Package ‘logicFS’

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R topics documented:

  data.logicfs .............................................................. 2
  getMatEval ............................................................. 3
  logic.bagging .......................................................... 3
  logic.oob ............................................................... 8
  logic.pimp ............................................................. 9
  logicFS ................................................................. 9
  logicFS-internal ...................................................... 14
  make.snp.dummy ...................................................... 14
Example Data of logicFS

data.logicfs contains two objects: a simulated matrix data.logicfs of 400 observations (rows)
and 15 variables (columns) and a vector cl.logicfs of length 400 containing the class labels of
the observations.

Each variable is categorical with realizations 1, 2 and 3. The first 200 observations are cases,
the remaining are controls. If one of the following expression is TRUE, then the corresponding
observation is a case:

SNP1 == 3
SNP2 == 1 AND SNP4 == 3
SNP3 == 3 AND SNP5 == 3 AND SNP6 == 1

where SNP1 is in the first column of data.logicfs, SNP2 in the second, and so on.

See Also

logic.bagging, logicFS
### getMatEval

**Evaluate Prime Implicants**

**Description**

Computes the values of prime implicants for observations for which the values of the variables composing the prime implicants are available.

**Usage**

```r
getMatEval(data, vec.primes, check = TRUE)
```

**Arguments**

- `data` a data frame in which each row corresponds to an observation, and each column to a binary variable.
- `vec.primes` a character vector naming the prime implicants that should be evaluated. Each of the variables composing these prime implicants must be represented by one column of `data`.
- `check` should some checks be done before the evaluation is performed? It is highly recommended not to change the default `check = TRUE`.

**Value**

A matrix in which each row corresponds to an observation (the same observations in the same order as in `data`, and each column to one of the prime implicants.

**Author(s)**

Holger Schwender, <holger.schwender@hhu.de>

### logic.bagging

**Bagged Logic Regression**

**Description**

A bagging and subsampling version of logic regression. Currently available for the classification, the linear regression, and the logistic regression approach of `logreg`. Additionally, an approach based on multinomial logistic regressions as implemented in `mlogreg` can be used if the response is categorical.
Usage

## Default S3 method:
logic.bagging(x, y, B = 100, useN = TRUE, ntrees = 1, nleaves = 8,
  glm.if.1tree = FALSE, replace = TRUE, sub.frac = 0.632,
  anneal.control = logreg.anneal.control(), oob = TRUE,
  onlyRemove = FALSE, prob.case = 0.5, importance = TRUE,
  score = c("DPO", "Conc", "Brier", "PL"), addMatImp = FALSE, fast = FALSE,
  neighbor = NULL, adjusted = FALSE, ensemble = FALSE, rand = NULL, ...)

## S3 method for class 'formula'
logic.bagging(formula, data, recdom = TRUE, ...)

Arguments

x
  a matrix consisting of 0's and 1's. Each column must correspond to a binary
  variable and each row to an observation. Missing values are not allowed.

y
  a numeric vector, a factor, or a vector of class Surv specifying the values of a
  response for all the observations represented in x, where no missing values are
  allowed in y. If a numeric vector, then y either contains the class labels (coded
  by 0 and 1) or the values of a continuous response depending on whether the
  classification or logistic regression approach of logic regression, or the linear
  regression approach, respectively, should be used. If the response is categorical,
  then y must be a factor naming the class labels of the observations. If the re-
  sponse is a (right-censored survival time), then y must be vector of class Surv
  (generated, e.g., with the function Surv from the R package survival).

B
  an integer specifying the number of iterations.

useN
  logical specifying if the number of correctly classified out-of-bag observations
  should be used in the computation of the importance measure. If FALSE, the
  proportion of correctly classified oob observations is used instead. Ignored if
  importance = FALSE. Also ignored in the survival case.

ntrees
  an integer indicating how many trees should be used.
  For a binary response: If ntrees is larger than 1, the logistic regression approach
  of logic regression will be used. If ntrees is 1, then by default the classification
  approach of logic regression will be used (see glm.if.1tree.)
  For a continuous response: A linear regression model with ntrees trees is fitted
  in each of the B iterations.
  For a categorical response: n.lev − 1 logic regression models with ntrees trees
  are fitted, where n.lev is the number of levels of the response (for details, see
  mlogreg).
  For a response of class Surv: A Cox proportional hazards regression model with
  ntrees trees is fitted in each of the B iterations.

nleaves
  a numeric value specifying the maximum number of leaves used in all trees
  combined. See the help page of the function logreg of the package LogicReg
  for details.

glm.if.1tree
  if ntrees is 1 and glm.if.1tree is TRUE the logistic regression approach of
  logic regression is used instead of the classification approach. Ignored if ntrees
  is not 1 or the response is not binary.
replace should sampling of the cases be done with replacement? If TRUE, a bootstrap sample of size length(cl) is drawn from the length(cl) observations in each of the B iterations. If FALSE, ceiling(sub.frac * length(cl)) of the observations are drawn without replacement in each iteration.

sub.frac a proportion specifying the fraction of the observations that are used in each iteration to build a classification rule if replace = FALSE. Ignored if replace = TRUE.

anneal.control a list containing the parameters for simulated annealing. See the help page of logreg.anneal.control in the LogicReg package.

oob should the out-of-bag error rate (classification and logistic regression) or the out-of-bag root mean square prediction error (linear regression), respectively, be computed?

onlyRemove should in the single tree case the multiple tree measure be used? If TRUE, the prime implicants are only removed from the trees when determining the importance in the single tree case. If FALSE, the original single tree measure is computed for each prime implicant, i.e. a prime implicant is not only removed from the trees in which it is contained, but also added to the trees that do not contain this interaction. Ignored in all other than the classification case.

prob.case a numeric value between 0 and 1. If the outcome of the logistic regression, i.e. the class probability, for an observation is larger than prob.case, this observation will be classified as case (or 1).

importance should the measure of importance be computed?

score a character string naming the score that should be used in the computation of the importance measure for a survival time analysis. By default, the distance between predicted outcomes (score = "DPO") proposed by Tietz et al (2018) is used in the determination of the importance of the variables. Alternatively, Harrell’s C-Index (“Conc”), the Brier score (“Brier”), or the predictive partial log-likelihood (“PL”) can be used.

addMatImp should the matrix containing the improvements due to the prime implicants in each of the iterations be added to the output? (For each of the prime implicants, the importance is computed by the average over the B improvements.) Must be set to TRUE, if standardized importances should be computed using vim.norm, or if permutation based importances should be computed using vim.signperm. If ensemble = TRUE and addMatImp = TRUE in the survival case, the respective score of the full model is added to the output instead of an improvement matrix.

fast should a greedy search (as implemented in logreg) be used instead of simulated annealing?

neighbor a list consisting of character vectors specifying SNPs that are in LD. If specified, all SNPs need to occur exactly one time in this list. If specified, the importance measures are adjusted for LD by considering the SNPs within a LD block as exchangeable.

adjusted logical specifying whether the measures should be adjusted for noise. Often, the interaction actually associated with the response is not exactly found in some iterations of logic bagging, but an interaction is identified that additionally contains one (or seldomly more) noise SNPs. If adjusted is set to TRUE, the values of the importance measure is corrected for this behaviour.
in the case of a survival outcome, should ensemble importance measures (as, e.g., in \texttt{randomSurvivalSRC} be used? If \texttt{FALSE}, importance measures analogous to the ones in the \texttt{logicFS} analysis of other outcomes are used (see Tietz et al., 2018).

\begin{verbatim}
logic.bagging

ensemble

in the case of a survival outcome, should ensemble importance measures (as, e.g., in \texttt{randomSurvivalSRC} be used? If \texttt{FALSE}, importance measures analogous to the ones in the \texttt{logicFS} analysis of other outcomes are used (see Tietz et al., 2018).

rand
numeric value. If specified, the random number generator will be set into a reproducible state.

formula
an object of class \texttt{formula} describing the model that should be fitted.

data
a data frame containing the variables in the model. Each row of data must correspond to an observation, and each column to a binary variable (coded by 0 and 1) or a factor (for details, see \texttt{recdom}) except for the column comprising the response, where no missing values are allowed in data. The response must be either binary (coded by 0 and 1), categorical, continuous, or a right-censored survival time. If a survival time, i.e. an object of class \texttt{Surv}, a Cox proportional hazard model is fitted in each of the B iterations of \texttt{logicFS}. If continuous, a linear model is fitted in each iterations. If categorical, the column of \texttt{data} specifying the response must be a factor. In this case, multinomial logic regressions are performed as implemented in \texttt{mlogreg}. Otherwise, depending on \texttt{ntrees} (and \texttt{glm.if.1tree}) the classification or the logistic regression approach of logic regression is used.

recdom
a logical value or vector of length \texttt{ncol(data)} comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If \texttt{recdom} is \texttt{TRUE} (and a logical value), then all factors/variables with three levels will be coded by two dummy variables as described in \texttt{make.snp.dummy}. Each level of each of the other factors (also factors specifying a SNP that shows only two genotypes) is coded by one indicator variable. If \texttt{recdom} is \texttt{FALSE} (and a logical value), each level of each factor is coded by an indicator variable. If \texttt{recdom} is a logical vector, all factors corresponding to an entry in \texttt{recdom} that is \texttt{TRUE} are assumed to be SNPs and transformed into two binary variables as described above. All variables corresponding to entries of \texttt{recdom} that are \texttt{TRUE} (no matter whether \texttt{recdom} is a vector or a value) must be coded either by the integers 1 (coding for the homozygous reference genotype), 2 (heterozygous), and 3 (homozygous variant), or alternatively by the number of minor alleles, i.e. 0, 1, and 2, where no mixing of the two coding schemes is allowed. Thus, it is not allowed that some SNPs are coded by 1, 2, and 3, and others are coded by 0, 1, and 2.

