CLUSTERING

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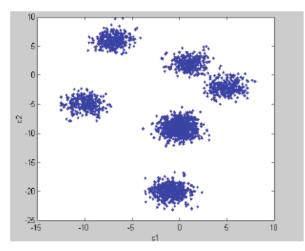
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MAGICMOTORSPORT - COURSE

Clustering

- Now, an **unsupervised task**.
- we have just x_i...
- We will see the k-means algorithm which is, in my opinion, the unsupervised version of the Nearest Neighbors (NNs) method.
- ▶ in this slides: number of data N.

What is clustering? Find the groups of samples and, if it is possible, The number of groups.



Type of clusters.... infinite....



Examples of application

Segmentation

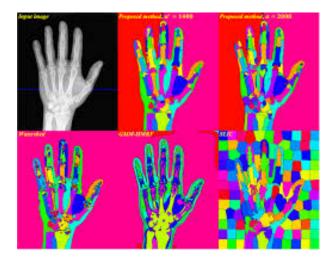


Examples of application

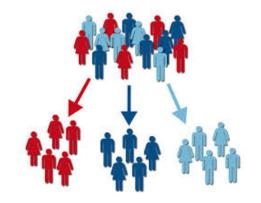
Segmentation



Examples of application Segmentation



Examples of application



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Main families of clustering algorithms

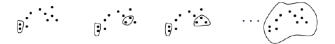
(a) partitional (partitioning) clustering(b) hierarchical clustering etc...

Las dos familias principales de algoritmos de agrupamiento, son:

• Agrupamiento particional (se suele fijar k, el número de grupos)



• Agrupamiento jerárquico (no se fija k)



The most famous clustering algorithm

The k-means algorithm.

k is the number of clusters....

Note that

 $1 \leq k \leq N$

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If we set k = N, each data should be a cluster....

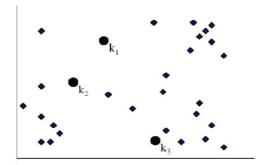
k-means algorithm

- Fix a number k (of clusters).
- Start randomly, choosing the positions of *k* centroids.
- Assign samples/data to each centroid as function of some distance.
- Move the centroids, doing the arithmetic means of the assigned samples/data....

k-means algorithm: starting

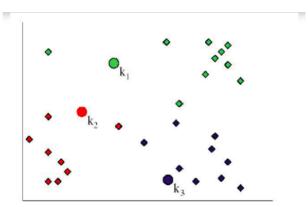
Fix a number k (of clusters).

Ejemplo del algoritmo k-medias (k-means) con k=3

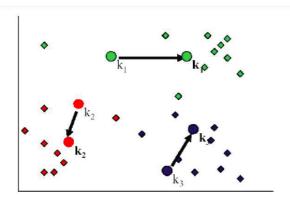


k= 3 centroides: k1, k2, k3

k-means algorithm: assignment/distribution step according to the distances....

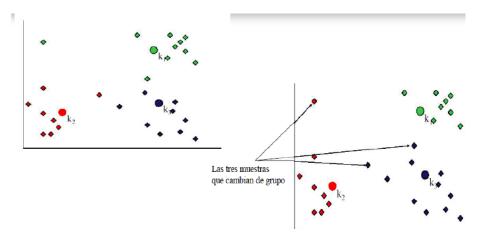


Se asigna cada muestra al centroide más cercano. Cada color representa un *cluster* distinto. k-means algorithm: moving step according to the means of the assigned samples...



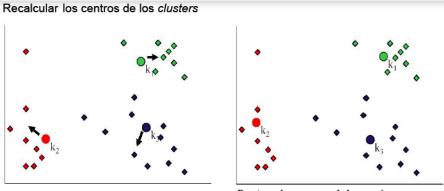
Se recalcula la posición de cada centroide como el promedio de las muestras/observaciones/ejemplos de cada *cluster*.

k-means algorithm: again, assign ...



