

# SAGx

March 24, 2012

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Fstat

*Calculation of F statistic by gene given a linear model*

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## Description

Calculates F statistic.

## Usage

```
Fstat(indata = M, formula1 = ~as.factor(g), formula0 = "mean", design1 = NULL,
```

## Arguments

<code>indata</code>	The data matrix
<code>formula1</code>	a formula describing the alternative linear model
<code>formula0</code>	a formula describing the nullmodel. Use linear models syntax, except for one-way ANOVA ("mean")
<code>design1</code>	the alternaive design matrix. If not NULL it overrides the formula argument
<code>design0</code>	the null design matrix. If not NULL it overrides the formula argument
<code>B</code>	the number of bootstrap replicates

## Value

A list with the components

<code>Fstat</code>	the value of the F statistic
<code>fnum</code>	the numerator degrees of freedom
<code>fdenom</code>	the denominator degrees of freedom
<code>design1</code>	the alternative design matrix
<code>design0</code>	the null design matrix
<code>SS1</code>	the sum of squares in the denominator of the F-statistic
<code>SS0</code>	the sum of squares in the numerator of the F-statistic
<code>pvalue</code>	the p-value for testing the alternative vs the null model

**Author(s)**

Per Broberg

**Examples**

```
## Annette Dobson (1990) "An Introduction to Generalized Linear Models".
## Page 9: Plant Weight Data.
ctl <- c(4.17,5.58,5.18,6.11,4.50,4.61,5.17,4.53,5.33,5.14)
trt <- c(4.81,4.17,4.41,3.59,5.87,3.83,6.03,4.89,4.32,4.69)
group <- gl(2,10,20, labels=c("Ctl","Trt"))
weight <- c(ctl, trt)
anova(lm.D9 <- lm(weight ~ group))
# Analysis of Variance Table

# Response: weight
#           Df Sum Sq Mean Sq F value Pr(>F)
#group      1  0.6882  0.6882  1.4191  0.249
#Residuals 18  8.7292  0.4850

# Fstat(indata = rbind(weight,weight),formulal=~group) # Fstat will need at least two genes
#$Fstat
# weight weight
#1.419101 1.419101

#$fnum
#[1] 18

#$fdenom
#[1] 1

#$design1
# (Intercept) groupTrt
#1           1         0
#2           1         0
#3           1         0
#4           1         0
#5           1         0
#6           1         0
#7           1         0
#8           1         0
#9           1         0
#10          1         0
#11          1         1
#12          1         1
#13          1         1
#14          1         1
#15          1         1
#16          1         1
#17          1         1
#18          1         1
#19          1         1
#20          1         1
#attr(,"assign")
#[1] 0 1

# $design0
```

```
# NULL

# $$$1
# weight weight
#8.72925 8.72925

#$$$0
# weight weight
#0.688205 0.688205
```

---

GSEA.mean.t

*Gene Set Enrichment Analysis using output from samroc*


---

### Description

Based on a list of gene sets, e.g. pathways, in terms Affymatrix identifiers, these sets are ranked with respect to regulation as measured by an effect in a linear model using the SAM statistic. Typical applications include two-group comparisons or simple linear regression to clinical variable or gene expression of a given gene.

### Usage

```
GSEA.mean.t(samroc = samroc.res, probeset = probeset,
pway = kegg, type = c("original", "absolute", "maxmean"), two.side = FALSE, cutoff
```

### Arguments

samroc	an object of class samroc.result
probeset	the Affymatrix identifiers
pway	a list of pathway or gene sets
type	if "absolute" value of the absolute value of the samroc test statistic is used. If "original" no transformation. "maxmean" not available.
two.side	if TRUE a two-sided test is performed. Currently only two-sided test when type = "original" and else one-sided
cutoff	Gene sets with the number of members not falling within the interval given by <i>cutoff</i> are excluded
restand	if TRUE a 'restandardization' following Efron and Tibshirani (2006) is performed

### Details

Restandardization based on Efron and Tibshirani (2006) introduced. For normal approximation of the gene set statistic both the mean of the statistic, or the variance (and likewise for the Wilcoxon statistic), are obtained from the permutation distribution included in the samroc.result object. Note that this will account for the dependency between genes.