... for the \texttt{formula} method, optional parameters to be passed to the low level function \texttt{logic.bagging.default}. Otherwise, ignored.

Value

\texttt{logic.bagging} returns an object of class \texttt{logicBagger} containing

\begin{verbatim}
logreg.model
a list containing the B logic regression models,

inbag
a list specifying the B Bootstrap samples,

vim
an object of class \texttt{logicFS} (if \texttt{importance} = \texttt{TRUE}),

oob.error
the out-of-bag error (if \texttt{oob} = \texttt{TRUE}),

...

further parameters of the logic regression.
\end{verbatim}
Author(s)

Holger Schwender, <holger.schwender@hhu.de>; Tobias Tietz, <tobias.tietz@hhu.de>

References


See Also

predict.logicBagg, plot.logicBagg, logicFS

Examples

## Not run:
# Load data.
data(data.logicfs)
# For logic regression and hence logic.bagging, the variables must be binary. data.logicfs, however, contains categorical data with realizations 1, 2 and 3. Such data can be transformed into binary data by
bin.snps<-make.snp.dummy(data.logicfs)
# To speed up the search for the best logic regression models only a small number of iterations is used in simulated annealing.
my.anneal<-logreg.anneal.control(start=2,end=-2,iter=10000)
# Bagged logic regression is then performed by
bagg.out<-logic.bagging(bin.snps,cl.logicfs,B=20,nleaves=10,
                       rand=123, anneal.control=my.anneal)
# The output of logic.bagging can be printed
bagg.out
# By default, also the importances of the interactions are computed
bagg.out$vim
# and can be plotted.
plot(bagg.out)
# The original variable names are displayed in
plot(bagg.out,coded=FALSE)
# New observations (here we assume that these observations are...
logic.oob

Prime Implicants

Description

Computes the out-of-bag error of the classification rule comprised by a logicBagg object.

Usage

logic.oob(log.out, prob.case = 0.5)

Arguments

log.out an object of class logicBagg, i.e. the output of logic.bagging.
prob.case a numeric value between 0 and 1. If the logic regression models are logistic regression models, i.e. if in logic.bagging ntree is set to a value larger than 1, or glm.if.1tree is set to TRUE, then an observation will be classified as case (or more exactly, as 1) if the class probability is larger than prob.case.

Value

The out-of-bag error estimate.

Author(s)

Holger Schwender, <holger.schwender@hhu.de>

See Also

logic.bagging
logic.pimp

**Prime Implicants**

**Description**

Determines the prime implicants contained in the logic regression models comprised in an object of class `logicBagg`.

**Usage**

`logic.pimp(log.out)`

**Arguments**

- `log.out`: an object of class `logicBagg`, i.e., the output of `logic.bagging`.

**Details**

Since we are interested in all potentially interested interactions and not in a minimum set of them, `logic.pimp` and returns all prime implicants and not a minimum number of them.

**Value**

A list consisting of the prime implicants for each of the B logic regression models of `log.out`.

**Author(s)**

Holger Schwender, <holger.schwender@hhu.de>

**See Also**

`logic.bagging, logicFS, prime.implicants`

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logicFS

**Feature Selection with Logic Regression**

**Description**

Identification of interesting interactions between binary variables using logic regression. Currently available for the classification, the linear regression and the logistic regression approach of `logreg` and for a multinomial logic regression as implemented in `mlogreg`.
Usage

```r
## Default S3 method:
logicFS(x, y, B = 100, useN = TRUE, ntrees = 1, nleaves = 8,
glm.if.1tree = FALSE, replace = TRUE, sub.frac = 0.632,
anneal.control = logreg.anneal.control(), onlyRemove = FALSE,
prob.case = 0.5, score = c("DPO", "Conc", "Brier", "PL"),
addMatImp = TRUE, fast = FALSE, neighbor = NULL,
adjusted = FALSE, ensemble = FALSE, rand = NULL, ...)
```

```r
## S3 method for class 'formula'
logicFS(formula, data, recdom = TRUE, ...)
```

```r
## S3 method for class 'logicBagg'
logicFS(x, neighbor = NULL, adjusted = FALSE,
prob.case = 0.5, score = c("DPO", "Conc", "Brier", "PL"),
ensemble = FALSE, addMatImp = TRUE, ...)
```

Arguments

- **x**: a matrix consisting of 0’s and 1’s. Alternatively, x can also be an object of class logicBagg, i.e. the output of logic.bagging. If a matrix, each column must correspond to a binary variable and each row to an observation. Missing values are not allowed.

- **y**: a numeric vector, a factor, or a vector of class Surv specifying the values of a response for all the observations represented in x, where no missing values are allowed in y. If a numeric vector, then y either contains the class labels (coded by 0 and 1) or the values of a continuous response depending on whether the classification or logistic regression approach of logic regression, or the linear regression approach, respectively, should be used. If the response is categorical, then y must be a factor naming the class labels of the observations. If the response is a (right-censored survival time), then y must be vector of class Surv (generated, e.g., with the function Surv from the R package survival).

- **B**: an integer specifying the number of iterations.

- **useN**: logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If FALSE, the proportion of correctly classified out-of-bag observations is used instead. Ignored in the survival case.

- **ntrees**: an integer indicating how many trees should be used.

For a binary response: If ntrees is larger than 1, the logistic regression approach of logic regression will be used. If ntrees is 1, then by default the classification approach of logic regression will be used (see glm.if.1tree.)

For a continuous response: A linear regression model with ntrees trees is fitted in each of the B iterations.

For a categorical response: n.lev − 1 logic regression models with ntrees trees are fitted, where n.lev is the number of levels of the response (for details, see mlogreg).
For a response of class Surv: A Cox proportional hazards regression model with \ntrees trees is fitted in each of the B iterations.

**nleaves**

a numeric value specifying the maximum number of leaves used in all trees combined. For details, see the help page of the function logreg of the package LogicReg.

**glm.if.1tree**

if \ntrees is 1 and glm.if.1tree is TRUE the logistic regression approach of logic regression is used instead of the classification approach. Ignored if \ntrees is not 1, or the response is not binary.

**replace**

should sampling of the cases be done with replacement? If TRUE, a Bootstrap sample of size length(y) is drawn from the length(y) observations in each of the B iterations. If FALSE, ceiling(sub.frac * length(y)) of the observations are drawn without replacement in each iteration.

**sub.frac**

a proportion specifying the fraction of the observations that are used in each iteration to build a classification rule if replace = FALSE. Ignored if replace = TRUE.

**anneal.control**

a list containing the parameters for simulated annealing. See the help of the function logreg.anneal.control in the LogicReg package.

**onlyRemove**

should in the single tree case the multiple tree measure be used? If TRUE, the prime implicants are only removed from the trees when determining the importance in the single tree case. If FALSE, the original single tree measure is computed for each prime implicant, i.e. a prime implicant is not only removed from the trees in which it is contained, but also added to the trees that do not contain this interaction. Ignored in all other than the classification case.

**prob.case**

a numeric value between 0 and 1. If the outcome of the logistic regression, i.e. the predicted probability, for an observation is larger than prob.case this observations will be classified as case (or 1).

**score**

a character string naming the score that should be used in the computation of the importance measure for a survival time analysis. By default, the distance between predicted outcomes (score = "DPO") proposed by Tietz et al. (2018) is used in the determination of the importance of the variables. Alternatively, Harrell’s C-Index ("Conc"), the Brier score ("Brier"), or the predictive partial log-likelihood ("PL") can be used.

**addMatImp**

should the matrix containing the improvements due to the prime implicants in each of the iterations be added to the output? (For each of the prime implicants, the importance is computed by the average over the B improvements.) Must be set to TRUE, if standardized importances should be computed using vim.norm, or if permutation based importances should be computed using vim.signperm. If ensemble = TRUE and addMatImp = TRUE in the survival case, the respective score of the full model is added to the output instead of an improvement matrix.

**fast**

should a greedy search (as implemented in logreg) be used instead of simulated annealing?

