Package ‘WeightedCluster’

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Author Matthias Studer [aut, cre]
Maintainer Matthias Studer <matthias.studer@unige.ch>
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Description Clusters state sequences and weighted data. It provides an optimized weighted PAM algorithm as well as functions for aggregating replicated cases, computing cluster quality measures for a range of clustering solutions and plotting (fuzzy) clusters of state sequences. Parametric bootstraps methods to validate typology of sequences are also provided.

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R topics documented:

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Build a clustrange object to compare different clustering solutions.

**Usage**

```r
as.clustrange(object, diss, weights=NULL, R=1, samplesize=NULL, ...)
```

## S3 method for class 'twins'
```
as.clustrange(object, diss, weights=NULL, R=1, samplesize=NULL, 
ncluster=20, ...)
```

## S3 method for class 'hclust'
```
as.clustrange(object, diss, weights=NULL, R=1, samplesize=NULL, 
ncluster=20, ...)
```

## S3 method for class 'dtclust'
```
as.clustrange(object, diss, weights=NULL, R=1, samplesize=NULL, 
ncluster=20, labels=TRUE, ...)
```

## S3 method for class 'clustrange'
```
plot(x, stat="noCH", legendpos="bottomright", 
norm="none", withlegend=TRUE, lwd=1, col=NULL, ylab="Indicators", 
xlab="N clusters", conf.int=0.9, ci.method="none", ci.alpha=.3, line="t0", ...)
```

**Arguments**

- **object**: The object to convert such as a data.frame.
- **diss**: A dissimilarity matrix or a dist object (see `dist`).
- **weights**: Optional numerical vector containing weights.
- **R**: Optional number of bootstrap that can be used to build confidence intervals.
- **samplesize**: Size of bootstrap sample. Default to sum of weights.
- **ncluster**: Integer. Maximum number of cluster. The range will include all clustering solution starting from two to ncluster.
- **labels**: Logical. If TRUE, rules to assign an object to a sequence is used to label the cluster (instead of a number).
- **x**: A clustrange object to be plotted.
as.clustrange

stat Character. The list of statistics to plot or "noCH" to plot all statistics except "CH" and "CHsq" or "all" for all statistics. See wcClusterQuality for a list of possible values. It is also possible to use "RHC" to plot the quality measure 1-HC. Unlike HC, RHC should be maximized as all other quality measures.

legendpos Character. legend position, see legend.
	norm Character. Normalization method of the statistics can be one of "none" (no normalization), "range" (given as (value -min)/(max-min)), "zscore" (adjusted by mean and standard deviation) or "zscoremed" (adjusted by median and median of the difference to the median).

withlegend Logical. If FALSE, the legend is not plotted.

lwd Numeric. Line width, see par.

col A vector of line colors, see par. If NULL, a default set of color is used.

xlab x axis label.

ylab y axis label.

conf.int Confidence to build the confidence interval (default: 0.9).

ci.method Method used to build the confidence interval (only if bootstrap has been used, see R above). One of "none" (do not plot confidence interval), "norm" (based on normal approximation), "perc" (based on percentile).

ci.alpha alpha color value used to plot the interval.

line Which value should be plotted by the line? One of "t0" (value for actual sample), "mean" (average over all bootstraps), "median" (median over all bootstraps).

... Additionnal parameters passed to/from methods.

Details

as.clustrange convert objects to clustrange objects. clustrange objects contains a list of clustering solution with associated statistics and can be used to find the optimal clustering solution.

If object is a data.frame or a matrix, each column should be a clustering solution to be evaluated.

If object is an hclust or twins objects (i.e. hierarchical clustering output, see hclust, diana or agnes), the function compute all clustering solution ranging from two to ncluster and compute the associated statistics.

Value

An object of class clustrange with the following elements:

clustering: A data.frame of all clustering solutions.

stats: A matrix containing the clustering statistics of each cluster solution.