Se reasignan las muestras al centroide más cercano

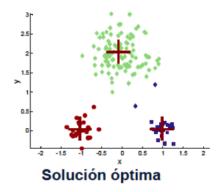
k-means algorithm: and move... and repeat...

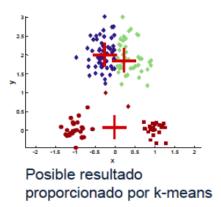


Reasignar las muestras al cluster más cercano ...

El criterio para detener el algoritmo puede ser un número máximo de iteraciones, la estabilización en la posición de los centroides, ...

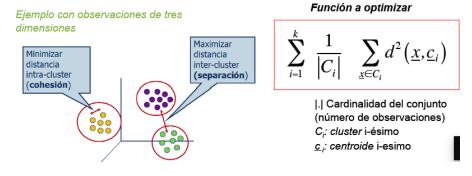
Possible results





Are we minimizing a cost function? Yes... We are minimizing the sum of the distances "inside each cluster"

Al considerar la distancia Euclídea y la media aritmética, se está **minimizando** la **variación** *intra-cluster*. Esta medida se usa, por tanto, como criterio del grado de ajuste (cohesión y separación) de los centroides.



Relationship with density estimation

We are minimizing the sum of the distances "inside each cluster"

This is related to density estimation, and variances (of components within a mixture of densities)....

It is can be shows that we are looking for a "good" mixture of Gaussians describing the data....

"Variance" inside the cluster

If the distance is Euclidean, we are minimizing the "variance" inside the cluster.

"... the basic idea behind partitioning methods, such as k-means clustering, is to define clusters such that the total intra-cluster variation (or total within-cluster sum of square) is minimized." "Variance" inside the cluster

If the distance is Euclidean, we are minimizing the "variance" inside the cluster.

j-th centroid \mathbf{c}_j of the *j*-th cluster C_j , then we want to minimize

 $\operatorname{Var}[\mathbf{x} \in C_j] = \operatorname{variance} \text{ inside } C_j \approx \frac{1}{|C_j|} \sum_{i \in C_j} ||\mathbf{x}_i - \mathbf{c}_j||^2.$

"Law of Total Variance"....

Clear the mean of all the centroids is the mean of the data

$$\begin{split} \mu &= \frac{1}{k} \sum_{j=1}^{k} \mathbf{c}_{j} = \frac{1}{k} \sum_{j=1}^{k} \left(\frac{1}{|C_{j}|} \sum_{i \in C_{j}} \mathbf{x}_{i} \right), \\ &= \frac{1}{N} \sum_{i=1}^{M} \mathbf{x}_{i}, \end{split}$$

Law of Total Variance:

$$Var[\mathbf{x}] = \left(\sum_{j=1}^{k} Var[inside the cluster C_j]\right) + Var[of "centroids"],$$
$$= \sum_{j=1}^{k} \underbrace{Var[\mathbf{x} \in C_j]}_{internal} + \underbrace{\sum_{j=1}^{k} ||\mathbf{c}_j - \boldsymbol{\mu}||^2}_{among the centroids}$$

"Law of Total Variance" as a consequence:

$$\mathsf{Var}[\mathbf{x}] \geq \sum_{j=1}^k \mathsf{Var}[\mathbf{x} \in \mathit{C}_j]$$

and it is also valid for the approximations:

$$rac{1}{N}\sum_{i=1}^{N}||\mathbf{x}_i-oldsymbol{\mu}||^2\geq \sum_{j=1}^k\left(rac{1}{|\mathit{C}_j|}\sum_{i\in \mathit{C}_j}||\mathbf{x}_i-\mathbf{c}_j||^2
ight)$$

Recall that

$$\boldsymbol{\mu} = \frac{1}{k} \sum_{j=1}^{k} \mathbf{c}_{j} = \frac{1}{k} \sum_{j=1}^{k} \left(\frac{1}{|C_{j}|} \sum_{i \in C_{j}} \mathbf{x}_{i} \right)$$

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as k grows...