**neighbor**

a list consisting of character vectors specifying SNPs that are in LD. If specified, all SNPs need to occur exactly one time in this list. If specified, the importance measures are adjusted for LD by considering the SNPs within a LD block as exchangable.
adjusted logical specifying whether the measures should be adjusted for noise. Often, the interaction actually associated with the response is not exactly found in some iterations of logic bagging, but an interaction is identified that additionally contains one (or seldomly more) noise SNPs. If adjusted is set to TRUE, the values of the importance measure is corrected for this behaviour.

ensemble in the case of a survival outcome, should ensemble importance measures (as, e.g., in randomSurvivalSRC) be used? If FALSE, importance measures analogous to the ones in the logicFS analysis of other outcomes are used (see Tietz et al., 2018).

rand numeric value. If specified, the random number generator will be set into a reproducible state.

formula an object of class formula describing the model that should be fitted.

data a data frame containing the variables in the model. Each row of data must correspond to an observation, and each column to a binary variable (coded by 0 and 1) or a factor (for details, see recdom) except for the column comprising the response, where no missing values are allowed in data. The response must be either binary (coded by 0 and 1), categorical, continuous, or a right-censored survival time. If a survival time, i.e., an object of class Surv, a Cox proportional hazard model is fitted in each of the B iterations of logicFS. If continuous, a linear model is fitted in each iterations. If categorical, the column of data specifying the response must be a factor. In this case, multinomial logic regressions are performed as implemented in mlogreg. Otherwise, depending on nntrees (and glm.if.1tree) the classification or the logistic regression approach of logic regression is used.

recdom a logical value or vector of length ncol(data) comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If recdom is TRUE (and a logical value), then all factors/variables with three levels will be coded by two dummy variables as described in make.snp.dummy. Each level of each of the other factors (also factors specifying a SNP that shows only two genotypes) is coded by one indicator variable. If recdom is FALSE (and a logical value), each level of each factor is coded by an indicator variable. If recdom is a logical vector, all factors corresponding to an entry in recdom that is TRUE are assumed to be SNPs and transformed into two binary variables as described above. All variables corresponding to entries of recdom that are TRUE (no matter whether recdom is a vector or a value) must be coded either by the integers 1 (coding for the homozygous reference genotype), 2 (heterozygous), and 3 (homozygous variant), or alternatively by the number of minor alleles, i.e. 0, 1, and 2, where no mixing of the two coding schemes is allowed. Thus, it is not allowed that some SNPs are coded by 1, 2, and 3, and others are coded by 0, 1, and 2.

... for the formula method, optional parameters to be passed to the low level function logicFS.default. Otherwise, ignored.

Value

An object of class logicFS containing

primes the prime implicants,
vim  
the proportion of logic regression models containing the prime implicants (or 
the neighbors of the prime implicants, if neighbor != NULL; or the extended 
primes of the prime implicants, if adjusted = TRUE; or the extended primes of 
the neighbors of the prime implicants, if neighbor != NULL and adjusted = 
TRUE),

prop  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

type  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

param  
the importance of the prime implicants,

mat.imp  
the importance of the prime implicants,

measure  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

neighbor  
the importance of the prime implicants,

useN  
the proportion of logic regression models containing the prime implicants (or 
the neighbors of the prime implicants, if neighbor != NULL; or the extended 
primes of the prime implicants, if adjusted = TRUE; or the extended primes of 
the neighbors of the prime implicants, if neighbor != NULL and adjusted = 
TRUE),

type  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

param  
the importance of the prime implicants,

mat.imp  
the proportion of logic regression models containing the prime implicants (or 
the neighbors of the prime implicants, if neighbor != NULL; or the extended 
primes of the prime implicants, if adjusted = TRUE; or the extended primes of 
the neighbors of the prime implicants, if neighbor != NULL and adjusted = 
TRUE),

measure  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

neighbor  
the importance of the prime implicants,

useN  
the proportion of logic regression models containing the prime implicants (or 
the neighbors of the prime implicants, if neighbor != NULL; or the extended 
primes of the prime implicants, if adjusted = TRUE; or the extended primes of 
the neighbors of the prime implicants, if neighbor != NULL and adjusted = 
TRUE),

threshold  
the type of model (1: classification, 2: linear regression, 3: logistic regression, 
4: Cox regression),

mu  
the importance of the prime implicants,
# To speed up the search for the best logic regression models
# only a small number of iterations is used in simulated annealing.
my.anneal<-logreg.anneal.control(start=2,end=-2,iter=10000)

# Feature selection using logic regression is then done by
log.out<-logicFS(bin.snps,cl.logicfs,B=20,nleaves=10,
rand=123,anneal.control=my.anneal)

# The output of logic.fs can be printed
log.out

# One can specify another number of interactions that should be
# printed, here, e.g., 15.
print(log.out,topX=15)

# The variable importance can also be plotted.
plot(log.out)

# And the original variable names are displayed in
plot(log.out,coded=FALSE)

## End(Not run)

---

### logicF5-internal

**Internal logicF5 functions**

**Description**

Internal logicF5 functions.

**Details**

These functions are not meant to be directly called by the user.

**Author(s)**

Holger Schwender, <holger.schwender@hhu.de>

---

### make.snp.dummy

**SNPs to Dummy Variables**

**Description**

Transforms SNPs into binary dummy variables.
Usage

```r
make.snp.dummy(data)
```  

Arguments

data

A matrix in which each column corresponds to a SNP and each row to an observation. The genotypes of all SNPs must be either coded by 1 (for the homozygous reference genotype), 2 (heterozygous), and 3 (homozygous variant) or by 0, 1, 2. It is not allowed that some SNPs following the 1, 2, 3 coding scheme and some SNPs the 0, 1, 2 coding. Missing values are allowed, but please note that neither `logic.bagging` nor `logicFS` can handle missing values so that the missing values need to be imputed (preferably before an application of `make.snp.dummy`).

Details

`make.snp.dummy` assumes that the homozygous dominant genotype is coded by 1, the heterozygous genotype by 2, and the homozygous recessive genotype by 3. Alternatively, the three genotypes can be coded by the number of minor alleles, i.e. by 0, 1, and 2. For each SNP, two dummy variables are generated:

- **SNP.1**: At least one of the bases explaining the SNP are of the recessive type.
- **SNP.2**: Both bases are of the recessive type.

Value

A matrix with `2*ncol(data)` columns containing 2 dummy variables for each SNP.

Note

See the R package `scrime` for more general functions for recoding SNPs.

Author(s)

Holger Schwender, <holger.schwender@hhu.de>

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**mlogreg**  

*Multinomial Logic Regression*

Description

Performs a multinomial logic regression for a nominal response by fitting a logic regression model (with logit as link function) for each of the levels of the response except for the level with the smallest value which is used as reference category.
Usage

```r
## S3 method for class 'formula'
mlogreg(formula, data, recdom = TRUE, ...)
## Default S3 method:
mlogreg(x, y, ntrees = 1, nleaves = 8, anneal.control = logreg.anneal.control(),
       select = 1, rand = NA, ...)
```

Arguments

- `formula`: an object of class `formula` describing the model that should be fitted.
- `data`: a data frame containing the variables in the model. Each column of `data` must correspond to a binary variable (coded by 0 and 1) or a factor (for details on factors, see `recdom`) except for the column comprising the response, and each row to an observation. The response must be a categorical variable with less than 10 levels. This response can be either a factor or of type numeric or character.
- `recdom`: a logical value or vector of length `ncol(data)` comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If `TRUE` (logical value), then all factors (variables) with three levels will be coded by two dummy variables as described in `make.snp.dummy`. Each level of each of the other factors (also factors specifying a SNP that shows only two genotypes) is coded by one indicator variable. If `FALSE` (logical value), each level of each factor is coded by an indicator variable. If `recdom` is a logical vector, all factors corresponding to an entry in `recdom` that is `TRUE` are assumed to be SNPs and transformed into the two binary variables described above. Each variable that corresponds to an entry of `recdom` that is `TRUE` (no matter whether `recdom` is a vector or a value) must be coded by the integers 1 (coding for the homozygous reference genotype), 2 (heterozygous), and 3 (homozygous variant).
- `x`: a matrix consisting of 0’s and 1’s. Each column must correspond to a binary variable and each row to an observation.
- `y`: either a factor or a numeric or character vector specifying the values of the response. The length of `y` must be equal to the number of rows of `x`.
- `ntrees`: an integer indicating how many trees should be used in the logic regression models. For details, see `logreg` in the LogicReg package.
- `nleaves`: a numeric value specifying the maximum number of leaves used in all trees combined. See the help page of the function `logreg` in the LogicReg package for details.
- `anneal.control`: a list containing the parameters for simulated annealing. For details, see the help page of `logreg.anneal.control` in the LogicReg package.
- `select`: numeric value. Either 0 for a stepwise greedy selection (corresponds to `select = 6` in `logreg`) or 1 for simulated annealing.
- `rand`: numeric value. If specified, the random number generator will be set into a reproducible state.
- `...`: for the `formula` method, optional parameters to be passed to the low level function `mlogreg.default`. Otherwise, ignored.
Value
An object of class mlogreg composed of

- **model**: a list containing the logic regression models,
- **data**: a matrix containing the binary predictors,
- **cl**: a vector comprising the class labels,
- **ntrees**: a numeric value naming the maximum number of trees used in the logic regressions,
- **nleaves**: a numeric value comprising the maximum number of leaves used in the logic regressions,
- **fast**: a logical value specifying whether the faster search algorithm, i.e., the greedy search, has been used.