See Also

See also wcKMedRange, wcClusterQuality.
Examples

data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)

## Compute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")

## Ward clustering
wardCluster <- hclust(as.dist(diss), method="ward", members=aggMvad$aggWeights)

## Computing clustrange from Ward clustering
wardRange <- as.clustrange(wardCluster, diss=diss,
weights=aggMvad$aggWeights, ncluster=15)

## Plot all statistics (standardized)
plot(wardRange, stat="all", norm="zscoremed", lwd=3)

## Plot HC, RHC and ASW
plot(wardRange, stat=c("HC", "RHC", "ASWw"), norm="zscore", lwd=3)

---

as.seqtree

Convert a hierarchical clustering object to a seqtree object.

Description

Convert a hierarchical clustering object to a seqtree object which can then be displayed using seqtreedisplay.

Usage

as.seqtree(object, seqdata, diss, weighted=TRUE, ...)

## S3 method for class 'twins'
as.seqtree(object, seqdata, diss, weighted=TRUE, ncluster, ...)

## S3 method for class 'hclust'
as.seqtree(object, seqdata, diss, weighted=TRUE, ncluster, ...)

Arguments

- **object**: An object to be converted to a seqtree.
- **seqdata**: State sequence object.
- **diss**: A dissimilarity matrix or a dist object (see dist)
- **weighted**: Logical. If TRUE, weights of the seqdata object are taken to build the tree.
fuzzyseqplot

Parameters

ncluster Maximum number of cluster. The tree will be builded until this number of cluster.

... Additional parameters passed to/from methods.

Details

By default as.seqtree try to convert the object to a data.frame assuming that it contains a list of nested clustering solutions. Be aware that seqtree and as.seqtree only support binary splits.

If object is an hclust or twins objects (i.e. hierarchical clustering output, see hclust, diana or agnes), the function returns a seqtree object reproducing the agglomerative schedule.

Value

A seqtree object.

Examples

data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)

## Compute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")

## Ward clustering
wardCluster <- hclust(as.dist(diss), method="ward", members=aggMvad$weight)

st <- as.seqtree(wardCluster, seqdata=mvad.seq, diss=diss, weighted=TRUE, ncluster=10)
print(st)

## You typically want to run (You need to install GraphViz before)
## seqtreedisplay(st, type="d", border=NA)

fuzzyseqplot

Plot sequences according to a fuzzy clustering.

Description

This function propose a graphical representation of a fuzzy clustering results where sequences are weighted according to their cluster membership strength.

Usage

fuzzyseqplot(seqdata, group = NULL, membership.threashold = 0, type = "i", members.weighted = TRUE, memb.exp = 1, ...)

Arguments

seqdata  State sequence object created with the seqdef function.
group  A fuzzy partition of the data, either as a membership matrix or as a fanny object.
membership.threashold  Numeric. Minimum membership strength to be included in plots.
type  the type of the plot. Available types are "d" for state distribution plots (chrono-
grams), "f" for sequence frequency plots, "i" for selected sequence index plots,
"I" for whole set index plots, "ms" for plotting the sequence of modal states,
"mt" for mean times plots, "pc" for parallel coordinate plots and "r" for rep-
resentative sequence plots.
members.weighted  Logical. Should the sequences be weighted by their membership strength in
each group before being plotted?
memb.exp  Optional. Fuzzyness parameter used in the fanny algorithm.
...  arguments to be passed to seqplot.

Details

The dataset is augmented by repeating the sequence $s_i$ of individual $i$ $k$ times (i.e., once per cluster). We therefore have $k$ sequences for individual $i$, denoted as $s_{i1}...s_{ik}$. These sequences are therefore weighted according to their membership degree $u_{i1}...u_{ik}$. Hence, even if the same sequence were repeated $k$ times, its total weight sum to 1. An additional categorical covariate is created in this augmented dataset that specifies the cluster (ranging from 1 to $k$) of the associated membership degree. This weighting strategy allows us to use any tools available for weighted sequence data (see seqplot).

For index plots, we additionally suggest ordering the sequences according to membership degree by setting sortv="membership" (see example). The most typical sequence lies at the top of the subfigures, with a high membership degree; meanwhile, the bottom shows less-characteristic patterns. Restricting to sequences with the highest membership degree can be achieved with the membership.threashold argument.

References


See Also

See also fanny for fuzzy clustering.

