Package 'WeightedCluster'

December 10, 2025

Version 2.0

Date 2025-12-08

Title Clustering of Weighted Data

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Depends R (>= 3.0.0), TraMineR (>= 2.0-6), cluster

Imports utils, RColorBrewer, foreach, progressr, future, doFuture, nnet, fastcluster, vegclust, lme4, margins

Suggests RUnit, knitr, isotone, vegan, lattice, rmarkdown, Cairo, progress, DirichletReg, betareg, fpc

VignetteBuilder knitr

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, sequence analysis typology validation using parametric bootstraps and plotting (fuzzy) clusters of state sequences. It further provides a fuzzy and crisp CLARA algorithm to cluster large database with sequence analysis, and a methodological framework for Robustness Assessment of Regressions using Cluster Analysis Typologies (RARCAT).

URL http://mephisto.unige.ch/weightedcluster/

NeedsCompilation yes

Repository CRAN

Date/Publication 2025-12-10 08:40:02 UTC

Contents

`as.clustrange` *Build a clustrange object to compare different clustering solutions.*

Description

Build a clustrange object to compare different clustering solutions.

Usage

```
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.
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 clustassoc (other cluster quality measures), 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.
ncluster	Maximum number of cluster. The tree will be builded until this number of cluster.
...	Additionnal 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 schedulde.

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)
```

bootclustrange *Cluster Quality Indices estimation by subsampling*

Description

bootclustrange estimates the quality of the clustering based on subsamples of the data to avoid computational overload.

Usage

```
bootclustrange(object, seqdata, seqdist.args = list(method = "LCS"),
               R = 100, sample.size = 1000, parallel = FALSE,
               progressbar = FALSE, sampling = "clustering",
               strata = NULL)
## S3 method for class 'bootclustrange'
plot(x, stat = "noCH", legendpos = "bottomright",
                              norm = "none", withlegend = TRUE, lwd = 1,
                              col = NULL, ylab = "Indicators",
                              xlab = "N clusters", conf.int = 0.95,
                              ci.method = "perc", ci.alpha = 0.3,
                              line = "median", ...)
## S3 method for class 'bootclustrange'
print(x, digits = 2, bootstat = c("mean"), ...)
```

Arguments

object	A seqclararange object or a data.frame with the clustering to be evaluated.
seqdata	State sequence object of class stslist. The sequence data to use. Use seqdef to create such an object.
seqdist.args	List of arguments passed to seqdist for computing the distances.
R	Numeric. The number of subsamples to use.
sample.size	Numeric. The size of the subsamples, values between 1000 and 10 000 are recommended.
parallel	Logical. Whether to initialize the parallel processing of the future package using the default multisession strategy. If FALSE (default), then the current plan is used. If TRUE, multisession plan is initialized using default values.
progressbar	Logical. Whether to initialize a progressbar using the future package. If FALSE (default), then the current progress bar handlers is used . If TRUE, a new global progress bar handlers is initialized.
sampling	Character. The sampling procedure to be used: "clustering" (default) the sampling is stratified by the maximum number of clusters, use "medoids" to add the medoids in each subsamples, "strata" to stratify by the strata arguments, or "random" for random sampling.
strata	An optional stratification variable.

x	A bootclustrange object to be plotted or printed.
stat	Character. The list of statistics to plot or "noCH" to plot all statistics except "CH" and "CHsq" or "all" for all statistics. See as.clustrange for a list of possible values.
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: 0.95).
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" (default, based on percentile).)
ci.alpha	alpha color value used to plot the interval.
line	Which value should be plotted by the line? One of "mean" (average over all bootstraps), "median"(default, median over all bootstraps).
digits	Number of digits to be printed.
bootstat	The summary statistic to use "mean" or "median".
...	Additionnal parameters passed to/from methods.

Details

bootclustrange estimates the quality of the clustering based on subsamples of the data to avoid computational overload. It randomly samples R times sample.size sequences from seqdata using the sampling procedure defined by the sampling arguments. In each subsample, a distance matrix is computed using the selected sequences and the seqdist.args arguments and the cluster quality indices are then estimated using as.clustrange.