Author(s)
Holger Schwender, <holger.schwender@hhu.de>

References

See Also
predict.mlogreg, logic.bagging, logicFS

---

**plot.logicFS**  
Variable Importance Plot

**Description**
Generates a dotchart of the importance of the most important interactions for an object of class logicFS or logicBagg.

**Usage**
```r
## S3 method for class 'logicFS'
plot(x, topX = 15, cex = 0.9, pch = 16, col = 1, show.prop = FALSE,
     force.topX = FALSE, coded = TRUE, add.thres = TRUE, thres = NULL,
     include0 = TRUE, add.v0 = TRUE, v0.col = "grey50", main = NULL, ...)

## S3 method for class 'logicBagg'
plot(x, topX = 15, cex = 0.9, pch = 16, col = 1, show.prop = FALSE,
     force.topX = FALSE, coded = TRUE, include0 = TRUE, add.v0 = TRUE,
     v0.col = "grey50", main = NULL, ...)
```
Arguments

- **x**: an object of either class `logicFS` or `logicBagg`.
- **topX**: integer specifying how many interactions should be shown. If `topX` is larger than the number of interactions contained in `x` all the interactions are shown. For further information, see `force.topX`.
- **cex**: a numeric value specifying the relative size of the text and symbols.
- **pch**: specifies the used symbol. See the help of `par` for details.
- **col**: the color of the text and the symbols. See the help of `par` for how colors can be specified.
- **show.prop**: if `TRUE` the proportions of models that contain the interactions of interest are shown. If `FALSE` (default) the importances of the interactions are shown.
- **force.topX**: if `TRUE` exactly `topX` interactions are shown. If `FALSE` (default) all interactions up to the `topX`th most important one and all interactions having the same importance as the `topX`th most important one are shown.
- **coded**: should the coded variable names be displayed? Might be useful if the actual variable names are pretty long. The coded variable name of the `j`-th variable is `Xj`.
- **add.thres**: should a vertical line marking the threshold for a prime implicant to be called important be drawn in the plot? If `TRUE`, this vertical line will be drawn at `NULL`.
- **thres**: non-negative numeric value specifying the threshold for a prime implicant to be called important. If `NULL` and `add.thres = TRUE`, the suggested threshold from `x` will be used.
- **include0**: should the x-axis include zero regardless whether the importances of the shown interactions are much higher than 0?
- **add.v0**: should a vertical line be drawn at `x = 0`? Ignored if `include0 = FALSE` and all importances are larger than zero.
- **v0.col**: the color of the vertical line at `x = 0`. See the help page of `par` for how colors can be specified.
- **main**: character string naming the title of the plot. If `NULL`, the name of the importance measure is used.
- **...**: Ignored.

Author(s)

Holger Schwender, <holger.schwender@hhu.de>

See Also

`logicFS`, `logic.bagging`
Description

Plots predicted survival or cumulative hazard curves of new observations for an object of class `predict.survivalFS`.

Usage

```r
## S3 method for class 'predict.survivalFS'
plot(x, select_obs, xlab = "time", ylab = NULL,
     ylim = NULL, type = "l", main = NULL, sub = NULL,
     vec_col = NULL, vec_lty = NULL, addLegend = TRUE, ...)
```

Arguments

- `x`: an object of class `predict.survivalFS` as generated by the function `predict.logicBagg`.
- `select_obs`: a numeric vector identifying the observations whose survival curves should be plotted. If `is.missing(select.obs)` the first five observations, or, if the number of observations is less than five, all observations are chosen.
- `xlab`: a title for the x axis: see `title`.
- `ylab`: a title for the y axis: see `title`. If `NULL`, the title is generated automatically.
- `ylim`: a numeric vector of length 2 that sets the limits of the y axis. If `NULL`, the limits are generated automatically.
- `type`: character indicating the type of plotting; actually any of the types as in `plot.default`.
- `main`: an overall title for the plot: see `title`. If `NULL`, the main title is generated automatically.
- `sub`: a sub title for the plot: see `title`. If `NULL`, the sub title is generated automatically.
- `vec_col`: a numeric or character vector that specifies the plotting colors of the survival curves (see `par`). Vector must have the same length as `select_obs`.
- `vec_lty`: a numeric or character vector that specifies the line types of the survival curves (see `par`). Vector must have the same length as `select_obs`.
- `addLegend`: should a legend be added to the plot automatically?
- `...`: Ignored.

Author(s)

Tobias Tietz, <tobias.tietz@hhu.de>
predict.logicBagg  

`predict.logicBagg`  

`Predict Method for logicBagg objects`

**Description**

Prediction for test data using an object of class `logicBagg`.

**Usage**

```r
## S3 method for class 'logicBagg'
predict(object, newData, prob.case = 0.5,
        type = c("class", "prob"), score = c("DPO", "Conc", "Brier"), ...)
```

**Arguments**

- `object`  
  an object of class `logicBagg`.

- `newData`  
  a matrix or data frame containing new data. If omitted `object\$data`, i.e. the original training data, are used. Each row of `newData` must correspond to a new observation. Each row of `newData` must contain the same variable as the corresponding column of the data matrix used in `logic.bagging`, i.e. `x` if the default method of `logic.bagging` has been used, or data without the column containing the response if the formula method has been used.

- `prob.case`  
  a numeric value between 0 and 1. A new observation will be classified as case (or more exactly, as 1) if the class probability, i.e. the average of the predicted probabilities of the models (if the logistic regression approach of logic regression has been used), or the percentage of votes for class 1 (if the classification approach of logic regression has been used) is larger than `prob.case`. Ignored if `type = "prob"` or the response is either quantitative or an object of class `Surv`.

- `type`  
  character vector indicating the type of output. If "class", a numeric vector of zeros and ones containing the predicted classes of the observations (using the specification of `prob.case`) will be returned. If "prob", the class probabilities or percentages of votes for class 1, respectively, for all observations are returned. Ignored if the response is quantitative or an object of class `Surv`.

- `score`  
  a character string naming the score that should be used to assess the performance of the prediction model in the survival case. By default, the distance between predicted outcomes (score = "DPO") proposed by Tietz et al. (2018) is used in the assessment of the prediction performance. Alternatively, Harrell’s C-Index ("Conc"), or the Brier score ("Brier") can be used. Furthermore, score determines whether a prediction for the cumulative hazard function (score = "DPO" or score = "Conc") or the survival function (score = "Brier") of the new observations should be made. Ignored in all other than the survival case.

- `...`  
  Ignored.
Value

A numeric vector containing the predicted classes (if type = "class") or the class probabilities (if type = "prob") of the new observations if the classification or the logistic regression approach of logic regression is used. If the response is quantitative, the predicted value of the response for all observations in the test data set is returned. If the response is of class Surv, an object of class predict.survivalFS with either an prediction for the cumulative hazard function or the survival function of the new observations is returned.

Author(s)

Holger Schwender, <holger.schwender@hhu.de>, Tobias Tietz, <tobias.tietz@hhu.de>

See Also

logic.bagging

predict.mlogreg  Predict Method for mlogreg Objects

Description

Prediction for test data using an object of class mlogreg.

Usage

```r
# S3 method for class 'mlogreg'
predict(object, newData, type = c("class", "prob"), ...)
```

Arguments

- **object**: an object of class mlogreg, i.e. the output of the function mlogreg.
- **newData**: a matrix or data frame containing new data. If omitted object\$data, i.e. the original training data, are used. Each row of newData must correspond to a new observation. Each row of newData must contain the same variable as the corresponding column of the data matrix used in mlogreg, i.e. x if the default method of mlogreg has been used, or data without the column containing the response if the formula method has been used.
- **type**: character vector indicating the type of output. If "class", a vector containing the predicted classes of the observations will be returned. If "prob", the class probabilities for each level and all observations are returned.
- **...**: Ignored.

Value

A numeric vector containing the predicted classes (if type = "class"), or a matrix composed of the class probabilities (if type = "prob").
Author(s)
Holger Schwender, <holger.schwender@hhu.de>

See Also
mlogreg

print.logicFS

Print a logicFS object

Description
Prints an object of class logicFS.

Usage
## S3 method for class 'logicFS'
print(x, topX = 5, show.prop = TRUE, coded = FALSE, digits = 2, ...)

Arguments

x
an object of either class logicFS.

topX
integer indicating how many interactions should be shown. Additionally to the topX most important interactions, any interaction having the same importance as the topX most important one are also shown.

show.prop
should the proportions of models containing the interactions of interest also be shown?

coded
should the coded variable names be displayed? Might be useful if the actual variable names are pretty long. The coded variable name of the $j$-th variable is $X_j$.

digits
number of digits used in the output.

... Ignored.

Author(s)
Holger Schwender, <holger.schwender@hhu.de>

See Also
logicFS, vim.logicFS
survivalFS

**Logic Feature Selection for Survival Data**

**Description**

Identification of interactions of binary variables associated with survival time using logic regression.

