WMMFB40: Traitement des données temps réel et données hétèrogènes

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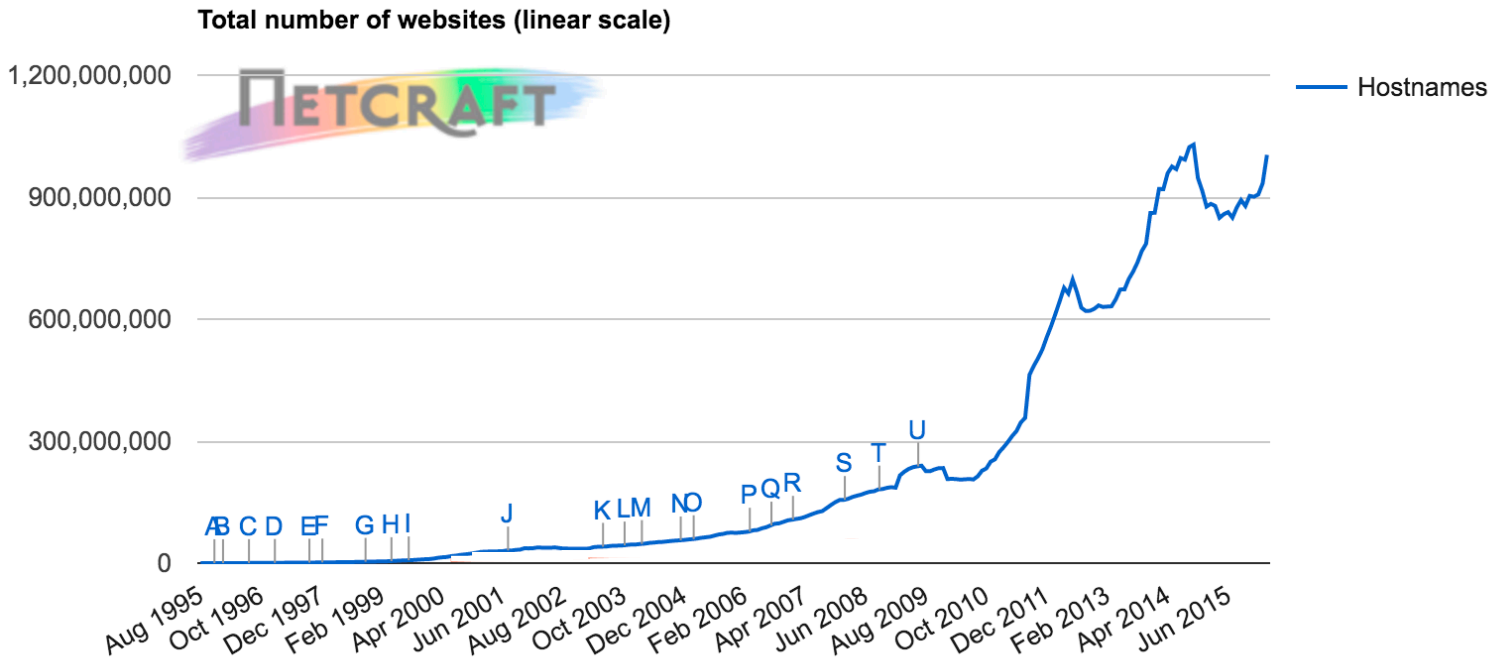
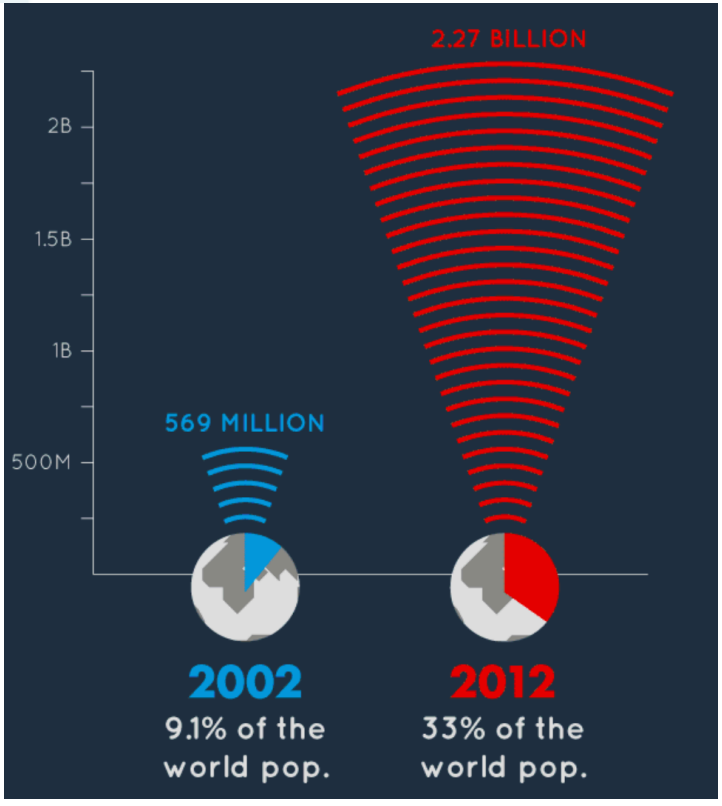
Era of Big Data

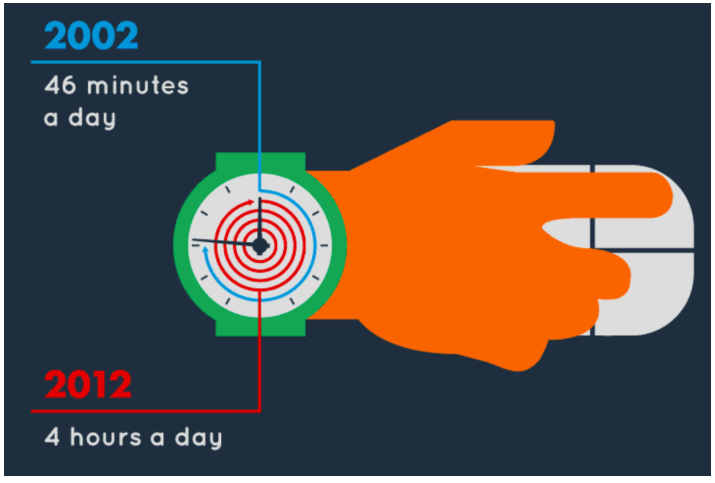
- In great part due to the rapid development of the Web this last 20 years,



Era of Big Data: New practices and habits

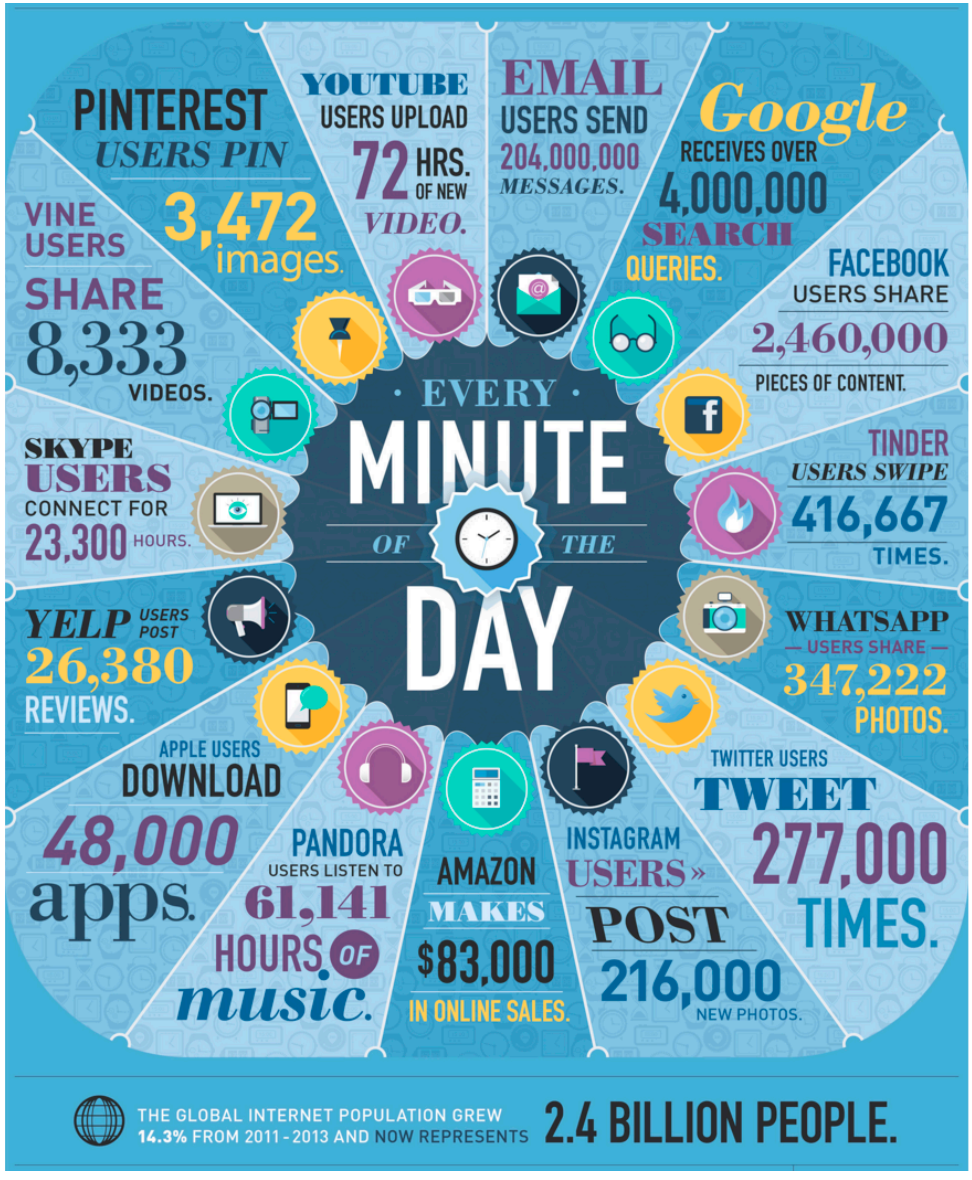


Nombre d'internautes



Temps de connexion

Era of Big Data: Increased data generation



Era of Big Data: value of the data

- According to the EMC project[1], in 2020 there will be 40 zetta bytes (40×10^{21} bytes) of unstructured data on the web.
- These data are considered as the oil of the XXI century.[2]
- Need to develop new automatic tools for information access.

[1] http://www.emc.com/leadership/digital-universe/index.htm

[2] http://www.lepoint.fr/technologie/les-data-petrole-du-xxie-siecle-14-03-2012-1441346_58.php

Recommender systems

- An effective way to exploit users' appetite on the Web.

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Plus de ...

- 60% of movies watched on Netflix are recommended movies,
- 35% of sales on Amazon are through recommendation,
- 38% of clicks on Google are generated over recommended products.

Outline

- Part I: Unsupervised learning techniques for automatic latent theme extraction,
- Part II: Recommender systems
- TP: Either clustering or a Machine Learning based technique for collaborative filtering.

