

# Package ‘logicFS’

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**Title** Identification of SNP Interactions

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**Depends** LogicReg, mcbiopi

**Suggests** genefilter, siggenes

**Description** Identification of interactions between binary variables using Logic Regression. Can, e.g., be used to find interesting SNP interactions. Contains also a bagging version of logic regression for classification.

**License** LGPL (>= 2)

**biocViews** SNP, Classification, Genetics

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data.logicfs	<i>Example Data of logicFS</i>
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### Description

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](#)

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getMatEval	<i>Evaluate Prime Implicants</i>
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### Description

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

### Usage

```
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@udo.edu>

---

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,
  addMatImp = FALSE, fast = 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 or a factor 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.
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.
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 <code>ntrees</code> trees is fitted in each of the <code>B</code> iterations.
	For a categorical response: $n.lev - 1$ logic regression models with <code>ntrees</code> trees are fitted, where $n.lev$ is the number of levels of the response (for details, see <a href="#">mlogreg</a> ).
<code>nleaves</code>	a numeric value specifying the maximum number of leaves used in all trees combined. See the help page of the function <code>logreg</code> of the package <code>LogicReg</code> for details.
<code>glm.if.1tree</code>	if <code>ntrees</code> is 1 and <code>glm.if.1tree</code> is TRUE the logistic regression approach of logic regression is used instead of the classification approach. Ignored if <code>ntrees</code> is not 1 or the response is not binary.
<code>replace</code>	should sampling of the cases be done with replacement? If TRUE, a bootstrap sample of size <code>length(c1)</code> is drawn from the <code>length(c1)</code> observations in each of the <code>B</code> iterations. If FALSE, <code>ceiling(sub.frac * length(c1))</code> of the observations are drawn without replacement in each iteration.
<code>sub.frac</code>	a proportion specifying the fraction of the observations that are used in each iteration to build a classification rule if <code>replace = FALSE</code> . Ignored if <code>replace = TRUE</code> .
<code>anneal.control</code>	a list containing the parameters for simulated annealing. See the help page of <code>logreg.anneal.control</code> in the <code>LogicReg</code> package.
<code>oob</code>	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?
<code>onlyRemove</code>	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.
<code>prob.case</code>	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 <code>prob.case</code> , this observations will be classified as case (or 1).
<code>importance</code>	should the measure of importance be computed?
<code>addMatImp</code>	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 <code>B</code> improvements.) Must be set to TRUE, if standardized importances should be computed using <a href="#">vim.norm</a> , or if permutation based importances should be computed using <a href="#">vim.signperm</a> .
<code>fast</code>	should a greedy search (as implemented in <code>logreg</code> ) be used instead of simulated annealing?
<code>rand</code>	numeric value. If specified, the random number generator will be set into a reproducible state.
<code>formula</code>	an object of class <code>formula</code> describing the model that should be fitted.
<code>data</code>	a data frame containing the variables in the model. Each row of <code>data</code> must correspond to an observation, and each column to a binary variable (coded by 0 and 1) or a factor (for details, see <code>recdom</code> ) except for the column comprising the response, where no missing values are allowed in <code>data</code> . The response must be either binary (coded by 0 and 1), categorical or continuous. If continuous, a linear model is fitted in each of the <code>B</code> iterations of <code>logicFS</code> . 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 `ntrees` (and `glm.if.1tree`) the classification or the logistic regression approach of logic regression is used.

<code>recdom</code>	a logical value or vector of length <code>ncol(data)</code> comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If <code>recdom</code> is TRUE (and a logical value), then all factors/variables with three levels will be coded by two dummy variables as described in <code>make.snp.dummy</code> . 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 <code>recdom</code> is FALSE (and a logical value), each level of each factor is coded by an indicator variable. If <code>recdom</code> is a logical vector, all factors corresponding to an entry in <code>recdom</code> that is TRUE are assumed to be SNPs and transformed into two binary variables as described above. All variables corresponding to entries of <code>recdom</code> that are TRUE (no matter whether <code>recdom</code> 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.
<code>...</code>	for the formula method, optional parameters to be passed to the low level function <code>logic.bagging.default</code> . Otherwise, ignored.

### Value

<code>logic.bagging</code>	returns an object of class <code>logicBagg</code> containing
<code>logreg.model</code>	a list containing the B logic regression models,
<code>inbagg</code>	a list specifying the B Bootstrap samples,
<code>vim</code>	an object of class <code>logicFS</code> (if <code>importance = TRUE</code> ),
<code>oob.error</code>	the out-of-bag error (if <code>oob = TRUE</code> ),
<code>...</code>	further parameters of the logic regression.

### Author(s)

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### References

- Ruczinski, I., Kooperberg, C., LeBlanc M.L. (2003). Logic Regression. *Journal of Computational and Graphical Statistics*, 12, 475-511.
- Schwender, H., Ickstadt, K. (2007). Identification of SNP Interactions Using Logic Regression. *Biostatistics*, 9(1), 187-198.

### 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
# in data.logicfs) are assigned to one of the classes by
predict(bagg.out,data.logicfs)

## End(Not run)
```