### Value

A matrix with columns normal approximation p-values, mean statistic, median statistic, and if type = "original", also Wilcoxon signed ranks statistic based p-value.

**Author(s)**

Per Broberg

**References**

Tian, Lu and Greenberg, Steven A. and Kong, Sek Won and Altschuler, Josiah and Kohane, Isaac S. and Park, Peter J. (2005) Discovering statistically significant pathways in expression profiling studies, *PNAS* Vol. 102, nr. 38, pp. 13544-13549

Bradley Efron and Robert Tibshirani (2006) On testing of the significance of sets of genes, Technical report, Stanford

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JT.test

*Jonckheere-Terpstra trend test*

---

**Description**

The test is testing for a monotone trend in terms of the class parameter. The number of times that an individual of a higher class has a higher gene expression forms a basis for the inference.

**Usage**

```
JT.test(data, class, labs = NULL, alternative = c("two-sided", "decreasing", "increasing"))
```

**Arguments**

<code>data</code>	A matrix with genes in rows and subjects in columns
<code>class</code>	the column labels, if not an ordered factor it will be redefined to be one.
<code>labs</code>	the labels of the categories coded by class
<code>alternative</code>	two-sided, decreasing or increasing
<code>ties</code>	Adjustment for ties

**Details**

Assumes that groups are given in increasing order, if the class variable is not an ordered factor, it will be redefined to be one. The p-value is calculated through a normal approximation.

The implementation owes to suggestions posted to R list.

The definition of predictive strength appears in Flandre and O'Quigley.

**Value**

an object of class JT-test, which extends the class htest, and includes the following slots

<code>statistic</code>	the observed JT statistic
<code>parameter</code>	the null hypothesis parameter, if other value than 0.
<code>p.value</code>	the p-value for the two-sided test of no trend.
<code>method</code>	Jonckheere-Terpstra

alternative	The relations between the levels: decreasing, increasing or two-sided
data.name	the name of the input data
median1 ...	mediann the medians for the n groups
trend	the rank correlation with category
S1	Predictive strength

**Author(s)**

Per Broberg, acknowledging input from Christopher Andrews at SUNY Buffalo

**References**

Lehmann, EH (1975) *Nonparametrics: Statistical Methods Based on Ranks* p. 233. Holden Day  
 Flandre, Philippe and O'Quigley, John, *Predictive strength of Jonckheere's test for trend: an application to genotypic scores in HIV infection*, *Statistics in Medicine*, 2007, 26, 24, 4441-4454

**Examples**

```
# Enter the data as a vector
A <- as.matrix(c(99,114,116,127,146,111, 125,143,148,157,133,139, 149, 160, 184))
# create the class labels
g <- c(rep(1,5), rep(2,5), rep(3,5))
# The groups have the medians
tapply(A, g, median)
# JT.test indicates that this trend is significant at the 5% level
JT.test(data = A, class = g, labs = c("GRP 1", "GRP 2", "GRP 3"), alternative = "two-side
```

---

R2BASE

*Produces a BASE file*


---

**Description**

The function produces a BASE file for import to Gene Data Viewer.

**Usage**

```
R2BASE(context.data = clingen, sample.ids = AZID, expression.data = dats,
annotation = annots, out = "u:/temp/temp.base")
```

**Arguments**

context.data	e.g. a clinical database
sample.ids	Sample Ids, that names the columns of the expression data.
expression.data	a matrix with the gene expression data, samples correspond to columns and probesets to rows. It is assumed that probeset identifiers are found in the first column.
annotation	annotations of the probesets, i.e. the rows in the expression.data. It is assumed that probeset identifiers are found in the first column.
out	the output file including path

**Value**

The file produced complies with an old BASE format. However, none of these formats are documented, as far as I know. So, essentially this function defines a data format that can be read by e.g. Gene Data Viewer.