Examples

data(mvad)
mvad.seq <- seqdef(mvad[1:100, 17:86])

## Compute distance using Hamming distance
seqclustname <- Automatic labeling of cluster using sequence medoids

Description
This function automatically name the cluster using the sequence medoid of each cluster.

Usage
seqclustname(seqdata, group, diss, weighted = TRUE, perc = FALSE)

Arguments
seqdata State sequence object (see seqdef).
group A vector of clustering membership.
diss a dissimilarity matrix or a dist object.
weighted Logical. If TRUE, weights of the seqdata object are taken to find the medoids.
perc Logical. If TRUE, the percentage of sequences in each cluster is added to the label of each group.

Value
A factor of clustering membership. The labels are defined using sequences medoids and optionally percentage of case in each cluster.

Examples
data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)

## Computing Hamming distance between sequence
diss <- seqdist(mvad.seq, method="HAM")

## KMedoids using PAMonce method (clustering only)
clust5 <- wcKMedoids(diss, k=5, weights=aggMvad$aggWeights)

clust5.labels <- seqclustname(mvad.seq, clust5$clustering, diss=diss, perc=TRUE)
seqdplot(mvad.seq, group=clust5.labels)
seqnull

Generate nonclustered sequence data according to different null models.

Description

This function generates sequence data that is similar to the original sequence data, but nonclustered on specific aspects related to the sequencing, timing or time spend in the different states. The function is typically used by only specifying a model among "combined", "duration", "sequencing", "stateindep" or "Markov". The "userpos" model allows to fully specify a sequence generating model using a starting distribution and a transition rate matrix.

Usage

seqnull(seqdata, model = c("combined", "duration", "sequencing", "stateindep", "Markov", "userpos"), imp.trans = NULL, imp.trans.limit = -1, trate = "trate", begin = "freq", time.varying = TRUE, weighted = TRUE)

Arguments

seqdata State sequence object of class stslist. The sequence data to use. Use seqdef to create such an object.

model String. The model used to generate the nonclustered data. It can be one of "combined", "duration", "sequencing", "stateindep", "Markov" or "userpos". See the Details section.

imp.trans Optional named character vector listing impossible transitions. Names indicates starting states, while value destinations. Only used for "combined", "duration" and "sequencing" models.

imp.trans.limit Numeric. Optional. All transitions with a transition rates below (or equal) this value are considered impossible. Only used for "combined", "duration" and "sequencing" models.

trate String, matrix or array. Only used to specify the "userpos" model. It can be either a method to compute the time-varying transition rates, a matrix of transition rates used for all time points, or a time-varying transition rates matrix specified as an array. String values "freq" to use state distribution or "trate" to use transition rates.

begin String or vector. Only used to specify the "userpos" model. Either a vector of probability for the first state in the sequence, or a method to compute it. String values "freq" to use state distribution at first time point or "ofreq" to use the overall (time-independent) state distribution.

time.varying Logical. If TRUE, the state distribution or the transition rate specified by the trate argument (using a string) are computed separately for each time point.

weighted Logical. If TRUE, state distribution and transition rates are computed using the weights specified in seqdata.
Details

This function generates sequence data that is similar to the original sequence data, but nonclustered on specific aspects related to the sequencing, timing or time spend in the different states. The function is typically used by only specifying a model among "combined", "duration", "sequencing", "stateindep" or "Markov". The models are shortly described below. More information about their usefulness can be found in Studer (2021) (see below).

The "combined", "duration" and "sequencing" models generate sequence in spell format, by generating a vector of state and their attached durations. The "combined" model generate random sequencing and duration. The "duration" model only randomizes duration, while keeping the original sequencing of the states found in the data. Finally, the "sequencing" only randomizes the sequencing of the states and keep the time spent in a state as found in the data.

The "stateindep" model generate sequence by randomly selecting a state at each time point without taking into account the previous one. It can generate highly unlikely sequence because it doesn’t account for coherence of trajectories over time.

The "Markov" model use a time-invariant (homogeneous) transition rate matrix to generate the sequences. It can reveals difference in the timing of transitions.

