Package ‘ranktreeEnsemble’

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**Type** Package

**Title** Ensemble Models of Rank-Based Trees with Extracted Decision Rules

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**BugReports** https://github.com/TransBioInfoLab/ranktreeEnsemble/issues/

**License** GPL (>= 2)

**Depends** R (>= 3.5.0)

**Imports** Rcpp (>= 1.0.10), randomForestSRC, gbm, methods, data.tree

**LinkingTo** Rcpp

**Description** Fast computing an ensemble of rank-based trees via boosting or random forest on binary and multi-class problems. It converts continuous gene expression profiles into ranked gene pairs, for which the variable importance indices are computed and adopted for dimension reduction. Decision rules can be extracted from trees.

**URL** https://github.com/TransBioInfoLab/ranktreeEnsemble/

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**R topics documented:**

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extract.rules

**Description**

Extract rules from a random forest (rfsrc) object

**Usage**

```r
eextract.rules(object, subtrees = 5,
              treedepth = 2,
              digit = 2,
              pairs = TRUE)
```

**Arguments**

- `object`: A random forest (rfsrc) object
- `subtrees`: Number of trees to extract rules
- `treedepth`: Tree depth. The larger the number, the longer the extracted rules are.
- `digit`: Digit to be displayed in the extracted rules.
- `pairs`: Are variables in (object) generated from the `pair` function? Set `pairs = FALSE` to extract rules from regular random forest (rfsrc) object with continuous predictors.

**Value**

- `rule`: Interpretable extracted rules. Note that the performance score displayed is inaccurate based on few samples.
- `rule.raw`: Rules directly extracted from trees for prediction purpose
- `data`: Data used to grow trees from the argument (object).

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importance

References


Examples

data(tnbc)
obj <- rforest(subtype~, data = tnbc[1:100,c(1:5,337)])
objr <- extract.rules(obj)
objr$rule[,1:3]

### extract rules from a regular random forest
library(randomForestSRC)
obj2 <- rfsrc(subtype~, data = tnbc[1:100,c(1:5,337)])
objr2 <- extract.rules(obj2, pairs = FALSE)
objr2$rule[,1:3]

importance

<table>
<thead>
<tr>
<th>importance</th>
<th>Variable Importance Index for Each Predictor</th>
</tr>
</thead>
</table>

Description

The function computes variable importance for each predictor from a rank-based random forests model or boosting model. A higher value indicates a more important predictor. The random forest implementation was performed via the function vimp directly imported from the randomForestSRC package. Use the command package?randomForestSRC for more information. The boosting implementation was performed via the function relative.influence directly imported from the gbm package. For technical details, see the vignette: utils::browseVignettes("gbm")

Usage

importance(object, ...)

Arguments

| object | An object of class rfsrc generated from the function rforest or gbm generated from the function rboost. |
| ...    | Further arguments passed to or from other methods. |

Value

For the boosting model, a vector of variable importance values is given. For the random forest model, a matrix of variable importance values is given for the variable importance index for all the class labels, followed by the index for each class label.
Transform Continuous Variables into Ranked Binary Pairs

Description

The function transforms a dataset with \( p \) continuous predictors into \( \frac{p(p-1)}{2} \) binary predictors of ranked pairs.

Usage

\[
\text{pair(data, yvar.name = NULL)}
\]

Arguments

- **data**: A dataset with \( p \) continuous variables or with \( p + 1 \) variables including a dependent variable.
- **yvar.name**: The column name of the independent variable in data. By default, there is no dependent variable.

Value

A data frame with the transformed data. The dependent variable is moved to the last column of the data.
Note

The function is efficiently coded in C++.

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References


Examples

data(tnbc)
datp <- pair(tnbc[101:105,c(1:5,337)],"subtype")
datp
datp <- pair(tnbc[105:110,1:5])
datp

predict

Prediction or Extract Predicted Values for Random Forest, Random Forest Rule or Boosting Models

Description

Obtain predicted values using a random forest (rfsrc), random forest extracted rule (rules) or boosting (gbm) object. If no new data is provided, it extracts the out-of-bag predicted values of the outcome for the training data.

Usage

predict(object,
        newdata = NULL,
        newdata.pair = FALSE, ...)

