Unsupervised Learning: Clustering

ML Instruction Team, Fall 2022

CE Department Sharif University of Technology

Clustering: An Overview

- Clustering algorithms can be classified into different categories, based on the following criteria:
 - ▶ Whether each point is assigned to exactly one cluster or several clusters with certain probabilities that add up to 1:
 - Hard
 - Soft
 - Whether all clusters are on the same level or several clusters are built in a hierarchical way:
 - Partitional
 - Hierarchical

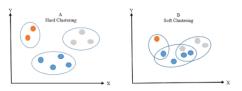


Figure: Hard vs Soft source.

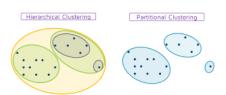


Figure: Partitional vs Heirarchical source.

Clustering: An Overview

- Hierarchical clustering is usually done in two different ways:
 - ▶ **Agglomerative**: This is a "bottom-up" approach, Each observation starts in its own cluster, and pairs of clusters are merged as one moves up the hierarchy.
 - ▶ **Divisive**: This is a "top-down" approach, All observations start in one cluster, and splits are performed recursively as one moves down the hierarchy.

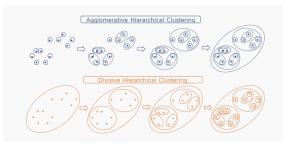


Figure: Agglomerative vs Divisive source.

- A particularly simple method for clustering is K-means, The idea is to represent each cluster k by a center point \mathbf{c}_k and assign each data point \mathbf{x}_n to one of the clusters k which can be written in terms of index sets \mathcal{C}_k
- The center points and the assignment are then chosen such that the mean squared distance between data points and center points is minimized:

$$J := \sum_{n=1}^N \sum_{k=1}^K r_{nk} \|\mathbf{x}_n - \mathbf{c}_k\|^2$$

- Here we introduced a corresponding binary indicator variable $r_{nk} \in \{0,1\}$ where $k=1,2,\ldots,K$ describing which of the K clusters the data point $\mathbf{x_n}$ is assigned to, so that if data point $\mathbf{x_n}$ is assigned to cluster k then $r_{nk}=1$, and $r_{nj}=0$ for $j\neq k$
- Now, Our goal is to find values for the $\{r_{nk}\}$ and the $\{\mathbf{c}_k\}$ so as to minimize J. we can do this through an **Iterative Procedure**



- \blacksquare To minimize J through iterating, we have to do the following algorithm:
 - **1** Initialize c_k with Random Value for all k = 1, 2, ..., K, It could be chosen from data values either.
 - ② Minimize J with respect to r_{nk} , keeping the \mathbf{c}_k fixed. because J is a linear function of r_{nk} this optmization can be performed easily to give a closed form solution:

$$r_{nk} = \begin{cases} 1 & \quad \text{if } k = \operatorname{argmin}_j \|\mathbf{x}_n - \mathbf{c}_j\|^2 \\ 0 & \quad \text{otherwise} \end{cases}$$

3 Minimize J with respect to \mathbf{c}_k , keeping the r_{nk} fixed. if the assignment is fixed, it is easy to show that the optimal choice of the center positions is given by:

$$\mathbf{c}_k = \frac{\sum_n r_{nk} \mathbf{x}_n}{\sum_n r_{nk}}$$

• Check the convergence criteria, otherwise go to step 2.



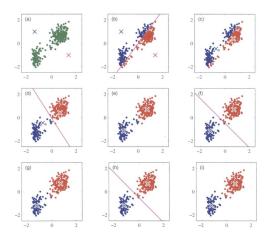


Figure: Illustration of K-Means with K = 2 [1].

- Note that the result of the algorithm is **not necessarily a global optimum** of the objective function J
 It is therefore advisable to **run the algorithm several times** with different initial center
- locations and pick the best result.

 A drawback of this and many other clustering algorithms is that the number of clusters
- A drawback of this and many other clustering algorithms is that **the number of clusters** is not determined.
- One has to decide on a proper *K* in advance, or one simply runs the algorithm with several different *K*-values and picks the best according to some criterion.

- The *K*-means algorithm is a very simple method with sharp boundaries between the clusters, and no particular characterization of the shape of individual clusters.
- In a more refined algorithm, one might want to model each cluster with a Gaussian, capturing the shape of the clusters.
- This leads naturally to a probabilistic interpretation of the data as a superposition of Gaussian probability distributions.

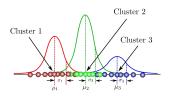


Figure: 1D Gaussian Mixture Model source.

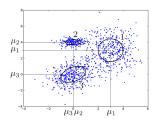


Figure: 2D Gaussian Mixture Model source.

