

Package: rfVarImpOOB (via r-universe)

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Title Unbiased Variable Importance for Random Forests

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Depends R (>= 3.2.2), stats, randomForest

Imports ggplot2, ggpubr, dplyr,titanic,magrittr,ranger

Suggests knitr,rmarkdown

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Description Computes a novel variable importance for random forests: Impurity reduction importance scores for out-of-bag (OOB) data complementing the existing inbag Gini importance, see also <doi:10.1080/03610926.2020.1764042>. The Gini impurities for inbag and OOB data are combined in three different ways, after which the information gain is computed at each split. This gain is aggregated for each split variable in a tree and averaged across trees.

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LazyData true

VignetteBuilder knitr

NeedsCompilation no

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Repository https://markusloecher.r-universe.dev

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Accuracy	<i>computes accuracy of a vector</i>
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Description

Accuracy is defined as the proportion of correct labels

Usage

```
Accuracy(y, yHat, dig = 8)
```

Arguments

y	vector of categorical/nominal values
yHat	prediction/estimate
dig	number of digits

Value

Accuracy defined as proportion of values equal to majority

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
Accuracy(c(rep(0,9),1), 1)
```

```
Accuracy(c(rep(0,9),1), 0)
```

arabidopsis

Arabidopsis thaliana

Description

RNA editing is the process whereby RNA is modified from the sequence of the corresponding DNA template [1]. For instance, cytidine-to-uridine conversion (abbreviated C-to-U conversion) is common in plant mitochondria. The mechanisms of this conversion remain largely unknown, although the role of neighboring nucleotides is emphasized. Cummings and Myers [1] suggest to use information from sequence regions flanking the sites of interest to predict editing in *Arabidopsis thaliana*, *Brassic napus* and *Oryza sativa* based on random forests. The *Arabidopsis thaliana* data of [1] can be loaded from the journal Web site.

For each of the 876 observations, the data set gives

the response at the site of interest (binary: edited/not edited) and as potential predictor variables the 40 nucleotides at positions -20 to 20, relative to the edited site (4 categories), cp: the codon position (4 categories), fe: the estimated folding energy (continuous) and dfe: the difference in estimated folding energy between pre- edited and edited sequences (continuous).

Usage

```
arabidopsis
```

Format

Data frame with columns

edit binary:the response at the site of interest

X.k nucleotides at positions -k, relative to the edited site (4 categories)

Xk nucleotides at positions k, relative to the edited site (4 categories)

cp the codon position (4 categories),

fe the estimated folding energy (continuous)

dfe the difference in estimated folding energy between pre- edited and edited sequences (continuous)

Source

[1] Cummings, Michael P, and Daniel S Myers. Simple Statistical Models Predict C-to-U Edited Sites in Plant Mitochondrial RNA. BMC Bioinformatics, 2004, 7.

Examples

```
arabidopsis
```

```
GiniImportanceForest  computes inbag and OOB Gini importance averaged over all trees in
                        a forest
```

Description

workhorse function of this package

Usage

```
GiniImportanceForest(RF, data, ylabel = "Survived", zeroLeaf = TRUE,
                      agg = c("mean", "median", "none")[1], score = c("PMDI21",
                              "MDI", "MDA", "MIA")[1], Predictor = Mode, verbose = 0)
```

Arguments

RF	object returned by call to randomForest()
data	data which was used to train the RF. NOTE: assumes setting of inbag=TRUE while training
ylabel	name of dependent variable
zeroLeaf	if TRUE discard the information gain due to splits resulting in n=1
agg	method of aggregating importance scores across trees. If "none" return the raw arrays (for debugging)
score	scoring method:MDI=mean decrease impurity (Gini),MDA=mean decrease accuracy (permutation),MIA=mean increase accuracy
Predictor	function to estimate node prediction, such as Mode or mean or median. Alternatively, pass an array of numbers as replacement for the yHat column of tree
verbose	level of verbosity

Value

matrix with variable importance scores and their stdevs

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
data("titanic_train", package = "rfVarImp00B", envir = environment())

set.seed(123)

ranRows=sample(nrow(titanic_train), 300)

data=titanic_train[ranRows,]

RF = randomForest::randomForest(formula = Survived ~ Sex + Pclass + PassengerId,

                                data=data,

                                ntree=5,importance=TRUE,

                                mtry=3,keep.inbag=TRUE,

                                nodesize = 20)

data$Survived = as.numeric(data$Survived)-1

VI_Titanic = GiniImportanceForest(RF, data,ylab="Survived")
```

Description

computes importance scores for an individual tree.