Clustering

- The aim of clustering is to identify disjoint groups of observations within a given collection.
  - $\Rightarrow$ The aim is to find homogenous groups, by assembling observations that are close one to another, and separating the best those that are different
- Let G be a partition found over the collection $\mathcal{C}$ of N observations. An element of G is called *group* (or *cluster*). A group, G_k, where $1 \leq k \leq |G|$, corresponds to a subset of observations in $\mathcal{C}$.
- A representative of a group G_k, generally its center of gravity $\mathbf{r}_k$, is called prototype.

Classification vs. Clustering

- In **classification**: we have pairs of examples constituted by observations and their associated class labels $(\mathbf{x}, y) \in \mathbb{R}^d \times \{1, \ldots, K\}$.
  - The class information is provided by an expert and the aim is to find a prediction function $f : \mathbb{R}^d \to \mathcal{Y}$ that makes the association between the inputs and the outputs following the ERM or the SRM principle
- In **clustering**: the class information does not exist and the aim is to find homogeneous clusters or groups reflecting the relationship between observations.
  - The main hypothesis here is that this relationship can be found with the disposition of examples in the characteristic space,
  - The exact number of groups for a problem is very difficult to be found and it is generally fixed before hand to some arbitrary value,
  - The partitioning is usually done iteratively and it mainly depends on the initialization.

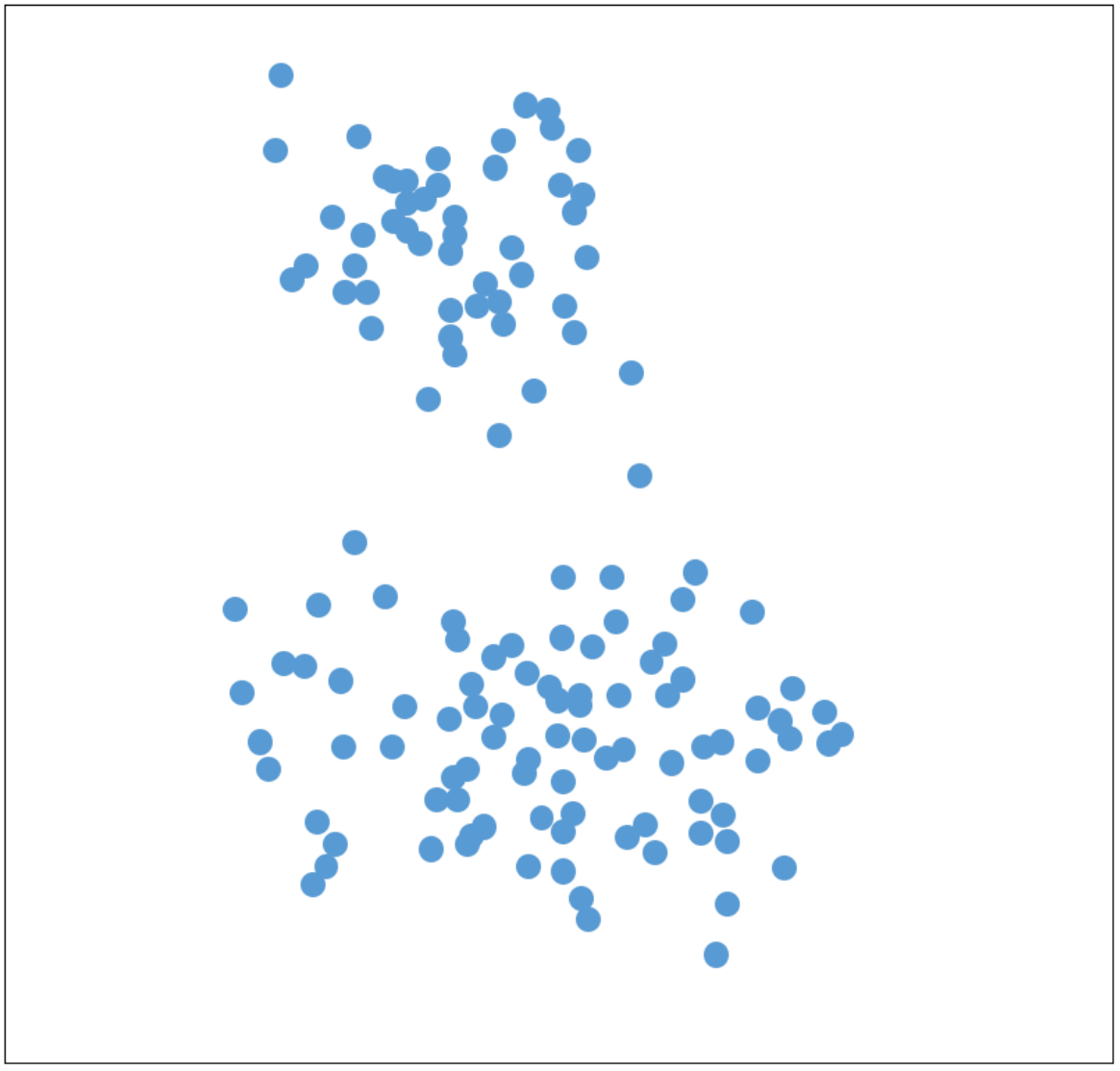
K-means algorithm [MacQueen, 1967]

- The K-means algorithm tends to find the partition for which the average distance between different groups is minimised:

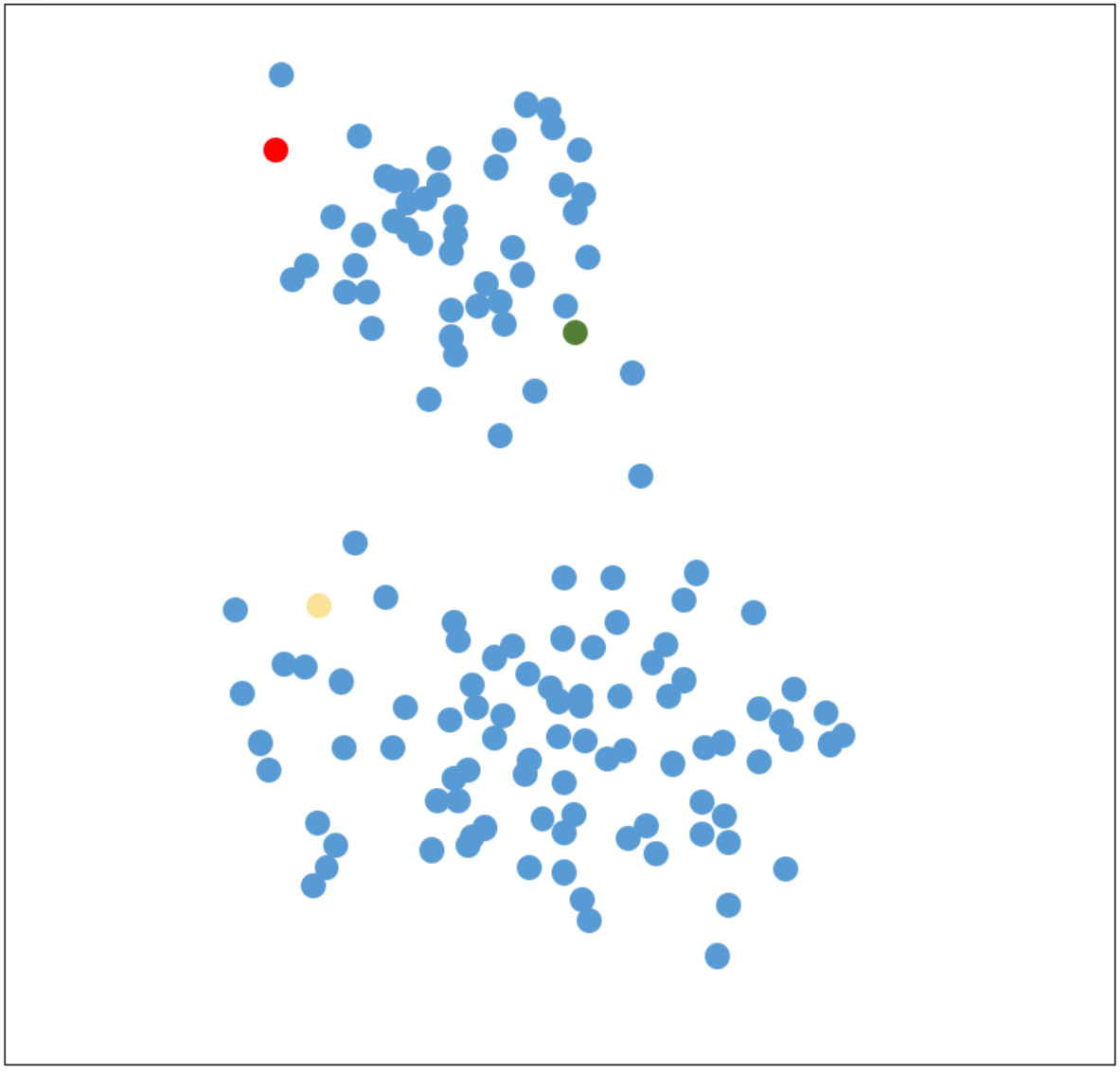
$$\text{argmin}_G \left(\sum_{k=1}^{K} \sum_{d \in G_k} ||\mathbf{x} - \mathbf{r}_k||_2^2 \right)$$

- From a given set of centroids, the algorithm then iteratively
  - affects each observation to the centroid to which it is the closest, resulting in new clusters;
  - estimates new centroids for the clusters that have been found.

