Package ‘C443’

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Description  Get insight into a forest of classification trees, by calculating similarities between the trees, and subsequently clustering them. Each cluster is represented by it’s most central cluster member. The package implements the methodology described in Sies & Van Mechelen (2020) <doi:10.1007/s00357-019-09350-4>.
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ClusterForest Clustering the classification trees in a forest based on similarities

Description
A function to get insight into a forest of classification trees by clustering the trees in a forest using Partitioning Around Medoids (PAM, Kaufman & Rousseeuw, 2009), based on user provided similarities, or based on similarities calculated by the package using a similarity measure chosen by the user (see Sies & Van Mechelen, 2020).

Usage
```r
clusterforest(
  observeddata, # The entire observed dataset
  treedata = NULL, # A list of dataframes on which the trees are based. Not necessary if the data set is included in the tree object.
  trees, # A list of trees of class party, classes inheriting from party (e.g., glmtree), or classes that can be coerced to party (i.e., rpart, Weka_tree, XMLnode).
  simmatrix = NULL,
  m = NULL,
  tol = NULL,
  weight = NULL,
  fromclus = 1,
  toclus = 1,
  treecov = NULL,
  sameobs = FALSE,
  seed = NULL
)
```

Arguments
- **observeddata**: The entire observed dataset
- **treedata**: A list of dataframes on which the trees are based. Not necessary if the data set is included in the tree object.
- **trees**: A list of trees of class party, classes inheriting from party (e.g., glmtree), or classes that can be coerced to party (i.e., rpart, Weka_tree, XMLnode).
simmatrix

A similarity matrix with the similarities between all trees. Should be square, symmetric and have ones on the diagonal. Default=NULL

m

Similarity measure that should be used to calculate similarities, in the case that no similarity matrix was provided by the user. Default=NULL. m=1 is based on counting common predictors; m=2 is based on counting common predictor-split point combinations; m=3 is based on common ordered sets of predictor-range part combinations (see Shannon & Banks (1999)); m=4 is based on the agreement of partitions implied by leaf membership (Chipman, 1998); m=5 is based on the agreement of partitions implied by class labels (Chipman, 1998); m=6 is based on the number of predictor occurrences in definitions of leaves with same class label; m=7 is based on the number of predictor-split point combinations in definitions of leaves with same class label m=8 measures closeness to logical equivalence (applicable in case of binary predictors only)

tol

A vector with for each predictor a number that defines the tolerance zone within which two split points of the predictor in question are assumed equal. For example, if the tolerance for predictor X is 1, then a split on that predictor in tree A will be assumed equal to a split in tree B as long as the splitpoint in tree B is within the splitpoint in tree A ± 1. Only applicable for m=1 and m=6. Default=NULL

weight

If 1, the number of dissimilar paths in the Shannon and Banks measure (m=2), should be weighted by 1/their length (Otherwise they are weighted equally). Only applicable for m=2. Default=NULL

fromclus

The lowest number of clusters for which the PAM algorithm should be run. Default=1.

toclus

The highest number of clusters for which the PAM algorithm should be run. Default=1.

treecov

A vector/dataframe with the covariate value(s) for each tree in the forest (1 column per covariate).

sameobs

Are the same observations included in every tree data set? For example, in the case of subsamples or bootstrap samples, the answer is no. Default=FALSE

seed

A seed number that should be used for the multi start procedure (based on which initial medoids are assigned). Default=NULL.

Details

The user should provide the number of clusters that the solution should contain, or a range of numbers that should be explored. In the latter case, the resulting clusterforest object will contain clustering results for each solution. On this clusterforest object, several methods, such as plot, print and summary, can be used.

Value

The function returns an object of class clusterforest, with attributes:

medoids

the position of the medoid trees in the forest (i.e., which element of the list of partytrees)

medoidtrees

the medoid trees
clusters
The cluster to which each tree in the forest is assigned

avgsilwidth
The average silhouette width for each solution (see Kaufman and Rousseeuw, 2009)

accuracy
For each solution, the accuracy of the predicted class labels based on the medoids.

agreement
For each solution, the agreement between the predicted class label for each observation based on the forest as a whole, and those based on the medoids only (see Sies & Van Mechelen, 2020)

within sim
Within cluster similarity for each solution (see Sies & Van Mechelen, 2020)

treesimilarities
Similarity matrix on which clustering was based

treecov
covariate value(s) for each tree in the forest

seed
seed number that was used for the multi start procedure (based on which initial medoids were assigned)

