

Package ‘networktree’

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Title Recursive Partitioning of Network Models

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Description Network trees recursively partition the data with respect to covariates. Two network tree algorithms are available: model-based trees based on a multivariate normal model and nonparametric trees based on covariance structures. After partitioning, correlation-based networks (psychometric networks) can be fit on the partitioned data. For details see Jones, Mair, Simon, & Zeileis (2020) <[doi:10.1007/s11336-020-09731-4](https://doi.org/10.1007/s11336-020-09731-4)>.

Depends R (>= 3.5.0)

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LazyData true

Imports partykit, qgraph, stats, utils, Matrix, mvtnorm, Formula, grid, graphics, gridBase, reshape2

RoxygenNote 7.1.1

Suggests R.rsp, knitr, rmarkdown, fxregime, zoo

URL <https://paytonjjones.github.io/networktree/>

BugReports <https://github.com/paytonjjones/networktree/issues>

NeedsCompilation no

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comparetree	<i>comparetree</i>
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Description

Quickly compares two partitions of a networktree object

Usage

```
comparetree(
  tree,
  id1 = 2L,
  id2 = 3L,
  transform = "detect",
  highlights = 5,
  plot = FALSE,
  plot.type = c("compare", "subtract"),
  layout = "constrained",
  ...
)
```

Arguments

tree	a networktree object
id1	the first partition
id2	the second partition
transform	should stored correlation matrices be transformed to partial correlations or graphical lasso? Can be set to "cor", "pcor", or "glasso". Defaults to automatic detection
highlights	the number of comparisons to highlight
plot	plot a comparison of the two partitions?

plot.type	"compare" or "subtract". "compare" plots the two networks side by side. "subtract" subtracts network 2 from network 1, and plots a network where edge weights indicate the difference
layout	layout for the plots. The default "constrained" uses a FR layout from the full dataset
...	additional arguments passed to qgraph

Examples

```

set.seed(1)
d <- data.frame(trend = 1:200, foo = runif(200, -1, 1))
d <- cbind(d, rbind(
  rmvnorm::rmvnorm(100, mean = c(0, 0, 0),
    sigma = matrix(c(1, 0.5, 0.5, 0.5, 1, 0.5, 0.5, 0.5, 1), ncol = 3)),
  rmvnorm::rmvnorm(100, mean = c(0, 0, 0),
    sigma = matrix(c(1, 0, 0.5, 0, 1, 0.5, 0.5, 0.5, 1), ncol = 3))
))
colnames(d)[3:5] <- paste0("y", 1:3)

## Generate a networktree
tree1 <- networktree(nodevars=d[,3:5], splitvars=d[,1:2])

## Print out the structure
tree1

## Compare any two partitions
compartree(tree1, id1=2, id2=3, highlights=3)

## Add a comparison plot
compartree(tree1, id1=2, id2=3, plot=TRUE)

```

cortrafo

cortrafo

Description

An influence function that transforms the response variables (y_1, y_2, y_3, \dots) into scores relevant to the correlations, means, and/or variances.

For example, in the case of correlations the variables are transformed into a matrix of $(n^2-n)/2$ columns (e.g., the number of total correlations), and i rows, where i is the # of observations of y_1 , where the mean of each vector is equal to the correlation between y_1 and y_2 , y_1 and y_3 , etc.

Used internally in when `method="ctree"`.

Usage

```
cortrafo(data, weights, control, model, ...)
```


Examples

```

head(dass)

## Example networktree with DASS
data(dass)
## Select depression subscale
nodeVars <- colnames(dass)[(grep("_D", colnames(dass)))]
splitVars <- c("gender", "orientation", "race", "married", "engnat")
myTree<-networktree(dass[,nodeVars], dass[,splitVars])
myTree
plot(myTree)

```

getnetwork

getnetwork

Description

Easily extract a network from one of the nodes in a networktree object

Usage

```
getnetwork(tree, id = 1L, transform = "detect", verbose = FALSE, ...)
```

Arguments

tree	a networktree object
id	the node in the tree to extract. Use <code>summary(tree)</code> to see id numbers for each split
transform	should stored correlation matrices be transformed to partial correlations or graphical lasso? Can be set to "cor", "pcor", or "glasso". Defaults to automatic detection
verbose	should warnings and messages from transformation functions (qgraph) be printed?
...	arguments passed to qgraph (e.g., "tuning", "threshold")

Examples

```

set.seed(1)
d <- data.frame(trend = 1:200, foo = runif(200, -1, 1))
d <- cbind(d, rbind(
  mvtnorm::rmvnorm(100, mean = c(0, 0, 0),
    sigma = matrix(c(1, 0.5, 0.5, 0.5, 1, 0.5, 0.5, 0.5, 1), ncol = 3)),
  mvtnorm::rmvnorm(100, mean = c(0, 0, 0),

```

```

        sigma = matrix(c(1, 0, 0.5, 0, 1, 0.5, 0.5, 0.5, 1), ncol = 3))
    ))
    colnames(d)[3:5] <- paste0("y", 1:3)

    ## Now use the function
    tree1 <- networktree(nodevars=d[,3:5], splitvars=d[,1:2])

    getnetwork(tree1, id=1)

```

mvnfit

Maximum Likelihood Estimation for Multivariate Normal Model

Description

Fit a multivariate normal model without covariates or covariance restrictions. In addition to the (straightforward) parameter estimates the fitted log-likelihood and corresponding score contributions are computed.