Value

A state sequence object of class stslist.

References


See Also

See Also seqnullcqi.

Examples

data(biofam)
bf.seq <- seqdef(biofam[1:200,10:25])

#Plot the sequences generated by different null models.
seqdplot(seqnull(bf.seq, model="combined"))
seqdplot(seqnull(bf.seq, model="duration"))
seqdplot(seqnull(bf.seq, model="sequencing"))
seqdplot(seqnull(bf.seq, model="stateindep"))
seqdplot(seqnull(bf.seq, model="Markov"))
Sequencing Analysis Typologies Validation Using Parametric Bootstrap

Description

seqnullcqi implements the methodology proposed by Studer (2021) for the validation of sequence analysis typologies using parametric bootstraps. The method works by comparing the cluster quality of an observed typology with the quality obtained by clustering similar but nonclustered data. Several models to test the different structuring aspects of the sequences important in life-course research, namely, sequencing, timing, and duration (see function seqnull). This strategy allows identifying the key structural aspects captured by the observed typology. Plot and print methods of the seqnullcqi results are also provide.

Usage

seqnullcqi(seqdata, clustrange, R, model=c("combined", "duration", "sequencing", "stateindep", "Markov", "userpos"), seqdist.args=list(), kmedoid = FALSE, hclust.method="ward.D", ...)

## S3 method for class 'seqnullcqi'
plot(x, stat, type = c("line", "density", "boxplot", "seqdplot"), quant = 0.95, norm = TRUE, legendpos = "topright", alpha = 0.2, ...)

## S3 method for class 'seqnullcqi'
print(x, norm=TRUE, quant=0.95, digits=2, ...)

Arguments

- seqdata: State sequence object of class stslist. The sequence data to use. Use seqdef to create such an object.
- clustrange: The clustering of the data to be validated as an object of class clustrange. See as.clustrange or wcKMedRange to create such an object.
- model: String. The model used to generate the similar but nonclustered data. It can be one of "combined", "duration", "sequencing", "stateindep", "Markov" or "userpos". See seqnull for more information.
- R: The number of bootstraps.
- seqdist.args: List of arguments passed to seqdist for computing the distances.
- kmedoid: Logical. If TRUE, the PAM algorithm is used to cluster the data using wcKMedRange. If FALSE, hclust is used.
- x: A seqnullcqi object to be plotted or printed.
- stat: Character. The statistic to plot or "all" for all statistics. See wcClusterQuality for a list of possible values.
The `seqnullcqi` function provides a validation method for sequence analysis typologies using parametric bootstraps as proposed in Studer (2021). This method works by comparing the value of the cluster quality of an observed typology with the cluster quality obtained by clustering similar but nonclustered data. More precisely it works as follows.

1. Cluster the observed sequence data and compute the associated cluster quality indices.
2. Repeat R times:
   (a) Generate similar but nonclustered data using a null model (see `seqnull` for available null models).
   (b) Cluster the generated data using the same distance measure and clustering algorithm as in step 1.
   (c) Record the quality indices values of this null clustering.
3. Compare the quality of the observed typology with the one obtained in the R bootstraps with the null sequence data using plot and print methods.
4. If the cluster quality measure of the observed typology is constantly higher than the ones obtained with null data, a “good” typology has been found.

Several null models are provided to test the different structuring aspects of the sequences important in life-course research, namely, sequencing, timing, and duration (see function `seqnull` and Studer, 2021). This strategy allows identifying the key structural aspects captured by the observed typology.

**Value**

`seqnullcqi` returns a "seqnullcqi" object with the following components:

- **seqdata**
  The sequence data generated by the null model (see `seqnull`)

- **stats**
  The cluster quality indices for the null data.

- **clustrange**
  The clustering of the data to be validated as an object of class clustrange.
The number of bootstraps

Logical. If TRUE, the PAM algorithm was used to cluster the data using \texttt{wcKMedRange}.

Hierarchical method to used with \texttt{hclust}.

List of arguments passed to \texttt{seqdist} for computing the distances.

List of arguments passed to \texttt{seqnull} to generate the sequence data under the null model.