**Author(s)**

Per Broberg

---

R2mim

*Output a script file to WinMIM*

---

**Description**

Given a candidate probe, it produces a script file for WinMIM by calculating means and covariances and for the N most highly correlated probes (in absolute value). Here N is an input parameter, but a recommended value 10. WinMIM can find a relevant graphical model for the dependencies between the probes.

**Usage**

```
R2mim(probe="12345_at", N=10, data=inm, out="u:/study/copd/mimscr.txt")
```

**Arguments**

probe	The name of the candidate probe
N	The number of highly correlated probes to be studied
data	The input data set
out	The MIM script file

**Value**

The correlation matrix

**Note**

David Edwards' program WinMIM can be found on StatLib (<http://lib.stat.cmu.edu/graphmod/>). In MIM issue input `mimscr.txt` and the calculations to find a model will start. When finished go to the Graphics menu and click on Independence Graph. The resulting graph can be exported both to WMF and LaTeX.

**Author(s)**

Per Broberg

**References**

Edwards, David (1995) *Introduction to Graphical Modelling*. Springer-Verlag  
 Lauritzen, Steffen (1996) *Graphical Models*. Oxford University Press  
 Whittaker, Joe (1990) *Graphical Models in Multivariate Analysis*. Wiley

---

`Xprep`*Fitting of a linear model*

---

**Description**

The function fits a linear model to a microarray data matrix.

**Usage**

```
Xprep(indata=M, formula=~as.factor(g), contrast=c(0,1), design=NULL)
```

**Arguments**

<code>indata</code>	The data matrix
<code>formula</code>	a linear model formula in the lm format
<code>contrast</code>	a vector defining the contrast of interest
<code>design</code>	the design matrix

**Value**

a list with the entries

<code>Mbar</code>	estimate of the contrast
<code>Vest</code>	the error variance
<code>k</code>	inverse of the scale factor turning Vest into a standard error
<code>f</code>	the degrees of freedom of Vest
<code>design</code>	the design matrix

**Author(s)**

Per Broberg

---

`Xprep.resid`*Calculation of input of residuals from linear model*

---

**Description**

The function fits a linear model to a microarray data matrix and calculates the residuals.

**Usage**

```
Xprep.resid(data=M, formula=~as.factor(g), design=NULL)
```

**Arguments**

<code>data</code>	The data matrix
<code>formula</code>	a linear model formula in the lm format
<code>design</code>	the design matrix

**Value**

A matrix with the residuals

**Author(s)**

Per Broberg

---

clin2mim

*Output a script file to WinMIM, linking clinical data and gene expression*

---

**Description**

Given a clinical variable, it produces a script file for WinMIM by calculating means and covariances and for the N most highly correlated probes (in absolute value). Here N is an input parameter, but a recommended value 10. WinMIM can find a relevant graphical model for the dependencies between the probes and the clinical variable.

**Usage**

```
clin2mim(variable="FEV1.ACTUAL", data=dbs, clindat=clinical, probes=probes, N=10, out
```

**Arguments**

variable	Clinical variable to be examined
data	The input data set, with subject id in first column.
clindat	The input clinical data, with subject id in first column
probes	The name of the probes in the order of <i>data</i>
N	The number of highly correlated probes to be studied
out	The MIM script file

**Value**

The correlation matrix

**Note**

David Edwards' program WinMIM can be found on StatLib (<http://lib.stat.cmu.edu/graphmod/>). In MIM issue input `mimscript.txt` and the calculations to find a model will start. When finished go to the Graphics menu and click on Independence Graph. The resulting graph can be exported both to WMF and LaTeX.