---

 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@udo.edu>

**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@udo.edu>

**See Also**

[logic.bagging](#), [logicFS](#), [prime.implicants](#)

## 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

```
## 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, addMatImp = TRUE, fast = FALSE, rand = NULL, ...)

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

## Arguments

<code>x</code>	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.
<code>y</code>	a numeric vector or a factor specifying the values of a response for all the observations represented in <code>x</code> , where missing values are not allowed in <code>y</code> . If a numeric vector, then <code>y</code> 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 <code>y</code> must be a factor naming the class labels of the observations.
<code>B</code>	an integer specifying the number of iterations.
<code>useN</code>	logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If <code>FALSE</code> , the proportion of correctly classified oob observations is used instead.
<code>ntrees</code>	an integer indicating how many trees should be used. For a binary response: If <code>ntrees</code> is larger than 1, the logistic regression approach of logic regression will be used. If <code>ntrees</code> is 1, then by default the classification approach of logic regression will be used (see <code>glm.if.1tree</code> .) For a continuous response: A linear regression model with <code>ntrees</code> trees is fitted in each of the <code>B</code> iterations. For a categorical response: $n.lev - 1$ logic regression models with <code>ntrees</code> trees are fitted, where $n.lev$ is the number of levels of the response (for details, see <a href="#">mlogreg</a> ).
<code>nleaves</code>	a numeric value specifying the maximum number of leaves used in all trees combined. For details, see the help page of the function <code>logreg</code> of the package <code>LogicReg</code> .



<code>glm.if.1tree</code>	if <code>ntrees</code> is 1 and <code>glm.if.1tree</code> is TRUE the logistic regression approach of logic regression is used instead of the classification approach. Ignored if <code>ntrees</code> is not 1, or the response is not binary.
<code>replace</code>	should sampling of the cases be done with replacement? If TRUE, a Bootstrap sample of size <code>length(c1)</code> is drawn from the <code>length(c1)</code> observations in each of the B iterations. If FALSE, <code>ceiling(sub.frac * length(c1))</code> of the observations are drawn without replacement in each iteration.
<code>sub.frac</code>	a proportion specifying the fraction of the observations that are used in each iteration to build a classification rule if <code>replace = FALSE</code> . Ignored if <code>replace = TRUE</code> .
<code>anneal.control</code>	a list containing the parameters for simulated annealing. See the help of the function <code>logreg.anneal.control</code> in the <code>LogicReg</code> package.
<code>onlyRemove</code>	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.
<code>prob.case</code>	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 <code>prob.case</code> this observations will be classified as case (or 1).
<code>addMatImp</code>	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 <code>vim.norm</code> , or if permutation based importances should be computed using <code>vim.signperm</code> .
<code>fast</code>	should a greedy search (as implemented in <code>logreg</code> ) be used instead of simulated annealing?
<code>rand</code>	numeric value. If specified, the random number generator will be set into a reproducible state.
<code>formula</code>	an object of class <code>formula</code> describing the model that should be fitted.
<code>data</code>	a data frame containing the variables in the model. Each row of <code>data</code> must correspond to an observation, and each column to a binary variable (coded by 0 and 1) or a factor (for details, see <code>recdom</code> ) except for the column comprising the response, where no missing values are allowed in <code>data</code> . The response must be either binary (coded by 0 and 1), categorical or continuous. If continuous, a linear model is fitted in each of the B iterations of <code>logicFS</code> . If categorical, the column of <code>data</code> specifying the response must be a factor. In this case, multinomial logic regressions are performed as implemented in <code>mlogreg</code> . Otherwise, depending on <code>ntrees</code> (and <code>glm.if.1tree</code> ) the classification or the logistic regression approach of logic regression is used.
<code>recdom</code>	a logical value or vector of length <code>ncol(data)</code> comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If <code>recdom</code> is TRUE (and a logical value), then all factors/variables with three levels will be coded by two dummy variables as described in <code>make.snp.dummy</code> . 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 <code>recdom</code> is FALSE (and a logical value), each level of each factor is coded by an indicator variable. If <code>recdom</code> is a logical vector, all factors corresponding to an entry in <code>recdom</code> 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

<code>primes</code>	the prime implicants,
<code>vim</code>	the importance of the prime implicants,
<code>prop</code>	the proportion of logic regression models that contain the prime implicants,
<code>type</code>	the type of model (1: classification, 2: linear regression, 3: logistic regression),
<code>param</code>	further parameters (if <code>addInfo = TRUE</code> ),
<code>mat.imp</code>	the matrix containing the improvements if <code>addMatImp = TRUE</code> , otherwise, <code>NULL</code> ,
<code>measure</code>	the name of the used importance measure,
<code>useN</code>	the value of <code>useN</code> ,
<code>threshold</code>	<code>NULL</code> ,
<code>mu</code>	<code>NULL</code> .

### Author(s)

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### References

- Ruczinski, I., Kooperberg, C., LeBlanc M.L. (2003). Logic Regression. *Journal of Computational and Graphical Statistics*, 12, 475-511.
- Schwender, H., Ickstadt, K. (2007). Identification of SNP Interactions Using Logic Regression. *Biostatistics*, 9(1), 187-198.

### See Also

[plot.logicFS](#), [logic.bagging](#)

### Examples