Usage

```

mvnfit(
  y,
  x = NULL,
  start = NULL,
  weights = NULL,
  offset = NULL,
  model = c("correlation", "mean", "variance"),
  ...,
  estfun = FALSE,
  object = FALSE
)

```

Arguments

y	A matrix or data.frame where each row corresponds to a k-dim observation.
x	Not used yet
start	Not used yet
weights	Not used yet
offset	Not used yet
model	Vector of characters. Specifies which estimated parameters are returned.
...	Not used yet
estfun	Logical. Should the matrix of score contributions (aka estimating functions) be returned?
object	Not used yet

Details

Used internally in when method="mob"

networktree

networktree: Partitioning of network models

Description

Computes a tree model with networks at the end of branches. Can use model-based recursive partitioning or conditional inference.

Wraps the mob() and ctree() functions from the partykit package.

Usage

```
networktree(...)

## Default S3 method:
networktree(
  nodevars,
  splitvars,
  method = c("mob", "ctree"),
  model = "correlation",
  transform = c("cor", "pcor", "glasso"),
  na.action = na.omit,
  weights = NULL,
  ...
)

## S3 method for class 'formula'
networktree(
  formula,
  data,
  transform = c("cor", "pcor", "glasso"),
  method = c("mob", "ctree"),
  na.action = na.omit,
  model = "correlation",
  ...
)
```

Arguments

...	additional arguments passed to mob_control (mob) or ctree_control (ctree)
nodevars	the variables with which to compute the network. Can be vector, matrix, or dataframe
splitvars	the variables with which to test split the network. Can be vector, matrix, or dataframe

method	"mob" or "ctree"
model	can be any combination of c("correlation", "mean", "variance") splits are determined based on the specified characteristics
transform	should stored correlation matrices be transformed to partial correlations or a graphical lasso for plotting? Can be set to "cor" (default), "pcor", or "glasso"
na.action	a function which indicates what should happen when the data contain missing values (NAs).
weights	weights
formula	A symbolic description of the model to be fit. This should either be of type $y_1 + y_2 + y_3 \sim x_1 + x_2$ with node vectors y_1 , y_2 , and y_3 or $y \sim x_1 + x_2$ with a matrix response y . x_1 and x_2 are used as partitioning variables.
data	a data frame containing the variables in the model

References

Jones, P.J., Mair, P., Simon, T., Zeileis, A. (2020). Network trees: A method for recursively partitioning covariance structures. *Psychometrika*, 85(4), 926-945. <https://doi.org/10.1007/s11336-020-09731-4>

Examples

```
set.seed(1)
d <- data.frame(trend = 1:200, foo = runif(200, -1, 1))
d <- cbind(d, rbind(
  mvtnorm::rmvnorm(100, mean = c(0, 0, 0),
    sigma = matrix(c(1, 0.5, 0.5, 0.5, 1, 0.5, 0.5, 0.5, 1), ncol = 3)),
  mvtnorm::rmvnorm(100, mean = c(0, 0, 0),
    sigma = matrix(c(1, 0, 0.5, 0, 1, 0.5, 0.5, 0.5, 1), ncol = 3))
))
colnames(d)[3:5] <- paste0("y", 1:3)

## Now use the function
tree1 <- networktree(nodevars=d[,3:5], splitvars=d[,1:2])

## Formula interface
tree2 <- networktree(y1 + y2 + y3 ~ trend + foo, data=d)

## plot
plot(tree2)
plot(tree2, terminal_panel = "box")
plot(tree2, terminal_panel = "matrix")

## Conditional version
tree3 <- networktree(nodevars=d[,3:5], splitvars=d[,1:2],
  method="ctree")

## Change control arguments
tree4 <- networktree(nodevars=d[,3:5], splitvars=d[,1:2],
```

```
alpha=0.01)
```

```
plot.networktree      Plotting 'networktree' objects
```

Description

Wraps plot.party to plot a tree model with networks on the ends. Networks are plotted with qgraph, and additional arguments are passed there

Usage

```
## S3 method for class 'networktree'
plot(
  x,
  terminal_panel = NULL,
  transform = NULL,
  layout = "lock",
  sdbars = FALSE,
  tnex = 3,
  partyargs = list(),
  na.rm = TRUE,
  ...
)
```