Recall the probability, we assume that the probability density function (pdf) of cluster *k* can be written as:

$$\mathcal{N}(\mathbf{x} \mid \mathbf{c}_k, \boldsymbol{\Sigma}_k) = \frac{1}{(2\pi)^{D/2}} \frac{1}{(\det(\boldsymbol{\Sigma}_k))^{1/2}} \exp \left(-\frac{1}{2} (\mathbf{x} - \mathbf{c}_k)^T \boldsymbol{\Sigma}_k^{-1} (\mathbf{x} - \mathbf{c}_k) \right)$$

Here \mathbf{c}_k, Σ_k are the mean and covariance matrix of the given k cluster respectively. There is also a prior probability $P(k) = \pi_k$ that a data point belongs to a particular cluster k. The overall pdf for the data is then given by the total probability:

$$p(\mathbf{x}) = \sum_{k=1}^K P(k) p(\mathbf{x} \mid k) = \sum_{k=1}^K \pi_k \mathcal{N}(\mathbf{x} \mid \mathbf{c}_k, \Sigma_k)$$

where
$$0 \le \pi_k \le 1$$
, $\sum_{k=1}^K \pi_k = 1$



- The problem now is that we do not know the parameters of the model, i.e. the values of the centers $\{\mathbf{c}_k\}$ and the covariance matrices $\{\Sigma_k\}$ of the Gaussians and the probabilities $\{\pi_k\}$ for the clusters.
- The simple idea is to choose the parameters such, that the **probability density of the data is maximized**. In other words we want to choose the model such that the data becomes most probable. This is referred to as **Maximum Likelihood Estimation**
- We know that our data points were drawn independently, assume that we put these $\{x_n\}$ into the rows of the $X_{n\times d}$, so as a result the likelihood function would be:

$$L\Big(\{(\mathbf{c}_k, \boldsymbol{\Sigma}_k, \boldsymbol{\pi}_k)\}\Big) = ln\Big(p(\mathbf{X} \mid \{(\mathbf{c}_k, \boldsymbol{\Sigma}_k, \boldsymbol{\pi}_k)\})\Big) = \sum_{n=1}^N ln\Big(\sum_{k=1}^K \boldsymbol{\pi}_k \mathcal{N}(\mathbf{x}_n \mid \mathbf{c}_k, \boldsymbol{\Sigma}_k)\Big)$$



- Unfortunately, the Maximum Likelihood Estimation has not a closed form solution. because the parameters on the left-hand side will occur implicitly also on the right-hand side.
- Beside of the lackness of a closed form solution, Maximum Likelihood Estimation would probably have singularity and identifiability problems.
- However, one can start with some initial parameter values and then iterate through these equations to improve the estimate.
- One can actually show that the likelihood increases with each iteration, if a change occurs. This iterative scheme is referred to as the expectation-maximization algorithm, or simply EM algorithm

- To maximize Likelihood function through EM, we have to do the following algorithm:
 - Initialize $\{\mathbf{c}_k\}$, $\{\Sigma_k\}$ and $\{\pi_k\}$ with Random Value and evaluate the initial value of log-likelihood.
 - 2 Evaluate the responsibilities using the current parameter values:

$$\gamma(\boldsymbol{z}_{nk}) \!\! = \!\! \frac{\boldsymbol{\pi}_k \mathcal{N}(\mathbf{x}_n | \mathbf{c}_k, \boldsymbol{\Sigma}_k)}{\sum_{j=1}^K \boldsymbol{\pi}_j \mathcal{N}(\mathbf{x}_n | \mathbf{c}_j, \! \boldsymbol{\Sigma}_j)}$$

Re-Estimate the parameters using the current responsibilities:

$$\begin{split} \mathbf{c}_k^{new} &= \frac{1}{N_k} \sum_{n=1}^N \gamma(z_{nk}) \mathbf{x}_n \\ \Sigma_k^{new} &= \frac{1}{N_k} \sum_{n=1}^N \gamma(z_{nk}) (\mathbf{x}_n - \mathbf{c}_k^{new}) (\mathbf{x}_n - \mathbf{c}_k^{new})^T \\ \pi_k^{new} &= \frac{N_k}{N} \quad \text{where} \quad N_k = \sum_{n=1}^N \gamma(z_{nk}) \end{split}$$

Evaluate the log-likelihood:

$$ln\bigg(p(\mathbf{X}|\{(\mathbf{c}_k,\!\Sigma_k,\!\pi_k)\})\bigg)\!=\!\!\sum_{n=1}^{N}ln\bigg(\sum_{k=1}^{K}\pi_k\mathcal{N}(\mathbf{x}_n|\mathbf{c}_k,\!\Sigma_k)\bigg)$$

Solution Check the convergence criteria, otherwise go to step 2.

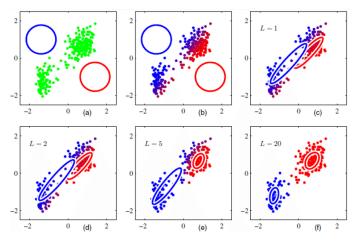


Figure: Illustration of EM using K = 2 [1].

References

[1]. Bishop, Christopher. Pattern Recognition and Machine Learning (Information Science and Statistics). 2018.

Thank You!

Any Question?