```
## Not run:
# Load data.
data(data.logicfs)

# For logic regression and hence logic.fs, 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)

# 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)

```

---

make.snp.dummy

*SNPs to Dummy Variables*


---

## Description

Transforms SNPs into binary dummy variables.

## Usage

```
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 <code>logic.bagging</code> nor <code>logicFS</code> can handle missing values so that the missing values need to be imputed (preferably before an application of <code>make.snp.dummy</code> ).
------	---

## 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  $2 * \text{ncol}(\text{data})$  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@udo.edu>

---

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**

```
## 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**

<code>formula</code>	an object of class <code>formula</code> describing the model that should be fitted.
<code>data</code>	a data frame containing the variables in the model. Each column of <code>data</code> must correspond to a binary variable (coded by 0 and 1) or a factor (for details on factors, see <code>recdom</code> ) 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 <code>numeric</code> or <code>character</code> .
<code>recdom</code>	a logical value or vector of length <code>ncol(data)</code> comprising whether a SNP should be transformed into two binary dummy variables coding for a recessive and a dominant effect. If <code>TRUE</code> (logical value), then all factors (variables) with three levels will be coded by two dummy variables as described in <code>make.snp.dummy</code> . 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 <code>FALSE</code> (logical value), each level of each factor is coded by an indicator variable. If <code>recdom</code> is a logical vector, all factors corresponding to an entry in <code>recdom</code> that is <code>TRUE</code> are assumed to be SNPs and transformed into the two binary variables described above. Each variable that corresponds to an entry of <code>recdom</code> that is <code>TRUE</code> (no matter whether <code>recdom</code> 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).

<code>x</code>	a matrix consisting of 0's and 1's. Each column must correspond to a binary variable and each row to an observation.
<code>y</code>	either a factor or a numeric or character vector specifying the values of the response. The length of <code>y</code> must be equal to the number of rows of <code>x</code> .
<code>ntrees</code>	an integer indicating how many trees should be used in the logic regression models. For details, see <code>logreg</code> in the <code>LogicReg</code> package.
<code>nleaves</code>	a numeric value specifying the maximum number of leaves used in all trees combined. See the help page of the function <code>logreg</code> in the <code>LogicReg</code> package for details.
<code>anneal.control</code>	a list containing the parameters for simulated annealing. For details, see the help page of <code>logreg.aneal.control</code> in the <code>LogicReg</code> package.
<code>select</code>	numeric value. Either 0 for a stepwise greedy selection (corresponds to <code>select = 6</code> in <code>logreg</code> ) or 1 for simulated annealing.
<code>rand</code>	numeric value. If specified, the random number generator will be set into a reproducible state.
<code>...</code>	for the <code>formula</code> method, optional parameters to be passed to the low level function <code>mlogreg.default</code> . Otherwise, ignored.

### Value

An object of class `mlogreg` composed of

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

### Author(s)

Holger Schwender, <holger.schwender@udo.edu>

### References

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

### 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

