Package 'ctgt'

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Type Package

Title Closed Testing with Globaltest for Pathway Analysis

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Description A shortcut procedure is proposed to implement closed testing for large-scale multiple testings, especially with the global test. This shortcut is asymptotically equivalent to closed testing and post hoc. Users could detect any possible sets of features or pathways with family-wise error rate controlled. The global test is powerful to detect associations between a group of features and an outcome of interest.

License GPL (>= 2)

Imports Rcpp (>= 1.0.3)

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Contents

`ctgt-package` *'Closed Testing with Globaltest for Pathway Analysis'*

Description

A shortcut procedure for closed testing with the global test is presented.

Details

See examples in actgt function.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541 Jelle J. Goeman, Sara A. van de Geer, Floor de Kort, Hans C. van Houwelingen, A global test for groups of genes: testing association with a clinical outcome, Bioinformatics, Volume 20, Issue 1, 1 January 2004, Pages 93-99, https://doi.org/10.1093/bioinformatics/btg382

`1-alpha quantile` *The 1-alpha quantile of globaltest*

Description

Robbins and Pitman Algorithm to calculate the criticalvalue given eigenvalue vector and alpha level.

Usage

```
criticalvalue(lam, alpha = 0.05)
```

Arguments

`lam`	The numeric vector with eigenvalues as elements.
`alpha`	The type I error rate allowed. The default is 0.05.

Value

Returns a real number.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541

`closed testing with globaltest`

Approximated Closed Testing with Global Test

Description

To detect the significance of the set of features after correcting for multiple global tests, with family-wise error rate controlled.

Usage

```
actgt (y, X, xs, hyps, maxit = 0, alpha = 0.05)
```

Arguments

`y`	The response vector (numeric vector).
`X`	The full design matrix, whose columns are named by the covariates.
`xs`	The name vector of all covariates (character vector).
`hyps`	The name vector of the covariates in the pathway of interest (character vector).
`maxit`	An optional integer to denote the maximal interations for branch and bound method. The default value 0 means the single-step shortcut without branch and bound method. Note that larger value is more time-consuming.
`alpha`	The type I error rate allowed. The default is 0.05.

Value

Returns a list of rejection indicator and the number of iterations.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541

Examples

```
#Generate the design matrix and response vector for logistic regression models
n= 100
m = 5
X = matrix(data = 0, nrow = n, ncol = m,byrow = TRUE )
for ( i in 1:n){
  set.seed(1234+i)
  X[i,] =  as.vector(arima.sim(model = list(order = c(1, 0, 0), ar = 0.2), n = m) )
}

y = rbinom(n,1,0.6)
X[which(y==1),1:3] = X[which(y==1),1:3] + 0.8


xs = paste("x",seq(1,m,1),sep="")
colnames(X) = xs

hyps=xs[1]

#The sinle-step ctgt procedure
actgt(y = y, X = X, xs = xs, hyps = hyps, maxit = 0, alpha = 0.05)
#Result Iterations
#"unsure"        "0"

# The iterative ctgt procedure with more iterations
actgt(y = y, X = X, xs = xs, hyps = hyps, maxit = 0, alpha = 0.05)
#Result Iterations
#"reject"       "2"
#which means that x1 is rejected by closed testing within two more iterations of the shortcut


# For a group of feature sets
mysets = list(xs[1:5], xs[c(1,4)], xs[c(1,4,5)])
sapply(mysets, function(i) actgt(y = y, X = X, xs = xs, hyps = i, maxit = 0, alpha = 0.05))
#Result     "reject" "unsure" "reject"
#Iterations "0"      "0"      "0"

mysets = list(xs[1:5], xs[c(1,4)], xs[c(1,4,5)])
sapply(mysets, function(i) actgt(y = y, X = X, xs = xs, hyps = i, maxit = 0, alpha = 0.05))
#Result     "reject" "reject" "reject"
#Iterations "0"      "2"          "0"
```

`internalfunctions` *'Internal Functions (ctgt)'*

Description

Internal functions of ctgt.