**Usage**

```r
## Default S3 method:
survivalFS(x, y, B = 20, replace = FALSE,
    sub.frac = 0.632, score = c("DPO", "Conc", "Brier", "PL"),
    addMatImp = TRUE, adjusted = FALSE, neighbor = NULL,
    ensemble = FALSE, rand = NULL, ...)

## S3 method for class 'formula'
survivalFS(formula, data, recdom = TRUE, ...)

## S3 method for class 'logicBagg'
survivalFS(x, score = c("DPO", "Conc", "Brier", "PL"),
    adjusted = FALSE, neighbor = NULL, ensemble = FALSE,
    addMatImp = TRUE, rand = NULL, ...)
```

**Arguments**

- `x`: a matrix consisting of 0’s and 1’s. Alternatively, `x` can also be an object of class `logicBagg`, i.e. the output of `logic.bagging`. If a matrix, each column must correspond to a binary variable and each row to an observation. Missing values are not allowed.

- `y`: a vector of class `Surv` specifying the right-censored survival time for all observations represented in `x`, where no missing values are allowed in `y`. This vector can, e.g., be generated using the function `Surv` from the R package `survival`.

- `B`: an integer specifying the number of iterations.

- `replace`: should sampling of the cases be done with replacement? If `TRUE`, a Bootstrap sample of size `length(y)` is drawn from the `length(y)` observations in each of the `B` iterations. If `FALSE`, ceiling(`sub.frac * length(y)`) of the observations are drawn without replacement in each iteration.

- `sub.frac`: a proportion specifying the fraction of the observations that are used in each iteration to build a classification rule if `replace = FALSE`. Ignored if `replace = TRUE`.

- `score`: a character string naming the score that should be used in the computation of the importance measure for a survival time analysis. By default, the distance between predicted outcomes (`score = "DPO"`) proposed by Tietz et al. (2018) is used in the determination of the importance of the variables. Alternatively, Harrell’s C-Index (“Conc”), the Brier score (“Brier”), or the predictive partial log-likelihood (“PL”) can be used.
addMatImp should the matrix containing the improvements due to the prime implicants in each of the iterations be added to the output if ensemble = FALSE? (For each of the prime implicants, the importance is computed by the average over the B improvements.) If ensemble = TRUE and addMatImp = TRUE, the respective score of the full model is added to the output instead of an improvement matrix.

adjusted logical specifying whether the measures should be adjusted for noise. Often, the interaction actually associated with the response is not exactly found in some iterations of logic bagging, but an interaction is identified that additionally contains one (or seldomly more) noise SNPs. If adjusted is set to TRUE, the values of the importance measure is corrected for this behaviour.

neighbor a list consisting of character vectors specifying SNPs that are in LD. If specified, all SNPs need to occur exactly one time in this list. If specified, the importance measures are adjusted for LD by considering the SNPs within a LD block as exchangable.

ensemble in the case of a survival outcome, should ensemble importance measures (as, e.g., in randomSurvivalSRC be used? If FALSE, importance measures analogous to the ones in the logicFS analysis of other outcomes are used (see Tietz et al., 2018).

rand numeric value. If specified, the random number generator will be set into a reproducible state.

formula an object of class formula describing the model that should be fitted.

data a data frame containing the variables in the model. Each row of data must correspond to an observation, and each column to a binary variable (coded by 0 and 1) or a factor (for details, see recdom) except for the column comprising the response, where no missing values are allowed in data. The response must be an object of class Surv.

recdom a logical value or vector of length ncol(data) comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If recdom is TRUE (and a logical value), then all factors/variables with three levels will be coded by two dummy variables as described in make.snp.dummy. Each level of each of the other factors (also factors specifying a SNP that shows only two genotypes) is coded by one indicator variable. If recdom isFALSE (and a logical value), each level of each factor is coded by an indicator variable. If recdom is a logical vector, all factors corresponding to an entry in recdom that is TRUE are assumed to be SNPs and transformed into two binary variables as described above. All variables corresponding to entries of recdom that are TRUE (no matter whether recdom is a vector or a value) must be coded either by the integers 1 (coding for the homozygous reference genotype), 2 (heterozygous), and 3 (homozygous variant), or alternatively by the number of minor alleles, i.e. 0, 1, and 2, where no mixing of the two coding schemes is allowed. Thus, it is not allowed that some SNPs are coded by 1, 2, and 3, and others are coded by 0, 1, and 2.

... further arguments of logicFS. Ignored, if x is an object of class logicBagg.

Value

An object of class logicFS containing
vim.approxPval

primes: the prime implicants,

vim: the importance of the prime implicants,

prop: the proportion of logic regression models containing the prime implicants, (or the neighbors of the prime implicants, if neighbor ! = NULL; or the extended primes of the prime implicants, if adjusted = TRUE; or the extended primes of the neighbors of the prime implicants, if neighbor ! = NULL and adjusted = TRUE),

type: the type of model (1: classification, 2: linear regression, 3: logistic regression, 4: Cox regression),

param: further parameters (if addInfo = TRUE),

mat.imp: either the matrix containing the improvements if addMatImp = TRUE and ensemble = FALSE, or the respective score of the full model if addMatImp = TRUE and ensemble = TRUE, or NULL if addMatImp = FALSE,

measure: the name of the used importance measure,

neighbor: neighbor,

useN: the value of useN,

threshold: NULL,

mu: NULL.

Author(s)

Tobias Tietz, <tobias.tietz@hhu.de>

References


See Also

logicFS, logic.bagging

vim.approxPval

Approximate P-Value Based Importance Measure

Description

Computes the importances based on an approximation to a t- or F-distribution.

Usage

vim.approxPval(object, version = 1, adjust = "bonferroni")
### Arguments

- **object**: an object of class `logicFS` which contains the values of standardized importances. Only in the linear regression case, the importances in `object` are allowed to be non-standardized.
- **version**: either 1 or 2. If 1, then the importance measure is computed by \( 1 - \text{padj} \), where `padj` is the adjusted p-value. If 2, the importance measure is determined by \(- \log_{10}(\text{padj})\), where a raw p-value equal to 0 is set to \( 1 / (10 \times \text{n.perm}) \) to avoid infinitive importances.
- **adjust**: character vector naming the method with which the raw permutation based p-values are adjusted for multiplicity. If "qvalue", the function `qvalue.cal` from the package `siggenes` is used to compute q-values. Otherwise, `p.adjust` is used to adjust for multiple comparisons. See `p.adjust` for all other possible specifications of `adjust`. If "none", the raw p-values will be used.

### Value

An object of class `logicFS` containing the same object as `object` except for
- **vim**: the values of the importance measure based on an approximation to the t- or F-distribution,
- **measure**: the name of the used importance measure,
- **threshold**: 0.95 if `version = 1`, and \(-\log_{10}(0.05)\) if `version = 2`.

### Author(s)

Holger Schwender, holger.schwender@hhu.de

### References


### See Also

- `logic.bagging`, `logicFS`, `vim.input`, `vim.set`, `vim.permSet`

---

**vim.chisq**  
*ChiSquare Based Importance*

### Description

Determining the importance of interactions found by `logic.bagging` or `logicFS` by Pearson’s ChiSquare Statistic. Only available for the classification and the logistic regression approach of logic regression.
vim.chisq

Usage

vim.chisq(object, data = NULL, cl = NULL)

Arguments

object

either an object of class logicFS or the output of an application of logic.bagging
with importance = TRUE.

data

a data frame or matrix consisting of 0's and 1's in which each column corre-
sponds to one of the explanatory variables used in the original analysis with
logic.bagging or logicFS, and each row corresponds to an observation. Must
be specified if object is an object of class logicFS, or cl is specified. If object
is an object of class logicBagg and neither data nor cl is specified, data and
cl stored in object is used to compute the ChiSquare statistics. It is, how-
ever, highly recommended to use new data to test the interactions contained in
object, as they have been found using the data stored in object, and it is very
likely that most of them will show up as interesting if they are tested on the same
data set.

c1

a numeric vector of 0's and 1's specifying the class labels of the observations
in data. Must be specified either if object is an object of class logicFS, or if
data is specified.

Details

Currently Pearson’s ChiSquare statistic is computed without continuity correction.

Contrary to vim.logicFS (and vim.norm and vim.signperm), vim.chisq does neither take
the logic regression models into account nor uses the out-of-bag observations for computing the
importances of the identified interactions. It “just” tests each of the found interactions on the whole data
set by calculating Pearson’s ChiSquare statistic for each of these interactions. It is, therefore, highly
recommended to use an independent data set for specifying the importances of these interactions
with vim.chisq.

Value

An object of class logicFS containing

primes

the prime implicants

vim

the values of Pearson’s ChiSquare statistic,

prop

NULL,

type

NULL,

param

further parameters (if object is the output of logicFS or vim.logicFS with
addInfo = TRUE),

mat.imp

NULL,

measure

"ChiSquare Based",

threshold

the 1 - 0.05/m quantile of the ChiSquare distribution with one degree of freedom,

mu

NULL.
**Author(s)**
Holger Schwender, <holger.schwender@hhu.de>

**See Also**
logic.bagging, logicFS, vim.logicFS, vim.norm, vim.ebam

---

**vim.ebam**  
*EBAM Based Importance*

**Description**
Determines the importance of interactions found by logic.bagging or logicFS by an Empirical Bayes Analysis of Microarrays (EBAM). Only available for the classification and the logistic regression approach of logic regression.