See Also

See Also \texttt{seqnull} for description of the null models.

Examples

```r
data(biofam)

## Create the sequence object
bf.seq <- seqdef(biofam[sample.int(nrow(biofam), 100), 10:25])

## Library fastcluster greatly improve computation time when using hclust
# library(fastcluster)
## Computing distances
diss <- seqdist(bf.seq, method="HAM")
## Hierarchical clustering
hc <- hclust(as.dist(diss), method="ward.D")
# Computing cluster quality measures.
clustqual <- as.clustrange(hc, diss=diss, ncluster=7)

# Compute cluster quality measure for the null model "combined"
# seqdist.args should be the same as for seqdist above except the sequence data.
# Clustering methods should be the same as above.
bcq <- seqnullcqi(bf.seq, clustqual, R=10, model=c("combined"),
seqdist.args=list(method="HAM"),
hclust.method="ward.D")

# Print the results
bcq

# Different kind of plots
plot(bcq, stat="ASW", type="line")
plot(bcq, stat="ASW", type="density")
plot(bcq, stat="ASW", type="boxplot")
```
seqpropclust

Monothetic clustering of state sequences

Description

Monothetic divisive clustering of the data using object properties. For state sequences object different set of properties are automatically extracted.

Usage

seqpropclust(seqdata, diss, properties = c("state", "duration", "spell.age", "spell.dur", "transition", "pattern", "AFtransition", "AFpattern", "Complexity"), other.prop = NULL, prop.only = FALSE, pmin.support = 0.05, max.k = -1, with.missing = TRUE, R = 1, weight.permutation = "diss", min.size = 0.01, max.depth = 5, maxcluster = NULL, ...)

wcPropertyClustering(diss, properties, maxcluster = NULL, ...)
dtcut(st, k, labels = TRUE)

Arguments

seqdata State sequence object (see seqdef).
diss a dissimilarity matrix or a dist object.
properties Character or data.frame. In seqpropclust, it can be a list of properties to be extracted from seqdata. It can also be a data.frame specifying the properties to use for the clustering.
other.prop data.frame. Additional properties to be considered to cluster the sequences.
prop.only Logical. If TRUE, the function returns a data.frame containing the extracted properties (without clustering the data).
pmin.support Numeric. Minimum support (as a proportion of sequences). See seqefsub.
max.k Numeric. The maximum number of events allowed in a subsequence. See seqefsub.
with.missing Logical. If TRUE, property of missing spell are also extracted.
R Number of permutations used to assess the significance of the split. See disstree.
weight.permutation Weight permutation method: "diss" (attach weights to the dissimilarity matrix), "replicate" (replicate cases using weights), "rounded-replicate" (replicate case using rounded weights), "random-sampling" (random assignment of covariate profiles to the objects using distributions defined by the weights.). See disstree.
min.size Minimum number of cases in a node, will be treated as a proportion if less than 1. See disstree.
max.depth Maximum depth of the tree. See disstree.
maxcluster  Maximum number of cluster to consider.
st        A divisive clustering tree as produced by seqpropclust
ek        The number of groups to extract.
labels    Logical. If TRUE, rules to assign an object to a sequence is used to label the
          cluster (instead of a number).
...        Arguments passed to/from other methods.

Details

The method implement the DIVCLUS-T algorithm.

Value

Return a seqpropclust object, which is (in fact) a distree object. See disstree.

References

Ritschard and M. Studer (Eds.), Sequence Analysis and Related Approaches: Innovative Methods

Piccarreta R, Billari FC (2007). Clustering work and family trajectories by using a divisive algo-


See Also

as.clustrange, seqtreedisplay, disstree.

Examples

data(mvad)
mvad.seq <- seqdef(mvad[1:100, 17:86])

## Compute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")

pclust <- seqpropclust(mvad.seq, diss=diss, maxcluster=5, properties=c("state", "duration"))

## Run it to visualize the results
##seqtreedisplay(pclust, type="d", border=NA, showdepth=TRUE)

pclustqual <- as.clustrange(pclust, diss=diss, ncluster=5)
wcAggregateCases

Aggregate identical cases.

Description
Function to aggregate identical cases.