Considering that k grows approaching N:

$$\sum_{j=1}^k \mathsf{Var}[\mathbf{x} \in \mathit{C}_j]
ightarrow \mathsf{0},$$

and

$$\sum_{j=1}^k ||\mathbf{c}_j - \boldsymbol{\mu}||^2
ightarrow \mathsf{Var}[\mathbf{x}].$$

When k = N (with a proper clustering: each data is a cluster),

$$\sum_{j=1}^{k} \operatorname{Var}[\mathbf{x} \in C_j] = 0, \quad \sum_{j=1}^{k} ||\mathbf{c}_j - \boldsymbol{\mu}||^2 = \operatorname{Var}[\mathbf{x}].$$

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when k = 1...

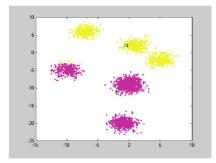
When k = 1: all the data in one unique cluster,

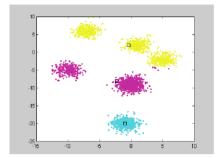
$$\sum_{j=1}^{k} \operatorname{Var}[\mathbf{x} \in C_j] = \operatorname{Var}[\mathbf{x} \in C_1] = \operatorname{Var}[\mathbf{x}],$$
$$\sum_{j=1}^{k} ||\mathbf{c}_j - \boldsymbol{\mu}||^2 = ||\mathbf{c}_1 - \boldsymbol{\mu}||^2 = 0.$$

The *k*-means algorithm is a parametric method

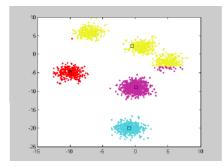
- Note that the k-means algorithm is a parametric method.
- We fix k and then decide....

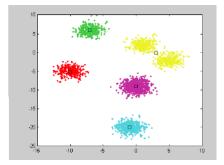
How many clusters? starting with k = 2 and then increase k...





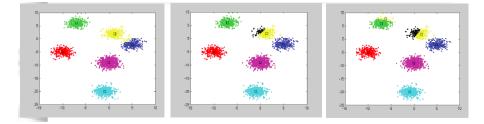
How many clusters? starting with k = 2 and then increase k...





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How many clusters? starting with k = 2 and then increase k...



and then use some criterium for the "optimal performance"...

Note that

$1 \leq k \leq N$

With k = N, each data is a cluster.... (k = 1 could/should be underfitting) (k = N could/should be overfitting)

However, in this unsupervised case, it is not "easy", straightforward, to apply Cross-Validation (CV)

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and then use some criterium for the "optimal performance"...

- We could use "marginal likelihood with probabilistic approaches....."
- Now we will see two methods:
 - Elbow method + AIC (Akaike information criterion)
 - Silhouette method

Elbow method + AIC (for deciding k...)

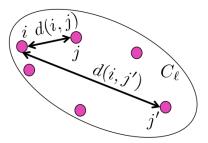
Find k^* which minimizes the following cost function

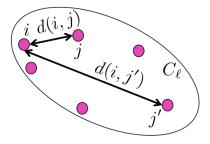
$$\mathsf{Cost}(k) = \sum_{j=1}^{k} \mathsf{Var}[\mathbf{x} \in C_j] + k$$
$$\mathsf{Cost}(k) = \sum_{\substack{j=1 \\ \text{fitting}}}^{k} \mathsf{Var}[\mathbf{x} \in C_j] + \underbrace{k}_{\texttt{model penalty (AIC)}}$$

When k grows: the first term $\sum_{j=1}^{k} \text{Var}[\mathbf{x} \in C_j]$ decreases, and the model penalty grows (k)

- Consider the ℓ -th cluster C_{ℓ} .
- ▶ For each *i*-th point in the ℓ -th cluster C_{ℓ} , then
 - $i = 1, ..., |C_{\ell}|$, we compute