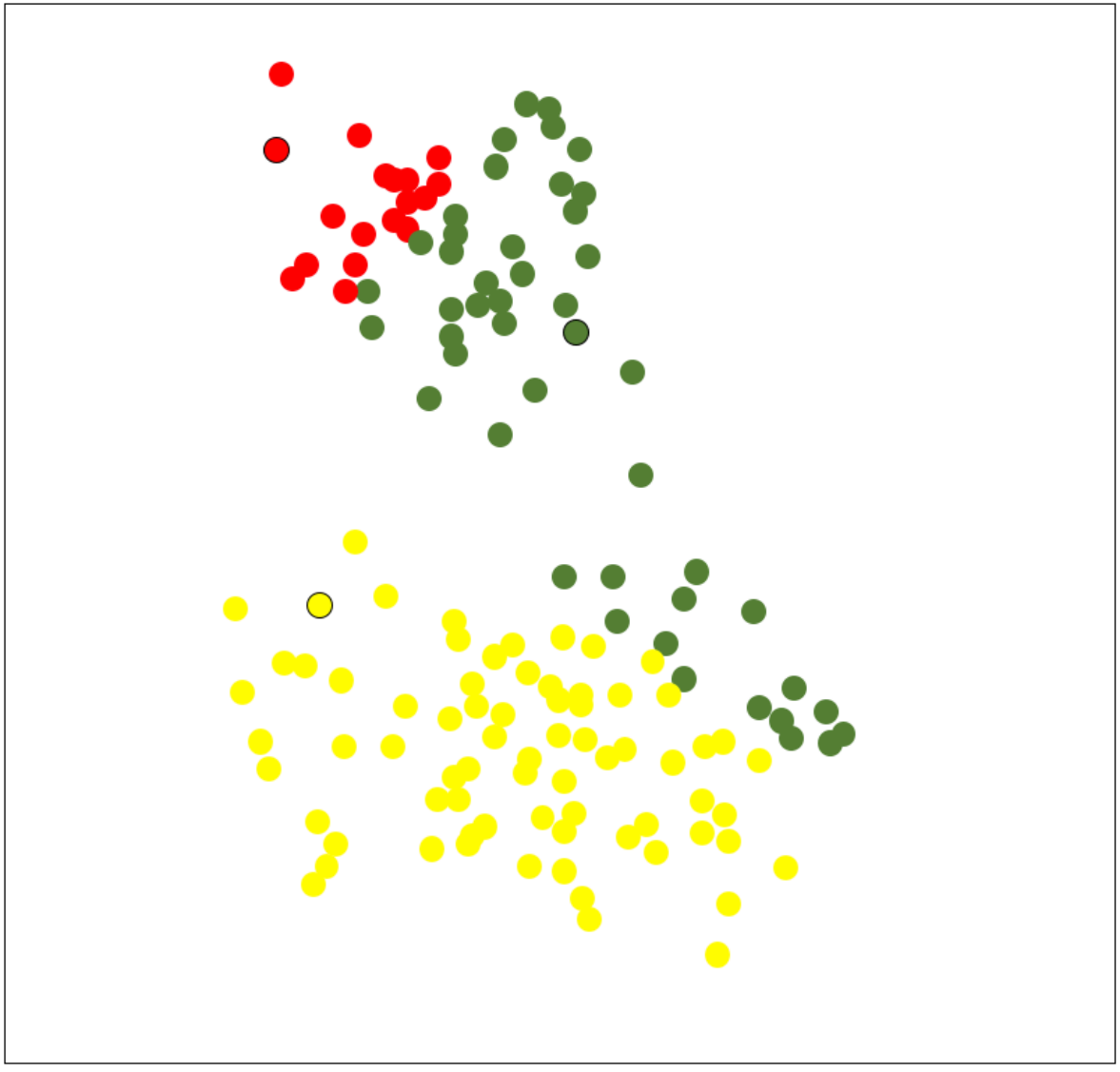
Clustering with K-means



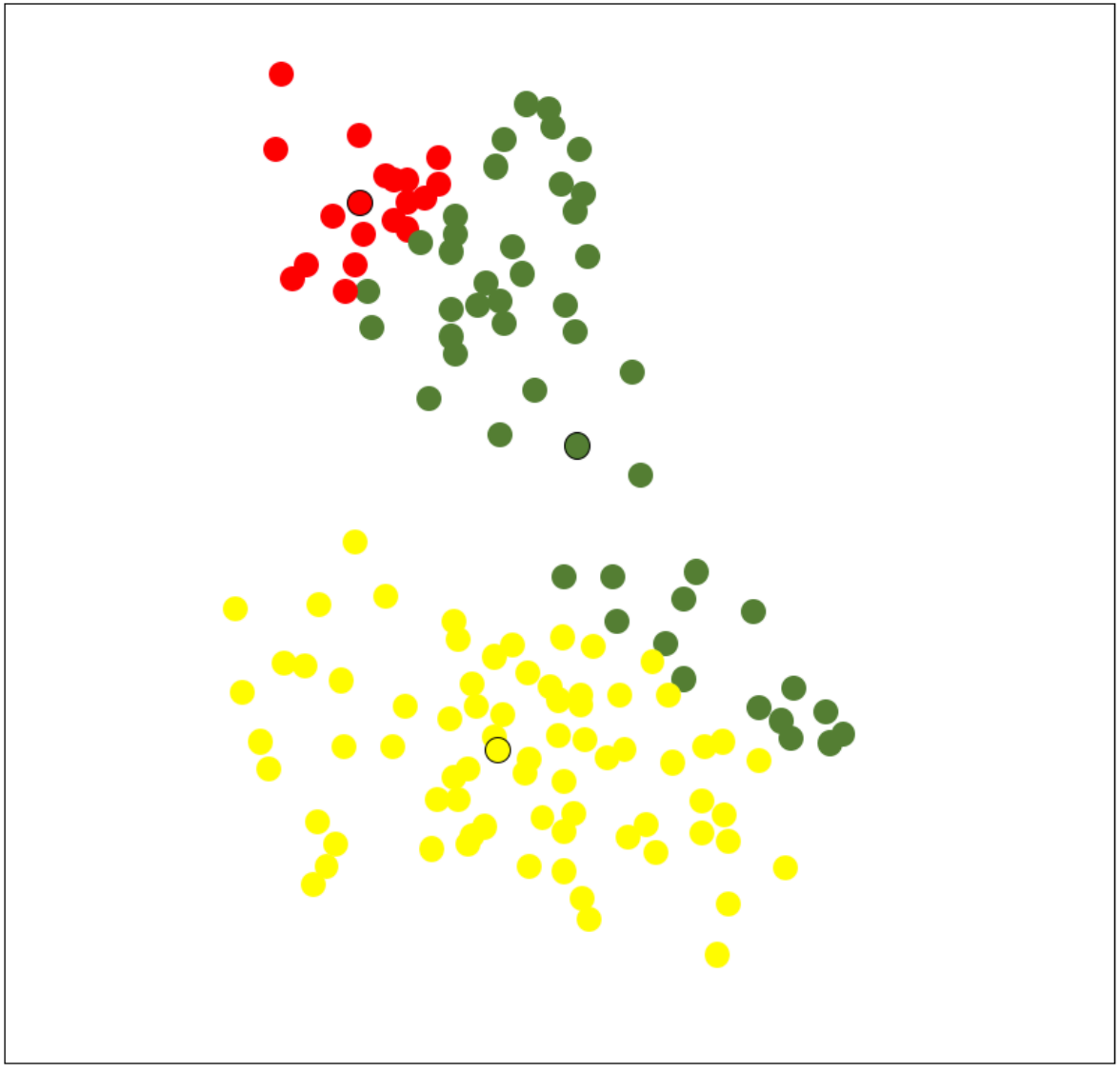
Clustering with K-means



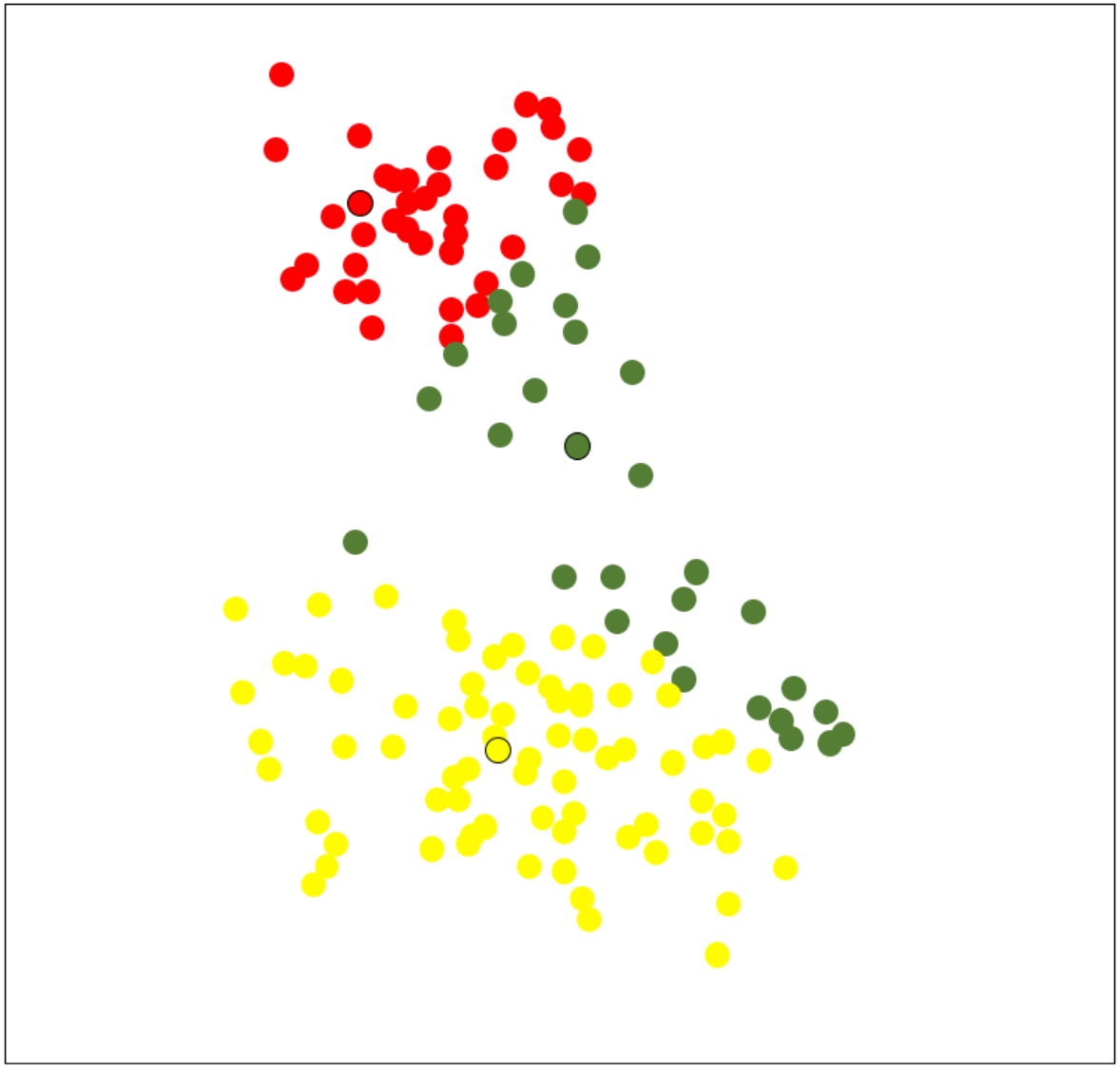
Clustering with K-means



Clustering with K-means



Clustering with K-means



