About the method - cluster\_pam: Partitioning Around Medoids. Similar to k-means but uses medoids (real points) instead of centroids, making it more robust to outliers.

# Clustering - pam  
  
# installation   
#install.packages("daltoolbox")  
  
# loading DAL  
library(daltoolbox)

Load data (iris).

# loading dataset  
data(iris)

Configure PAM with k=3.

# clustering method configuration  
model <- cluster\_pam(k=3)

Fit and generate cluster labels.

# model fitting and labeling  
model <- fit(model, iris[,1:4])  
clu <- cluster(model, iris[,1:4])  
table(clu)

## clu  
## 1 2 3   
## 50 62 38

External evaluation using Species.

# evaluate model using external metric  
eval <- evaluate(model, clu, iris$Species)  
eval

## $clusters\_entropy  
## # A tibble: 3 × 4  
## x ce qtd ceg  
## <fct> <dbl> <int> <dbl>  
## 1 1 0 50 0   
## 2 2 0.771 62 0.319   
## 3 3 0.297 38 0.0754  
##   
## $clustering\_entropy  
## [1] 0.3938863  
##   
## $data\_entropy  
## [1] 1.584963

References - Kaufman, L. and Rousseeuw, P. J. (1990). Finding Groups in Data: An Introduction to Cluster Analysis.