**Usage**

```r
text <- vim.ebam(object, data = NULL, cl = NULL, storeEBAM = FALSE, ...)
```

**Arguments**

- **object**  
either an object of class logicFS or the output of an application of logic.bagging with importance = TRUE.

- **data**  
a data frame or matrix consisting of 0's and 1's in which each column corresponds to one of the explanatory variables used in the original analysis with logic.bagging or logicFS, and each row corresponds to an observation. Must be specified if object is an object of class logicFS, or cl is specified. If object is an object of class logicBagg and neither data nor cl is specified, data and cl stored in object is used to compute the ChiSquare statistics. It is, however, highly recommended to use new data to test the interactions contained in object, as they have been found using the data stored in object, and it is very likely that most of them will show up as interesting if they are tested on the same data set.

- **cl**  
a numeric vector of 0’s and 1’s specifying the class labels of the observations in data. Must be specified either if object is an object of class logicFS, or if data is specified.

- **storeEBAM**  
logical specifying whether the output of the EBAM analysis should be stored in the output of vim.ebam.

- **...**  
further arguments of ebam and cat.ebam. For details, see the help files of these functions from the package siggenes.
Details

For each interaction found by logic.bagging or logicFS, the posterior probability that this interaction is significant is computed using the Empirical Bayes Analysis of Microarrays (EBAM). These posterior probabilities are used as the EBAM based importances of the interactions.

The test statistic underlying this EBAM analysis is Pearson’s ChiSquare statistic. Currently, the value of this statistic is computed without continuity correction.

Contrary to vim.logicFS (and vim.norm and vim.signperm), vim.ebam does neither take the logic regression models into account nor uses the out-of-bag observations for computing the importances of the identified interactions. It "just" tests each of the found interactions on the whole data set by calculating Pearson’s ChiSquare statistic for each of these interactions and performing an EBAM analysis. It is, therefore, highly recommended to use an independent data set for specifying the importances of these interactions with vim.ebam.

Value

An object of class logicFS containing

- `primes` the prime implicants,
- `vim` the posterior probabilities of the interactions,
- `prop` NULL,
- `type` NULL,
- `param` further parameters (if object is the output of logicFS or vim.logicFS with addInfo = TRUE),
- `mat.imp` NULL,
- `measure` "EBAM Based",
- `threshold` the value of delta used in the EBAM analysis (see help files for ebam); by default: 0.9,
- `mu` NULL,
- `ebam` an object of class EBAM (only available if storeEBAM = TRUE).

Author(s)

Holger Schwender, <holger.schwender@hhu.de>

References


See Also

logic.bagging, logicFS, vim.logicFS, vim.norm, vim.chisq
Description

Quantifies the importance of each input variable occurring in at least one of the logic regression models found in the application of `logic.bagging`.

Usage

```r
vim.input(object, useN = NULL, iter = NULL, prop = TRUE,
          standardize = NULL, mu = 0, addMatImp = FALSE,
          prob.case = 0.5, rand = NA)
```

Arguments

- **object**: an object of class `logicBagg`, i.e., the output of `logic.bagging`.
- **useN**: logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If `FALSE`, the proportion of correctly classified oob observations is used instead. If `NULL` (default), then the specification of `useN` in `object` is used.
- **iter**: integer specifying the number of times the values of the considered variable are permuted in the computation of its importance. If `NULL` (default), the values of the variable are not permuted, but the variable is removed from the model.
- **prop**: should the proportion of logic regression models containing the respective variable also be computed?
- **standardize**: should a standardized version of the importance measure for a set of variables be returned? By default, `standardize = TRUE` is used in the classification and the (multinomial) logistic regression case, and `standardize` is set to `FALSE` in the linear regression case. For details, see `mu`.
- **mu**: a non-negative numeric value. Ignored if `standardize = FALSE`. Otherwise, a t-statistic for testing the null hypothesis that the importance of the respective variable is equal to `mu` is computed.
- **addMatImp**: should the matrix containing the improvements due to each of the variables in each of the logic regression models be added to the output?
- **prob.case**: a numeric value between 0 and 1. If the logistic regression approach of logic regression has been used in `logic.bagging`, then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than `prob.case`. Otherwise, `prob.case` is ignored.
- **rand**: an integer for setting the random number generator in a reproducible case.
Value

An object of class logicFS containing

- `vim` the importances of the variables,
- `prop` the proportion of logic regression models containing the respective variable (if `prop = TRUE`) or NULL (if `prop = FALSE`),
- `primes` the names of the variables,
- `type` the type of model (1: classification, 2: linear regression, 3: logistic regression),
- `param` further parameters (if `addInfo = TRUE` in the previous call of logic.bagging),
- `mat.imp` either a matrix containing the improvements due to the variables for each of the models (if `addMatImp = TRUE`), or NULL (if `addMatImp = FALSE`),
- `measure` the name of the used importance measure,
- `useN` the value of `useN`,
- `threshold` NULL if `standardize = FALSE`, otherwise the $1 - 0.05/m$ quantile of the t-distribution with $B - 1$ degrees of freedom, where $m$ is the number of variables and $B$ is the number of logic regression models composing object,
- `mu` `mu` (if `standardize = TRUE`), or NULL (otherwise),
- `iter` `iter`.

Author(s)

Holger Schwender, <holger.schwender@hhu.de>

References


See Also

- logic.bagging, logicFS, vim.logicFS, vim.set, vim.ebam, vim.chisq

<table>
<thead>
<tr>
<th>vim.logicFS</th>
<th>Importance Measures</th>
</tr>
</thead>
</table>

Description

Computes the value of the single or the multiple tree measure, respectively, for each prime implicant contained in a logic bagging model to specify the importance of the prime implicant for classification, if the response is binary. If the response is quantitative, the importance is specified by a measure based on the log2-transformed mean square prediction error. If the response is a time to an event, performance measures for time-to-event models are employed to determine the importance measures.
Usage

```r
vim.logicFS(log.out, neighbor = NULL, adjusted = FALSE, useN = TRUE,
onlyRemove = FALSE, prob.case = 0.5, addInfo = FALSE,
score = c("DPO", "Conc", "Brier", "PL"), ensemble = FALSE,
addMatImp = TRUE)
```

Arguments

- **log.out**: an object of class `logicBagg`, i.e., the output of `logic.bagging`.
- **neighbor**: a list consisting of character vectors specifying SNPs that are in LD. If specified, all SNPs need to occur exactly one time in this list. If specified, the importance measures are adjusted for LD by considering the SNPs within a LD block as exchangeable.
- **adjusted**: logical specifying whether the measures should be adjusted for noise. Often, the interaction actually associated with the response is not exactly found in some iterations of logic bagging, but an interaction is identified that additionally contains one (or seldomly more) noise SNPs. If adjusted is set to TRUE, the values of the importance measure is corrected for this behaviour.
- **useN**: logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If FALSE, the proportion of correctly classified oob observations is used instead. Ignored in the survival case.
- **onlyRemove**: should in the single tree case the multiple tree measure be used? If TRUE, the prime implicants are only removed from the trees when determining the importance in the single tree case. If FALSE, the original single tree measure is computed for each prime implicant, i.e., a prime implicant is not only removed from the trees in which it is contained, but also added to the trees that do not contain this interaction. Ignored in all other than the classification case.
- **prob.case**: a numeric value between 0 and 1. If the logistic regression approach of logic regression is used (i.e., if the response is binary, and in `logic.bagging` `ntrees` is set to a value larger than 1, or `glm.if.1tree` is set to TRUE), then an observation will be classified as a case (or more exactly as 1), if the class probability of this observation estimated by the logic bagging model is larger than prob.case.
- **addInfo**: should further information on the logic regression models be added?
- **score**: a character string naming the score that should be used in the computation of the importance measure for a survival time analysis. By default, the distance between predicted outcomes (score = "DPO") proposed by Tietz et al. (2018) is used in the determination of the importance of the variables. Alternatively, Harrell’s C-Index ("Conc"), the Brier score ("Brier"), or the predictive partial log-likelihood ("PL") can be used.
- **ensemble**: in the case of a survival outcome, should ensemble importance measures (as, e.g., in `randomSurvivalSRC` be used? If FALSE, importance measures analogous to the ones in the logicFS analysis of other outcomes are used (see Tietz et al., 2018).
- **addMatImp**: should the matrix containing the improvements due to the prime implicants in each of the iterations be added to the output? (For each of the prime implicants,
the importance is computed by the average over the B improvements.) Must be set to TRUE, if standardized importances should be computed using `vim.norm`, or if permutation based importances should be computed using `vim.signperm`. If ensemble = TRUE and addMatImp = TRUE in the survival case, the respective score of the full model is added to the output instead of an improvement matrix.