**Author(s)**

Per Broberg

**References**

Edwards, David (1995) *Introduction to Graphical Modelling*. Springer-Verlag  
 Laittzen, Steffen (1996) *Graphical Models*. Oxford University Press  
 Whittaker, Joe (1990) *Graphical Models in Multivariate Analysis*. Wiley



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cluster.q

*Clustering Goodness measured by Q2*


---

**Description**

Calculates a goodness of clustering measure based prediction sum squares.

**Usage**

```
cluster.q(data, cluster)
```

**Arguments**

data	The data matrix
cluster	a vector describing the cluster memberships

**Value**

The clustering mean Q2

**Author(s)**

Per Broberg

**References**

Eriksson, L., Johansson, E., Kettaneh-Wold, N. and Wold, S. (1999) *Introduction to Multi- and Megavariate Data Analysis using Projection Methods (PCA & PLS)*, Umetrics

---

estimatep0

*Estimate proportion unchanged genes*


---

**Description**

The function uses the vector of p-values to estimate p0.

**Usage**

```
estimatep0(ps = pp, B = 500, range = seq(0, 0.95, by = 0.05))
```

**Arguments**

ps	the vector of p-values, e.g. from firstpass
B	the number of Bootstrap samples
range	the values considered

**Value**

the value of p0, the proportion unchanged genes

**Author(s)**

Per Broberg

**References**

Storey, J. A Direct Approach to the False Discovery Rate, Technical Report Stanford (2001)

---

fetchSignal	<i>Fetch data from the GATC database</i>
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---

**Description**

Fetch FILENAME, PROBESET, SIGNAL and ABS\_CALL from the GATC database

**Usage**

```
fetchSignal(experiment="AZ33 ALI", channel, chip="HG_U95Av2")
```

**Arguments**

experiment	The name of the experiment corresponding to an individual chip
channel	The channel to the database
chip	the chip type

**Value**

dataframe with columns

**Author(s)**

Ported to R by Per Broberg. Original Oracle code by Petter Hallgren, with input from Petra Johansson.

**Examples**

```
## Not run:
# Do not run example 1. Fetch Probeset, Signal, ABS_CALL and CHIP for one sample.
library(RODBC)
(channel<-odbcConnect("DSN",uid="USERID",pwd="PASSWORD"))
ali.data <- fetchSignal(experiment="AZ33 ALI", channel, chip="hg_u95a")
colnames(ali.data)
#[1] "FILENAME" "PROBESET" "SIGNAL" "ABS_CALL" "CHIP"

# Do not run example 2
t1 <- paste("select q1.name as name from experiment q1, physical_chip q2, chip_design q3")
t2 <- paste("where q1.physical_chip_id=q2.id and q3.id=q2.design_id and ")
t3 <- paste("upper(q1.name) like '")
Ids <- sqlQuery(channel,paste(t1,t2,t3) )
# fetch Signal from GATC corresponding to the U95A chip for all samples in experiment. #
tmp <- apply(Ids,1,toupper)
probes <- data.frame(fetchSignal(experiment=tmp[1],channel, chip="hg_u95a"), "PROBESET")
test <- matrix(nrow=nrow(as.data.frame(probes)), ncol=nrow(Ids))
```

```

for(i in 1:nrow(as.data.frame(tmp))) {
  test[,i] <- fetchSignal(experiment=tmp[i],channel, chip="hg_u95a")[, "SIGNAL"]
}
codes <- data.frame(apply(Ids,1,code<-function(x) substr(x,1,5)))
colnames(test) <- as.character(t(codes))
test <- test[,order(colnames(test))]

## End(Not run)

```

---

firstpass

*First pass description of GeneChip data*


---

## Description

Does a first-pass analysis for a comparative experiment. This includes the calculation of means and confidence intervals for the groups, and finally a Kruskal-Wallis p-value for the null hypothesis of no difference

