GMMHC

Description

The function provides a clustering method combining the agglomerative hierarchical clustering method and the Gaussian mixture model.

Usage

```
GMMHC(X_array, ks, min.nc=2, max.nc=15, maxiter = 100,
                distance = "euclidean", method="average",index_nb = "kl")
```

Arguments

X_array	a 3-d array
ks	the range of number of clusters for gaussian mixture model
min.nc	minimal number of clusters for NbClust
max.nc	maximal number of clusters for NbClust
maxiter	the maximal steps for solving the gaussian mixture model with EM algorithm
distance	parameter for NbClust. The distance measure to be used to compute the dissimilarity matrix. This must be one of: "euclidean", "maximum", "manhattan", "canberra", "binary", "minkowski" or "NULL". By default, distance="euclidean". If the distance is "NULL", the dissimilarity matrix (diss) should be given by the user. If distance is not "NULL", the dissimilarity matrix should be "NULL".
method	parameter for NbClust. The cluster analysis method to be used. This should be one of: "ward.D", "ward.D2", "single", "complete", "average", "mcquitty", "median", "centroid", "kmeans".
index_nb	parameter for NbClust. The index to be calculated. This should be one of : "kl", "ch", "hartigan", "ccc", "scott", "marriot", "trcow", "tracew", "friedman", "rubin", "cindex", "db", "silhouette", "duda", "pseudot2", "beale", "ratkowsky", "ball", "ptbiserial", "gap", "frey", "mcclain", "gamma", "gplus", "tau", "dunn", "hubert", "sdindex", "dindex", "sdbw", "all" (all indices except GAP, Gamma, Gplus and Tau), "alllong" (all indices with Gap, Gamma, Gplus and Tau included).

Value

best_num	the best number of clusters
class_est	partition that corresponds to the best number of clusters