```
## 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 topXth most important one and all interactions having the same importance as the topXth 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 $X_j$ .
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@udo.edu>

**See Also**

[logicFS](#), [logic.bagging](#)

---

predict.logicBagg      *Predict Method for logicBagg objects*

---

**Description**

Prediction for test data using an object of class logicBagg.

**Usage**

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

**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 <a href="#">logic.bagging</a> , i.e.\ $x$ if the default method of <a href="#">logic.bagging</a> has been used, or data <i>without</i> 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 quantitative.
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.
...	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.

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**See Also**

[logic.bagging](#)

---

predict.mlogreg	<i>Predict Method for mlogreg Objects</i>
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---

**Description**

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

**Usage**

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

**Arguments**

object	an object of class <code>mlogreg</code> , i.e. the output of the function <code>mlogreg</code> .
newData	a matrix or data frame containing new data. If omitted <code>object\$data</code> , i.e. the original training data, are used. Each row of <code>newData</code> must correspond to a new observation. Each row of <code>newData</code> must contain the same variable as the corresponding column of the data matrix used in <code>mlogreg</code> , i.e. <code>x</code> if the default method of <code>mlogreg</code> has been used, or data <i>without</i> the column containing the response if the formula method has been used.
type	character vector indicating the type of output. If <code>"class"</code> , a vector containing the predicted classes of the observations will be returned. If <code>"prob"</code> , 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@udo.edu>

**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 <i>j</i> -th variable is X <sub>j</sub> .
digits	number of digits used in the output.
...	Ignored.

### Author(s)

Holger Schwender, <holger.schwender@udo.edu>

### See Also

[logicFS](#), [vim.logicFS](#)

---

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 <code>logicFS</code> which contains the values of standardized importances. Only in the linear regression case, the importances in <code>object</code> are allowed to be non-standardized.
version	either 1 or 2. If 1, then the importance measure is computed by $1 - \text{padj}$ , where <code>padj</code> 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 $1 / (10 * n.\text{perm})$ to avoid infinitive importances.
adjust	character vector naming the method with which the raw permutation based p-values are adjusted for multiplicity. If <code>"qvalue"</code> , the function <code>qvalue.cal</code> from the package <code>siggenes</code> is used to compute q-values. Otherwise, <code>p.adjust</code> is used to adjust for multiple comparisons. See <code>p.adjust</code> for all other possible specifications of <code>adjust</code> . If <code>"none"</code> , 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 <code>version = 1</code> , and $-\log_{10}(0.05)$ if <code>version = 2</code> .