## Usage

```
firstpass(data = D, probes = probes , g, log = FALSE, present = NULL, labels = N
```

## Arguments

data	A data frame with one array in each column
probes	a vector containing the names of the probes in the same order as rows in D
g	A vector with the groups for the arrays, eg. TREATMENT and CONTROL
present	A dataframe with the Present calls, 3 = P, 2 = M, 1 = A.
log	if TRUE then data are log transformed through $t(x) = \log(1+x)$ and geometric means are calculated
labels	a vector of labels given the group means
output.data	if T the raw data are included in the output

## Details

A speed-up for Wilcoxon based on Kronecker products was put in place with SAGx v.1.4.5. Ties are currently not taken into account in Wilcoxon.

## Value

A dataframe with the columns PROBES, followed by group means and sd's, lower confidence intervals and then, upper confidence interval (confidence level 95%), and followed a Kruskal-Wallis p-value, and finally the input data,. If present names a dataframe holding the present calls the proportion present is calculated. Furthermore, if there are two groups the difference in group means is added.

**Examples**

```
## Not run:
# not run
g <- c(rep(1,4),rep(2,4)); labs <- c("Mean Diet","Mean Control"); probes <- paste("Probe",
  firstpass(data = utmat[1:2,], probes = probes[1:2], g, log = FALSE, labels = labs)
# Probesets      Mean Diet      Mean Control      LCL.1      LCL.2
#1  Probe 1 -12.3444460036497 -11.7495704973055 -12.9047961446666 -12.2832657957485 -11.
#2  Probe 2 -7.99773926405627 -8.02799133391929 -8.47704512876227 -8.19487551919835 -7.5
#      Difference Subject 1 Subject 2 Subject 3 Subject 4 Subject 5 Subject 6
#1 -0.594875506344176 -12.345150 -11.805071 -12.776232 -12.451332 -11.595748 -12.320430 -
#2 0.0302520698630131 -7.660097 -8.157944 -8.404433 -7.768484 -7.979951 -8.017327

## End(Not run)
```

fom

*Clustering Figure of Merit***Description**

Goodness of clustering measure based on prediction error.

**Usage**

```
fom(data, cluster)
```

**Arguments**

data	The data matrix
cluster	a vector describing the cluster memberships

**Details**

The criterion in the Reference is not correct in the article (i.e. does not follow from the premises), but has been corrected here.

**Value**

The Figure of Merit measure of the current clustering

**Author(s)**

Per Broberg

**References**

Yeung, K.Y., Haynor, D.R. and Ruzzo, W.L. (2001) Validating clustering for gene expression data. *Bioinformatics* Vol. 17, pp. 309-318

---

 fp.fn

*Calculation of fp and fn based on a vector of p-values*


---

**Description**

Based on a vector of p-values the proportion false positive (fp) and the proportion false negative are calculated for each entry, assuming that one to be the last to be called significant. The sum of fp and fn is also calculated (errors). Furthermore, an estimate of the proportion unchanged together with the number of the entry with minimum errors.

**Usage**

```
fp.fn(ps = pvals, B = 100)
```

**Arguments**

ps	a vector of p-values
B	the number of bootstrap loops done by the function estimatep0 called by fp.fn

**Value**

A list with components

p0	the estimated proportion unchanged
fp	the estimated proportion false positives
fn	the estimated proportion false negatives
N	the number of the p-value (significance level) that gives minimum fp + fn

**Author(s)**

Per Broberg

---

 gap

*GAP statistic clustering figure of merit*


---

**Description**

Calculates a goodness of clustering measure based on the average dispersion compared to a reference distribution.

**Usage**

```
gap(data = swiss, class = g, B = 500, cluster.func = myclus)
```

**Arguments**

<code>data</code>	The data matrix, with samples (observations) in rows and genes (variables) in columns
<code>class</code>	a vector describing the cluster memberships of the rows of data
<code>B</code>	the number of bootstrap samples
<code>cluster.func</code>	a function taking the arguments <code>data</code> and <code>k</code> (number of clusters) and outputs cluster assignments as list elements <code>cluster</code> (accessed by <code>object\$cluster</code> ).