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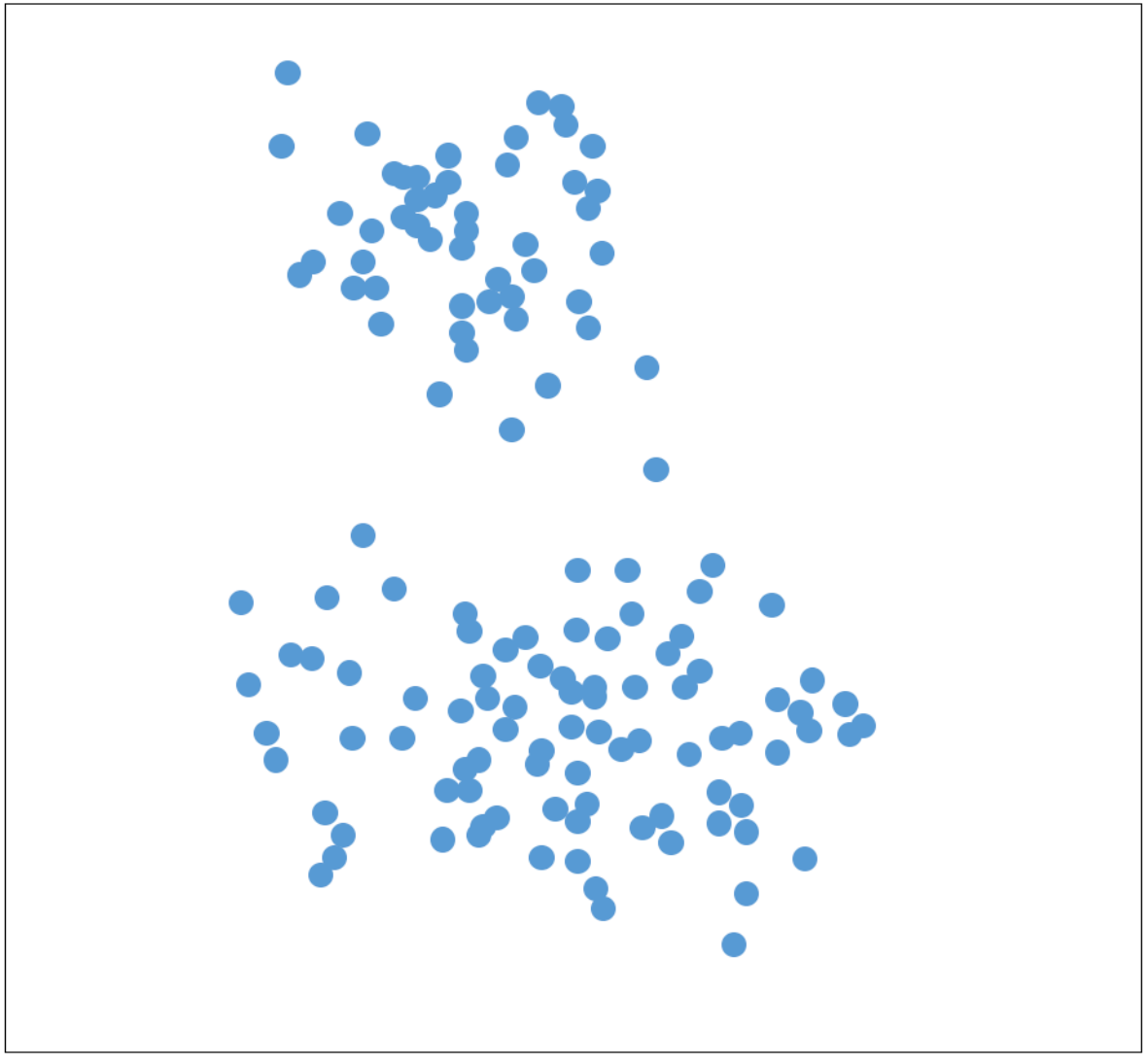

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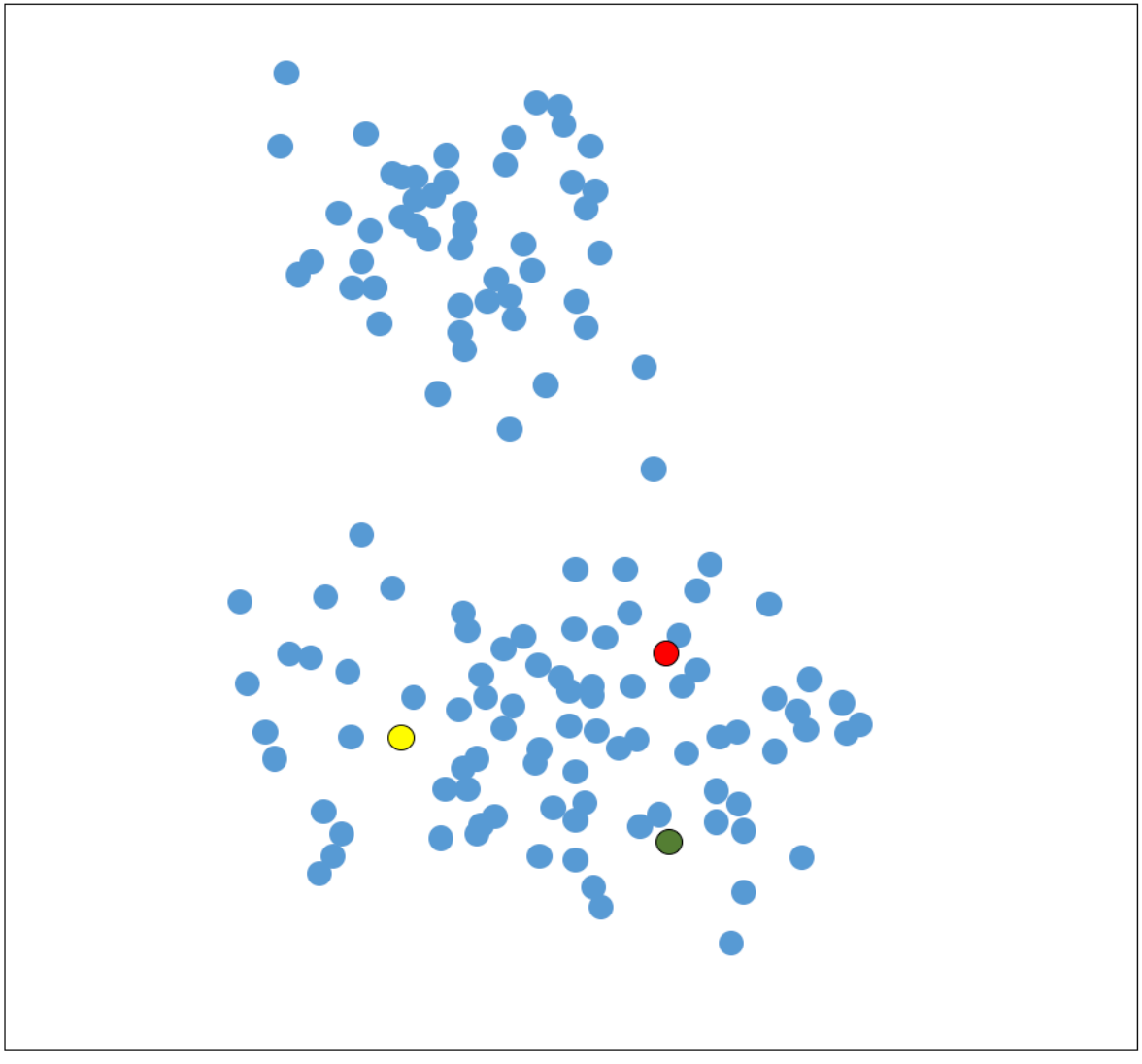

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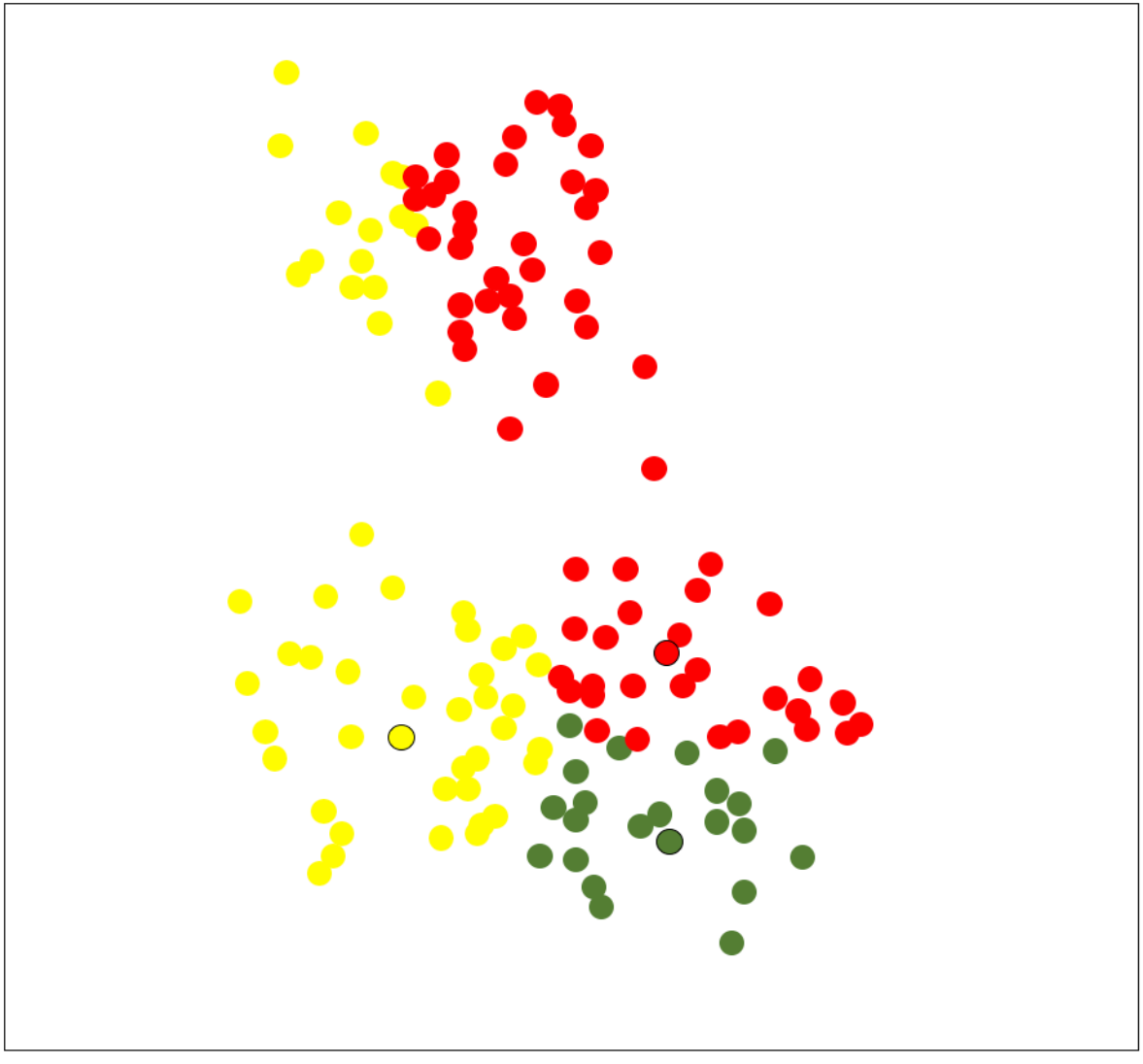