The clustering can be specified either as a seqclararange object or a data.frame.

Value

A clustrange object, see as.clustrange with the bootrapped values.

References

Studer, M., R. Sadeghi and L. Tochon (2024). Sequence Analysis for Large Databases. *LIVES Working Papers 104* doi:10.12682/lives.22961658.2024.104

See Also

See Also as.clustrange for the list of cluster quality indices that are computed, and seqclararange for example of use

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clustassoc *Share of an association between an object (described by a dissimilarity matrix) and a covariate that is reproduced by a clustering solution.*

Description

The clustassoc measures to which extent a clustering solution can account for the relationship between a covariate and the objects of interest, i.e. the sequences or any other object described by a dissimilarity matrix. It can be used to guide the choice of the number of groups ensuring that the clustering captures the relevant information to account for a statistical relationship of interest. This is useful when the clustering is used in subsequent analyses, such as regressions. In this case, the within-cluster variation is ignored, as objects clustered together are described by a single value. Ensuring that the association is accounted for by the clustering can avoid drawing wrong conclusions (see Unterlerchner et al. 2023).

Usage

```
clustassoc(clustrange, diss, covar, weights = NULL)
## S3 method for class 'clustassoc'
plot(x, stat=c("Unaccounted", "Remaining", "BIC"), type="b", ...)
```

Arguments

clustrange	A clustrange object regrouping the different clustering solutions to be evaluated.
diss	A dissimilarity matrix or a dist object (see dist).
covar	Vector (Numeric or factor): the covariate of interest. The type of the vector matters for the computation of the BIC (see details). If Numeric, a linear regression is used, while a multinomial regression is used for categorical/factor variables.
weights	Optional numerical vector containing weights.
x	A clustassoc object to be plotted.
stat	The information to be plotted according to the number of groups. "Unaccounted" (default) plots the share of the association that is NOT accounted for by the clustering solution. "Remaining" plots the share of the overall variability/discrepancy of the object remaining when controlling for the clustering. "BIC" plots the BIC of a regression predicting the covariate using the clustering solution (see details).
type	character indicating the type of plotting (see plot.default). "b" plots points and lines.
...	Additionnal parameters passed to/from methods.

Details

The clustassoc measures to which extent a clustering solution can account for the relationship between a covariate and the objects of interest. It can be used to guide the choice of the number of groups of the clustering to ensure that it captures the relevant information to account for a statistical relationship of interest.

The method works as follows. The relationship between trajectories (or any objects described by a distance matrix) and covariates can be studied directly using discrepancy analysis (see Studer et al. 2011). It measures the strength of the relationship with a Pseudo-R2, measuring the share of the variation of the object explained by a covariate. The method works without prior clustering, and therefore, without data simplification. The method is provided by the dissmfacw function from the TraMineR package.

Multifactor discrepancy analysis allows measuring a relationship while controlling for other covariates. the clustassoc function measures the remaining association between the objects and the covariate while controlling for the clustering. If the covariate Pseudo-R2 remains high (or at the same level), it means that the clustering does not capture the relationship between covariates and the objects. In other words, the clustering has simplified the relevant information to capture this relationship. Conversely, if the Pseudo-R2 is much lower, it means that the clustering reproduces the key information to understand the relationship. Using this strategy, the clustassoc measure the share of the original Pseudo-R2 that is taken into account by our clustering.

The function also compute the BIC of a regression predicting the covariate using the clustering solution as proposed by Han et al. 2017. A lower BIC is to be preferred. The method is, however, less reliable than the previous one.

Value

A clustassoc object containing the following information for each clustering:

Unaccounted	The share of the original association that is NOT accounted for by the clustering solution.
Remaining	The remaining strength of the association (share of the variability of the object) that is not accounted for by the clustering solution.
BIC	The BIC of a model explaining the covariate using the clustering as explanatory variable.
Remaining	The remaining strength of the association (share of the variability of the object) that is not accounted for by the clustering solution.
numcluster	The number of clusters (and 1 means no clustering).