Arguments

x	an object of type 'networktree'
terminal_panel	an optional panel function of the form function(node) plotting the terminal nodes. Alternatively, a panel generating function of class "grapcon_generator" that is called with arguments x and tp_args to set up a panel function. Or, a character choosing one of the implemented standard plots "graph", "box", "matrix" or "bar". The default (NULL) chooses an appropriate panel function depending on the "model" argument.
transform	"cor", "pcor", or "glasso". If set to NULL, transform detected from x
layout	network layout, passed to qgraph. Default "lock" computes spring layout for the full sample and applies this to all graphs
sdbars	if using a barplot, should std deviation error bars be plotted?
tnex	terminal node extension (passed to plot.party). To make the terminal plots bigger, increase this value.
partyargs	additional arguments (list format) passed to partykit::plot.party plotting function that takes partitioned data as input
na.rm	should NA values be removed prior to calculating relevant parameters?
...	additional arguments passed to qgraph or barplot

`predict.networktree` *Predict 'networktree' objects*

Description

Wraps `predict.party`

Usage

```
## S3 method for class 'networktree'
predict(object, newdata = NULL, type = c("node", "parameter"), ...)
```

Arguments

<code>object</code>	a fitted 'networktree'
<code>newdata</code>	An optional data frame in which to look for variables with which to predict. If omitted, the fitted values are used.
<code>type</code>	"node", or "parameter". Specifies whether to predict nodes (return value is a vector) or parameters (matrix).
<code>...</code>	not used

`print.networktree` *Printing 'networktree' objects*

Description

Wraps `print.modelparty` to print a tree model with networks on the ends.

Usage

```
## S3 method for class 'networktree'
print(x, parameters = FALSE, FUN = NULL, ...)
```

Arguments

<code>x</code>	an object of type 'networktree'
<code>parameters</code>	print parameters for each partition? See <code>getnetwork</code> function for extracting parameters conveniently
<code>FUN</code>	only evaluated if <code>parameters=TRUE</code> , passed to <code>print.modelparty</code>
<code>...</code>	additional arguments passed <code>print.modelparty</code>

tipi

Ten Item Personality Questionnaire

Description

This dataset includes 1899 online participants who participated in a questionnaire available through the Open Source Psychometrics Project (<https://openpsychometrics.org/>), an organization that maintains an open website for the public to take psychometric tests for educational and entertainment purposes

Usage

tipi

Format

a dataframe. Columns represent questionnaire items and rows represent individuals

Details

The Ten Item Personality Questionnaire (TIPI) is a brief inventory of the Big Five personality domains. Each personality domain is assessed with two items. One item measures the domain normally and the other item measures the domain in reverse (e.g., "reserved, quiet" for reverse extraversion).

Labels for TIPI items in this dataset correspond to the first letter of each Big Five personality domain (Extraversion, Neuroticism, Conscientiousness, Agreeableness, and Openness to experience), with the character "r" indicating items that measure the domain in reverse.

Also includes demographics such as education level, rearing environment (urban/suburban/rural), gender, English as a native language, age, religion, sexual orientation, race, voting status, marriage status, and number of children in one's family during childhood.

The dataset is publicly available at http://openpsychometrics.org/_rawdata/GCBS.zip and can be cited as:

OpenPsychometrics (2019). Generic Conspiracist Beliefs Scale Survey. Retrieved from http://openpsychometrics.org/_rawdata

Examples

```
head(tipi)
```

```
## Example networktree with TIPI
data(tipi)
nodeVars <- c("E", "A_r", "C", "N", "O", "E_r", "A", "C_r", "N_r", "O_r")
splitVars <- c("gender", "education", "engnat")
myTree<-networktree(tipi[,nodeVars], tipi[,splitVars])
myTree
plot(myTree)
```

`workaholic`*Workaholism and Psychiatric Symptoms*

Description

This dataset includes 16,426 workers who were assessed on symptoms of psychiatric disorders (ADHD, OCD, anxiety, depression) and workaholism.

Usage`workaholic`**Format**

a dataframe. Columns represent symptoms and rows represent individuals

Details

Scales: Adult ADHD Self-Report Scale, Obsession-Compulsive Inventory-Revised, Hospital Anxiety and Depression Scale, and the Bergen Work Addiction Scale.

Also includes demographics such as age, gender, work status, position, sector, annual income.

The dataset is publicly available at <https://doi.org/10.1371/journal.pone.0152978> and can be cited as:

Andreassen, C. S., Griffiths, M. D., Sinha, R., Hetland, J., & Pallesen, S. (2016). The relationships between workaholism and symptoms of psychiatric disorders: a large-scale cross-sectional study. *PLoS One*, 11, e0152978.

Examples

```
head(workaholic)
```

```
## Example networktree with OCI-R scale
data(workaholic)
nodeVars <- paste("OCIR", 1:18, sep="")
splitVars <- c("Workaholism_diagnosis", "Gender")
myTree<-networktree(workaholic[,nodeVars], workaholic[,splitVars])
myTree
plot(myTree)
```

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