**Value**

The GAP statistic and the standard deviation

**Author(s)**

Per Broberg

**References**

Tishirani, R., Walther, G. and Hastie, T. (2000) Estimating the number of clusters in a dataset via the Gap statistic. *Technical Report* Stanford

**Examples**

```
library("MASS")
data(swiss)
cl <- myclus(data = swiss, k = 3)
gap(swiss, cl$cluster)
```

---

```
list.experiments Display all experiment names and id's
```

---

**Description**

Display all experiment names and id's in the GATC database

**Usage**

```
list.experiments(channel, chip = "HG_U95Av2")
```

**Arguments**

<code>channel</code>	the ODBC channel set up through RODBC
<code>chip</code>	the chip type

**Details**

The GATC database has caused some problems by switching between upper and lower case in an erratic manner. To solve this all names are changed to upper case in the identification of experiments. Thus the function will not distinguish between the experiments 'A' and 'a', but with any sensible naming strategy, the restriction is without consequence

**Value**

dataframe with column EXPERIMENT

**Examples**

```
# Not run
## Not run: library(Rodbc)
channel <- odbcConnect(DBN, USRID, PWD)
ut <- list.experiments(channel, chip = "hu6800")
colnames(ut)
#[1] "EXPERIMENT"

## End(Not run)
```

---

```
list.intersection.p
```

*p-value for intersection of two gene lists.*

---

**Description**

Calculates a p-value for observing a number of probe sets common to two lists drawn from the same chip.

**Usage**

```
list.intersection.p(N = 14000, N1 = 100, N2 = 200, common = 30)
```

**Arguments**

N	The selectable number of probe sets
N1	the number of probe sets on the first list.
N2	the number of probe sets on the second list
common	the number of probe sets in common to the two lists.

**Value**

the p-value giving the probability of observing by chance at least as many in common as was actually observed.

**Author(s)**

Per Broberg

---

 mat2TeX

*Ouput matrix to LaTeX*


---

**Description**

The function outputs a matrix to a LaTeX table

**Usage**

```
mat2TeX(mat, digits = 4, rowNameTitle = "", file = "",
        roundNum = NULL, rowNameAlign = "l", matAlign = "r",
        prtHead = TRUE, prtEnd = TRUE, extraTitle = NULL,
        rowNameCols = 1, append = FALSE)
```

**Arguments**

mat	a matrix
digits	number of digits
rowNameTitle	title above row names
file	output file
roundNum	integer indicating the precision
rowNameAlign	alignment of row names, default is "l"
matAlign	alignment of columns, default is "r"
prtHead	if TRUE the begin{tabular} line is produced
prtEnd	if TRUE the end{tabular} line is produced
extraTitle	extra title
rowNameCols	the row name column, default is 1
append	if TRUE the output is appended to file, deafuld is FALSE

**Author(s)**

Juerg Kindermann; code found on R list

---

 myclus

*A clustering function*


---

**Description**

Uses a hierarchical clustering to initiate a kmeans clustering.

**Usage**

```
myclus(data = swiss, k = 3)
```



**Arguments**

data	The data matrix
k	the number of clusters

**Value**

a list from function kmeans

**Author(s)**

From Ripley and Venables

**References**

Venables, W.N. and Ripley, B.D (2000) *Modern Applied Statistics with S-PLUS*, Springer

**Examples**

```
library(MASS)
data(swiss)
cl <- myclus(data = swiss, k = 3)
gap(swiss, cl$cluster)
```

---

normalise

*Normalise arrays*

---

**Description**

Normalises arrays against a calculated average array, and calibrated linearly in a cube-root scatter plot.

**Usage**

```
normalise(x, linear=TRUE)
```

**Arguments**

x	The data matrix
linear	if linear=TRUE then the matrix elements are raised to the power of 3.