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**References**

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

**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.

**Usage**

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

**Arguments**

object	either an object of class <code>logicFS</code> or the output of an application of <code>logic.bagging</code> with <code>importance = TRUE</code> .
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 <code>logic.bagging</code> or <code>logicFS</code> , and each row corresponds to an observation. Must be specified if object is an object of class <code>logicFS</code> , or <code>cl</code> is specified. If object is an object of class <code>logicBagg</code> and neither data nor <code>cl</code> is specified, data and <code>cl</code> 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 <code>logicFS</code> , 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

<code>primes</code>	the prime implicants
<code>vim</code>	the values of Pearson's ChiSquare statistic,
<code>prop</code>	NULL,
<code>type</code>	NULL,
<code>param</code>	further parameters (if object is the output of <code>logicFS</code> or <code>vim.logicFS</code> with <code>addInfo = TRUE</code> ),
<code>mat.imp</code>	NULL,
<code>measure</code>	"ChiSquare Based",
<code>threshold</code>	the 1 - 0.05/m quantile of the ChiSquare distribution with one degree of freedom,
<code>mu</code>	NULL.

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**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**

```
vim.ebam(object, data = NULL, cl = NULL, storeEBAM = FALSE, ...)
```

**Arguments**

<code>object</code>	either an object of class <code>logicFS</code> or the output of an application of <code>logic.bagging</code> with <code>importance = TRUE</code> .
<code>data</code>	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 <code>logic.bagging</code> or <code>logicFS</code> , and each row corresponds to an observation. Must be specified if <code>object</code> is an object of class <code>logicFS</code> , or <code>cl</code> is specified. If <code>object</code> is an object of class <code>logicBagg</code> and neither <code>data</code> nor <code>cl</code> is specified, <code>data</code> and <code>cl</code> stored in <code>object</code> is used to compute the ChiSquare statistics. It is, however, highly recommended to use new data to test the interactions contained in <code>object</code> , as they have been found using the data stored in <code>object</code> , and it is very likely that most of them will show up as interesting if they are tested on the same data set.
<code>cl</code>	a numeric vector of 0's and 1's specifying the class labels of the observations in <code>data</code> . Must be specified either if <code>object</code> is an object of class <code>logicFS</code> , or if <code>data</code> is specified.
<code>storeEBAM</code>	logical specifying whether the output of the EBAM analysis should be stored in the output of <code>vim.ebam</code> .
<code>...</code>	further arguments of <code>ebam</code> and <code>cat.ebam</code> . For details, see the help files of these functions from the package <code>siggenes</code> .

**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@udo.edu>

**References**

Schwender, H. and Ickstadt, K. (2008). Empirical Bayes Analysis of Single Nucleotide Polymorphisms. *BMC Bioinformatics*, 9:144.

**See Also**

[logic.bagging](#), [logicFS](#), [vim.logicFS](#), [vim.norm](#), [vim.chisq](#)

---

vim.input

*VIM for Inputs*

---

**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**

```
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 <code>logicBagg</code> , i.e.\ the output of <code>logic.bagg</code>
useN	logical specifying if the number of correctly classified out-of-bag observations should be used in the computation of the importance measure. If <code>FALSE</code> , the proportion of correctly classified oob observations is used instead. If <code>NULL</code> (default), then the specification of <code>useN</code> 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 <code>NULL</code> (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, <code>standardize = TRUE</code> is used in the classification and the (multinomial) logistic regression case, and <code>standardize</code> is set to <code>FALSE</code> in the linear regression case. For details, see <code>mu</code> .
mu	a non-negative numeric value. Ignored if <code>standardize = FALSE</code> . Otherwise, a t-statistic for testing the null hypothesis that the importance of the respective variable is equal to <code>mu</code> 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 <code>logic.bagg</code> , then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than <code>prob.case</code> . Otherwise, <code>prob.case</code> is ignored.
rand	an integer for setting the random number generator in a reproducible case.

**Value**

	An object of class <code>logicFS</code> containing
vim	the importances of the variables,
prop	the proportion of logic regression models containing the respective variable (if <code>prop = TRUE</code> ) or <code>NULL</code> (if <code>prop = FALSE</code> ),
primes	the names of the variables,
type	the type of model (1: classification, 2:linear regression, 3: logistic regression),
param	further parameters (if <code>addInfo = TRUE</code> in the previous call of <code>logic.bagg</code> ),
mat.imp	either a matrix containing the improvements due to the variables for each of the models (if <code>addMatImp = TRUE</code> ), or <code>NULL</code> (if <code>addMatImp = FALSE</code> ),
measure	the name of the used importance measure,
useN	the value of <code>useN</code> ,
threshold	<code>NULL</code> if <code>standardize = FALSE</code> , 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	<code>mu</code> (if <code>standardize = TRUE</code> ), or <code>NULL</code> (otherwise),
iter	<code>iter</code> .

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**References**

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

**See Also**

[logic.bagging](#), [logicFS](#), [vim.logicFS](#), [vim.set](#), [vim.ebam](#), [vim.chisq](#)

---

 vim.logicFS

*Importance Measures*


---

**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.

**Usage**