Usage

```
## iterative shortcut with branch and bound
actgt_it(y,Tmatrix, Cmatrix,fxs, sxs,Tf,Lamf,Cf,Ts,Lams,Cs,count=1,maxIt=1,a = 0.05)

## to check whether tmin is above cmax
tacmax(tmins,levels,tw, cf,lf,ls,alp )

## to check whether tmin is above ctrue
tactrue(tmins,hyxs,cfull,Wmatrix,alp )
```

Arguments

y	The response vector (numeric vector).
Tmatrix	The matrix used to calculate the test statistics.
Cmatrix	The matrix used to calculate the critical values.
fxs	The name vector of upper model (character vector).
sxs	The name vector of lower model (character vector).
Tf, Lamf, Cf	Test statistic, eigenvalues, and critical value of fxs.
Ts, Lams, Cs	Test statistic, eigenvalues, and critical value of sxs.
count	count the branches, default is 1.
maxIt	maximal number of branches chosen by user, default is 1.
a, alp	alpha level.
tmins	Minimum test statistics.
levels	levels
tw, cf, lf, ls	sorted weights, critical values and level for fxs and sxs.
hyxs	The name vector of the covariates of interest (character vector).
cfull	critical value of full model.
Wmatrix	matrix to calculate majorizing vector.

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majorizing vector *The majorizing vector*

Description

To get the majorizing vector at a specific level, given the upbound and lowbound.

Usage

```
getL (ub, lb, level)
```

Arguments

ub	upper bound.
lb	lower bound.
level	level of interest.

Value

Returns a numeric vector with the same length as ub and lb.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541

non-standardized globaltest *'Non-standardized globaltest'*

Description

This is the sencond version of the globaltest, the non-standardized globaltest

Usage

```
## a powerful variant of globaltest
gt2 (y, X, hyps, alpha = 0.05)
```

Arguments

y	The response vector (numeric vector).
X	The full design matrix, whose columns are named by the covariates.
hyps	The name vector of the covariates in the pathway of interest (character vector).
alpha	The type I error rate allowed. The default is 0.05.

Value

Returns the p-value, the observed and expected test statistics and the number of covariates.

Author(s)

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References

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Examples

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#Generate the design matrix and response vector for logistic regression models
n= 100
m = 5
X = matrix(data = 0, nrow = n, ncol = m,byrow = TRUE )
for ( i in 1:n){
  set.seed(1234+i)
  X[i,] =  as.vector(arima.sim(model = list(order = c(1, 0, 0), ar = 0.2), n = m) )
}

y = rbinom(n,1,0.6)
X[which(y==1),1:3] = X[which(y==1),1:3] + 0.8


xs = paste("x",seq(1,m,1),sep="")
colnames(X) = xs

hyps=xs[1]

#The raw p-values of globaltest
gt2(y = y, X = X, hyps = hyps, alpha = 0.05)
#p-value Statistic  Expected      #Cov
#7.64e-03  2.30e+02  1.24e+02  1.00e+00
```

`p-value` *p-value of globaltest*

Description

Robbins and Pitman Algorithm to calculate the p-value given the observed value and the eigenvalue vector.

Usage

```
pv(x, lam)
```

Arguments

`x`	The observed value that is used to calculate the coresponding the p-value.
`lam`	The numeric vector with eigenvalues as elements.

Value

Returns a value between 0 and 1.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541

`true discoveries` *True discoveries*

Description

To count the number of true discoveries within a given pathway or feature set of interest.

Usage

```
discoveries (y, X, xs, hyps, maxit = 0, alpha = 0.05)
```

Arguments

y	The response vector (numeric vector).
X	The full design matrix, whose columns are named by the covariates.
xs	The name vector of all covariates (character vector).
hyps	The name vector of the covariates in the pathway of interest (character vector).
maxit	An optional integer to denote the maximal interations for branch and bound method. The default value 0 means the single-step shortcut without branch and bound method. Note that larger value is more time-consuming.
alpha	The type I error rate allowed. The default is 0.05.

Value

Returns a non-negative interger.

Author(s)

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References

Ningning Xu, Aldo solari, Jelle Goeman, Clsoed testing with global test, with applications on metabolomics data, arXiv:2001.01541, https://arxiv.org/abs/2001.01541

Examples

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#Generate the design matrix and response vector for logistic regression models
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  set.seed(1234+i)
  X[i,] =  as.vector(arima.sim(model = list(order = c(1, 0, 0), ar = 0.2), n = m) )
}

y = rbinom(n,1,0.6)
X[which(y==1),1:3] = X[which(y==1),1:3] + 0.8


xs = paste("x",seq(1,m,1),sep="")
colnames(X) = xs

# For standarized data
X = scale(x = X,center = FALSE,scale = TRUE)/sqrt(n-1)
interest = xs

discoveries(y=y, X = X, xs = xs, hyps = interest)
#2
discoveries(y=y, X = X, xs = xs, hyps = interest, maxit=10)
#2
```

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