Package ‘binomialRF’

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Type  Package
Title  Binomial Random Forest Feature Selection
Version  0.1.0
URL  https://www.biorxiv.org/content/10.1101/681973v1.abstract

Description  The ‘binomialRF’ is a new feature selection technique for decision trees that aims at providing an alternative approach to identify significant feature subsets using binomial distributional assumptions (Rachid Zaim, S., et al. (2019)) <doi:10.1101/681973>. Treating each splitting variable selection as a set of exchangeable correlated Bernoulli trials, ‘binomialRF’ then tests whether a feature is selected more often than by random chance.

License  GPL-2
Encoding  UTF-8
LazyData  true

biocViews  Software, GenePrediction, StatisticalMethod, DecisionTree, DimensionReduction, ExperimentalDesign

Imports  randomForest, data.table, stats, rlist
Suggests  foreach, knitr, rmarkdown, correlbinom

RoxygenNote  7.0.2
VignetteBuilder  knitr

NeedsCompilation  no

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cv_binomialRF is the cross-validated form of the binomialRF, where K-fold crossvalidation is conducted to assess the feature’s significance. Using the cvFolds=K parameter, will result in a K-fold cross-validation where the data is ‘chunked’ into K-equally sized groups and then the averaged result is returned.

**Usage**

```r
.cv_binomialRF(X, y, cvFolds = 5, fdr.threshold = 0.05, 
 fdr.method = "BY", ntrees = 2000, keep.both = FALSE)
```

**Arguments**

- `X` design matrix
- `y` class label
- `cvFolds` how many times should we perform cross-validation
- `fdr.threshold` fdr.threshold for determining which set of features are significant
- `fdr.method` how should we adjust for multiple comparisons (i.e., `p.adjust.methods` =c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none")
- `ntrees` how many trees should be used to grow the randomForest? (Defaults to 5000)
- `keep.both` should we keep the naive binomialRF as well as the correlated adjustment

**Value**

a data.frame with 4 columns: Feature Name, cross-validated average for Frequency Selected, CV Median (Probability of Selecting it randomly), CV Median(Adjusted P-value based on fdr.method), and averaged number of times selected as significant.

**References**

Examples

```r
set.seed(324)

# Generate simulation data
X = matrix(rnorm(1000), ncol=10)
trueBeta = c(rep(10,5), rep(0,5))
z = 1 + X %*% trueBeta
pr = 1/(1+exp(-z))
y = as.factor(rbinom(100,1,pr))

# Run cross-validation
```

---

**binomialRF**

*random forest feature selection based on binomial exact test*

**Description**

`binomialRF` is the R implementation of the feature selection algorithm by (Zaim 2019)

**Usage**

```r
binomialRF(X,y, fdr.threshold = .05, fdr.method = 'BY',
nTrees = 2000, percent_features = .5,
keep.both = FALSE, user_cbinom_dist = NULL,
sampsize = round(nrow(X) *.63))
```

**Arguments**

- `X`: design matrix
- `y`: class label
- `fdr.threshold`: fdr.threshold for determining which set of features are significant
- `fdr.method`: how should we adjust for multiple comparisons (i.e., `p.adjust.methods` = c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY","fdr", "none"))
- `ntrees`: how many trees should be used to grow the `randomForest`?
- `percent_features`: what percentage of L do we subsample at each tree? Should be a proportion between (0,1)
- `keep.both`: should we keep the naive `binomialRF` as well as the correlated adjustment
- `user_cbinom_dist`: insert either a pre-specified correlated binomial distribution or calculate one via the R package `correlbinom`.
- `sampsize`: how many samples should be included in each tree in the `randomForest`
calculateBinomialP

Value

a data.frame with 4 columns: Feature Name, Frequency Selected, Probability of Selecting it randomly, Adjusted P-value based on fdr.method

References


Examples

set.seed(324)

###############################
### Generate simulation data
###############################

X = matrix(rnorm(1000), ncol=10)
trueBeta= c(rep(10,5), rep(0,5))
z = 1 + X %*% trueBeta
pr = 1/(1+exp(-z))
y = as.factor(rbinom(100,1,pr))

###############################
### Run binomialRF
###############################

require(correlbinom)
 rho = 0.33
ntrees = 250

cbinom = correlbinom(rho, successprob = calculateBinomialP(10, .5), trials = ntrees,
                     precision = 1024, model = 'kuk')

binom.rf <- binomialRF(X,y, fdr.threshold = .05,fdr.method = 'BY',
                     ntrees = ntrees,percent_features = .5,
                     keep.both=FALSE, user_cbinom_dist=cbinom,
                     sampsize=round(nrow(X)*rho))

print(binom.rf)

calculateBinomialP

calculate the probability, p, to conduct a binomial exact test

Description

calculateBinomialP returns a probability of randomly selecting a feature as the root node in a decision tree. This is a generic function that is called internally in binomialRF but that may also be called directly if needed. The arguments ... should be, L= Total number of features in X, and percent_features= what percent of L is subsampled in the randomForest call.
calculateBinomialP_Interaction

