Package 'GSA'

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Title Gene Set Analysis

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Description Gene Set Analysis.

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Contents

GSA *Gene set analysis*

Description

Determines the significance of pre-defined sets of genes with respect to an outcome variable, such as a group indicator, a quantitative variable or a survival time

Usage

```
GSA(x,y, genesets, genenames,
method=c("maxmean","mean","absmean"),
resp.type=c("Quantitative","Two class unpaired","Survival","Multiclass",
            "Two class paired", "tCorr", "taCorr"),
censoring.status=NULL,random.seed=NULL,  knn.neighbors=10,
s0=NULL, s0.perc=NULL,minsize=15,maxsize=500,
restand=TRUE,restand.basis=c("catalog","data"),
 nperms=200,
xl.mode=c("regular","firsttime","next20","lasttime"),
xl.time=NULL, xl.prevfit=NULL)
```

Arguments

x	Data x: p by n matrix of features (expression values), one observation per column (missing values allowed); y: n-vector of outcome measurements
y	Vector of response values: 1,2 for two class problem, or 1,2,3 ... for multiclass problem, or real numbers for quantitative or survival problems
genesets	Gene set collection (a list)
genenames	Vector of genenames in expression dataset
method	Method for summarizing a gene set: "maxmean" (default), "mean" or "absmean"
resp.type	Problem type: "quantitative" for a continuous parameter; "Two class unpaired" ; "Survival" for censored survival outcome; "Multiclass" : more than 2 groups, coded 1,2,3...; "Two class paired" for paired outcomes, coded -1,1 (first pair), -2,2 (second pair), etc
censoring.status	Vector of censoring status values for survival problems, 1 mean death or failure, 0 means censored
random.seed	Optional initial seed for random number generator (integer)
knn.neighbors	Number of nearest neighbors to use for imputation of missing features values
s0	Exchangeability factor for denominator of test statistic; Default is automatic choice
s0.perc	Percentile of standard deviation values to use for s0; default is automatic choice; -1 means s0=0 (different from s0.perc=0, meaning s0=zeroeth percentile of standard deviation values= min of sd values)

minsize	Minimum number of genes in genesets to be considered
maxsize	Maximum number of genes in genesets to be considered
restand	Should restandardization be done? Default TRUE
,	
restand.basis	What should be used to do the restandardization? The set of genes in the genesets ("catalog", the default) or the genes in the data set ("data")
nperms	Number of permutations used to estimate false discovery rates
xl.mode	Used by Excel interface
xl.time	Used by Excel interface
xl.prevfit	Used by Excel interface

Details

Carries out a Gene set analysis, as described in the paper by Efron and Tibshirani (2006). It differs from a Gene Set Enrichment Analysis (Subramanian et al 2006) in its use of the "maxmean" statistic: this is the mean of the positive or negative part of gene scores in the gene set, whichever is large in absolute values. Efron and Tibshirani shows that this is often more powerful than the modified KS statistic used in GSEA. GSA also does "restandardization" of the genes (rows), on top of the permutation of columns (done in GSEA). Gene set analysis is applicable to microarray data and other data with a large number of features. This is also the R package that is called by the "official" SAM Excel package v3.0. The format of the response vector y and the calling sequence is illustrated in the examples below. A more complete description is given in the SAM manual at http://www-stat.stanford.edu/~tibs/SAM

Value

A list with components

GSA.scores	Gene set scores for each gene set
GSA.scores.perm	Matrix of Gene set scores from permutions, one column per permutation
fdr.lo	Estimated false discovery rates for negative gene sets (negative means lower expression correlates with class 2 in two sample problems, lower expression correlates with increased y for quantitative problems, lower expression correlates with higher risk for survival problems)
fdr.hi	Estimated false discovery rates for positive gene sets; positive is opposite of negative, as defined above
pvalues.lo	P-values for negative gene sets
pvalues.hi	P-values for positive gene sets
stand.info	Information from restandardization process
stand.info.star	Information from restandardization process in permutations
ngenes	Number of genes in union of gene sets
nperms	Number of permutations used

gene.scores	Individual gene scores (eg t-statistics for two class problem)
s0	Computed exchangeability factor
s0.perc	Computed percentile of standard deviation values. s0= s0.perc percentile of the gene standard deviations
call	The call to GSA
x	For internal use
y	For internal use
genesets	For internal use
genenames	For internal use
r.obs	For internal use
r.star	For internal use
gs.mat	For internal use
gs.ind	For internal use
catalog	For internal use
catalog.unique	For internal use