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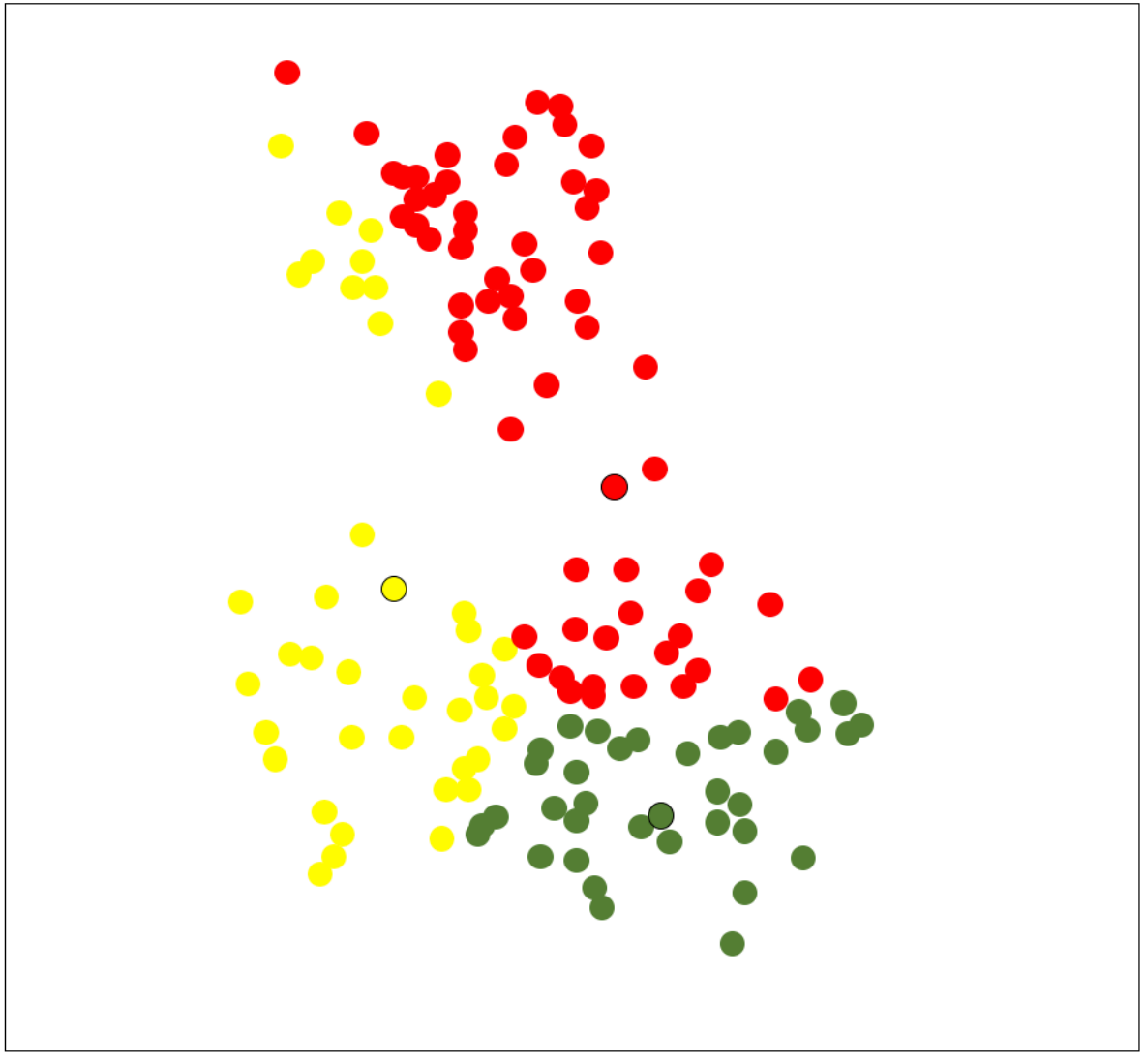

Different forms of clustering

There are two main forms of clustering:

1. *Flat* partitioning, where groups are supposed to be independent one from another. The user then chooses a number of clusters and a threshold over the similarity measure.
2. *Hierarchical* partitioning, where the groups are structured in the form of a taxonomy, which in general is a binary tree (each group has two siblings).

Hierarchical partitioning

- The hierarchical tends to construct a tree and it can be realized
  - in *bottom-up* manner, by creating a tree from the observations (agglomerative techniques), or *top-down*, by creating a tree from its root (divisives techniques).
- Hierarchical methods are purely determinists and do not require that a number of groups to be fixed before hand.

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- Hierarchical methods are purely determinists and do not require that a number of groups to be fixed before hand.
- In opposite, their complexity is in general quadratique in the number of observations (N) !

Steps of clustering

Clustering is an iterative process including the following steps:

1. Choose a similarity measure and eventually compute a similarity matrix.
2. Clustering.
    a. Choose a family of partitioning methods.
    b. Choose an algorithm within that family.
3. Validate the obtained groups.
4. Return to step 2, by modifying the parameters of the clustering algorithm or the family of the partitioning family.

Similarity measures

There exists several similarity measures or distance, the most common ones are:

- *Jaccard* measure, which estimates the proportion of common termes within two documents. In the case where the feature characteristics are between 0 and 1, this measure takes the form:

$$\text{sim}_{\text{Jaccard}}(\mathbf{x}, \mathbf{x}') = \frac{\sum_{i=1}^{d} x_i x'_i}{\sum_{i=1}^{d} x_i + x'_i - x_i x'_i}$$

- *Dice* coefficient takes the form:

$$\text{sim}_{\text{Dice}}(\mathbf{x}, \mathbf{x}') = \frac{\sum_{i=1}^{d} x_i x'_i}{\sum_{i=1}^{d} x_i^2 + (x'_i)^2}$$

Similarity measures

- *cosine* similarity, writes:

$$\text{sim}_{\cos}(\mathbf{x}, \mathbf{x}') = \frac{\sum_{i=1}^{d} x_i x'_i}{\sqrt{\sum_{i=1}^{d} x_i^2} \sqrt{\sum_{i=1}^{d} (x'_i)^2}}$$

- *Euclidean* distance is given by:

$$\text{dist}_{\text{eucl}}(\mathbf{x}, \mathbf{x}') = ||\mathbf{x} - \mathbf{x}'||_2 = \sqrt{\sum_{i=1}^{d} (x_i - x'_i)^2}$$

This distance is then transformed into a similarity measure, by using for example its opposite.

Mixture models

- With the probabilistic approaches, we suppose that each group G_k is generated by a probability density of parameters θ_k
- Following the formula of total probabilities, an observation $\mathbf{x}$ is then supposed to be generated with a probability

$$P(\mathbf{x}, \Theta) = \sum_{k=1}^{K} \underbrace{P(y = k)}_{\pi_k} P(\mathbf{x} \mid y = k, \theta_k)$$

  where $\Theta = \{\pi_k, \theta_k; k \in \{1, \ldots, K\}\}$ are the parameters of the mixture.
- The aim is then to find the parameters Θ with which the mixture models fits the best the observations

Mixture models (2)

- If we have a collection of N observations, $\mathbf{x}_{1:N}$, the log-likelihood writes

$$\mathcal{L}_M(\Theta) = \sum_{i=1}^{N} \ln \left[\sum_{k=1}^{K} \pi_k P(\mathbf{x}_i \mid y = k, \theta_k) \right]$$

- The aim is then to find the parameters Θ^* that maximize this criterion

$$\Theta^* = \underset{\Theta}{\operatorname{argmax}}\, \mathcal{L}_M(\Theta)$$

- The direct maximisation of this criterion is impossible because it implies a sum of a logarithm of a sum.

Mixture models (3)

- We use then iterative methods for its maximisation (e.g. the EM algorithm).
- Once the optimal parameters of the mixture are found, each document is then assigned to a group following the Bayesian decision rule:

$$\mathbf{x} \in G_k \Leftrightarrow P(y = k \mid \mathbf{x}, \Theta^*) = \underset{\ell}{\operatorname{argmax}}\, P(y = \ell \mid \mathbf{x}, \Theta^*)$$

where

$$\begin{aligned} \forall \ell \in \{1, \ldots, K\}, P(y = \ell \mid \mathbf{x}, \Theta^*) &= \frac{\pi_\ell^* P(\mathbf{x} \mid y = \ell, \theta_k^*)}{P(\mathbf{x}, \Theta^*)} \\ &\propto \pi_\ell^* P(\mathbf{x} \mid y = \ell, \theta_k^*) \end{aligned}$$

EM algorithm [Dempster, 1977]

- The idea behind the algorithm is to introduce hidden random variables Z such that if Z were known, the value of parameters maximizing the likelihood would be simple to be find:

$$\mathcal{L}_M(\Theta) = \ln \sum_Z P(\mathbf{x}_{1:N} \mid Z, \Theta) P(Z \mid \Theta)$$

- by denoting the current estimates of the parameters at time t by $\Theta^{(t)}$, the next iteration $t+1$ consists in finding the new parameters Θ that maximize $\mathcal{L}_M(\Theta) - \mathcal{L}_M(\Theta^{(t)})$

$$\mathcal{L}_M(\Theta) - \mathcal{L}_M(\Theta^{(t)}) = \ln \sum_Z P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)}) \frac{P(\mathbf{x}_{1:N} \mid Z, \Theta) P(Z \mid \Theta)}{P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)}) P(\mathbf{x}_{1:N} \mid \Theta^{(t)})}$$

EM algorithm [Dempster, 1977]

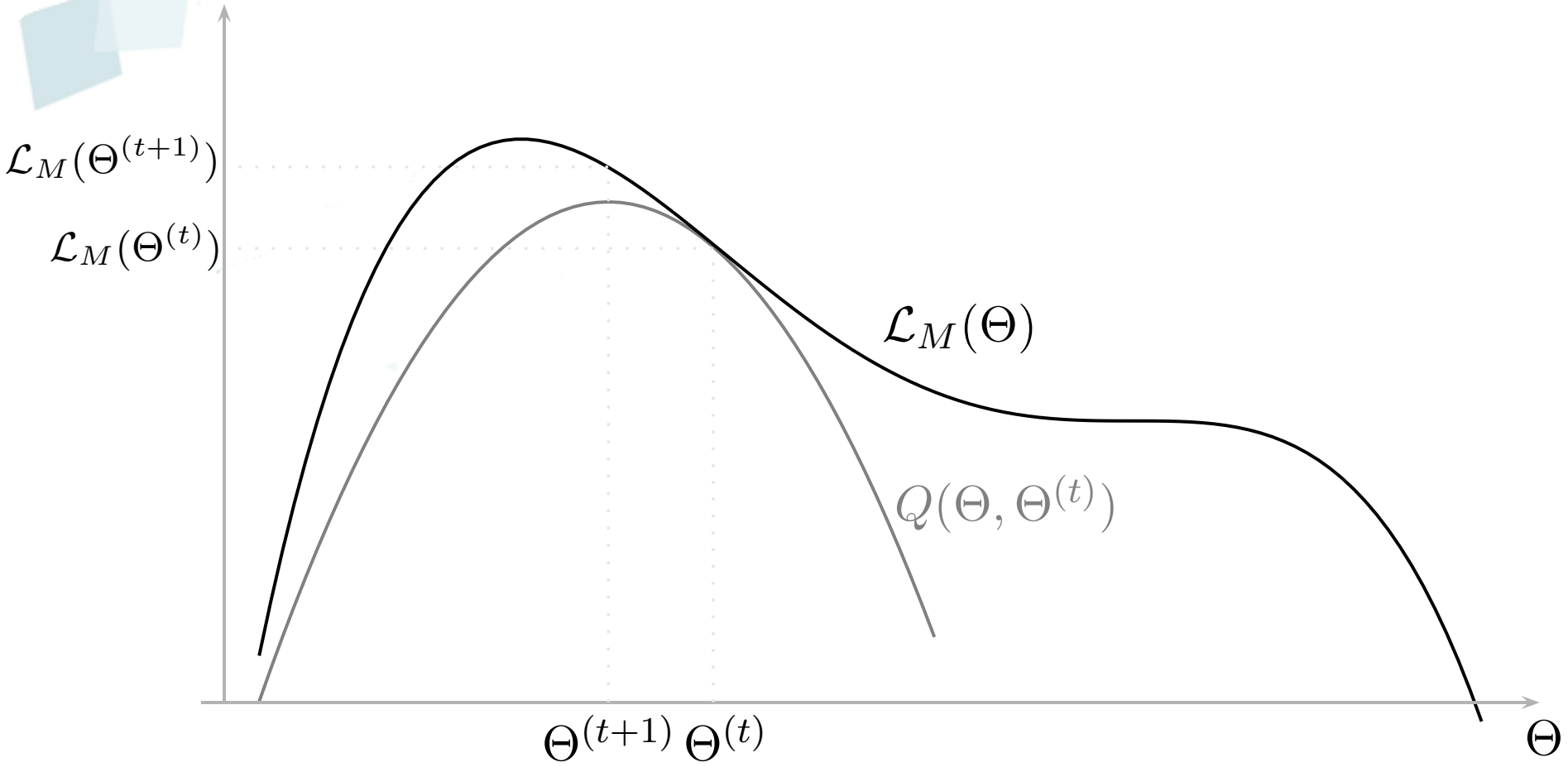
- From the Jensen inequality and the concavity of the logarithm it comes:

$$\mathcal{L}_M(\Theta) - \mathcal{L}_M(\Theta^{(t)}) \geq \sum_Z P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)}) \ln \frac{P(\mathbf{x}_{1:N} \mid Z, \Theta) P(Z \mid \Theta)}{P(\mathbf{x}_{1:N} \mid \Theta^{(t)}) P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)})}$$