Author(s)

Matthias Studer

References

Unterlerchner, L., M. Studer and A. Gomensoro (2023). Back to the Features. Investigating the Relationship Between Educational Pathways and Income Using Sequence Analysis and Feature Extraction and Selection Approach. *Swiss Journal of Sociology*.

Studer, M. 2013. WeightedCluster Library Manual: A Practical Guide to Creating Typologies of Trajectories in the Social Sciences with R.*LIVES Working Papers 2013(24)*: 1-32.

Studer, M., G. Ritschard, A. Gabadinho and N. S. Mueller (2011). Discrepancy analysis of state sequences, *Sociological Methods and Research*, Vol. 40(3), 471-510, doi:10.1177/0049124111415372.

Han, Y., A. C. Liefbroer and C. H. Elzinga. 2017. Comparing Methods of Classifying Life Courses: Sequence Analysis and Latent Class Analysis. *Longitudinal and Life Course Studies 8(4)*: 319-41.

See Also

See Also `as.clustrange` for cluster quality indexes, and the `dissmfacw` function from the `TraMineR` package.

Examples

```
data(mvad)

## Small subsample to reduce computations
mvad <- mvad[1:50,]

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

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

## Ward clustering
wardCluster <- hclust(as.dist(diss), method="ward.D")

## Computing clustrange from Ward clustering up to 5 groups
wardRange <- as.clustrange(wardCluster, diss=diss, ncluster=5)

## Compute clustassoc
## How many groups are required to account for the relationship
## between trajectories and the gcse5eq covariate
assoc <- clustassoc(wardRange, covar=mvad$gcse5eq, diss=diss)

## Plot unaccounted share of the association
## A value close to zero means that the relationship is accounted for.
## Here at least 2-4 groups are required
plot(assoc)

## Plot BIC
## A low value means that an association between trajectories and the covariate is identified.
## 2-3 groups show best results.
plot(assoc, stat="BIC")


## Plot remaining share of the variability of the sequences not explained by clustering
## A value close to zero means that there is no association left (similar)
## Here at least 2-4 groups are required
plot(assoc, stat="Remaining")
```

`fuzzyseqplot` *Plot sequences according to a fuzzy clustering.*

Description

This funciton 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 (chronograms), `"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 representative 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.treashold` argument.

References

Studer, M. (2018). Divisive property-based and fuzzy clustering for sequence analysis. In G. Ritschard and M. Studer (Eds.), *Sequence Analysis and Related Approaches: Innovative Methods and Applications*, Life Course Research and Social Policies.

See Also

See also `fanny` for fuzzy clustering.

Examples

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

## COmpute distance using Hamming distance
diss <- seqdist(mvad.seq, method="HAM")
library(cluster)
fclust <- fanny(diss, k=2, diss=TRUE)

fuzzyseqplot(mvad.seq, group=fclust, type="d")
fuzzyseqplot(mvad.seq, group=fclust, type="I", sortv="membership")
fuzzyseqplot(mvad.seq, group=fclust, type="f")
```

---

plot.seqclararange *Plot of cluster quality of CLARA algorithm.*

Description

Plot of the cluster quality of a `seqclararange` `object`.

Usage