Value

An object of class `logicFS` containing

- `primes` the prime implicants,
- `vim` the importance of the prime implicants,
- `prop` the proportion of logic regression models containing the prime implicants (or the neighbors of the prime implicants, if neighbor != NULL; or the extended primes of the prime implicants, if adjusted = TRUE; or the extended primes of the neighbors of the prime implicants, if neighbor != NULL and adjusted = TRUE),
- `type` the type of model (1: classification, 2: linear regression, 3: logistic regression, 4: Cox regression),
- `param` further parameters (if addInfo = TRUE),
- `mat.imp` either the matrix containing the improvements if addMatImp = TRUE and ensemble = FALSE, or the respective score of the full model if addMatImp = TRUE and ensemble = TRUE, or NULL if addMatImp = FALSE,
- `measure` the name of the used importance measure,
- `neighbor` neighbor,
- `useN` the value of useN,
- `threshold` NULL,
- `mu` NULL.

Author(s)

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References


See Also

`logic.bagging`, `logicFS`, `vim.norm`, `vim.signperm`
**vim.norm**

*Standardized and Sign-Permutation Based Importance Measure*

**Description**

Computes a standardized or a sign-permutation based version of either the Single Tree Measure, the Quantitative Response Measure, or the Multiple Tree Measure.

**Usage**

```r
vim.norm(object, mu = 0)

vim.signperm(object, mu = 0, n.perm = 10000, n.subset = 1000,
version = 1, adjust = "bonferroni", rand = NA)
```

**Arguments**

- `object` either the output of `logicFS` or `vim.logicFS` with `addMatImp = TRUE`, or the output of `logic.bagging` with `importance = TRUE` and `addMatImp = TRUE`.
- `mu` a non-negative numeric value against which the importances are tested. See Details.
- `n.perm` the number of sign permutations used in `vim.signperm`.
- `n.subset` an integer specifying how many permutations should be considered at once.
- `version` either 1 or 2. If 1, then the importance measure is computed by 1 - padj, where padj is the adjusted p-value. If 2, the importance measure is determined by -log10(padj), where a raw p-value equal to 0 is set to 1 / (10 * n.perm) to avoid infinitive importances.
- `adjust` character vector naming the method with which the raw permutation based p-values are adjusted for multiplicity. If "qvalue", the function `qvalue.cal` from the package `siggenes` is used to compute q-values. Otherwise, `p.adjust` is used to adjust for multiple comparisons. See `p.adjust` for all other possible specifications of `adjust`. If "none", the raw p-values will be used. For more details, see Details.
- `rand` an integer for setting the random number generator in a reproducible case.

**Details**

In both `vim.norm` and `vim.signperm`, a paired t-statistic is computed for each prime implicant, where the numerator is given by $VIM - \mu$ with VIM being the single or the multiple tree importance, and the denominator is the corresponding standard error computed by employing the B improvements of the considered prime implicant in the B logic regression models, where VIM is the mean over these B improvements.

Note that in the case of a quantitative response, such a standardization is not necessary. Thus, `vim.norm` returns a warning when the response is quantitative, and `vim.signperm` does not divide $VIM - \mu$ by its sample standard error.
Using $\mu = 0$ might lead to calling a prime implicant important, even though it actually shows only improvements of 1 or 0. When considering the prime implicants, it might be therefore be helpful to set $\mu$ to a value slightly larger than zero.

In vim.norm, the value of this t-statistic is returned as the standardized importance of a prime implicant. The larger this value, the more important is the prime implicant. (This applies to all importance measures – at least for those contained in this package.) Assuming normality, a possible threshold for a prime implicant to be considered as important is the $1 - 0.05/m$ quantile of the t-distribution with $B - 1$ degrees of freedom, where $m$ is the number of prime implicants.

In vim.signperm, the sign permutation is used to determine $n$.perm permuted values of the one-sample t-statistic, and to compute the raw p-values for each of the prime implicants. Afterwards, these p-values are adjusted for multiple comparisons using the method specified by adjust. The permutation based importance of a prime implicant is then given by $1 - $ these adjusted p-values. Here, a possible threshold for calling a prime implicant important is 0.95.

Value

An object of class logicFS containing

- **primes**: the prime implicants,
- **vim**: the respective importance of the prime implicants,
- **prop**: NULL,
- **type**: the type of model (1: classification, 2: linear regression, 3: logistic regression),
- **param**: further parameters (if addInfo = TRUE),
- **mat.imp**: NULL,
- **measure**: the name of the used importance measure,
- **useN**: the value of useN from the original analysis with, e.g., logicFS,
- **threshold**: the threshold suggested in Details,
- **mu**

Author(s)

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References


See Also

logic.bagging, logicFS, vim.logicFS, vim.chisq, vim.ebam
Permutation Based Importance Measures

Description
Computes the importances of input variables, SNPs, or sets of SNPs, respectively, based on permutations of the response. Currently only available for the classification and the logistic regression approach of logic regression.

Usage
vim.permInput(object, n.perm = NULL, standardize = TRUE, rebuild = FALSE, prob.case = 0.5, useAll = FALSE, version = 1, adjust = "bonferroni", addMatPerm = FALSE, rand = NA)

vim.permSNP(object, n.perm = NULL, standardize = TRUE, rebuild = FALSE, prob.case = 0.5, useAll = FALSE, version = 1, adjust = "bonferroni", addMatPerm = FALSE, rand = NA)

vim.permSet(object, set = NULL, n.perm = NULL, standardize = TRUE, rebuild = FALSE, prob.case = 0.5, useAll = FALSE, version = 1, adjust = "bonferroni", addMatPerm = FALSE, rand = NA)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>object</td>
<td>an object of class logicBagg, i.e. the output of logic.bagging.</td>
</tr>
<tr>
<td>set</td>
<td>either a list or a character or numeric vector.</td>
</tr>
<tr>
<td></td>
<td>If NULL (default), then it will be assumed that data, i.e. the data set used in the application of logic.bagging, has been generated using make.snp.dummy or similar functions for coding variables by binary variables, i.e. with a function that splits a variable, say SNPx, into the dummy variables SNPx.1, SNPx.2, ... (where the &quot;.&quot; can also be any other sign, e.g., an underscore).</td>
</tr>
<tr>
<td></td>
<td>If a character or a numeric vector, then the length of set must be equal to the number of variables used in object, i.e. the number of columns of data in the logicBagg object, and must specify the set to which a variable belongs either by an integer between 1 and the number of sets, or by a set name. If a variable should not be included in any of the sets, set the corresponding entry of set to NA. Using this specification of set it is not possible to assign a variable to more than one sets. For such a case, set set to a list (as follows).</td>
</tr>
<tr>
<td></td>
<td>If set is a list, then each object in this list represents a set of variables. Therefore, each object must be either a character or a numeric vector specifying either the names of the variables that belongs to the respective set or the columns of data that contains these variables. If names(set) is NULL, generic names will be employed as names for the sets. Otherwise, names(set) are used.</td>
</tr>
<tr>
<td>n.perm</td>
<td>number of permutations used in the computation of the importances. By default (i.e. if n.perm = NULL), 100 permutations are used if rebuild = TRUE and the</td>
</tr>
</tbody>
</table>
regression approach of logic regression has been used in `logic.bagging` (by setting `ntrees` to an integer larger than 1, or `glm.if.1tree = TRUE`). Otherwise, 1000 permutation are employed. Note that actually much more permutations should be used.

`standardize` should the standardized importance measure be used?

`rebuild` logical indicating whether the logic regression models should be rebuild (i.e., the parameters $\beta$ of the generalized linear models should be recomputed) after removing a variable or a set of variables from the logic trees and for each permutation of the response. Note that setting `rebuild = TRUE` increases the computation time substantially.

`prob.case` a numeric value between 0 and 1. If the logistic regression approach of logic regression has been used in `logic.bagging`, then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than `prob.case`. Otherwise, `prob.case` is ignored.

`useAll` logical indicating whether all $m \times n$.perm permuted values should be used in the computation of the permutation based p-values, where $m$ is the number of variables or sets of variables, respectively. If `FALSE`, the $n$.perm permuted values corresponding to the respective variable (or set of variables) are employed in the determination of the p-value of this variable (or set of variables).

`version` either 1 or 2. If 1, then the importance measure is computed by $1 - \text{padj}$, where \( \text{padj} \) is the adjusted p-value. If 2, the importance measure is determined by $-\log_{10}(\text{padj})$, where a raw p-value equal to 0 is set to $1 / (10 \times n$.perm) to avoid infinitive importances.

`adjust` character vector naming the method with which the raw permutation based p-values are adjusted for multiplicity. If “qvalue”, the function `qvalue.cal` from the package `siggenes` is used to compute q-values. Otherwise, `p.adjust` is used to adjust for multiple comparisons. See `p.adjust` for all other possible specifications of `adjust`. If “none”, the raw p-values will be used.

`addMatPerm` should the $(n$.perm + 1) x $m$ matrix containing the original values (first column) and the permuted values (the remaining columns) of the importance measure for the $m$ variables or $m$ sets of variables be added to the output?