- Let

$$Q(\Theta, \Theta^{(t)}) = \mathcal{L}_M(\Theta^{(t)}) + \sum_Z P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)}) \ln \frac{P(\mathbf{x}_{1:N} \mid Z, \Theta) P(Z \mid \Theta)}{P(\mathbf{x}_{1:N} \mid \Theta^{(t)}) P(Z \mid \mathbf{x}_{1:N}, \Theta^{(t)})}$$

EM algorithm [Dempster, 1977]



EM algorithm [Dempster, 1977]

- At iteration $t+1$, we look for parameters Θ that maximise $Q(\Theta, \Theta^{(t)})$:

$$\Theta^{(t+1)} = \underset{\Theta}{\operatorname{argmax}}\, \mathbb{E}_{Z|\mathbf{d}_{1:N}} \left[\ln P(\mathbf{d}_{1:N}, Z \mid \Theta) \mid \Theta^{(t)} \right]$$

- The EM algorithm is an iterative

Algorithm 1 The EM algorithm

1: Input: A collection $\mathbf{x}_{1:N} = \{\mathbf{x}_1, \cdots, \mathbf{x}_N\}$
2: Initialize randomly the parameters $\Theta^{(0)}$
3: **for** $t \geq 0$ **do**
4: **E**-step: Estimate $\mathbb{E}_{Z|\mathbf{d}_{1:N}} \left[\ln P(\mathbf{d}_{1:N}, Z \mid \Theta) \mid \Theta^{(t)} \right]$
5: **M**-step: Find new parameters $\Theta^{(t+1)}$ that maximise $Q(\Theta, \Theta^{(t)})$
6: **end for**

EM algorithm [Dempster, 1977]

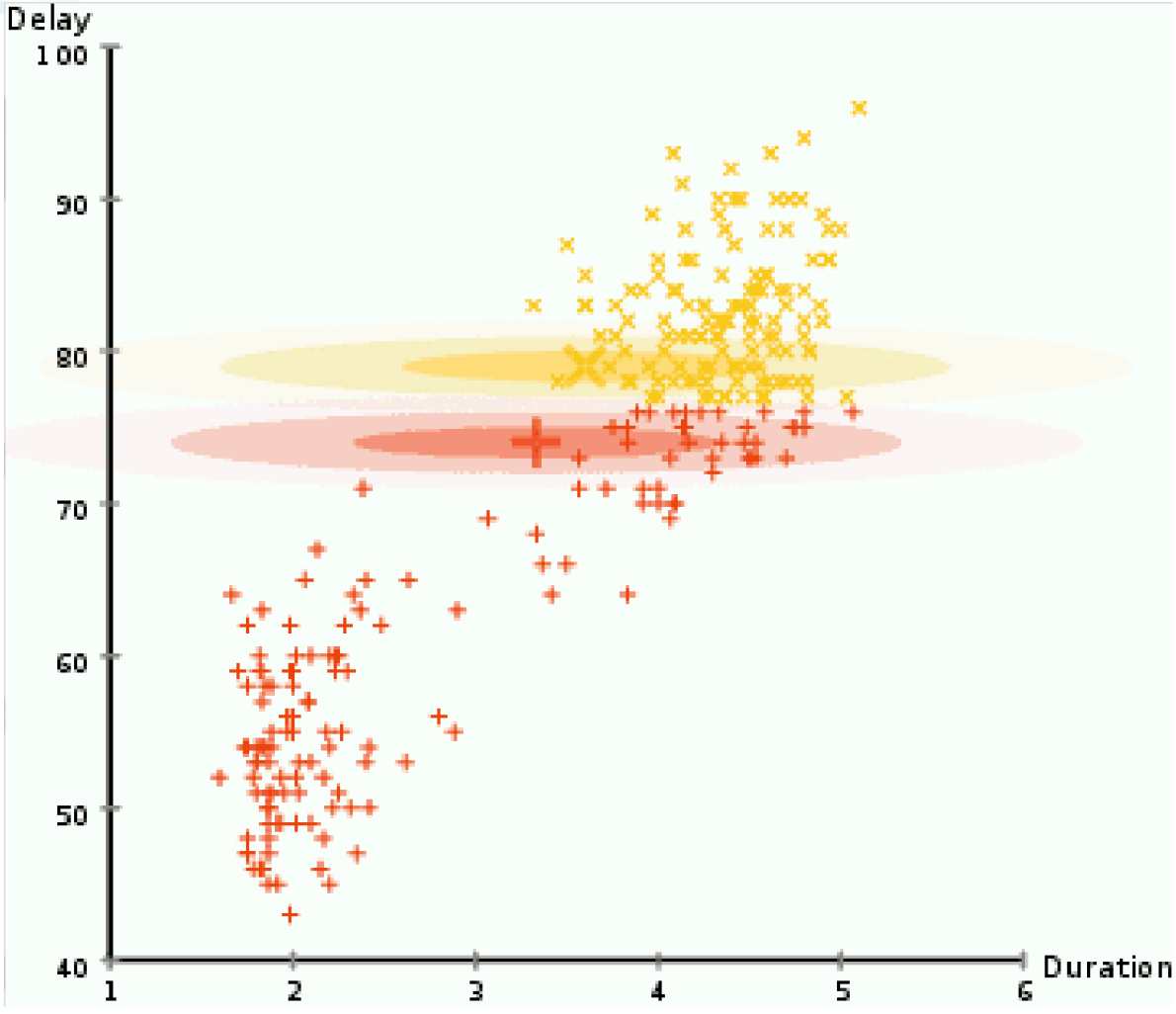


Figure from

https://en.wikipedia.org/wiki/Expectation%E2%80%93maximization_algorithm

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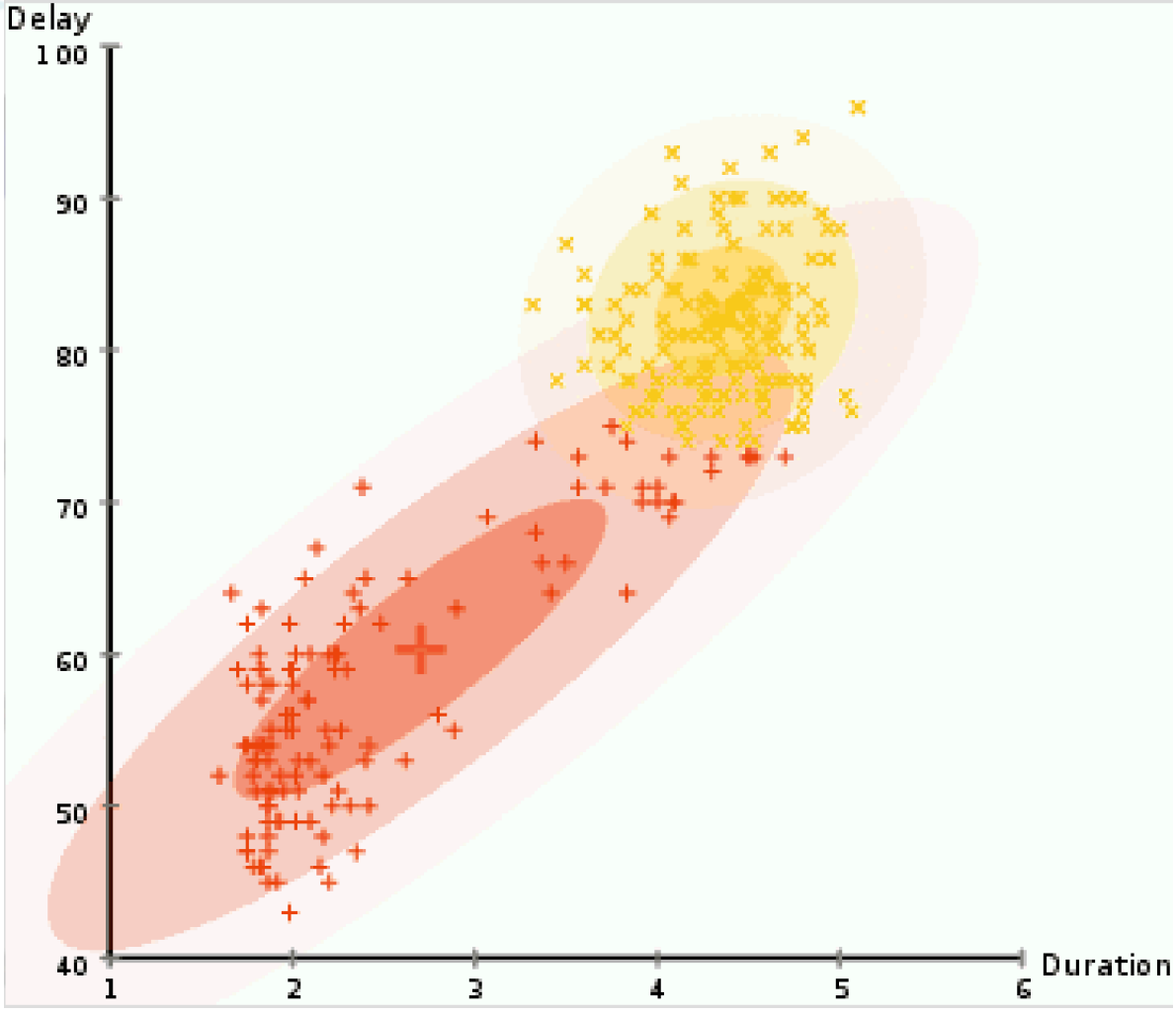