```
## S3 method for class 'seqclararange'
plot(x, stat = "CQI", type = "o", main = NULL,
  xlab = "Number of clusters", ylab = stat, col = "blue",
legend.pos = "topright", pch = 19, norm = "none", ...)
```

Arguments

`x`	`seqclararange` object, see `seqclararange`
`stat`	Character. The cluster quality indice to plot, namely one of `"CQI"` (default) to plot the value of the cluster quality indices by number of groups, `"stability"` to count the number of recovery of the best partition or `"stabmean"` to presents the average stability of the clustering.
`type`	Character. The type of line to draw. Possible types are `"l"` (lines), `"p"` points or `"o"` to plot both.
`main`	Character. The overall title of the plot: see `title`.

xlab	x axis label.
ylab	y axis label.
col	A vector of line colors, see par. If NULL, a default set of color is used.
legend.pos	Character. legend position, see legend.
pch	The plotting characters or symbols: see points.
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).
...	Additionnal parameters passed to/from methods.

References

Studer, M., R. Sadeghi and L. Tochon (2024). Sequence Analysis for Large Databases. *LIVES Working Papers 104* doi:10.12682/lives.22961658.2024.104

See Also

See seqclararange to produce a clustering objects.

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rarcat *Robustness Assessment of Regressions using Cluster Analysis Typologies (RARCAT)*

Description

rarcat is a wrapper for the functions regressboot and bootpool that performs the entire RARCAT procedure on all possible associations between a typology and covariates of interest. See Roth et al. (2024) or the R tutorial as WeightedCluster vignette for all details on the corresponding methods and their utility.

Usage

```
rarcat(formula, data, diss,
        robust=TRUE, R=500,
        kmedoid=FALSE, hclust.method="ward.D",
        fixed=FALSE, ncluster=10, cqi="HC",
        parallel=FALSE, progressbar=FALSE,
        fisher.transform=FALSE,
lmerCtrl=lme4::lmerControl())
## S3 method for class 'rarcat'
plot(x, what="AME", covar=x$factorName[1],
pooled.ame=TRUE, naive.ame=TRUE,
with.legend=TRUE, legend.prop=NA, rows=NA,
cols=NA, main=NULL,
```