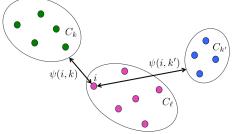
$$\mathsf{a}(i) = rac{1}{|\mathcal{C}_\ell| - 1} \sum_{j \in \mathcal{C}_\ell; j
eq i} \mathsf{d}(i, j).$$





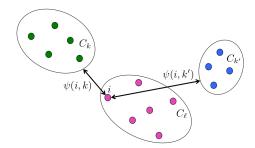
- a(i) measures how dissimilar is i-th data to its own cluster....
- ▶ high a(i) ==> great dissimilarity

For each *i*-th point in the ℓ -th cluster C_{ℓ} , then $i = 1, ..., |C_{\ell}|$, we also compute $\psi(i, k) = \frac{1}{|C_k|} \sum_{j \in C_k} d(i, j)$, with $k \neq \ell$. $b(i) = \min_k \psi(i, k)$, with $k \neq \ell$.



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high b(i) ==> the other clusters are different and do not explain the *i*-th data; the *i*-th data is not similar to other cluster

We now define a silhouette (value) of one data point i

$$s(i) = rac{b(i)-a(i)}{\max\{a(i),b(i)\}}$$
, if $|C_i|>1$

and

s(i)=0, if $|C_i|=1$

Which can be also written as:

$$s(i) = egin{cases} 1-a(i)/b(i), & ext{if}\ a(i) < b(i) \ 0, & ext{if}\ a(i) = b(i) \ b(i)/a(i) - 1, & ext{if}\ a(i) > b(i) \end{cases}$$

From the above definition it is clear that

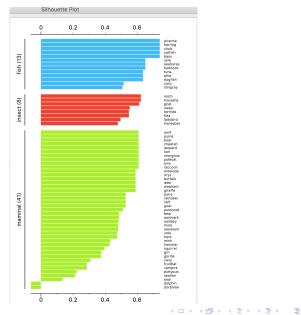
$$-1 \leq s(i) \leq 1$$

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Also, note that score is 0 for clusters with size = 1. This constraint is added to prevent the number of clusters from increasing significantly.

For s(i) to be close to 1 we require $a(i) \ll b(i)$. As a(i) is a measure of how dissimilar i is to its own cluster, a small value means it is well matched. Furthermore, a large b(i) implies that i is badly matched to its neighbouring cluster. Thus an s(i) close to one means that the data is appropriately clustered. If s(i) is close to negative one, then by the same logic we see that i would be more appropriate if it was clustered in its neighbouring cluster. An s(i) near zero means that the datum is on the border of two natural clusters.

- ▶ $s(i) \approx 1$ then the *i*-th data has been properly clustered.
- ► s(i) ≈ 0 then the i-th data could belong to different clusters....
- ► s(i) ≈ −1 then the i-th data should belong to another cluster....



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Consider the mean s(i) inside one cluster C_{ℓ} ,

$$ar{s}_\ell = rac{1}{|\mathcal{C}_\ell|} \sum_{i \in |\mathcal{C}_\ell|} s(i).$$

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if \bar{s}_{ℓ} is high ==> the points in the cluster are well-grouped (i punti del cluster C_{ℓ} sono effettivamente simili tra loro)

Consider now the mean of s(i) over all the clusters,

$$\begin{split} \widetilde{s}(k) &= \frac{1}{k} \sum_{\ell=1}^{k} \overline{s}_{\ell} = \frac{1}{k} \sum_{\ell=1}^{k} \left(\frac{1}{|C_{\ell}|} \sum_{i \in |C_{\ell}|} s(i) \right) \\ &= \frac{1}{N} \sum_{i=1}^{N} s(i), \end{split}$$

is a measure of how our clustering is "good".

Note that $\tilde{s}(k)$ depends on the number of clusters that we choose at the beginning.