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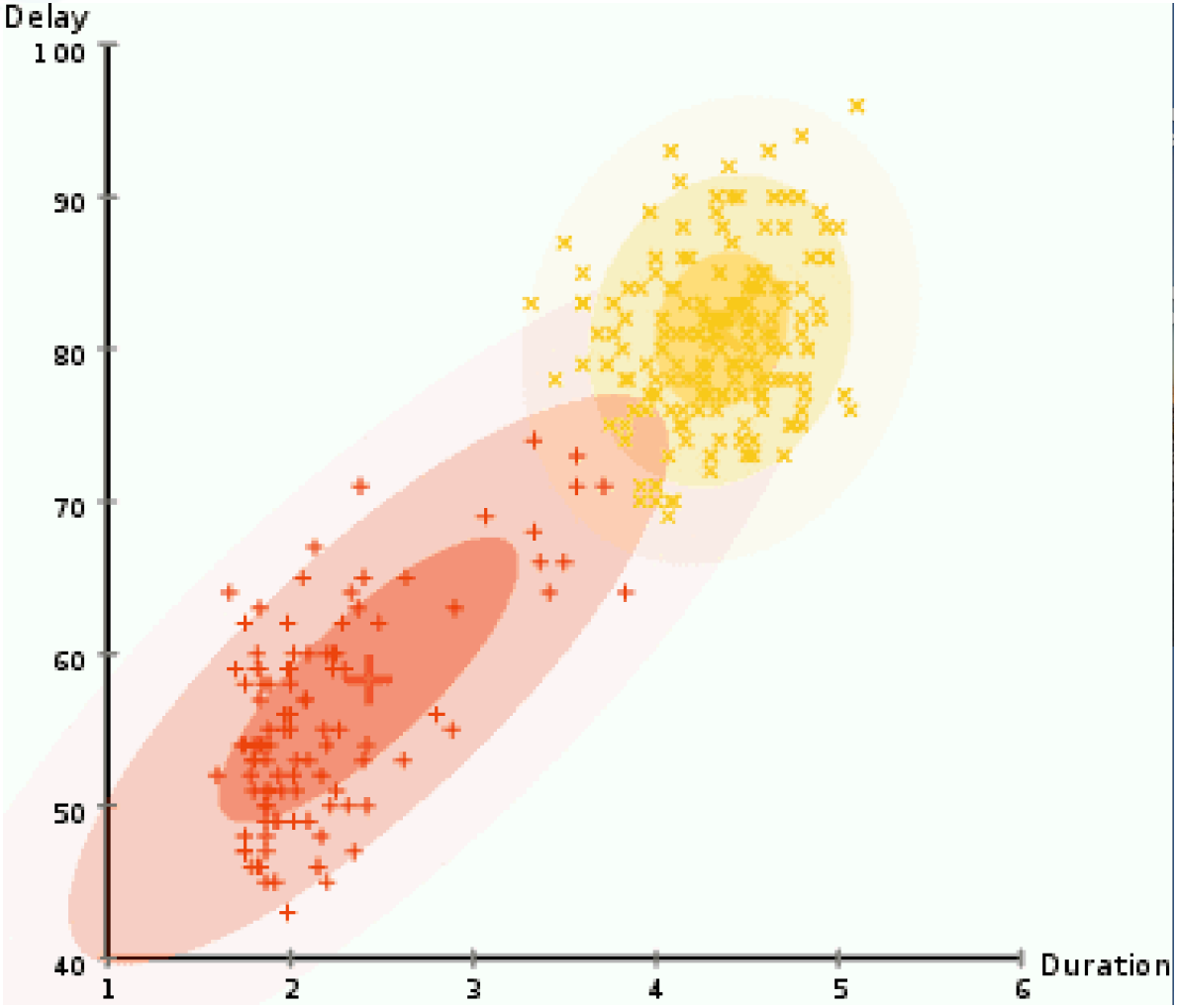

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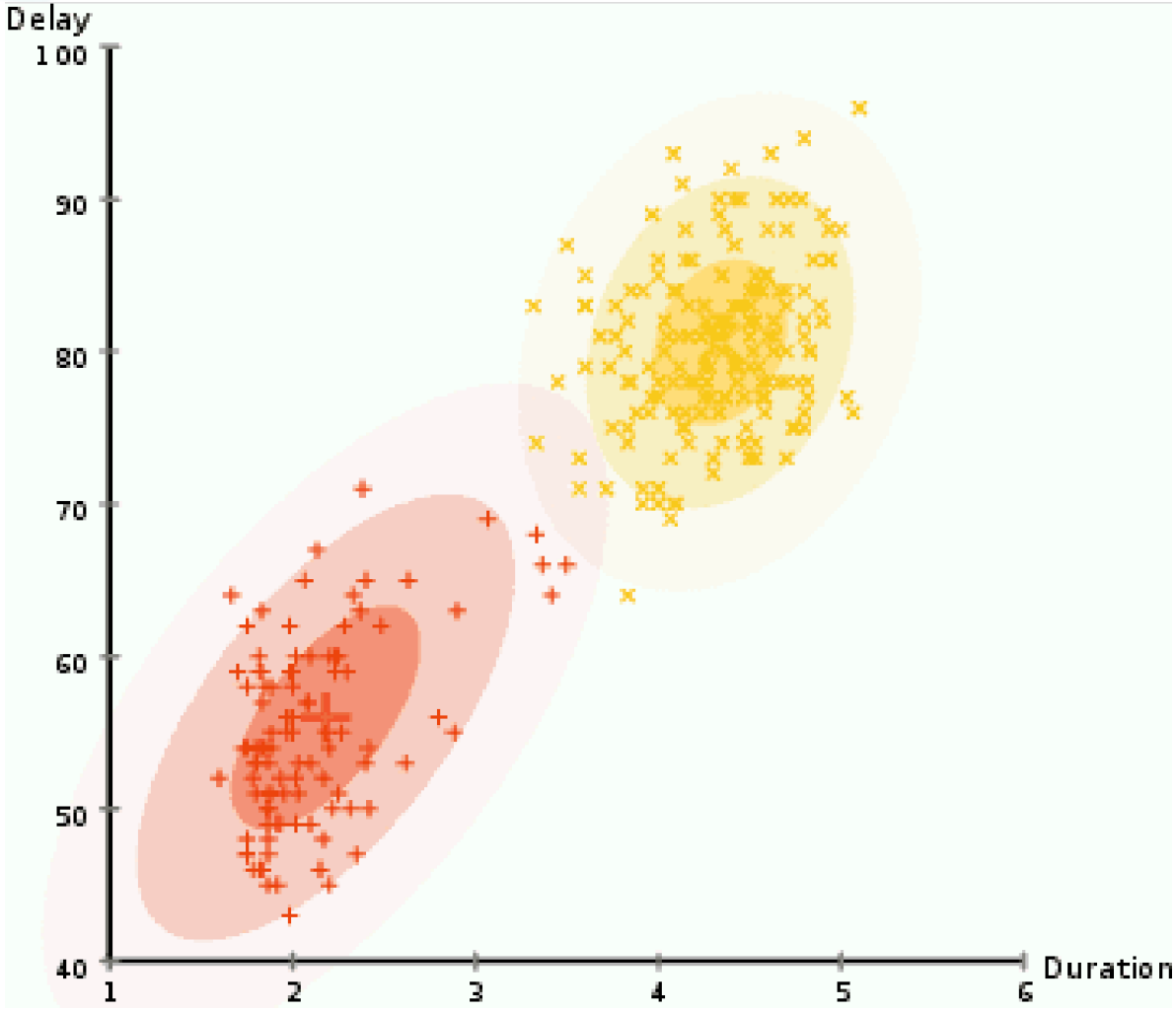

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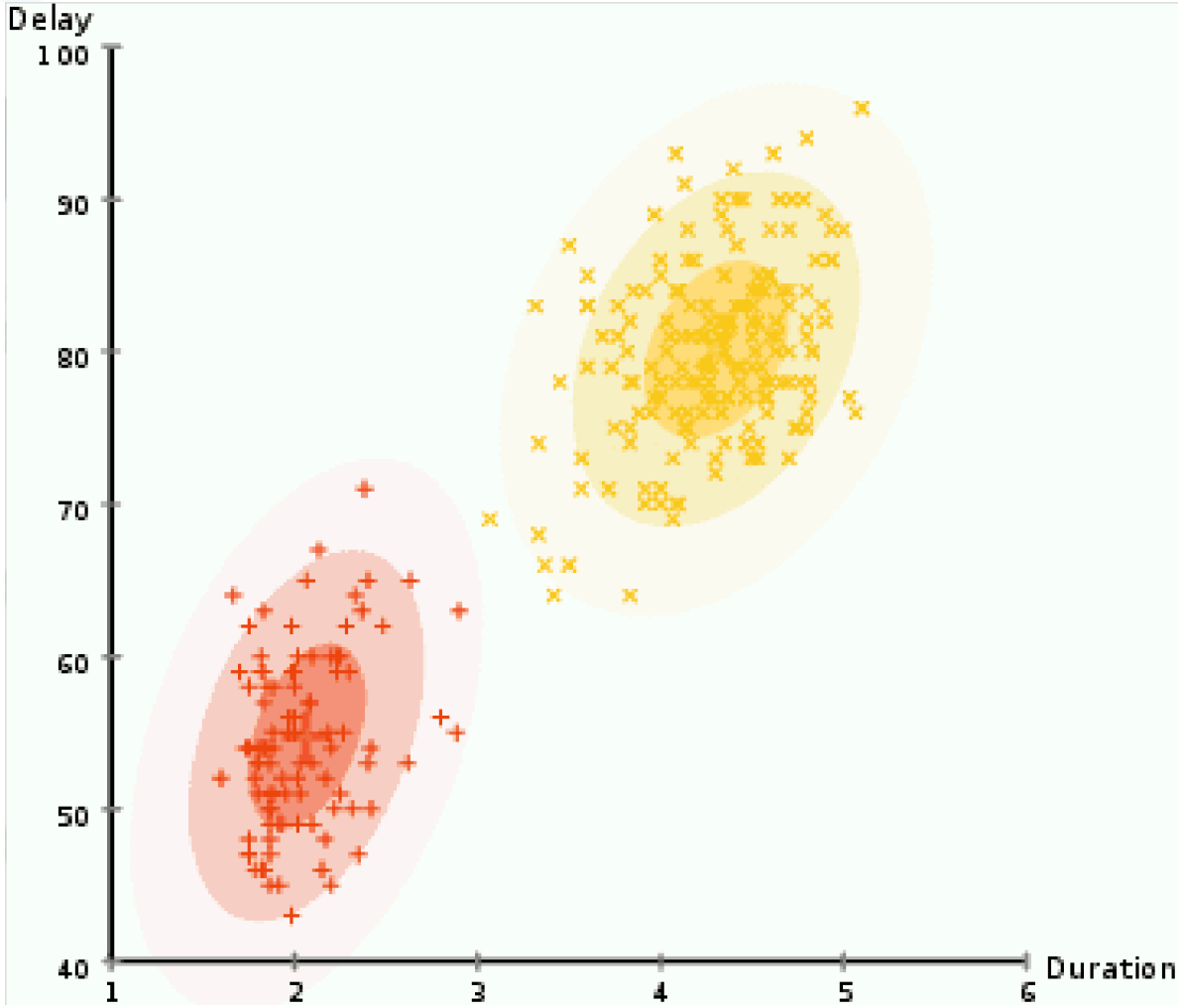