References


Examples
try(require(MASS))
require(rpart)
#Function to draw a bootstrap sample from a dataset
DrawBoots <- function(dataset, i){
  set.seed(2394 + i)
  Boot <- dataset[sample(1:nrow(dataset), size = nrow(dataset), replace = TRUE),]
  return(Boot)
}

#Function to grow a tree using rpart on a dataset
GrowTree <- function(x,y,BootsSample, minsplit = 40, minbucket = 20, maxdepth =3){
  controlrpart <- rpart.control(minsplit = minsplit, minbucket = minbucket, maxdepth = maxdepth,
  maxsurrogate = 0, maxcompete = 0)
  tree <- rpart(as.formula(paste(noquote(paste(y, "~")), noquote(paste(x, collapse="+")))),
  data = BootsSample, control = controlrpart)
  return(tree)
}

#Use functions to draw 20 bootstrapsamples and grow a tree on each sample
Boots<- lapply(1:10, function(k) DrawBoots(Pima.tr ,k))
Trees <- lapply(1:10, function (i) GrowTree(x=c(“npreg”, “glu”, “bp”, “skin”,

```
clusters

"bmi", "ped", "age"), y="type", Boots[[i]] ))

# Clustering the trees in this forest
ClusterForest <- clusterforest(observations=Pima.tr, treedata=Boots, trees=Trees, m=1,
fromclus=1, toclus=5, sameobs=FALSE)

clusters

Get the cluster assignments for a solution of a clusterforest object

Description

A function to get the cluster assignments for a given solution of a clusterforest object.

Usage

clusters(clusterforest, solution)

Arguments

clusterforest A clusterforest object
solution The solution for which cluster assignments should be returned. Default = 1

clusters.clusterforest

Get the cluster assignments for a solution of a clusterforest object

Description

A function to get the cluster assignments for a given solution of a clusterforest object.

Usage

## S3 method for class 'clusterforest'
clusters(clusterforest, solution = 1)

Arguments

clusterforest The clusterforest object
solution The solution
clusters.default  

Get the cluster assignments for a solution of a clusterforest object

Description

A function to get the cluster assignments for a given solution of a clusterforest object.

Usage

```r
## Default S3 method:
clusters(clusterforest, solution)
```

Arguments

- `clusterforest`: The clusterforest object
- `solution`: The solution

drugs  

Drug consumption data set

Description

A dataset collected by Fehrman et al. (2017), freely available on the UCI Machine Learning Repository (Lichman, 2013) containing records of 1885 respondents regarding their use of 18 types of drugs, and their measurements on 12 predictors. All predictors were originally categorical and were quantified by Fehrman et al. (2017). The meaning of the values can be found on https://archive.ics.uci.edu/ml/datasets/Drug+consumption+%28quantified%29. The original response categories for each drug were: never used the drug, used it over a decade ago, or in the last decade, year, month, week, or day. We transformed these into binary response categories, where 0 (non-user) consists of the categories never used the drug and used it over a decade ago and 1 (user) consists of all other categories.

Usage