Arguments

object An object of class rfsrc generated from the function rforest or gbm generated from the function rboost.
newdata Test data. If missing, the original training data is used for extracting the out-of-bag predicted values without running the model again.
newdata.pair Is newdata already converted into binary ranked pairs from the pair function?
... Further arguments passed to or from other methods.
Details

For the boosting (gbm) object, the cross-validation predicted values are provided if cv.folds>=2.

Value

value: Predicted value of the outcome. For the random forest (rfsrc) object, it is the predicted probability. For the boosting (gbm) object, it is the fitted values on the scale of regression function (e.g. log-odds scale). For the random forest extracted rule (rules) object, it is empty.

label: Predicted label of the outcome.

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References


Examples

data(tnbc)

# Random Forest

obj <- rforest(subtype~., data = tnbc[1:100,c(1:5,337)])
predict(obj)$label

predict(obj, tnbc[101:110,1:5])$label

datp <- pair(tnbc[101:110,1:5])
predict(obj, datp, newdata.pair = TRUE)$label

# Random Forest Extracted Rule

objr <- extract.rules(obj)
predict(objr)$label[1:5]
predict(obj, tnbc[101:110,1:5])$label

# Boosting

obj <- rboost(subtype~., data = tnbc[1:100,c(1:5,337)])
predict(obj)$label
predict(obj, tnbc[101:110,1:5])$label
Description

The package ranktreeEnsemble implements an ensemble of rank-based trees in boosting with the LogitBoost cost and random forests on both binary and multi-class problems. It converts continuous gene expression profiles into ranked gene pairs, for which the variable importance indices are computed and adopted for dimension reduction. Interpretable rules can be extracted from trees.

Author(s)

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References


Examples

```r
library(ranktreeEnsemble)
data(tnbc)
# performance of Random Rank Forest
obj <- rforest(subtype~., data = tnbc[,c(1:10,337)])
obj
# variable importance
importance(obj)
# predict new data from Random Rank Forest
predict(obj, tnbc[101:110,1:10])$label
# extract decision rules from rank-based trees
objr <- extract.rules(obj)
objr$rule[1:5,]
predict(objr, tnbc[101:110,1:10])$label
# filter decision rules with higher performance
objrs <- select.rules(objr,tnbc[110:130,c(1:10,337)])
predict(objrs, tnbc[101:110,1:10])$label
```
Generalized Boosted Modeling via Rank-Based Trees for Single Sample Classification with Gene Expression Profiles

Description

The function fits generalized boosted models via Rank-Based Trees on both binary and multi-class problems. It converts continuous gene expression profiles into ranked gene pairs, for which the variable importance indices are computed and adopted for dimension reduction. The boosting implementation was directly imported from the \texttt{gbm} package. For technical details, see the vignette: \texttt{utils::browseVignettes("gbm")}.

Usage

\begin{verbatim}
 rboost(
   formula, 
   data, 
   dimreduce = TRUE, 
   datrank = TRUE, 
   distribution = "multinomial", 
   weights, 
   ntree = 100, 
   nodedepth = 3, 
   nodesize = 5, 
   shrinkage = 0.05, 
   bag.fraction = 0.5, 
   train.fraction = 1, 
   cv.folds = 5, 
   keep.data = TRUE, 
   verbose = TRUE, 
   class.stratify.cv = TRUE, 
   n.cores = NULL
 )
\end{verbatim}

Arguments

- \texttt{formula}: Object of class 'formula' describing the model to fit.
- \texttt{data}: Data frame containing the y-outcome and x-variables.
- \texttt{dimreduce}: Dimension reduction via variable importance weighted forests. \texttt{FALSE} means no dimension reduction; \texttt{TRUE} means reducing 75\% variables before binary rank conversion and then fitting a weighted forest; a numeric value x\% between 0 and 1 means reducing x\% variables before binary rank conversion and then fitting a weighted forest.
- \texttt{datrank}: If using ranked raw data for fitting the dimension reduction model.
distribution  Either a character string specifying the name of the distribution to use: if the response has only 2 unique values, bernoulli is assumed; otherwise, if the response is a factor, multinomial is assumed.

weights  an optional vector of weights to be used in the fitting process. It must be positive but does not need to be normalized.