Usage
wcAggregateCases(x, weights = NULL, ...)
## S3 method for class 'data.frame'
wcAggregateCases(x, weights=NULL, ...)
## S3 method for class 'matrix'
wcAggregateCases(x, weights=NULL, ...)
## S3 method for class 'wcAggregateCases'
print(x, ...)

Arguments
x The object to aggregate.
weights Numeric. An optional case weights vector.
... Optional additional arguments.

Value
A wcAggregateCases object with the following components:

aggIndex Index of the unique cases in the original object data.
aggWeights Aggregated case weights
disaggIndex Index of the original object data in the unique cases.
disaggWeights Original weights used.

Examples
data(mvad)
## Taking only the father unemployment and
## success at the end of compulsory schooling.
myData <- mvad[, c("funemp", "gcse5eq")]
## Computing aggregated cases informations
ac <- wcAggregateCases(myData, weights=mvad$weight)
print(ac)
## Retrieving unique cases in the original data set
uniqueData <- myData[ac$aggIndex, ]
## Table from original data
table.orig <- xtabs(mvad$weight~funemp+gcse5eq, data=myData)
## Table from aggregated data
table.agg <- xtabs(ac$aggWeights~funemp+gcse5eq, data=uniqueData)

## Both table are equal, no information is lost
## (only the call command is different)
all(table.orig == table.agg)

---

wcClusterQuality  

Cluster quality statistics

Description

Compute several quality statistics of a given clustering solution.

Usage

wcClusterQuality(diss, clustering, weights = NULL)

Arguments

diss       A dissimilarity matrix or a dist object (see dist)
clustering Factor. A vector of clustering membership.
weights    optional numerical vector containing weights.

Details

Compute several quality statistics of a given clustering solution. See value for details.

Value

A list with two elements stats and ASW:

stats with the following statistics:

- **PBC** Point Biserial Correlation. Correlation between the given distance matrice and a distance which equal to zero for individuals in the same cluster and one otherwise.
- **HG** Hubert’s Gamma. Same as previous but using Kendall’s Gamma coefficient.
- **HGSD** Hubert’s Gamma (Somers’D). Same as previous but using Somers’ D coefficient.
- **ASW** Average Silhouette width (observation).
- **ASWw** Average Silhouette width (weighted).
- **CH** Calinski-Harabasz index (Pseudo F statistics computed from distances).
- **R2** Share of the discrepancy explained by the clustering solution.
- **CHsq** Calinski-Harabasz index (Pseudo F statistics computed from squared distances).
- **R2sq** Share of the discrepancy explained by the clustering solution (computed using squared distances).
- **HC** Hubert’s C coefficient.

ASW: The Average Silhouette Width of each cluster, one column for each ASW measure.
Examples

```r
data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)
## Computing Hamming distance between sequence
diss <- seqdist(mvad.seq, method="HAM")

## KMedoids using PAMonce method (clustering only)
clust5 <- wcKMedoids(diss, k=5, weights=aggMvad$aggWeights, cluster.only=TRUE)

## Compute the silhouette of each observation
qual <- wcClusterQuality(diss, clust5, weights=aggMvad$aggWeights)
print(qual)
```

Description

Automatically compute different clustering solutions and associated quality measures to help identifying the best one.

Usage

```r
wcCmpCluster(diss, weights = NULL, maxcluster, method = "all", pam.combine = TRUE)
```

Arguments

- `diss` A dissimilarity matrix or a dist object (see `dist`).
- `weights` Optional numerical vector containing weights.
- `maxcluster` Integer. Maximum number of cluster. The range will include all clustering solution starting from two to `ncluster`. 
method  A vector of hierarchical clustering methods to compute or "all" for all methods. Possible values include "ward", "single", "complete", "average", "mcquitty", "median", "centroid" (using hclust), "pam" (using wcKMedRange), "diana" (only for unweighted datasets using diana), "beta.flexible" (only for unweighted datasets using agnes)

pam.combine Logical. Should we try all combinations of hierarchical and PAM clustering?