```r
drugs
```

Format

A data frame with 1185 rows and 32 variables:

- **ID**: Respondent ID
- **Age**: Age of respondent
- **Gender**: Gender of respondent, where 0.48 denotes female and -0.48 denotes male
- **Edu**: Level of education of participant
Country  Country of current residence of participant  
Ethn   Ethnicity of participant  
Neuro  NEO-FFI-R Neuroticism score  
Extr   NEO-FFI-R Extraversion score  
Open   NEO-FFI-R Openness to experience score  
Agree  NEO-FFI-R Agreeableness score  
Consc  NEO-FFI-R Conscientiousness score  
Impul  Impulsiveness score measured by BIS-11  
Sensat Sensation seeking score measured by ImpSS  
Alc   Alcohol user (1) or non-user (0)  
Amphet  Amphetamine user (1) or non-user (0)  
Amyl   Amyl nitrite user (1) or non-user (0)  
Benzos Benzodiazepine user (1) or non-user (0)  
Caff   Caffeine user (1) or non-user (0)  
Can    Cannabis user (1) or non-user (0)  
Choco  Chocolate user (1) or non-user (0)  
Coke   Coke user (1) or non-user (0)  
Crack  Crack user (1) or non-user (0)  
Ecst   Ecstacy user (1) or non-user (0)  
Her    Heroine user (1) or non-user (0)  
Ket    Ketamine user (1) or non-user (0)  
Leghighs Legal Highs user (1) or non-user (0)  
LSD    LSD user (1) or non-user (0)  
Meth   Methadone user (1) or non-user (0)  
Mush   Magical Mushroom user (1) or non-user (0)  
Nico   Nicotine user (1) or non-user (0)  
Semeron Semeron user (1) or non-user (0), fictitious drug to identify over-claimers  
VSA    volatile substance abuse user(1) or non-user (0)

Source


References

medoidtrees (clusterforest)

Get the medoid trees for a solution of a clusterforest object

Description

A function to get the medoid trees for a given solution of a clusterforest object.

Usage

medoidtrees(clusterforest, solution)

Arguments

clusterforest  A clusterforest object
solution       The solution for which medoid trees should be returned. Default = 1
medoidtrees.default  Get the medoid trees for a solution of a clusterforest object

Description
A function to get the medoid trees for a given solution of a clusterforest object.

Usage
## Default S3 method:
medoidtrees(clusterforest, solution)

Arguments
clustemoer forest A clusterforest object
solution The solution for which medoid trees should be returned. Default = 1

plot.clusterforest  Plot a clusterforest object

Description
A function that can be used to plot a clusterforest object, either by returning plots with information on the cluster solutions (e.g., average silhouette width), or plots of the medoid trees of each solution.

Usage
## S3 method for class 'clusterforest'
plot(x, ..., solution = NULL, predictive_plots = FALSE)

Arguments
x A clusterforest object
... Additional arguments
solution The solution to plot the medoid trees from. Default = NULL
predictive_plots Indicating whether predictive plots should be returned: A plot showing the predictive accuracy when making predictions based on the medoid trees, and a plot of the agreement between the class label for each object predicted on the basis of the random forest as a whole versus based on the medoid trees. Default = FALSE.
Details

This function can be used to plot a clusterforest object in two ways. If it’s used with as only argument the clusterforest object, then the average silhouette width, agreement in predicted labels between medoids in solution and forest, and within cluster similarity measures are plotted for each solution. These plots may be helpful in deciding how many clusters are needed to summarize the forest (see Sies & Van Mechelen, 2020).

If the function is used with two arguments (the clusterforest object and the number of the solution), then the medoid tree(s) of that solution are plotted.

References


Examples

```r
require(MASS)
require(rpart)

#Function to draw a bootstrap sample from a dataset
DrawBoots <- function(dataset, i){
  set.seed(2394 + i)
  Boot <- dataset[sample(1:nrow(dataset), size = nrow(dataset), replace = TRUE),]
  return(Boot)
}

#Function to grow a tree using rpart on a dataset
GrowTree <- function(x,y,BootsSample, minsplit = 40, minbucket = 20, maxdepth =3){
  controlrpart <- rpart.control(minsplit = minsplit, minbucket = minbucket,
     maxdepth = maxdepth, maxsurrogate = 0, maxcompete = 0)
  tree <- rpart(as.formula(paste(noquote(paste(y, "~")),
     noquote(paste(x, collapse="+")))), data = BootsSample,
    control = controlrpart)
  return(tree)
}

#Use functions to draw 20 bootstrapsamples and grow a tree on each sample
Boots<- lapply(1:10, function(k) DrawBoots(Pima.tr ,k))
Trees <- lapply(1:10, function (i) GrowTree(x=c("npreg", "glu", "bp",
  "skin", "bmi", "ped", "age"), y="type",
  Boots[[i]] ))