ntree  Integer specifying the total number of trees to fit. This is equivalent to the number of iterations and the number of basis functions in the additive expansion, which matches n.tree in the gbm package.

nodedepth  Integer specifying the maximum depth of each tree. A value of 1 implies an additive model. This matches interaction.depth in the gbm package.

nodesize  Integer specifying the minimum number of observations in the terminal nodes of the trees, which matches n.minobsinnode in the gbm package. Note that this is the actual number of observations, not the total weight.

shrinkage  a shrinkage parameter applied to each tree in the expansion. Also known as the learning rate or step-size reduction; 0.001 to 0.1 usually work, but a smaller learning rate typically requires more trees. Default is 0.05.

bag.fraction  the fraction of the training set observations randomly selected to propose the next tree in the expansion. This introduces randomness into the model fit. If bag.fraction < 1 then running the same model twice will result in similar but different fits. gbm uses the R random number generator so set.seed can ensure that the model can be reconstructed. Preferably, the user can save the returned gbm.object using save. Default is 0.5.

train.fraction  The first train.fraction * nrows(data) observations are used to fit the gbm and the remaining observations are used for computing out-of-sample estimates of the loss function.

cv.folds  Number of cross-validation folds to perform. If cv.folds>1 then gbm, in addition to the usual fit, will perform cross-validation and calculate an estimate of generalization error returned in cv.error.

keep.data  a logical variable indicating whether to keep the data and an index of the data stored with the object. Keeping the data and index makes subsequent calls to gbm.more faster at the cost of storing an extra copy of the dataset.

verbose  Logical indicating whether or not to print out progress and performance indicators (TRUE). If this option is left unspecified for gbm.more, then it uses verbose from object. Default is TRUE.

class.stratify.cv  Logical indicating whether or not the cross-validation should be stratified by class. The purpose of stratifying the cross-validation is to help avoid situations in which training sets do not contain all classes.

n.cores  The number of CPU cores to use. The cross-validation loop will attempt to send different CV folds off to different cores. If n.cores is not specified by the user, it is guessed using the detectCores function in the parallel package. Note that the documentation for detectCores makes clear that it is not failsafe and could return a spurious number of available cores.
Value

fit A vector containing the fitted values on the scale of regression function (e.g. log-odds scale for bernoulli).

train.error A vector of length equal to the number of fitted trees containing the value of the loss function for each boosting iteration evaluated on the training data.

valid.error A vector of length equal to the number of fitted trees containing the value of the loss function for each boosting iteration evaluated on the validation data.

cv.error If cv.folds < 2 this component is NULL. Otherwise, this component is a vector of length equal to the number of fitted trees containing a cross-validated estimate of the loss function for each boosting iteration.

oobag.improve A vector of length equal to the number of fitted trees containing an out-of-bag estimate of the marginal reduction in the expected value of the loss function. The out-of-bag estimate uses only the training data and is useful for estimating the optimal number of boosting iterations. See gbm.perf.

cv.fitted If cross-validation was performed, the cross-validation predicted values on the scale of the linear predictor. That is, the fitted values from the i-th CV-fold, for the model having been trained on the data in all other folds.

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References


Examples

data(tnbc)
obj <- rboost(subtype~, data = tnbc[,c(1:10,337)])
obj

---

rforest Random Forest via Rank-Based Trees for Single Sample Classification with Gene Expression Profiles

Description

The function implements the ensembled rank-based trees in random forests on both binary and multi-class problems. It converts continuous gene expression profiles into ranked gene pairs, for which the variable importance indices are computed and adopted for dimension reduction. The random forest implementation was directly imported from the randomForestSRC package. Use the command package?randomForestSRC for more information.
Usage

rforest(formula, data,
    dimreduce = TRUE,
    datrank = TRUE,
    ntree = 500, mtry = NULL,
    nodesize = NULL, nodedepth = NULL,
    splitrule = NULL, nsplit = NULL,
    importance = c(FALSE, TRUE, "none", "anti", "permute", "random"),
    bootstrap = c("by.root", "none"),
    membership = FALSE,
    na.action = c("na.omit", "na.impute"), nimpute = 1,
    perf.type = NULL,
    xvar.wt = NULL, yvar.wt = NULL, split.wt = NULL, case.wt = NULL,
    forest = TRUE,
    var.used = c(FALSE, "all.trees", "by.tree"),
    split.depth = c(FALSE, "all.trees", "by.tree"),
    seed = NULL,
    statistics = FALSE,
    ...
)

## convenient interface for growing a rank-based tree
rforest.tree(formula, data, dimreduce = FALSE,
    ntree = 1, mtry = ncol(data),
    bootstrap = "none", ...)