```
vim.logicFS(log.out, useN = TRUE, onlyRemove = FALSE, prob.case = 0.5,
            addInfo = FALSE, addMatImp = TRUE)
```

**Arguments**

log.out	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.
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 ntree 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?
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 <a href="#">vim.norm</a> , or if permutation based importances should be computed using <a href="#">vim.signperm</a> .

**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,
type	the type of model (1: classification, 2: linear regression, 3: logistic regression),
param	further parameters (if addInfo = TRUE),
mat.imp	the matrix containing the improvements if addMatImp = TRUE, otherwise, NULL,
measure	the name of the used importance measure,
useN	the value of useN,
threshold	NULL,
mu	NULL.

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**References**

Schwender, H., Ickstadt, K. (2007). Identification of SNP Interactions Using Logic Regression. *Biostatistics*, 9(1), 187-198.

**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**

```
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 <code>logicFS</code> or <code>vim.logicFS</code> with <code>addMatImp = TRUE</code> , or the output of <code>logic.bagging</code> with <code>importance = TRUE</code> and <code>addMatImp = TRUE</code> .
mu	a non-negative numeric value against which the importances are tested. See <code>Details</code> .
n.perm	the number of sign permutations used in <code>vim.signperm</code> .
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 $1 - \text{padj}$ , where <code>padj</code> 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 $1 / (10 * \text{n.perm})$ 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 <code>qvalue.cal</code> from the package <code>siggenes</code> is used to compute q-values. Otherwise, <code>p.adjust</code> is used to adjust for multiple comparisons. See <code>p.adjust</code> for all other possible specifications of <code>adjust</code> . If "none", the raw p-values will be used. For more details, see <code>Details</code> .
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

<code>primes</code>	the prime implicants,
<code>vim</code>	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., <a href="#">logicFS</a> ,
threshold	the threshold suggested in Details,
mu	mu.

**Author(s)**

Holger Schwender, <holger.schwender@udo.edu>

**References**

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

**See Also**

[logic.bagging](#), [logicFS](#), [vim.logicFS](#), [vim.chisq](#), [vim.ebam](#)

---

 vim.permSNP

*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**

object	an object of class <code>logicBagg</code> , i.e.\ the output of <code>logic.baggging</code> .
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 <code>logic.baggging</code> , has been generated using <code>make.snp.dummy</code> or similar functions for coding variables by binary variables, i.e.\ with a function that splits a variable, say <code>SNPx</code> , into the dummy variables <code>SNPx.1</code> , <code>SNPx.2</code> , ... (where the "." can also be any other sign, e.g., an underscore). If a character or a numeric vector, then the length of <code>set</code> must be equal to the number of variables used in <code>object</code> , i.e.\ the number of columns of data in the <code>logicBagg</code> 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 <code>set</code> to NA. Using this specification of <code>set</code> it is not possible to assign a variable to more than one sets. For such a case, set <code>set</code> to a list (as follows). If <code>set</code> 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 <code>names(set)</code> is NULL, generic names will be employed as names for the sets. Otherwise, <code>names(set)</code> are used.
n.perm	number of permutations used in the computation of the importances. By default (i.e.\ if <code>n.perm = NULL</code> ), 100 permutations are used if <code>rebuild = TRUE</code> and the regression approach of logic regression has been used in <code>logic.baggging</code> (by setting <code>ntrees</code> to an integer larger than 1, or <code>glm.if.1tree = TRUE</code> ). 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 <code>rebuild = TRUE</code> 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 <code>logic.baggging</code> , then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than <code>prob.case</code> . Otherwise, <code>prob.case</code> is ignored.
useAll	logical indicating whether all $m * n.perm$ 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 $1 - padj$ , where $padj$ is the adjusted p-value. If 2, the importance measure is determined by $-\log_{10}(padj)$ , 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 <code>qvalue.cal</code> from the package <code>siggenes</code> is used to compute q-values. Otherwise, <code>p.adjust</code> is used to adjust for multiple comparisons. See <code>p.adjust</code> for all other possible specifications of <code>adjust</code> . If "none", the raw p-values will be used.