`rand` an integer for setting the random number generator in a reproducible state.

**Value**

An object of class `logicFS` containing

- `vim` the values of the importance measure for the input variables, the SNPs, or the sets of SNPs, respectively,
- `prop` `NULL`,
- `primes` the names of the inputs, SNPs, or sets of variables, respectively,
- `type` the type of model (1: classification, 3: logistic regression),
- `param` `NULL`,
- `mat.imp` `NULL`,
- `measure` the name of the used importance measure,
threshold 0.95, i.e.
the suggested threshold for calling an input, SNP or set of SNPs, respectively, important (this is just used as default value when plotting the importances, see argument thres of plot.logicFS),
mu NULL,
useN TRUE,
name either "Variable", "SNP", or "Set",
mat.perm if addMatPerm = FALSE, NULL; otherwise, a matrix containing the original and the permuted values of the respective importance measure.

Author(s)

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References


See Also

logic.bagging, vim.input, vim.set, vim.signperm

vim.set  VIM for SNPs and Sets of Variables

Description

Quantifies the importances of SNPs or sets of variables, respectively, contained in a logic bagging model.

Usage

vim.snp(object, useN = NULL, iter = NULL, standardize = NULL, mu = 0, addMatImp = FALSE, prob.case = 0.5, score = c("DPO", "Conc", "Brier", "PL"), ensemble = FALSE, rand = NULL)

vim.set(object, set = NULL, useN = NULL, iter = NULL, standardize = NULL, mu = 0, addMatImp = FALSE, prob.case = 0.5, score = c("DPO", "Conc", "Brier", "PL"), ensemble = FALSE, rand = NULL)
Arguments

object  
an object of class `logicBagger`, i.e., the output of `logic.bagging`.

set  
either a list or a character or numeric vector.

If `NULL` (default), then it will be assumed that `data`, i.e., the data set used in the application of `logic.bagging`, has been generated using `make.snp.dummy` or similar functions for coding variables by binary variables, i.e., with a function that splits a variable, say SNPx, into the dummy variables SNPx.1, SNPx.2, ... (where the "." can also be any other sign, e.g., an underscore).

If a character or a numeric vector, then the length of `set` must be equal to the number of variables used in `object`, i.e., the number of columns of `data` in the `logicBagger` object, and must specify the set to which a variable belongs either by an integer between 1 and the number of sets, or by a set name. If a variable should not be included in any of the sets, set the corresponding entry of `set` to `NA`. Using this specification of `set` it is not possible to assign a variable to more than one sets. For such a case, set `set` to a list (as follows).

If `set` is a list, then each object in this list represents a set of variables. Therefore, each object must be either a character or a numeric vector specifying either the names of the variables that belongs to the respective set or the columns of `data` that contains these variables. If `names(set)` is `NULL`, generic names will be employed as names for the sets. Otherwise, `names(set)` are used.

useN  
logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If `FALSE`, the proportion of correctly classified oob observations is used instead. If `NULL` (default), then the specification of `useN` in `object` is used. In the survival case, `useN` is ignored.

iter  
integer specifying the number of times the values of the variables in the respective set are permuted in the computation of the importance of this set. If `NULL` (default), the values of the variables are not permuted, but all variables belonging to the set are removed from the model. Permutation of variables is not available in the survival case, i.e. `iter` is set to `NULL`.

standardize  
should a standardized version of the importance measure for a set of variables be returned? By default, `standardize = TRUE` is used in the classification and the (multinomial) logistic regression case, and `standardize` is set to `FALSE` in the linear regression case. Standardization is not available in the survival case. For details, see `mu`.

mu  
a non-negative numeric value. Ignored if `standardize = FALSE`. Otherwise, a t-statistic for testing the null hypothesis that the importance of the respective set is equal to `mu` is computed.

addMatImp  
should the matrix containing the improvements due to each of the sets in each of the logic regression models be added to the output? If `ensemble = TRUE` and `addMatImp = TRUE` in the survival case, the respective score of the full model is added to the output instead of an improvement matrix.

prob.case  
a numeric value between 0 and 1. If the logistic regression approach of logic regression has been used in `logic.bagging`, then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than `prob.case`. Otherwise, `prob.case` is ignored.
score a character string naming the score that should be used in the computation of the importance measure for a survival time analysis. By default, the distance between predicted outcomes (score = "DPO") proposed by Tietz et al. (2018) is used in the determination of the importance of the variables. Alternatively, Harrell’s C-Index ("Conc"), the Brier score ("Brier"), or the predictive partial log-likelihood ("PL") can be used.

ensemble in the case of a survival outcome, should ensemble importance measures (as, e.g., in randomSurvivalSRC be used? If FALSE, importance measures analogous to the ones in the logicFS analysis of other outcomes are used (see Tietz et al., 2018).

rand an integer for setting the random number generator in a reproducible state.

Value
An object of class logicFS containing

vim the importances of the sets of variables,
prop NULL,
primes the names of the sets of variables,
type the type of model (1: classification, 2: linear regression, 3: logistic regression, 4: Cox regression),
param further parameters (if addInfo = TRUE in the previous call of logic.bagging), or NULL (otherwise),
mat.imp either a matrix containing the improvements due to the sets of variables for each of the models (if addMatImp = TRUE and ensemble = FALSE), or the respective score of the full model (if addMatImp = TRUE and ensemble = TRUE, or NULL (if addMatImp = FALSE)),
measure the name of the used importance measure,
useN the value of useN,
threshold NULL if standardize = FALSE, otherwise the $1 - 0.05/m$ quantile of the t-distribution with $B - 1$ degrees of freedom, where $m$ is the number of sets and $B$ is the number of logic regression models composing object,
mu mu (if standardize = TRUE), or NULL (otherwise),
iter iter,
name "Set".

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References

vim.set

See Also

tagic.bagging, logicFS, vim.logicFS, vim.input, vim.ebam, vim.chisq
Index

* datasets
data.logicfs, 2
* hplot
  plot.logicFS, 17
* htest
  logic.oob, 8
  vim.approxPval, 25
  vim.chisq, 26
  vim.ebam, 28
  vim.input, 30
  vim.logicFS, 31
  vim.norm, 34
  vim.permSNP, 36
  vim.set, 38
* internal
  logicFS-internal, 14
* logic
  logic.pimp, 9
  vim.approxPval, 25
  vim.chisq, 26
  vim.ebam, 28
  vim.input, 30
  vim.logicFS, 31
  vim.norm, 34
  vim.permSNP, 36
  vim.set, 38
* manip
  make.snp.dummy, 14
* multivariate
  logicFS, 9
  survivalFS, 23
* print
  print.logicFS, 22
* regression
  logic.bagging, 3
  logicFS, 9
  mlogreg, 15
  predict.logicBagg, 20
  predict.mlogreg, 21
  survivalFS, 23
* survival
  plot.predict.survivalFS, 19
* tree
  logic.bagging, 3
  logicFS, 9
  mlogreg, 15
  survivalFS, 23
* utilities
  getMatEval, 3
  logic.oob, 8
  logic.pimp, 9
cl.logicfs(data.logicfs), 2
contr.none (logicFS-internal), 14
contr.snps (logicFS-internal), 14
data.logicfs, 2
getMatEval, 3
g getXy (logicFS-internal), 14
logic.bagging, 2, 3, 8–10, 13, 15, 17, 18, 20, 21, 23, 25, 26, 28, 29, 31, 33–38, 41
logic.oob, 8
logic.pimp, 9
logicFS, 2, 7, 9, 15, 17, 18, 22, 24–26, 28, 29, 31, 33–35, 41
logicFS-internal, 14
make.snp.dummy, 6, 12, 14, 16, 24, 36, 39
mlogreg, 4, 6, 10, 12, 15, 21, 22
par, 19
plot.default, 19
plot.logicBagg, 7
plot.logicBagg (plot.logicFS), 17
plot.logicFS, 13, 17, 38
plot.predict.survivalFS, 19
predict.logicBagg, 7, 20
INDEX

predict.logregmodel (logicFS-internal), 14
predict.mlogreg, 17, 21
prime.implicants, 9
print.logicBagg (logic.bagging), 3
print.logicFS, 22
print.mlogreg (mlogreg), 15
print.predict.survivalFS
(plot.predict.survivalFS), 19

survivalFS, 23
title, 19

vim.approxPval, 25
vim.chisq, 26, 29, 31, 35, 41
vim.ebam, 28, 28, 31, 35, 41
vim.individual (vim.input), 30
vim.input, 26, 30, 38, 41
vim.logicFS, 22, 27–29, 31, 31, 34, 35, 41
vim.norm, 5, 11, 27–29, 33, 34
vim.permInput (vim.permSNP), 36
vim.permSet, 26
vim.permSet (vim.permSNP), 36
vim.permSNP, 36
vim.set, 26, 31, 38, 38
vim.signperm, 5, 11, 27, 29, 33, 38
vim.signperm (vim.norm), 34
vim.singleBoth (logicFS-internal), 14
vim.singleRemove (logicFS-internal), 14
vim.snp (vim.set), 38