These can be based on Gini impurity or Accuracy or logloss

Usage

```
GiniImportanceTree(bag, RF, k, ylabel = "Survived", returnTree = FALSE,
                    zeroLeaf = TRUE, score = c("PMDI21", "MDI", "MDA", "MIA")[1],
                    Predictor = Mode, verbose = 0)
```

Arguments

bag	data to compute the Gini gain for
RF	object returned by call to randomForest()
k	which tree
ylabel	name of dependent variable
returnTree	if TRUE returns the tree data frame otherwise the aggregated Gini importance grouped by split variables
zeroLeaf	if TRUE discard the information gain due to splits resulting in n=1
score	scoring method: PMDI=mean decrease penalized Gini impurity (note: the last digit is the exponent of the penalty!), MDI=mean decrease impurity (Gini), MDA=mean decrease accuracy (permutation), MIA=mean increase accuracy
Predictor	function to estimate node prediction, such as Mode or mean or median. Alternatively, pass an array of numbers as replacement for the yHat column of tree
verbose	level of verbosity

Value

if returnTree==TRUE returns the tree data frame otherwise the aggregated Gini importance grouped by split variables

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
rfTit = rfTitanic(nRows = 500,nodesize=10)

rfTit$data$Survived = as.numeric(rfTit$data$Survived)-1

k=1

tmp <- InOutBags(rfTit$RF, rfTit$data, k)

IndivTree =getTree(rfTit$RF,k)

#plot(as.party(tmp))#does not work

InTree = GiniImportanceTree(tmp$inbag,rfTit$RF,k,returnTree=TRUE)

OutTree = GiniImportanceTree(tmp$outbag,rfTit$RF,k,returnTree=TRUE)
```

gini_index

compute Gini impurity for binary values only

Description

simple function to compute simple or penalized Gini impurity

The "penalty" compares the class probabilities pHat with a reference estimate pEst which would typically serve as a prediction (e.g. in a tree node).

Usage

```
gini_index(pHat, pEst = NULL, k = 2, kind = 1, w = 2)
```

Arguments

pHat	probabilities from the current data,
pEst	estimated class probabilities (typically from an earlier inbag estimation). Only pass if you intend to compute the "validation-penalized Gini"
k	exponent of penalty term: $\text{abs}(\text{pHat}-\text{pEst})^k$
kind	kind of penalty
w	weights, default is 2 if you pass just a single probability instead of the vector (p,1-p)

Value

simple or penalized Gini impurity

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
#Test binary case:
```

```
gini_index(0.5,0.5,kind=1)
```

```
gini_index(0.9,0.1,kind=1)
```

```
gini_index(0.1,0.9,kind=1)
```

```
gini_index(0.5,0.5,kind=2)
```

```
gini_index(0.9,0.1,kind=2)
```

```
gini_index(0.1,0.9,kind=2)
```



```
gini_index(0.5,0.5,kind=3)
```

```
gini_index(0.9,0.1,kind=3)
```

```
gini_index(0.1,0.9,kind=3)
```

<code>gini_process</code>	<i>computes Gini index</i>
---------------------------	----------------------------

Description

computes Gini index

Usage

```
gini_process(classes, splitvar = NULL)
```

Arguments

<code>classes</code>	vector of factors/categorical vars
<code>splitvar</code>	split variable