Arguments

formula Object of class 'formula' describing the model to fit. Interaction terms are not supported.
data Data frame containing the y-outcome and x-variables.
dimreduce Dimension reduction via variable importance weighted forests. FALSE means no dimension reduction; TRUE means reducing 75% variables before binary rank conversion and then fitting a weighted forest; a numeric value x% between 0 and 1 means reducing x% variables before binary rank conversion and then fitting a weighted forest.
datrank If using ranked raw data for fitting the dimension reduction model.
tree Number of trees.
mtry Number of variables to possibly split at each node. Default is number of variables divided by 3 for regression. For all other families (including unsupervised settings), the square root of number of variables. Values are rounded up.
nodesize Minimum size of terminal node. The defaults are: survival (15), competing risk (15), regression (5), classification (1), mixed outcomes (3), unsupervised (3). It is recommended to experiment with different nodesize values.
nodedepth Maximum depth to which a tree should be grown. Parameter is ignored by default.
splitrule Splitting rule (see below).
nsplit
Non-negative integer specifying number of random splits for splitting a variable. When zero, all split values are used (deterministic splitting), which can be slower. By default 10 is used.

importance
Method for computing variable importance (VIMP); see below. Default action is importance="none" but VIMP can be recovered later using vimp or predict.

bootstrap
Bootstrap protocol. Default is by.root which bootstraps the data by sampling without replacement. If none, the data is not bootstrapped (it is not possible to return OOB ensembles or prediction error in this case).

membership
Should terminal node membership and inbag information be returned?

na.action
Action taken if the data contains NA’s. Possible values are na.omit or na.impute. The default na.omit removes the entire record if any entry is NA. Selecting na.impute imputes the data (see below for details). Also see the function impute for fast imputation.

nimpute
Number of iterations of the missing data algorithm. Performance measures such as out-of-bag (OOB) error rates are optimistic if nimpute is greater than 1.

perf.type
Optional character value specifying metric used for predicted value, variable importance (VIMP), and error rate. Reverts to the family default metric if not specified. Values allowed for univariate/multivariate classification are: perf.type="misclass" (default), perf.type="brier" and perf.type="gmean".

xvar.wt
Vector of non-negative weights (does not have to sum to 1) representing the probability of selecting a variable for splitting. Default is uniform weights.

yvar.wt
Used for sending in features with custom splitting. For expert use only.

split.wt
Vector of non-negative weights used for multiplying the split statistic for a variable. A large value encourages the node to split on a specific variable. Default is uniform weights.

case.wt
Vector of non-negative weights (does not have to sum to 1) for sampling cases. Observations with larger weights will be selected with higher probability in the bootstrap (or subsampled) samples. It is generally better to use real weights rather than integers. See the breast data example below illustrating its use for class imbalanced data.

forest
Save key forest values? Used for prediction on new data and required by many of the package functions. Turn this off if you are only interested in training a forest.

var.used
Return statistics on number of times a variable split? Default is FALSE. Possible values are all.trees which returns total number of splits of each variable, and by.tree which returns a matrix of number a splits for each variable for each tree.

split.depth
Records the minimal depth for each variable. Default is FALSE. Possible values are all.trees which returns a matrix of the average minimal depth for a variable (columns) for a specific case (rows), and by.tree which returns a three-dimensional array recording minimal depth for a specific case (first dimension) for a variable (second dimension) for a specific tree (third dimension).

seed
Negative integer specifying seed for the random number generator.

statistics
Should split statistics be returned? Values can be parsed using stat.split.

...
Further arguments passed to or from other methods.
Details

Splitting

1. Splitting rules are specified by the option `splitrule`.
2. For all families, pure random splitting can be invoked by setting `splitrule="random"`.
3. For all families, computational speed can be increased using randomized splitting invoked by the option `nsplit`. See Improving Computational Speed.