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Subramanian, A. and Tamayo, P. Mootha, V. K. and Mukherjee, S. and Ebert, B. L. and Gillette, M. A. and Paulovich, A. and Pomeroy, S. L. and Golub, T. R. and Lander, E. S. and Mesirov, J. P. (2005) A knowledge-based approach for interpreting genome-wide expression profiles. PNAS. 102, pg 15545-15550.

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some random gene sets
```

```
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.obj<-GSA(x,y, genenames=genenames, genesets=genesets,
             resp.type="Two class unpaired", nperms=100)


GSA.listsets(GSA.obj, geneset.names=geneset.names,FDRcut=.5)



#to use  "real" gene set collection, we read it in from a gmt file:
#
# geneset.obj<- GSA.read.gmt("file.gmt")
#
# where file.gmt is a gene set collection from GSEA collection or
#  or the website http://www-stat.stanford.edu/~tibs/GSA, or one
# that you have created yourself. Then

#   GSA.obj<-GSA(x,y, genenames=genenames, genesets=geneset.obj$genesets,
#                resp.type="Two class unpaired", nperms=100)
#
#
```

`GSA.correlate` *"Correlates" a gene set collection with a given list of gene nams*

Description

"Correlates" a gene set collection with a given list of gene names. Gives info on the overlap between the collection and the list of genes

Usage

```
GSA.correlate(GSA.genesets.obj, genenames)
```

Arguments

`GSA.genesets.obj`	Gene set collection, created for example by GSA.read.gmt
`genenames`	Vector of gene names in expression daatset

Details

Gives info on the overlap between a gene set collection and the list of gene names. This is for information purposes, to find out, for example, how many genes in the list of genes appear in the gene set collection.

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some random gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.correlate(genesets, genenames)
```

GSA.func *Gene set analysis without permutations*

Description

Determines the significance of pre-defined sets of genes with respect to an outcome variable, such as a group indicator, quantitative variable or survival time. This is the basic function called by GSA.

Usage

```
GSA.func(x,y, genesets, genenames,geneset.names=NULL,
 method=c("maxmean","mean","absmean"),
 resp.type=c("Quantitative","Two class unpaired","Survival","Multiclass",
             "Two class paired",  "tCorr", "taCorr" ),
censoring.status=NULL,
 first.time = TRUE, return.gene.ind = TRUE,
ngenes = NULL, gs.mat =NULL, gs.ind = NULL,
 catalog = NULL, catalog.unique =NULL,
s0 = NULL, s0.perc = NULL, minsize = 15, maxsize= 500, restand = TRUE,
restand.basis=c("catalog","data"))
```

Arguments

x	Data x: p by n matrix of features, one observation per column (missing values allowed)
y	Vector of response values: 1,2 for two class problem, or 1,2,3 ... for multiclass problem, or real numbers for quantitative or survival problems
genesets	Gene set collection (a list)
genenames	Vector of genenames in expression dataset
geneset.names	Optional vector of gene set names
method	Method for summarizing a gene set: "maxmean" (default), "mean" or "absmean"
resp.type	Problem type: "quantitative" for a continuous parameter; "Two class unpaired" ; "Survival" for censored survival outcome; "Multiclass" : more than 2 groups; "Two class paired" for paired outcomes, coded -1,1 (first pair), -2,2 (second pair), etc
censoring.status	Vector of censoring status values for survival problems, 1 mean death or failure, 0 means censored)
first.time	internal use
return.gene.ind	internal use
ngenes	internal use
gs.mat	internal use
gs.ind	internal use
catalog	internal use
catalog.unique	internal use
s0	Exchangeability factor for denominator of test statistic; Default is automatic choice

s0.perc	Percentile of standard deviation values to use for s0; default is automatic choice; -1 means s0=0 (different from s0.perc=0, meaning s0=zeroeth percentile of standard deviation values= min of sd values
minsize	Minimum number of genes in genesets to be considered
maxsize	Maximum number of genes in genesets to be considered
restand	Should restandardization be done? Default TRUE
restand.basis	What should be used to do the restandardization? The set of genes in the genesets ("catalog", the default) or the genes in the data set ("data")

Details

Carries out a Gene set analysis, computing the gene set scores. This function does not do any permutations for estimation of false discovery rates. GSA calls this function to estimate FDRs.