ClusterForest<- clusterforest(observeddata=Pima.tr,treedata=Boots,trees=Trees,m=1,
fromclus=1, toclus=5, sameobs=FALSE)
plot(ClusterForest)
plot(ClusterForest,2)
```
print.clusterforest  
\textit{Print a clusterforest object}\n
\textbf{Description}\n
A function that can be used to print a clusterforest object.

\textbf{Usage}\n
\begin{verbatim}
## S3 method for class 'clusterforest'
print(x, ..., solution = 1)
\end{verbatim}

\textbf{Arguments}\n
\begin{itemize}
  \item \texttt{x} A clusterforest object
  \item \texttt{...} Additional arguments
  \item \texttt{solution} The solution to print the medoid trees from. Default = NULL
\end{itemize}

\textit{summary.clusterforest}  \textit{Summarize a clusterforest object}\n
\textbf{Description}\n
A function to summarize a clusterforest object.

\textbf{Usage}\n
\begin{verbatim}
## S3 method for class 'clusterforest'
summary(object, ...)
\end{verbatim}

\textbf{Arguments}\n
\begin{itemize}
  \item \texttt{object} A clusterforest object
  \item \texttt{...} Additional arguments
\end{itemize}
treesimilarities

Get the similarity matrix that was used to create a clusterforest object

Description

A function to get the similarity matrix used to obtain a clusterforest object.

Usage

treesimilarities(clusterforest)

Arguments

clusterforest  A clusterforest object
treesimilarities.default

Get the similarity matrix that was used to create a clusterforest object

Description

A function to get the similarity matrix used to obtain a clusterforest object.

Usage

## Default S3 method:
treesimilarities(clusterforest)

Arguments

clusterforest A clusterforest object

treesource

Mapping the tree clustering solution to a known source of variation underlying the forest

Description

A function that can be used to get insight into a clusterforest solution, in the case that there are known sources of variation underlying the forest. In case of a categorical covariate, it visualizes the number of trees from each value of the covariate that belong to each cluster. In case of a continuous covariate, it returns the mean and standard deviation of the covariate in each cluster.

Usage

treesource(clusterforest, solution)

Arguments

clusterforest The clusterforest object
solution The solution

Value

multiplot In case of categorical covariate, for each value of the covariate, a bar plot with the number of trees that belong to each cluster
heatmap In case of a categorical covariate, a heatmap with for each value of the covariate, the number of trees that belong to each cluster
clustermeans In case of a continuous covariate, the mean of the covariate in each cluster
clusterstds In case of a continuous covariate, the standard deviation of the covariate in each cluster
Examples

```r
require(rpart)

#Function to draw a bootstrap sample from a dataset
DrawBoots <- function(dataset, i){
  set.seed(2394 + i)
  Boot <- dataset[sample(1:nrow(dataset), size = nrow(dataset), replace = TRUE),]
  return(Boot)
}

#Function to grow a tree using rpart on a dataset
GrowTree <- function(x,y,BootsSample, minsplit = 40, minbucket = 20, maxdepth =3){
  controlrpart <- rpart.control(minsplit = minsplit, minbucket = minbucket, maxdepth = maxdepth,
                              maxsurrogate = 0, maxcompete = 0)
  tree <- rpart(as.formula(paste(noquote(paste(y, "~")), noquote(paste(x, collapse="+")))),
                data = BootsSample, control = controlrpart)
  return(tree)
}

#Draw bootstrap samples and grow trees
BootsA<- lapply(1:5, function(k) DrawBoots(data_Amphet,k))
BootsC<- lapply(1:5, function(k) DrawBoots(data_cocaine,k))
Boots = c(BootsA,BootsC)
TreesA <- lapply(1:5, function (i) GrowTree(x=c("Age", "Gender", "Edu", "Neuro", "Extr", "Open", "Agree", "Consc", "Impul","Sensat"), y="Amphet", BootsA[[i]])
TreesC <- lapply(1:5, function (i) GrowTree(x=c( "Age", "Gender", "Edu", "Neuro", "Extr", "Open", "Agree", "Consc", "Impul", "Sensat"), y="Coke", BootsC[[i]])
Trees=c(TreesA,TreesC)

#Cluster the trees
ClusterForest<- clusterforest(observeddata=drugs,treedata=Boots,trees=Trees,m=1,
fromclus=2, toclus=2, treecov=rep(c("Amphet","Coke"),each=5), sameobs=FALSE)

#Link cluster result to known source of variation
treesource(ClusterForest, 2)
```

**treesource.clusterforest**

Mapping the tree clustering solution to a known source of variation underlying the forest
Description

A function that can be used to get insight into a clusterforest solution, in the case that there is a known source of variation underlying the forest. It visualizes the number of trees from each source that belong to each cluster.

Usage

```r
## S3 method for class 'clusterforest'
treesource(clusterforest, solution)
```

Arguments

- `clusterforest`: The clusterforest object
- `solution`: The solution

Description

A function that can be used to get insight into a clusterforest solution, in the case that there is a known source of variation underlying the forest. It visualizes the number of trees from each source that belong to each cluster.

Usage

```r
## Default S3 method:
treesource(clusterforest, solution)
```

Arguments

- `clusterforest`: The clusterforest object
- `solution`: The solution
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