```
xlab=paste(covar, "Average Marginal Effect"),
xlim=NULL, conf.level=0.95,...)
## S3 method for class 'rarcat'
print(x, conf.level=0.95, single.row = FALSE, digits = 3, ...)
## S3 method for class 'rarcat'
summary(object, ...)
```

Arguments

formula	A formula object with the clustering solution on the left side and the covariates of interest on the ride side.
data	The dataset (data frame) with column names corresponding to the information in formula. The number of individuals (row number) should match the dimension of diss.
diss	The numerical dissimilarity matrix used for clustering. Only a pre-computed matrix (i.e., where pairwise dissimilarities do not depend on the resample) is currently supported.
robust	Logical. TRUE (the default) indicates that RARCAT should be performed. FALSE implies a much faster function run but only output the original analysis, which is a standard regression analysis for all combinations of reference clusters and covariates.
R	The integer number of bootstrap. Set to 500 by default to attain a satisfactory precision around the estimates as the procedure involves multiple steps.
kmedoid	The clustering algorithm as a character string. Currently only "pam" (calling the function wcKMedRange) and "hierarchical" (calling the function fastcluster::hclust) are supported. By default "pam".
hclust.method	A character string with the method argument of hclust, "ward.D" by default.
fixed	Logical. TRUE implies that the number of clusters is the same in every bootstrap. FALSE (default) implies that an optimal number of clusters is evaluated each time.
ncluster	Integer. Either the number of clusters in every bootstrap if fixed is TRUE or the maximum number of clusters (starting from 2) to be evaluated in each bootstrap if fixed is FALSE.
cqi	A character string with the cluster quality index to be evaluated for each new partition. Any column of as.clustrange is supported, "CH" (the Calinski-Harabasz index) by default. Also works with algo= "pam".
parallel	Logical. Whether to initialize the parallel processing of the future package using the default multisession strategy. If FALSE (default), then the current plan is used. If TRUE, multisession plan is initialized using default values.
progressbar	Logical. Whether to initialize a progressbar using the future package. If FALSE (default), then the current progress bar handlers is used . If TRUE, a new global progress bar handlers is initialized.
fisher.transform	Logical. TRUE means that a Fisher transformation is applied in the multilevel model estimation step. This can be recommended in case of extreme associations (close to the -1 or 1 boundaries). FALSE by default.

lmerCtrl	Control parameter for lme4 (see lmerControl
x	rarcat object to be printed or plotted.
object	rarcat object for summary (diagnostic tools).
conf.level	Confidence level for the confidence intervals. 0.95 by default.
digits	Number of significant digits to print (3 by default).
single.row	Logical. Whether to show confidence interval on the same or separate line (Default=FALSE).
what	Character. Information to plot. With "AME" (default), the boostrapped AME are shown. Set to "ranef" to view the distribution of observation-level random effect (usefull to identify potentially influential unstable observation).
covar	Character. The covariate of interest.
pooled.ame	Logical. Whether to add a vertical line and confidence interval for the pooled AME.
naive.ame	Logical. Whether to add a vertical line and confidence interval for the naive AME.
with.legend	Logical. If FALSE, the legend is not plotted.
legend.prop	Real in range [0,1]. Proportion of the graphic area devoted to the legend plot with.legend=TRUE. Default value is set according to the place (bottom or right of the graphic area) where the legend is plotted.
rows	Integers. Number of rows of the plot panel.
cols	Integers. Number of columns of the plot panel.
main	Character string. Title of the graphic.
xlab	x axis label.
xlim	Numerics. Limits of the x-axis.
...	Additionnal parameters passed to/from methods.

Details

The rarcat function runs a standard typology-based association study and evaluates the impact of sampling uncertainty on the results, thus assessing the reproducibility of the analysis.

Value

The output of rarcattables contains the following tables:

The output of bootpool is a list with the following components:

nobs	An integer with the number of observations (i.e., number of estimated AMES from the function regressboot) used to compute the robust estimates in the multilevel model. Due to missing observations when an individual does not appear in a bootstrap, nobs < m x B, where m < M is the number of individuals in a given cluster, M is the total number of individuals and B is the total number of bootstrap in regressboot.

`pooled.ame` A numeric value indicating the pooled AME, which is the mean change in cluster membership probability for a change in the level of the covariate of interest over all bootstraps and all individuals belonging to the reference cluster in the original typology.

`standard.error` Standard error of the pooled AME, which diminishes asymptotically as the number of bootstrap increases.

`bootstrap.stddev`
The estimate for the standard deviation of the bootstrap random effect. This can be used to construct a prediction interval for the association of interest (see Roth et al. 2024 for details on how to compute this).

`observation.stddev`
The estimate for the standard deviation of the bootstrap random effect.

`bootstrap.ranef`
A vector of size `B` containing the estimated random effects for each bootstrap.

`observation.ranef`
A vector of size `m` containing the estimated random effects for each observation in the reference cluster.

`original.analysis`
Average Marginal Effects (AMEs) estimated with multivariable logistic regressions and representing the expected change in the probability of belonging to a trajectory group (a reference cluster) for a change in the level of a variable (a covariate of interest), together with their confidence intervals.

`robust.analysis`
Pooled AMEs from the bootstrap procedure and their prediction intervals, representing the range of expected values if the clustering and associated regressions were performed on a new sample from the same underlying distribution. This table provide robust estimates for a typology-based association study.

Author(s)

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References

Roth, L., Studer, M., Zuercher, E., & Peytremann-Bridevaux, I. (2024). Robustness assessment of regressions using cluster analysis typologies: a bootstrap procedure with application in state sequence analysis. BMC medical research methodology, 24(1), 303. https://doi.org/10.1186/s12874-024-02435-8.

Examples

```
## Loading the data (TraMineR package)
data(mvad)