Value

A list with components

scores	Gene set scores for each gene set
,	
norm.scores	Gene set scores transformed by the inverse Gaussian cdf
,	
mean	Means of gene expression values for each sample
sd	Standard deviation of gene expression values for each sample
gene.ind	List indicating whch genes in each positive gene set had positive individual scores, and similarly for negative gene sets
geneset.names	Names of the gene sets
nperms	Number of permutations used
gene.scores	Individual gene scores (eg t-statistics for two class problem)
s0	Computed exchangeability factor
s0.perc	Computed percentile of standard deviation values
stand.info	Information computed used in the restandardization process
method	Method used (from call to GSA.func)
call	The call to GSA

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some random gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.func.obj<-GSA.func(x,y, genenames=genenames, genesets=genesets,  resp.type="Two class unpaired")



#to use  "real" gene set collection, we read it in from a gmt file:
#
# geneset.obj<- GSA.read.gmt("file.gmt")
#
# where file.gmt is a gene set collection from GSEA collection or
#  or the website http://www-stat.stanford.edu/~tibs/GSA, or one
# that you have created yourself. Then

#   GSA.func.obj<-GSA.func(x,y, genenames=genenames,
#                          genesets=geneset.obj$genesets,
#                          resp.type="Two class unpaired")
#
#
```

GSA.genescores *Individual gene scores from a gene set analysis*

Description

Compute individual gene scores from a gene set analysis

Usage

```
GSA.genescores(geneset.number, genesets,  GSA.obj,  genenames, negfirst=FALSE)
```

Arguments

geneset.number	Number indicating which gene set is to examined
genesets	The gene set collection
GSA.obj	Object returned by function GSA
genenames	Vector of gene names for gene in expression dataset
negfirst	Should negative genes be listed first? Default FALSE

Details

Compute individual gene scores from a gene set analysis. Useful for looking "inside" a gene set that has been called significant by GSA.

Value

A list with components

res	Matrix of gene names and gene scores (eg t-statistics) for each gene in the gene set

,

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")
```

```
#create some random gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.obj<-GSA(x,y, genenames=genenames, genesets=genesets,
             resp.type="Two class unpaired", nperms=100)

# look at 10th gene set

GSA.genescores(10, genesets, GSA.obj, genenames)
```

GSA.listsets *List the results from a Gene set analysis*

Description

List the results from a call to GSA (Gene set analysis)

Usage

```
GSA.listsets(GSA.obj, geneset.names = NULL, maxchar = 20, FDRcut = 0.2)
```

Arguments

GSA.obj	Object returned by GSA function
.	
geneset.names	Optional vector of names for the gene sets
maxchar	Maximum number of characters in printed output
FDRcut	False discovery rate cutpoint for listed sets. A value of 1 will cause all sets to be listed
.	

Details

This function list the sigificant gene sets, based on a call to the GSA (Gene set analysis) function.

Value

A list with components

FDRcut	The false discovery rate threshold used.
negative	A table of the negative gene sets. "Negative" means that lower expression of most genes in the gene set correlates with higher values of the phenotype y. Eg for two classes coded 1,2, lower expression correlates with class 2. For survival data, lower expression correlates with higher risk, i.e shorter survival (Be careful, this can be confusing!)
positive	A table of the positive gene sets. "Positive" means that higher expression of most genes in the gene set correlates with higher values of the phenotype y. See "negative" above for more info.
nsets.neg	Number of negative gene sets
nsets.pos	Number of positive gene sets

