'green'])
plt.scatter(T[:,0], T[:,1], color=colors[y])
plt.show()
```