## Reducing sample size to speed up computations
mvad <- mvad[1:200,]
```

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

## Distance computation
diss <- seqdist(mvad.seq, method="LCS")

## Hierarchical clustering
hc <- fastcluster::hclust(as.dist(diss), method="ward.D")

## Computing cluster quality measures
clustqual <- as.clustrange(hc, diss=diss, ncluster=6)

## A six clusters solution is chosen here
mvad$clustering <- clustqual$clustering$cluster2

## The formula should include the typology (dependent) and the covariates of interest
## As in the original analysis, hierarchical clustering with Ward method is implemented
## The number of clusters is fixed to 2 here, larger values should often be used.
## For illustration purposes, the number of bootstrap is smaller than what it ought to be
rarcatout <- rarcat(clustering ~ Grammar + gcse5eq, mvad, diss, R = 30,
                    kmedoid=TRUE, fixed = TRUE, ncluster = 2)

## Assess the robustness of the original analysis
rarcatout
#plot(rarcatout, covar="gcse5eqyes")
#plot(rarcatout, covar="gcse5eqyes", what="ranef")
#summary(rarcatout)
```

`seqclararange` *CLARA Clustering for Sequence Analysis*

Description

Cluster large databases of sequences for a different number of groups using the CLARA algorithm based on subsampling to reduce computational burden. Crisp, fuzzy and representativeness clustering are available. The function further computes several cluster quality measures.

Usage

```
seqclararange(seqdata, R = 100, sample.size = 40 + 2 * max(kvals),
  kvals = 2:10,  seqdist.args = list(method = "LCS"),
  method=c("crisp", "fuzzy", "representativeness", "noise"),
  m = 1.5, criteria = c("distance"), stability = FALSE, dnoise=NULL,
  parallel = FALSE, progressbar = FALSE, keep.diss = FALSE,
  max.dist = NULL)
```

Arguments

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

R	Numeric. The number of subsamples to use.
sample.size	Numeric. The size of the subsamples, the default values is the one proposed by Kaufmann and Rousseuuw (1990). However, larger values (typically between 1000 and 10 000) are recommended.
kvals	Numeric vector. The different number of groups to compute.
seqdist.args	List of arguments passed to seqdist for computing the distances.
method	Character. The clustering approach to use, with default to "crisp" clustering. "fuzzy", "noise" or "representativeness" approaches can also be used.
m	Numeric. Only used for fuzzy clustering, the value of the fuzzifier.
criteria	Character. The name of the criteria used for selecting the best clustering among the different runs. The following values are accepted: "distance" (Default, average value to cluster medoids), "db" (Davies-Bouldin Index), "xb" (Xie-Beni index), "pbm" (PBM Index), "ams" (Average medoid silhouette value).
stability	Logical. If TRUE, stability measures are computed (can be time consuming, especially for fuzzy clustering). Default to FALSE.
dnoise	Numerical. The theoretically defined distance to the noise cluster. Mandatory for noise clustering.
parallel	Logical. Whether to initialize the parallel processing of the future package using the default multisession strategy. If FALSE (default), then the current plan is used. If TRUE, multisession plan is initialized using default values.
progressbar	Logical. Whether to initialize a progressbar using the future package. If FALSE (default), then the current progress bar handlers is used . If TRUE, a new global progress bar handlers is initialized.
keep.diss	Logical. Whether to keep the distances to the medoids. Set to FALSE by default.
max.dist	Numeric. Maximal theoretical distance value between sequences. Required for method="representativeness" clustering.

Details

seqclararange relies on the CLARA algorithm to cluster large database. The algorithm works as follows.

1. Randomly take a subsample of the data of size sample.size.
2. Cluster the subsample using the PAM algorithm initialized using Ward to speed up the computations (see wcKmedoids).
3. Use the identified medoids to assign cluster membership in the whole dataset.
4. Evaluate the resulting clustering using a criteria (see argument), the average distances to the medoids by default.

These steps are repeated R times and the best solution according to the given criterion is kept.

To minimize the computation, the operation is repeated for different number of groups, which then allows to choose the best number of groups according to different cluster quality indices. The following indices are computed automatically: "Avg dist" (Average distance to cluster medoids), "PBM"(PBM Index), "DB" (Davies-Bouldin Index), "XB" (Xie-Beni Index), "AMS" (Average medoid silhouette width), "ARI>0.8" (Number of iteration similar to the current best, only if stability=TRUE, "JC>0.8" (Number of iteration similar to the current best, only if stability=TRUE.