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some radnom gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.obj<-GSA(x,y, genenames=genenames, genesets=genesets,
             resp.type="Two class unpaired", nperms=100)
```

```
GSA.listsets(GSA.obj, geneset.names=geneset.names,FDRcut=.5)
```

GSA.make.features *Creates features from a GSA analysis that can be used in other procedures*

Description

Creates features from a GSA analysis that can be used in other procedures, for example, sample classification.

Usage

```
GSA.make.features(GSA.func.obj, x, genesets, genenames)
```

Arguments

GSA.func.obj	Object returned by GSA.func
x	Expression dataset from which the features are to be created
genesets	Gene set collection
genenames	Vector of gene names in expression dataset

Details

Creates features from a GSA analysis that can be used in other procedures, for example, sample classification. For example, suppose the GSA analysis computes a maxmean score for gene set 1 that is positive, based on the mean of the positive part of the scores in that gene set. Call the subset of genes with positive scores "A". Then we compute a new feature for this geneset, for each sample, by computing the mean of the scores for genes in A, setting other gene scores to zero.

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some random gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.func.obj<-GSA.func(x,y, genenames=genenames, genesets=genesets, resp.type="Two class unpaired")


GSA.make.features(GSA.func.obj, x, genesets, genenames)
```

GSA.plot *Plot the results from a Gene set analysis*

Description

Plots the results from a call to GSA (Gene set analysis)

Usage

```
GSA.plot(GSA.obj, fac=1, FDRcut = 1)
```

Arguments

GSA.obj	Object returned by GSA function
.	
fac	value for jittering points in plot ("factor" in called to jitter()

FDRcut — False discovery rate cutpoint for sets to be plotted. A value of 1 (the default) will cause all sets to be plotted

.

Details

This function makes a plot of the significant gene sets, based on a call to the GSA (Gene set analysis) function.

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
######### two class unpaired comparison
# y must take values 1,2

set.seed(100)
x<-matrix(rnorm(1000*20),ncol=20)
dd<-sample(1:1000,size=100)

u<-matrix(2*rnorm(100),ncol=10,nrow=100)
x[dd,11:20]<-x[dd,11:20]+u
y<-c(rep(1,10),rep(2,10))


genenames=paste("g",1:1000,sep="")

#create some radnom gene sets
genesets=vector("list",50)
for(i in 1:50){
 genesets[[i]]=paste("g",sample(1:1000,size=30),sep="")
}
geneset.names=paste("set",as.character(1:50),sep="")

GSA.obj<-GSA(x,y, genenames=genenames, genesets=genesets,
             resp.type="Two class unpaired", nperms=100)


GSA.listsets(GSA.obj, geneset.names=geneset.names,FDRcut=.5)

GSA.plot(GSA.obj)
```

GSA.read.gmt *Read in a gene set collection from a .gmt file*

Description

Read in a gene set collection from a .gmt file

Usage

```
GSA.read.gmt(filename)
```

Arguments

filename	The name of a file to read data values from. Should be a tab-separated text file, with one row per gene set. Column 1 has gene set names (identifiers), column 2 has gene set descriptions, remaining columns are gene ids for genes in that geneset

.

Details

This function reads in a geneset collection from a .gmt text file, and creates an R object that can be used as input into GSA. We use UniGene symbols for our gene set names in our .gmt files and expression datasets, to match the two. However the user is free to use other identifiers, as long as the same ones are used in the gene set collections and expression datasets.

Value

A list with components

genesets	List of gene names (identifiers) in each gene set

,

geneset.names	Vector of gene set names (identifiers)

,

geneset.descriptions	Vector of gene set descriptions

Author(s)

Robert Tibshirani

References

Efron, B. and Tibshirani, R. On testing the significance of sets of genes. Stanford tech report rep 2006. http://www-stat.stanford.edu/~tibs/ftp/GSA.pdf

Examples

```
# read in  functional pathways gene set file from Broad institute GSEA website
# http://www.broad.mit.edu/gsea/msigdb/msigdb_index.html
# You have to register first and then download the file C2.gmt from
#   their site

#GSA.read.gmt(C2.gmt)
```

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