x A clustrangefamily object to plot or print

object A clustrangefamily object to summarize

max.rank Integer. The different number of solution to print/summarize

group One of "stat" or "method". If "stat", plots are grouped by statistics, otherwise by clustering methods.

stat Character. The list of statistics to plot or "noCH" to plot all statistics except "CH" and "CHsq" or "all" for all statistics. See wcClusterQuality for a list of possible values. It is also possible to use "RHC" to plot the quality measure 1-HC. Unlike HC, RHC should be maximized as all other quality measures.

cxnorm Character. Normalization method of the statistics can be one of "none" (no normalization), "range" (given as (value -min)/(max-min), "zscore" (adjusted by mean and standard deviation) or "zscoremed" (adjusted by median and median of the difference to the median).

withlegend Logical. If FALSE, the legend is not plotted.

lwd Numeric. Line width, see par.

col A vector of line colors, see par. If NULL, a default set of color is used.

legend.prop When withlegend=TRUE, sets the proportion of the graphic area used for plotting the legend. Default value is set according to the place (bottom or right of the graphic area) where the legend is plotted. Values from 0 to 1.

rows,cols optional arguments to arrange plots.

xlab x axis label.

ylab y axis label.

main main title of the plot.

... Additional parameters passed to lines.

Value

An object of class clustrangefamily with the following elements:

Method name: the results of as.clustrange objects under each method name (see argument method for a list of possible values)

allstats: A matrix containing the clustering statistics for each cluster solution and method.

param: The parameters set when the function was called.

See Also

See Also as.clustrange
Examples

```r
data(mvad)

# Creating state sequence object
mvad.seq <- seqdef(mvad[, 17:86])

# Compute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")

# Ward clustering
allClust <- wcCmpCluster(diss, maxcluster=15, method=c("average", "pam", "beta.flexible"),
                         pam.combine=FALSE)

summary(allClust, max.rank=3)

# Plot PBC, RHC and ASW
plot(allClust, stat=c("PBC", "RHC", "ASW"), norm="zscore", lwd=2)

# Plot PBC, RHC and ASW grouped by cluster method
plot(allClust, group="method", stat=c("PBC", "RHC", "ASW"), norm="zscore", lwd=2)
```

wcKMedoids

*K-Medoids or PAM clustering of weighted data.*

**Description**

K-Medoids or PAM clustering of weighted data.

**Usage**

```r
wcKMedoids(diss, k, weights=NULL, npass = 1, initialclust=NULL,
            method="PAMonce", cluster.only = FALSE, debuglevel=0)
```

**Arguments**

- **diss**: A dissimilarity matrix or a dist object (see `dist`).
- **k**: Integer. The number of cluster.
- **weights**: Numeric. Optional numerical vector containing case weights.
- **npass**: Integer. Number of random start solution to test.
- **initialclust**: An integer vector, a factor, an "hclust" or a "twins" object. Can be either the index of the initial medoids (length should equal to k) or a vector specifying an initial clustering solution (length should then be equal to the number of observation.). If `initialclust` is an "hclust" or a "twins" object, then the initial clustering solution is taken from the hierarchical clustering in k groups.
- **method**: Character. One of "KMedoids", "PAM" or "PAMonce" (default). See details.
- **cluster.only**: Logical. If FALSE, the quality of the retained solution is computed.
- **debuglevel**: Integer. If greater than zero, print some debugging messages.
Details

K-Medoids algorithms aim at finding the best partition of the data in a k predefined number of groups. Based on a dissimilarity matrix, those algorithms seeks to minimize the (weighted) sum of distance to the medoid of each group. The medoid is defined as the observation that minimize the sum of distance to the other observations of this group. The function wcKMedoids support three different algorithms specified using the method argument:

"KMedoids" Start with a random solution and then iteratively adapt the medoids using an algorithm similar to kmeans. Part of the code is inspired (but completely rewritten) by the C clustering library (see de Hoon et al. 2010). If you use this solution, you should set npass>1 to try several solution.

"PAM" See pam in the cluster library. This code is based on the one available in the cluster library (Maechler et al. 2011). The advantage over the previous method is that it try to minimize a global criteria instead of a local one.