Value

A `seqclararange` object with the following components:

`kvals:`	The different number of groups evaluated.
`clustering:`	The retained clustering for each number of groups. For `"crisp"` clustering, a `data.frame` with the clustering in column named clusterX, with X the number of groups. For `"fuzzy"` and `"representativeness"`, a list of membership matrix, with each elements named clusterX, with X the number of groups.
`stats:`	A `matrix` containing the clustering statistics of each cluster solution.
`clara:`	Detailed information on the best clustering for each number of groups, in the same order as kvals.

References

Studer, M., R. Sadeghi and L. Tochon (2024). Sequence Analysis for Large Databases. *LIVES Working Papers 104* doi:10.12682/lives.22961658.2024.104

See Also

See also as `plot.seqclararange` to plot the results.

Examples

```
data(biofam) #load illustrative data
## Defining the new state labels
statelab <- c("Parent", "Left", "Married", "Left/Married",  "Child",
            "Left/Child", "Left/Married/Child", "Divorced")
## Creating the state sequence object,
biofam.seq <- seqdef(biofam[1:100, 10:25], alphabet=0:7, states=statelab)



## Clara clustering
bfclara <- seqclararange(biofam.seq, R = 3, sample.size = 10, kvals = 2:3,
  seqdist.args = list(method = "HAM"), parallel=FALSE,
  stability=TRUE)


#Show the cluster quality measures.
bfclara
#Plot and normalize the values for easier identification of minimum and maximum values.
plot(bfclara, norm="range")
## Stability values.
plot(bfclara, stat="stabmean")
plot(bfclara, stat="stability")

seqdplot(biofam.seq, group=bfclara$clustering$cluster3)

## Cluster quality indices estimation using boostrap
```

```
bCQI <- bootclustrange(bfclara, biofam.seq, seqdist.args = list(method = "HAM"),
  R = 3, sample.size = 10,  parallel=FALSE)

bCQI
plot(bCQI, norm="zscore")

## Not run:
## Fuzzy clustering
bfclaraf <- seqclararange(biofam.seq, R = 3, sample.size = 20, kvals = 2:3,
  method="fuzzy", seqdist.args = list(method = "HAM"),
parallel=FALSE)


bfclaraf
plot(bfclaraf, norm="zscore")


fuzzyseqplot(biofam.seq, group=bfclaraf$clustering$cluster3, type="I",
  sortv="membership", membership.threashold=0.2)

## Noise clustering
bfclaran <- seqclararange(biofam.seq, R = 3, sample.size = 20, kvals = 2:3,
  method="noise", seqdist.args = list(method = "HAM"), dnoise=6,
parallel=FALSE)

fuzzyseqplot(biofam.seq, group=bfclaran$clustering$cluster3, type="I",
  sortv="membership", membership.threashold=0.2)


## End(Not run)
```

`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 optionnaly 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 nonclusterd 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` arguement (using a string) are computed separately for each time point.

`weighted` Logicel. 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 nonclusterd 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 (homogeneouns) 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

Studer, M. (2021). Validating Sequence Analysis Typologies Using Parametric Bootstrap. *Sociological Methodology*. doi:10.1177/00811750211014232