addMatPerm	should the $(n.\text{perm} + 1) \times m$ 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 <code>thres</code> of <code>plot.logicFS</code> ),
mu	NULL,
useN	TRUE,
name	either "Variable", "SNP", or "Set",
mat.perm	if <code>addMatPerm = FALSE</code> , NULL; otherwise, a matrix containing the original and the permuted values of the respective importance measure.

### Author(s)

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### References

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

### 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, rand = NA)
```

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

**Arguments**

object	an object of class <code>logicBagg</code> , i.e.\ the output of <code>logic.bagging</code> .
set	either a list or a character or numeric vector. If <code>NULL</code> (default), then it will be assumed that data, i.e.\ the data set used in the application of <code>logic.bagging</code> , has been generated using <code>make.snp.dummy</code> or similar functions for coding variables by binary variables, i.e.\ with a function that splits a variable, say <code>SNPx</code> , into the dummy variables <code>SNPx.1</code> , <code>SNPx.2</code> , ... (where the "." can also be any other sign, e.g., an underscore). If a character or a numeric vector, then the length of <code>set</code> must be equal to the number of variables used in <code>object</code> , i.e.\ the number of columns of data in the <code>logicBagg</code> 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 <code>set</code> to <code>NA</code> . Using this specification of <code>set</code> it is not possible to assign a variable to more than one sets. For such a case, set <code>set</code> to a list (as follows). If <code>set</code> 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 <code>names(set)</code> is <code>NULL</code> , generic names will be employed as names for the sets. Otherwise, <code>names(set)</code> 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 <code>FALSE</code> , the proportion of correctly classified oob observations is used instead. If <code>NULL</code> (default), then the specification of <code>useN</code> in <code>object</code> is used.
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 <code>NULL</code> (default), the values of the variables are not permuted, but all variables belonging to the set are removed from the model
standardize	should a standardized version of the importance measure for a set of variables be returned? By default, <code>standardize = TRUE</code> is used in the classification and the (multinomial) logistic regression case, and <code>standardize</code> is set to <code>FALSE</code> in the linear regression case. For details, see <code>mu</code> .

mu	a non-negative numeric value. Ignored if <code>standardize = FALSE</code> . 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?
prob.case	a numeric value between 0 and 1. If the logistic regression approach of logic regression has been used in <code>logic.bagging</code> , then an observation will be classified as a case (or more exactly, as 1), if the class probability of this observation is larger than <code>prob.case</code> . Otherwise, <code>prob.case</code> is ignored.
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),
param	further parameters (if <code>addInfo = TRUE</code> in the previous call of <code>logic.bagging</code> ), or NULL (otherwise),
mat.imp	either a matrix containing the improvements due to the sets of variables for each of the models (if <code>addMatImp = TRUE</code> ), or NULL (if <code>addMatImp = FALSE</code> ),
measure	the name of the used importance measure,
threshold	NULL if <code>standardize = FALSE</code> , 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 <code>standardize = TRUE</code> ), or NULL (otherwise),
iter	iter.

### Author(s)

Holger Schwender, <holger.schwender@udo.edu>

### References

Schwender, H., Ruczinski, I., Ickstadt, K. (2011). Testing SNPs and Sets of SNPs for Importance in Association Studies. *Biostatistics*, 12, 18-32.

### See Also

[logic.bagging](#), [logicFS](#), [vim.logicFS](#), [vim.input](#), [vim.ebam](#), [vim.chisq](#)

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