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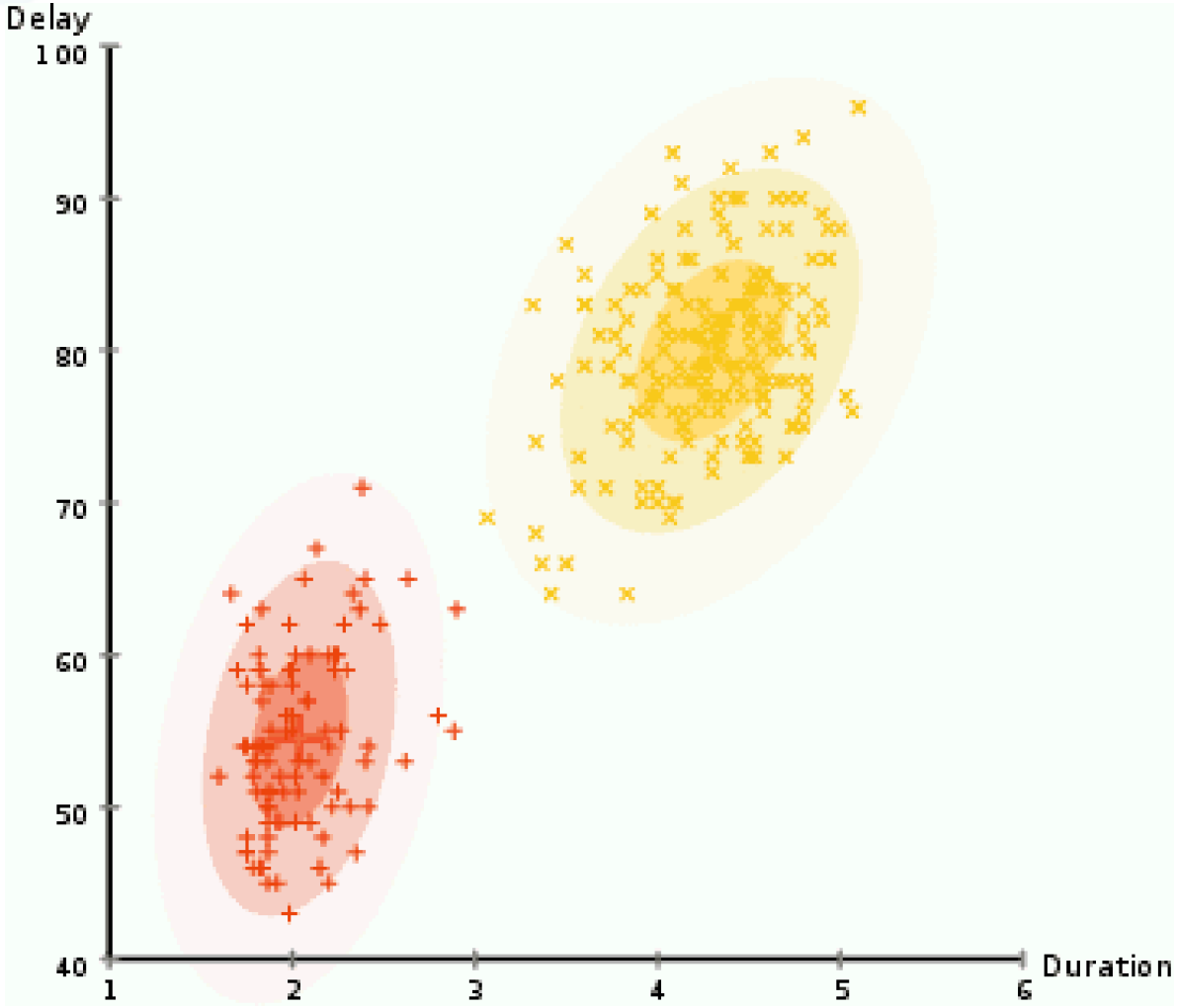

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CEM algorithm [?]

We suppose that

- Each group $k \in \{1, ..., K\}$ is generated by a distribution of probabilities of parameters θ_k,
- observations are supposed to be identically and independently distributed according to a probability distribution,
- each observation $\mathbf{x}_i \in \mathcal{C}$ belongs to one and only one group, we define a indicator cluster vector $\mathbf{t}_i = (t_{i1}, \ldots, t_{iK})$

$$\mathbf{x}_i \in G_\ell \Leftrightarrow y_i = \ell \Leftrightarrow t_{ik} = \begin{cases} 1, & \text{if } k = \ell, \\ 0, & \text{otherwise.} \end{cases}$$

The aim is to find the parameters $\Theta = \{\theta_k; k \in \{1, \ldots, K\}\}$ qui that maximizes the complete log-likelihood

$$\mathcal{V}(\mathcal{C}, \pi, \Theta, G) = \prod_{i=1}^{N} P(\mathbf{x}_i, y_i = \ell, \theta_k) = \prod_{i=1}^{N} \prod_{k=1}^{K} P(\mathbf{x}_i, y_i = k, \theta_k)^{t_{ik}}$$

Objectif

In general the parameters Θ are those that maximize

$$\begin{aligned}\mathcal{L}(\mathcal{C},\Theta,G) &= \sum_{i=1}^{N}\sum_{k=1}^{K} t_{ik}\log P(\mathbf{x}_i, y_i = k, \theta_k) \\ &= \sum_{i=1}^{N}\sum_{k=1}^{K} t_{ik}\log \underbrace{P(y_i = k)}_{\pi_k} P(\mathbf{x}_i \mid y_i = k, \theta_k)\end{aligned}$$

The maximization can be carried out using the classification

EM (CEM) algorithm.

CEM algorithm [?]

Begin with an initial partition $G^{(0)}$.
$t \leftarrow 0$
while $\mathcal{L}(\mathcal{C}, \Theta^{(t+1)}, G^{(t+1)}) - \mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t)}) > \epsilon$ **do**

E-step Estimate the posterior probabilities using the current parameters $\Theta^{(t)}$:

$$\forall \ell = \{1, \ldots, K\} \mathbb{E}[t_{i\ell} \mid \mathbf{x}_i, G^{(t)}, \Theta^{(t)}] = \frac{\pi_\ell^{(t)} P(\mathbf{x}_i \mid G_\ell^{(t)}, \theta_\ell^{(t)})}{\sum_{k=1}^{K} \pi_k^{(t)} P(\mathbf{x}_i \mid G_k^{(t)}, \theta_k^{(t)})}$$

C-step Assign to each example $\mathbf{x}_i$ its partition, the one for which the posterior probability is maximum. Note $G^{(t+1)}$ this new partition

M-step Estimate the new parameters $\Theta^{(t+1)}$ qui maximisent $\mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t+1)})$

$t \leftarrow t + 1$
end while

CEM algorithm (convergence)

The algorithm converges to a local maxima of the completer log-likelihood.

- At the **C**-step we choose the new partition $G^{(t+1)}$ using the current set of parameters $\Theta^{(t)}$, according the Bayesian decision rule

$$\mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t+1)}) \geq \mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t)})$$

- At the **M**-step new parameters are found $\Theta^{(t+1)}$ by maximising $\mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t+1)})$:

$$\mathcal{L}(\mathcal{C}, \Theta^{(t+1)}, G^{(t+1)}) \geq \mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t+1)})$$

- At each iteration t we have :

$$\mathcal{L}(\mathcal{C}, \Theta^{(t+1)}, G^{(t+1)}) \geq \mathcal{L}(\mathcal{C}, \Theta^{(t)}, G^{(t)})$$

As there is a finite number of partitions, the iterations between these two steps is guaranteed to converge.

Study case: document clustering

- Documents are usually represented using the Vector Space Model (VSM) proposed By Salton;
  - In this case, the feature characteristics of a document translate the presence of the terms of the vocabulary $\mathcal{V} = (t_1, \ldots, t_V)$ in that document.
  - If these features are based on term frequencies, a document d is then represented by a vector of dimension V:

$$\mathbf{d} = (\mathrm{tf}_{1,d}, \ldots, \mathrm{tf}_{V,d})$$

- In the case where, the presence of the terms in a document is supposed to be independent one from another. The probability distributions are Multinomials

$$\forall \ell \in \{1, \ldots, K\}, P(\mathbf{d} \mid y = \ell) = \frac{\mathrm{tf}_d!}{\mathrm{tf}_{1,d}! \ldots \mathrm{tf}_{V,d}!} \prod_{j=1}^{V} \theta_{j|\ell}^{\mathrm{tf}_{j,d}}$$

where, $tf_d = \mathrm{tf}_{1,d} + \ldots + \mathrm{tf}_{V,d}$

Study case: document clustering

- The parameters of the Mixture model are then

$$\Theta = \left\{\theta_{j|k}; j \in \{1,\ldots,V\}, k \in \{1,\ldots,K\}; \pi_k; j \in \{1,\ldots,K\}\right\}$$

- By neglecting the multinomial terms, the optimization of the complete log-likelihood over a document collection of N documents $\mathcal{C} = \{d_1,\ldots,d_N\}$ writes

$$\max_{\Theta} \sum_{i=1}^{N}\sum_{k=1}^{K} t_{ik}\left(\ln \pi_k + \sum_{j=1}^{V} \mathrm{tf}_{j,d} \ln \theta_{j|k}\right)$$

$$u.c. \sum_{k=1}^{K} \pi_k = 1, \forall k, \sum_{j=1}^{V} \theta_{j|k} = 1$$

Study case: document clustering

- The maximization of the complete log-likelihood with respect to model parameters is then carried out by these esitmates

$$\forall j, \forall k, \theta_{j|k} = \frac{\sum_{i=1}^{N} t_{ik} \mathrm{tf}_{j,d_i}}{\sum_{j=1}^{V} \sum_{i=1}^{N} t_{ik} \mathrm{tf}_{j,d_i}}$$

$$\forall k, \pi_k = \frac{\sum_{i=1}^{N} t_{ik}}{N}$$

Evaluation

- The results of clustering can be evaluated using a labeled training set.
- The two common measures are *purity* and *Normalised Mutual Information*.
- The purity measure tends to quantify the ability of the clustering method to regroupe the observations of the same class into the same partitions. Let G be the partition found and C the set of classes found over G. The purity measure is then defined by:

$$\text{pure}(G, C) = \frac{1}{N} \sum_{k} \max_{l} |G_k \cap C_l|$$

Evaluation

- The Normalised Mutual Information is defined by:

$$\mathrm{IMN}(G,C) = \frac{2 \times I(G,C)}{H(G) + H(C)}$$

where I is the mutual information and H the entropy. These two quantities can be computed as:

$$\begin{aligned} I(G,C) &= \sum_k \sum_l P(G_k \cap C_l) \log \frac{P(G_k \cap C_l)}{P(G_k)P(C_l)} \\ &= \sum_k \sum_l \frac{|G_k \cap C_l|}{N} \log \frac{N|G_k \cap C_l|}{|G_k||C_l|} \end{aligned}$$

and:

$$\begin{aligned} H(G) &= -\sum_k P(G_k) \log P(G_k) \\ &= -\sum_k \frac{|G_k|}{N} \log \frac{|G_k|}{N} \end{aligned} \quad (1)$$

NMI is equal to 1 if the two sets G and C are identical

References

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