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"))
```

---

seqnullcqi *Sequence 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",
parallel=FALSE, progressbar=FALSE, ...)

## 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.
hclust.method	String. Hierarchical method to use with hclust.
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.
type	Character. The type of graphic to be plotted. If type="line" (default), a transparent line representing the cluster quality index for each bootstrap is plotted using a separate line. If type="density", the density of the maximum cluster quality index values among the different number of groups is plotted as well as the original cluster quality values. If type="beanplot", beanplot of the distribution of the cluster quality index values for each number of groups is plotted separately. If type="seqdplot", a state distribution sequence plot of the sequences generated with the null model is plotted (see seqdplot).
quant	Numeric. Quantile to use for the confidence intervals.
norm	Logical. If TRUE, cluster quality indices are standardized using the mean and standard deviation of the null distribution.
legendpos	Character. legend position, see legend.
alpha	Transparency parameter for the lines to be drawn (only for type="line").
digits	Number of digits to be printed.
parallel	Logical. Whether to initialize the parallel processing of the future package using the default multisession strategy. If FALSE (default), then the current plan is used. If TRUE, multisession plan is initialized using default values.
progressbar	Logical. Whether to initialize a progressbar using the future package. If FALSE (default), then the current progress bar handlers is used . If TRUE, a new global progress bar handlers is initialized.
...	Additionnal parameters passed to seqnull (for seqnullcqi) or plot or print.

Details

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.
R	The number of bootstraps
kmedoid	Logical. If TRUE, the PAM algorithm was used to cluster the data using wcKMedRange.
hclust.method	Hierarchical method to used with hclust.
seqdist.args	List of arguments passed to seqdist for computing the distances.
nullmodel	List of arguments passed to seqnull to generate the sequence data under the null model.

References

Studer, M. (2021). Validating Sequence Analysis Typologies Using Parametric Bootstrap. *Sociological Methodology*. doi:10.1177/00811750211014232

A brief introduction to the R code needed to use parametric bootstraps for typology validation in sequence analysis is provided here https://sequenceanalysis.org/2023/10/19/validating-sequence-analysis-typo

See Also

See Also seqnull for description of the null models.

Examples

```
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=5, 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 automoatically 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 divise clustering tree as produced by seqpropclust
k	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

Studer, M. (2018). Divisive property-based and fuzzy clustering for sequence analysis. In G. Ritschard and M. Studer (Eds.), *Sequence Analysis and Related Approaches: Innovative Methods and Applications*, Life Course Research and Social Policies. Springer.

Piccarreta R, Billari FC (2007). Clustering work and family trajectories by using a divisive algorithm. *Journal of the Royal Statistical Society: Series A (Statistics in Society)*, 170(4), 1061-1078.

Chavent M, Lechevallier Y, Briant O (2007). DIVCLUS-T: A monothetic divisive hierarchical clustering method. *Computational Statistics & Data Analysis*, 52(2), 687-701.

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 'stslist'
wcAggregateCases(x, weights=NULL, weighted=TRUE, ...)
## S3 method for class 'wcAggregateCases'
print(x,  ...)
```

Arguments

`x`	The object to aggregate.
`weights`	Numeric. An optional case weights vector.
`weighted`	Logical. If `TRUE`, the `weights` are taken from the sequence object (see `seqdef`).
`...`	Optional additionnal 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

```
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)
```

wcCmpCluster *Automatic comparison of clustering methods.*

Description

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

Usage

```
wcCmpCluster(diss, weights = NULL, maxcluster, method = "all", pam.combine = TRUE)
## S3 method for class 'clustrangefamily'
print(x, max.rank=1, ...)
## S3 method for class 'clustrangefamily'
summary(object, max.rank=1, ...)
## S3 method for class 'clustrangefamily'
plot(x, group="stat", method="all", pam.combine=FALSE,
    stat="noCH", norm="none", withlegend=TRUE, lwd=1, col=NULL, legend.prop=NA,
rows=NA, cols=NA, main=NULL, xlab="", ylab="", ...)
```

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.
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.
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.
...	Additionnal 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

```
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

```
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 differents 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

Maechler, M., P. Rousseeuw, A. Struyf, M. Hubert and K. Hornik (2011). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.1 — For new features, see the 'Changelog' file (in the package source).

Hoon, M. d.; Imoto, S. & Miyano, S. (2010). The C Clustering Library. Manual

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

Maechler, M., P. Rousseeuw, A. Struyf, M. Hubert and K. Hornik (2011). cluster: Cluster Analysis Basics and Extensions. R package version 1.14.1 — For new features, see the 'Changelog' file (in the package source).

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 ordred by silhouette width,
## best classified are draw on the top.
seqIplot(mvad.seq, group=clust5, sortv=sil)
```

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