"PAMonce" Same as previous but with two optimizations. First, the optimization presented by Reynolds et al. 2006. Second, only evaluate possible swap if the dissimilarity is greater than zero. This algorithm is used by default.

wcKMedoids works differently according to the diss argument. It may be faster using a matrix but require more memory (since all distances are stored twice). All combination between method and diss argument are possible, except for the "PAM" algorithm were only distance matrix may be used (use the "PAMonce" algorithm instead).

Value

An integer vector with the index of the medoids associated with each observation.

References


See Also

pam in the cluster library, wcClusterQuality, wcKMedRange.

Examples

data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[, aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)
## Computing Hamming distance between sequence
diss <- seqdist(mvad.seq, method="HAM")
## K-Medoids

clust5 <- wcKMedoids(diss, k=5, weights=aggMvad$aggWeights)

## clust5$clustering contains index number of each medoids
## Those medoids are unique(clust5$clustering)

## Print the medoids sequences
print(mvad.seq[unique(clust5$clustering), ], informat="SPS")

## Some info about the clustering
print(clust5)

## Plot sequences according to clustering solution.
seqdplot(mvad.seq, group=clust5$clustering)

---

### wcKMedRange

**Compute** *wcKMedoids* clustering for different number of clusters.

#### Description

Compute *wcKMedoids* clustering for different number of clusters.

#### Usage

```
wcKMedRange(diss, kvals, weights=NULL, R=1, samplesize=NULL, ...)
```

#### Arguments

- **diss**: A dissimilarity matrix or a dist object (see `dist`).
- **kvals**: A numeric vector containing the number of cluster to compute.
- **weights**: Numeric. Optional numerical vector containing case weights.
- **R**: Optional number of bootstrap that can be used to build confidence intervals.
- **samplesize**: Size of bootstrap sample. Default to sum of weights.
- **...**: Additionnal parameters passed to `wcKMedoids`.

#### Details

Compute a clustrange object using the `wcKMedoids` method. clustrange objects contains a list of clustering solution with associated statistics and can be used to find the optimal clustering solution. See `as.clustrange` for more details.

#### See Also

See `as.clustrange`.
Examples

data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)

## Compute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")

## Pam clustering
pamRange <- wcKMedRange(diss, 2:15)

## Plot all statistics (standardized)
plot(pamRange, stat="all", norm="zscoremed", lwd=3)

## Plotting sequences in 3 groups
seqdplot(mvad.seq, group=pamRange$clustering$cluster3)

---

**wcSilhouetteObs**

Compute the silhouette of each object using weighted data.

Description

Compute the silhouette of each object using weighted data.

Usage

wcSilhouetteObs(diss, clustering, weights = NULL, measure="ASW")

Arguments

diss
clusterings
weights
measure

A dissimilarity matrix or a dist object (see dist)
Factor. A vector of clustering membership.
onoptional numerical vector containing weights.
"ASW" or "ASWw", the measure of the silhouette. See the WeightedCluster vignettes.

Details

See the silhouette function in the cluster package for a detailed explanation of the silhouette.

Value

A numeric vector containing the silhouette of each observation.
References

See Also
See also silhouette.

Examples

data(mvad)
## Aggregating state sequence
aggMvad <- wcAggregateCases(mvad[, 17:86], weights=mvad$weight)

## Creating state sequence object
mvad.seq <- seqdef(mvad[aggMvad$aggIndex, 17:86], weights=aggMvad$aggWeights)
## Computing Hamming distance between sequence
diss <- seqdist(mvad.seq, method="HAM")

## KMedoids using PAMonce method (clustering only)
clust5 <- wcKMedoids(diss, k=5, weights=aggMvad$aggWeights, cluster.only=TRUE)

## Compute the silhouette of each observation
sil <- wcSilhouetteObs(diss, clust5, weights=aggMvad$aggWeights, measure="ASWw")

## If you want to compute the average silhouette width,
## you should take weights into account
weighted.mean(sil, w=aggMvad$aggWeights)

## Plotting sequences ordered by silhouette width,
## best classified are drawn on the top.
seqIplot(mvad.seq, group=clust5, sortv=sil)
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