Value

Gini index

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
#Test binary case:
```

```
#50/50split
```

```
gini_process(c(rep(0,10),rep(1,10)))#0.5 CORRECT !
```

```
#10/90split
```

```
gini_process(c(rep(0,1),rep(1,9)))#0.18= CORRECT !
```

```
#0/100split
```

```
gini_process(factor(c(rep(0,0),rep(1,10)), levels=c(0,1)))#0
```

```
#Test binary case:
```

```
#25/25/25/25 split
```

```
gini_process(factor(c(rep(0,5),rep(1,5),rep(2,5),
```

```
rep(3,5)), levels=c(0:3)))#0.75 = 4*0.25*0.75 CORRECT !
```

```
#10/10/10/70 split
```

```
gini_process(factor(c(rep(0,1),rep(1,1),rep(2,1),
```

```
rep(3,7)), levels=c(0:3)))#0.48 = 3*0.1*0.9+0.7*0.3 CORRECT !
```

```
#0/0/0/100 split
```

```
gini_process(factor(c(rep(0,0),rep(1,0),rep(2,0),
```

```
rep(3,20)), levels=c(0:3))#0. CORRECT !
```

InOutBags	<i>separates data into inbag and outbag</i>
-----------	---

Description

convenience function to mitigate risk of improperly disentangling train/test

NOTE: the original row names (too dangerous for repeated rows) are not kept but instead recorded in a separate column

Usage

```
InOutBags(RF, data, k, inclRowNames = TRUE, NullRowNames = TRUE,
          verbose = 0)
```

Arguments

RF	object returned by call to randomForest()
data	data which was used to train the RF. NOTE: assumes setting of inbag=TRUE while training
k	tree number
inclRowNames	create extra column of original row names
NullRowNames	if TRUE set row names to NULL
verbose	level of verbosity

Value

inbag and outbag subsets of the original data

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
rfTit = rfTitanic(nRows = 200,nodesize=10, ntree = 5)
```

```
k=1
```

```
tmp <- InOutBags(rfTit$RF, rfTit$data, k)
```

lpnorm*Compute the Lp norm of a vector.*

Description

Compute the Lp norm of a vector.

Usage

```
lpnorm(x, p = 2)
```

Arguments

x	vector to compute the Lp norm of
p	parameter of p norm

Value

Lp norm of a vector or NA

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
lpnorm(1:10)
```

```
lpnorm(matrix(1:25, 5, 5))
```

```
lpnorm(split(1:25, rep(1:5, each = 5)))
```

```
lpnorm(1:10, 1)
```

```
lpnorm(matrix(1:25, 5, 5), 1)
```

```
lpnorm(split(1:25, rep(1:5, each = 5)), 1)
```

```
lpnorm(rnorm(10), 0)
```

```
lpnorm(matrix(rnorm(25), 5, 5), 0)
```

```
lpnorm(split(rnorm(25), rep(1:5, each = 5)), 0)
```

```
lpnorm(-5:5, Inf)
```

```
lpnorm(matrix(-25:-1, 5, 5), Inf)
```

```
lpnorm(split(-25:-1, rep(1:5, each = 5)), Inf)
```

Description

computes log loss for multiclass problem

Usage

```
mlogloss(actual, pred_m, eps = 0.001)
```

Arguments

actual	integer vector with truth labels, values range from 0 to n - 1 classes
pred_m	predicted probs: column 1 => label 0, column 2 => label 1 and so on
eps	numerical cutoff taken very high

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
# require(nnet)

# set.seed(1)

# actual = as.integer(iris$Species) - 1

# fit = nnet(Species ~ ., data = iris, size = 2)

# pred = predict(fit, iris)#note this is a 3-column prediction matrix!

#

# mlogloss(actual, pred) # 0.03967

#library(titanic)

#baseline prediction
```

```
#data(titanic_train, package="titanic")

yHat = mean(titanic_train$Survived)#0.383838

mlogloss(titanic_train$Survived,yHat)

#try factors

titanic_train$Survived = as.factor(titanic_train$Survived)

mlogloss(titanic_train$Survived,yHat)
```

Mode	<i>computes the mode of an array</i>
------	--------------------------------------

Description

returns the mode of a vector

Usage

```
Mode(x)
```

Arguments

x vector to find mode of

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
Mode(rep(letters[1:3],1:3))
```

```
Mode(c(TRUE, TRUE, FALSE))
```

```
Mode(c(TRUE, TRUE, FALSE, FALSE))
```

plotVI *creates barplots for variable importances*

Description

creates barplots for variable importances

Usage