Usage

calculateBinomialP(L, percent_features)

Arguments

L the total number of features in X. Should be a positive integer >1
percent_features what percentage of L do we subsample at each tree? Should be a proportion between (0,1)

Value

If L is an integer returns a probability value for selecting predictor Xj randomly

Examples

calculateBinomialP(110, .4)
calculateBinomialP(13200, .5)

calculateBinomialP_Interaction

calculate the probability, p, to conduct a binomial exact test

Description

calculateBinomialP_Interaction returns a probability of randomly selecting a feature as the root node in a decision tree. This is a generic function that is called internally in binomialRF but that may also be called directly if needed. The arguments ... should be, L= Total number of features in X, and percent_features= what percent of L is subsampled in the randomForest call.

Usage

calculateBinomialP_Interaction(L, percent_features, K = 2)

Arguments

L the total number of features in X. Should be a positive integer >1
percent_features what percentage of L do we subsample at each tree? Should be a proportion between (0,1)
K interaction level

Value

If L is an integer returns a probability value for selecting predictor Xj randomly

Examples

calculateBinomialP_Interaction(110, .4, 2)
Description

binomialRF is the R implementation of the feature selection algorithm by (Zaim 2019).

Usage

geneset_binomialRF(binomialRF_object, gene_ontology, cutoff = 0.2)

Arguments

- binomialRF_object: the binomialRF object output
- gene_ontology: a two- or three-column representation of a gene ontology with gene and geneset names
- cutoff: a real-valued number between 0 and 1, used as a p-value threshold

Value

a data.frame with 4 columns: Geneset Name, P-value, Adjusted P-value based on fdr.method

References


Description

k_binomialRF is the R implementation of the interaction feature selection algorithm by (Zaim 2019). k_binomialRF extends the binomialRF algorithm by searching for k-way interactions.

Usage

k_binomialRF(X, y, fdr.threshold = 0.05, fdr.method = "BY", ntrees = 2000, percent_features = 0.3, K = 2, cbinom_dist = NULL, sampsize = nrow(X) * 0.4)
**Arguments**

- **X**: design matrix
- **y**: class label
- **fdr.threshold**: fdr.threshold for determining which set of features are significant
- **fdr.method**: how should we adjust for multiple comparisons (i.e., `p.adjust.methods = c("holm", "hochberg", "hommel", "bonferroni", "BH", "BY","fdr", "none")`)
- **ntrees**: how many trees should be used to grow the `randomForest`? (Defaults to 5000)
- **percent_features**: what percentage of L do we subsample at each tree? Should be a proportion between (0,1)
- **K**: for multi-way interactions, how deep should the interactions be?
- **cbinom_dist**: user-supplied correlated binomial distribution
- **sampsize**: user-supplied sample size for random forest

**Value**

A data.frame with 4 columns: Feature Name, Frequency Selected, Probability of Selecting it randomly, Adjusted P-value based on fdr.method

**References**


**Examples**

```r
set.seed(324)

# Generate simulation data
X = matrix(rnorm(1000), ncol=10)
trueBeta = c(rep(10,5), rep(0,5))
z = 1 + X %*% trueBeta
pr = 1/(1+exp(-z))
y = rbinom(100,1,pr)

# Run interaction model
require(correlbinom)
rho = 0.33
ntrees = 250
cbinom = correlbinom(rho, successprob = calculateBinomialP_Interaction(10, .5,2),
trials = ntrees, precision = 1024, model = 'kuk')
```
k.binom.rf <- k_binomialRF(X, y, fdr.threshold = .05, fdr.method = 'BY',
    ntrees = ntrees, percent_features = .5,
cbinom_dist = cbinom,
sampsize = round(nrow(X)*rho))

pmf_list

Description

This data contains probability mass functions (pmf’s) for correlated binary data for various parameters. The sum of correlated exchangeable binary data is a generalization of the binomial distribution that deals with correlated trials. The correlation in decision trees occurs as the subsampling and bootstrapping step in random forests touch the same data, creating a co-dependency. This data contains some pre-calculated distributions for random forests with 500, 1000, and 2000 trees with 10, 100, and 1000 features. For more distributions, they can be calculated via the correlbinom R package.

Usage

pmf_list

Format

A list of lists

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