Choose the number of clusters such that

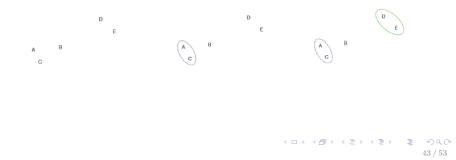
 $k^* = \arg \max_k \widetilde{s}(k).$

Recall that $\tilde{s}(k)$ represents the mean of the s(i) over all the data of the entire dataset for a specific number of clusters k.

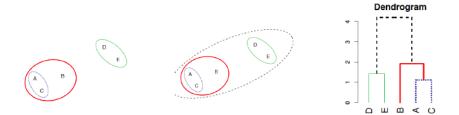
(agglomerative) Hierarchical clustering

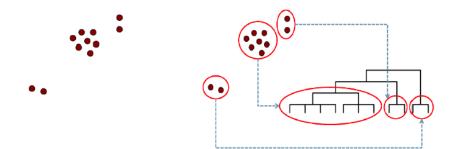
we always consider the two closest "clusters" or "super-clusters".

Hierarchical clustering starts by treating each observation as a separate cluster. Then, it repeatedly executes the following two steps: (1) identify the two clusters that are closest together, and (2) merge the two most similar clusters. This iterative process continues until all the clusters are merged together. This is illustrated in the diagrams below.

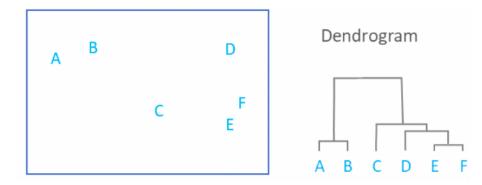


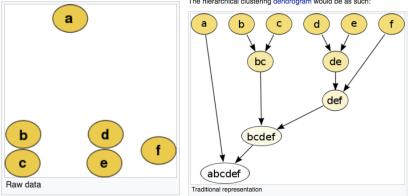
different resolutions....





The main output of Hierarchical Clustering is a *dendrogram*, which shows the hierarchical relationship between the clusters:



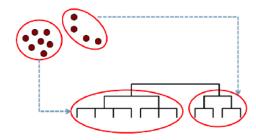


The hierarchical clustering dendrogram would be as such:

Agglomerative versus divisive algorithms

Hierarchical clustering typically works by sequentially merging similar clusters, as shown above. This is known as *agglomerative hierarchical clustering*. In theory, it can also be done by initially grouping all the observations into one cluster, and then successively splitting these clusters. This is known as *divisive hierarchical clustering*. Divisive clustering is rarely done in practice.



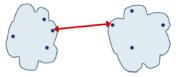




How do you consider a "distance" between clusters? (linkage)

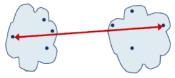
Single-link

Mínima distancia/disimilitud inter-cluster



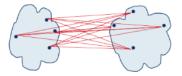
Complete-link

Máxima distancia/disimilitud inter-cluster



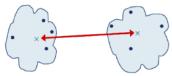
Average

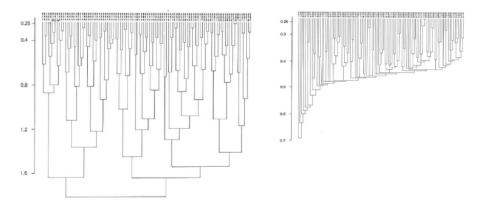
Distancia/disimilitud media inter-cluster

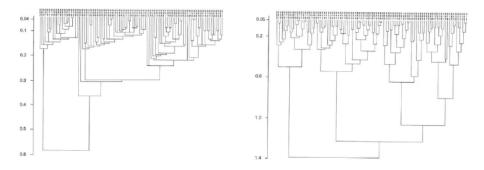


Centroids

Disimilitud o distancia entre centroides







(ロ)
 (日)
 (日)

Better with non-convex stuffs....