```
plotVI(VIbench, order_by = "Gini_00B", decreasing = TRUE)
```

Arguments

VIbench	matrix with importance scores as returned by GiniImportanceForest
order_by	how to order
decreasing	which direction to sort

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
data("titanic_train", package = "rfVarImp00B", envir = environment())
```

```
set.seed(123)
```

```
ranRows=sample(nrow(titanic_train), 300)
```

```
data=titanic_train[ranRows,]
```

```
RF = randomForest::randomForest(formula = Survived ~ Sex + Pclass + PassengerId,
```

```
data=data,
```



```

ntree=5, importance=TRUE,

mtry=3, keep.inbag=TRUE,

nodesize = 20)

data$Survived = as.numeric(data$Survived)-1

VI_Titanic = GiniImportanceForest(RF, data, ylab="Survived")

plotVI(VI_Titanic, decreasing = TRUE)

```

plotVI2 *creates barplots for variable importances*

Description

creates barplots for variable importances including permutation scores

Usage

```

plotVI2(VIbench, decreasing = TRUE, with_MDA = TRUE, ordered_by = "inbag",

score = "Gini Importance", horizontal = TRUE, fill = "order",

labelSize = 10, nrow = 3)

```

Arguments

VIbench	matrix with importance scores as returned by GiniImportanceForest
decreasing	which direction to sort
with_MDA	also visualize mean decrease in accuracy (permutation importance)
ordered_by	how to order
score	type of importance score: Gini, MIA,...

horizontal	horizontal barplot instead of vertical ?
fill	fill style for barplots; use e.g. <code>shQuote("blue")</code> to pass color strings
labelSize	size of axis labels
nrow	number of rows of ploztz arrangement

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
data("titanic_train", package = "rfVarImp00B", envir = environment())

set.seed(123)

ranRows=sample(nrow(titanic_train), 300)

data=titanic_train[ranRows,]

RF = randomForest::randomForest(formula = Survived ~ Sex + Pclass + PassengerId,

                                data=data,

                                ntree=5,importance=TRUE,

                                mtry=3,keep.inbag=TRUE,

                                nodesize = 20)

data$Survived = as.numeric(data$Survived)-1

VI_Titanic = GiniImportanceForest(RF, data,ylab="Survived")

plotVI2(VI_Titanic,decreasing = TRUE)
```



```
mtry=3,keep.inbag=TRUE,
nodesize = 1)

k=2

tree = randomForest::getTree(RF, k, labelVar = TRUE)

tree$node=NA

attr(tree, "rflib") = "randomForest"
inbag = rep(rownames(RF$inbag),time=RF$inbag[,k])

#trainBag=titanic_train[inbag,]

trainBag=titanic_train[ranRows,][inbag,]

tree=preorder2(1,trainBag,tree)
```

rfTitanic

fit a random forest model on the titanic data

Description

convenience function to reduce overhead of repeatedly fitting RF to titanic data

Usage

```
rfTitanic(formel = Survived ~ Sex + Pclass + PassengerId, nRows = 500,

ntree = 10, mtry = 3, nodesize = 1)
```

Arguments

formel	formula
nRows	subsampling size
ntree	number of trees
mtry	mtry
nodesize	nodesize

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

Examples

```
rfTit = rfTitanic(nRows = 500,nodesize=10)
```

splitBag	<i>splits the data from parent node into left and right children</i>
----------	--

Description

The function properly splits on factor levels

Usage

```
splitBag(treeRow, bag, tree)
```

Arguments

treeRow	current row of tree dataframe to be
bag	The data for the current row
tree	tree (from randomForest::getTree)

Value

list with elements left_daughter, right_daughter

Author(s)

Markus Loecher <Markus.Loecher@gmail.com>

titanic_train	<i>Titanic train data.</i>
---------------	----------------------------

Description

Titanic train data.

Usage

```
titanic_train
```

Format

Data frame with columns

PassengerId Passenger ID

Survived Passenger Survival Indicator

Pclass Passenger Class

Name Name

Sex Sex

Age Age

SibSp Number of Siblings/Spouses Aboard

Parch Number of Parents/Children Aboard

Ticket Ticket Number

Fare Passenger Fare

Cabin Cabin

Embarked Port of Embarkation

Source

<https://www.kaggle.com/c/titanic/data>

Examples

titanic_train

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