

Objectives



Learn

- 1. The basic concept of cluster analysis
- 2. Popular clustering algorithms
 - Core idea
 - Determining the number of clusters
 - Visualization







Basic concept of cluster analysis



- Goal: Group observations into clusters such that those in the same cluster are more "similar" than those of other clusters.
- Reduction in number of rows
- No distinction between dependent and independent variables.
- What exactly constitutes a cluster is not clear and many different concepts exist.
- We are going to discuss two popular concepts:
 - Centroid based: K-Means
 - Connectivity based: Hierarchical clustering





K-Means



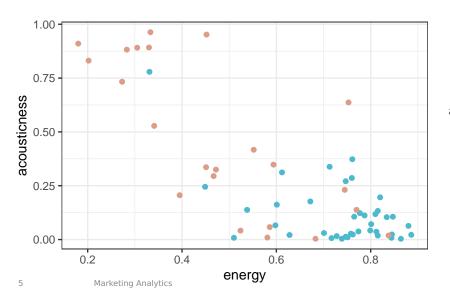
- Assigns each observation to one of K clusters.
- Iterative procedure repeated until cluster assignments no longer change:
 - 1. Assign each observation to the cluster with the closest mean
 - Re-calculate the cluster means taking into account the changed assignments
- The number of clusters K is a priori unclear (more later)





A first example





artist

- Adele
- Robin Schulz

A first example



- Example: two artists and two variables, K = 2.
- Important: scale all variables before clustering to ensure equal contribution to distance

```
tracks_scale <- data.frame(
   artist = example_tracks$artist,
   energy = scale(example_tracks$energy),
   acousticness = scale(example_tracks$acousticness))
kmeans_clusters <- kmeans(tracks_scale[-1], 2)
kmeans_clusters$centers</pre>
```

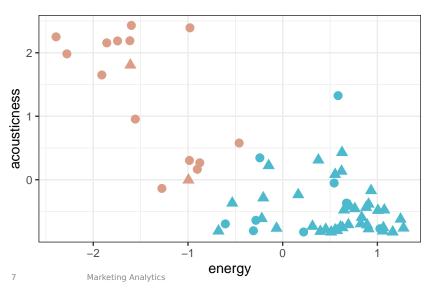






A first example





artist

- Adele
- ▲ Robin Schulz

cluster

- 1
- 2

Choosing the number of clusters



- If we extend the sample to the more interesting case of multiple artists the optimal K is unclear
- We can calculate varying indices for the optimal K and use the one that is optimal for the most indices
- In this case 3 is the best number of clusters according to the majority rule, chosen by 13 indices

```
library(NbClust)
opt_K <- NbClust(famous_tracks_scale,</pre>
                  method = "kmeans", max.nc = 10)
```

```
table(opt_K$Best.nc["Number_clusters", ])
```







Extended example



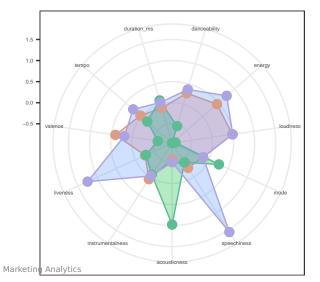
```
kmeans_tracks <- kmeans(famous_tracks_scale, 3)
kmeans_tracks$centers</pre>
```

```
danceability
                       loudness
                                       mode speechiness
             energy
  0.2758301 0.4526214 0.4853302 -0.1461378
                                             -0.2576401
                                             -0.4147683
 -0.5385548 -0.9566495 -0.8742383
                                  0.2632910
  0.3678342 0.7543900
                       0.4954862 -0.1492974 1.5546155
acousticness instrumentalness
                              liveness
                                          valence
  -0.5618965
                  0.06266324 -0.2524251 0.4012080
0.9772843
                 -0.06816719 -0.2728148 -0.6158085
  -0.5015270
                 -0.02849344 1.2469257
                                        0.1885188
     tempo duration_ms
0.03789976 -0.09047459
-0.17761023 0.09754255
0.26482862 0.04295692
```

Extended example



Characterize clusters





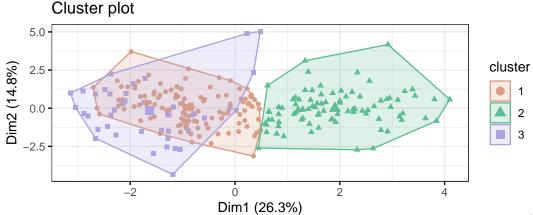




2D-Visualization



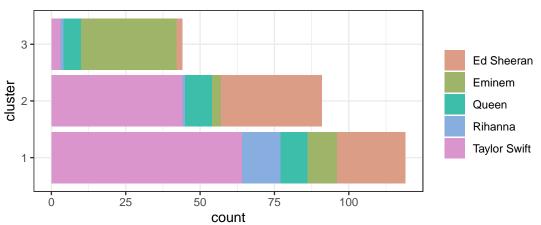
- Reduce dimensions with PCA and plot 2 components
- Gives a partial picture



Extended example



Characterize artists







Making a recommendation



Given a liked song, recommend songs in the same cluster

famous_tracks[famous_tracks\$trackName=="The Archer","cluster"]

[1] 2 Levels: 1 2 3

trackName	artistName	cluster
Bohemian Rhapsody - Remastered 2011 Photograph The A Team I See Fire - From "The Hobbit - The Desolation Of Smaug" Give Me Love Tenerife Sea	La Silectail	2 2 2

Hierarchical clustering

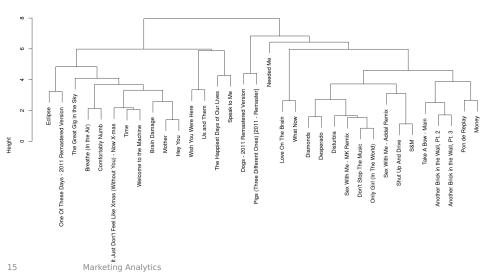


- Idea: similar observations can be "merged" to one cluster
- Starts out merging pairs of the most similar or closest observations
- Iteratively merges the most similar clusters until there is only one cluster left
- Does not require a priori setting of the number of clusters
- Number of clusters is determined post-hoc by "cutting-off" at some iteration

Visualization



Cluster Dendrogram



Example



- Calculate distances between observations (default: Euclidean) using dist
- Use distances in hclust to perform a hierarchical cluster analysis

```
hclust_tracks <- hclust(dist(pf_ri_scale))
hclust_tracks</pre>
```

```
Call:
hclust(d = dist(pf_ri_scale))
```

Cluster method : complete
Distance : euclidean

Number of objects: 34







Characterize clusters



- Decide on cut-off based on dendrogram. Specify the desired number of clusters using cutree.
- Calculate summary statistics for cluster

```
hclusters <- cutree(hclust_tracks,4)
pf_ri_hier <- data.frame(pf_ri_scale)</pre>
pf_ri_hier$cluster <- as.factor(hclusters)</pre>
aggregate(. ~ cluster, pf_ri_hier, mean)[,1:5]
```

```
cluster danceability
                                    loudness
                                                   mode
                           energy
             0.6301558 -0.8423205
                                   0.4931387 -1.1087884
             0.6793570 0.7636001
                                   0.6540518 -0.2407238
3
            -0.6149044 -0.7835601
                                  -0.7125465
                                              0.4785297
            -1.1381509 0.1890603 -0.1348845 -1.1087884
```