Available splitting rules

1. `splitrule="gini"` (default splitrule): Gini index splitting (Breiman et al. 1984, Chapter 4.3).
2. `splitrule="auc"`: AUC (area under the ROC curve) splitting for both two-class and multi-class settings. AUC splitting is appropriate for imbalanced data. See imbalanced for more information.
3. `splitrule="entropy"`: entropy splitting (Breiman et al. 1984, Chapter 2.5, 4.3).

Value

An object of class (`rfsrc`, `grow`) with the following components:

- **call**: The original call to `rfsrc` for growing the random forest object.
- **family**: The family used in the analysis.
- **n**: Sample size of the data (depends upon NA’s, see `na.action`).
- **ntree**: Number of trees grown.
- **mtry**: Number of variables randomly selected for splitting at each node.
- **nodesize**: Minimum size of terminal nodes.
- **nodedepth**: Maximum depth allowed for a tree.
- **splitrule**: Splitting rule used.
- **nsplit**: Number of randomly selected split points.
- **yvar**: y-outcome values.
- **yvar.names**: A character vector of the y-outcome names.
- **xvar**: Data frame of x-variables.
- **xvar.names**: A character vector of the x-variable names.
- **xvar.wt**: Vector of non-negative weights for dimension reduction which specify the probability used to select a variable for splitting a node.
- **split.wt**: Vector of non-negative weights specifying multiplier by which the split statistic for a covariate is adjusted.
- **cause.wt**: Vector of weights used for the composite competing risk splitting rule.
- **leaf.count**: Number of terminal nodes for each tree in the forest. Vector of length `ntree`. A value of zero indicates a rejected tree (can occur when imputing missing data). Values of one indicate tree stumps.
proximity Proximity matrix recording the frequency of pairs of data points occur within the same terminal node.

forest If forest=TRUE, the forest object is returned. This object is used for prediction with new test data sets and is required for other R-wrappers.

membership Matrix recording terminal node membership where each column records node membership for a case for a tree (rows).

splitrule Splitting rule used.

inbag Matrix recording inbag membership where each column contains the number of times that a case appears in the bootstrap sample for a tree (rows).

var.used Count of the number of times a variable is used in growing the forest.

imputed.indv Vector of indices for cases with missing values.

imputed.data Data frame of the imputed data. The first column(s) are reserved for the y-outcomes, after which the x-variables are listed.

split.depth Matrix (i,j) or array (i,j,k) recording the minimal depth for variable j for case i, either averaged over the forest, or by tree k.
	node.stats Split statistics returned when statistics=TRUE which can be parsed using stat.split.

err.rate Tree cumulative OOB error rate.

importance Variable importance (VIMP) for each x-variable.

predicted In-bag predicted value.

predicted.oob OOB predicted value.

class In-bag predicted class labels.

class.oob OOB predicted class labels.

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References


Examples

data(tnbc)

########### performance of Random Rank Forest
obj <- rforest(subtype~, data = tnbc[,c(1:10,337)])
obj
select.rules

Select Decision Rules to Achieve Higher Prediction Accuracy

Description

Select rules from a extrat.rules (rules) object

Usage

select.rules(object, data, data.pair = FALSE)

Arguments

object
An extracted rule (rules) object generated from the extract.rules function.
data
A validation dataset for selecting rules.
data.pair
Is data already converted into binary ranked pairs from the pair function?

Value

rule
Interpretable selected rules. Note that the performance score displayed is inaccurate based on few samples from the original argument object.
rule.raw
Rules directly extracted from trees for prediction purpose
data
Data used to grow trees from the argument (object).

Author(s)

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References


Examples

data(tnbc)
obj <- rforest(subtype~., data = tnbc[1:100,c(1:5,337)])
objr <- extract.rules(obj)
predict(objr, tnbc[101:110,1:5])$label
objrs <- select.rules(objr,tnbc[110:130,c(1:5,337)])
predict(objrs, tnbc[101:110,1:5])$label
Gene expression profiles in triple-negative breast cancer cell

Description
Gene expression profiles in triple-negative breast cancer cells with 215 observations and 337 variables. Gene expression values were randomly chosen from the original dataset. The outcome variable is subtype.

Usage
data(tnbc)

Source

Examples
data(tnbc)
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