**Value**

normalised version of indata

**Author(s)**

Per Broberg

**References**

Tusher, V.G., Tibshirani, R., and Chu, G. (2001) Significance analysis of microarrays applied to the ionizing radiation response. *PNAS* Vol. 98, no.9, pp. 5116-5121

---

```
one.probeset.per.gene
```

*Select the best probeset per gene*

---

### Description

This function takes a vector of probeset identifiers, a vector of gene identifiers and a vector of present rates, and outputs the probeset id per gene that corresponds to the highest present rate.

### Usage

```
one.probeset.per.gene(probeset = probeset, present = present, symbol = symbol)
```

### Arguments

probeset	a vector of probeset id's
present	a vector of present rates
symbol	a vector of gene symbols

### Details

It is assumed that missing gene symbol is coded as "". Note also that other measurements than present rate may be useful as selection criterion, such some variation measure. The function only assumes that high values are desirable.

### Value

A vector of probeset id's.

### Note

Experimental function. Feedback appreciated.

### Author(s)

Per Broberg

---

```
outlier
```

*Identify outliers in the multivariate distribution*

---

### Description

A PCA model is fitted to data and two statistics as measures of extremity are calculated. These are the Hotelling t-square and DMODX, the first is a measure of how far away from the centre of the projection subspace the projection of the observation is. The second one measures how remote from the projection the actual observation is. SVD is done directly on the data matrix. The number of significant dimensions is defined as the number of eigenvalues greater than 1. Typically arrays are in different columns.

**Usage**

```
outlier(M)
```

**Arguments**

```
M          matrix
```

**Value**

Dataframe with columns Hotelling and DMODX

**Author(s)**

Per Broberg

**References**

Jackson, J.E. (1991) *A User's Guide to Principal Components*. Wiley

**Examples**

```
## Not run:
# not run
ut<-outlier(M)
#[1] "The number of significant dimensions is 19"
colnames(ut)
#[1] "Hotelling" "DMODX"

## End(Not run)
```

---

p0.mom

*Estimate proportion unchanged genes*

---

**Description**

The function uses the vector of p-values to estimate p0.

**Usage**

```
p0.mom(ps = pvalues)
```

**Arguments**

```
ps          the vector of p-values, e.g. from firstpass
```

**Value**

the value of p0, the proportion unchanged genes as a list with components

```
mgf          estimate from the mgf method
PRE          estimate from the PRE method
experimental1
experimental2
```

**Author(s)**

Per Broberg

**References**

Broberg, P. A new estimate of the proportion unchanged genes, 2005, *Genome Biology* 5:p10  
 Broberg, P. A comparative review of estimates of the proportion unchanged genes and the false discovery rate, submitted (2004)

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 pava.fdr

---

*Estimate of the FDR and the proportion unchanged genes*


---

**Description**

Estimates tail area and local false discovery rate using isotonic regression

**Usage**

```
pava.fdr(ps = pvalues, p0 = NULL)
```

**Arguments**

ps	the vector of p-values, e.g. from firstpass
p0	an estimate of the proportion unchanged genes

**Details**

If p0 = NULL the PRE estimate of p0 is calculated.

**Value**

a list with components

pava.fdr	estimate of the FDR
p0	estimate of p0
pava.local.fdr	estimate of the local fdr

**Author(s)**

Per Broberg

**References**

Broberg, P : A comparative review of estimates of the proportion unchanged genes and the false discovery rate, *BMC Bioinformatics* 2005, 5(1):199  
 Aubert J, Bar-Hen A, Daudin J-J, Robin S: Determination of the differentially expressed genes in microarray experiments using local FDR. *BMC Bioinformatics* 2004, 6(1):125

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pava *Pooling of Adjacent Violators*

---

**Description**

The PAVA algorithm

**Usage**

```
pava(x, wt = rep(1, length(x)))
```

**Arguments**

x	A numeric sequence
wt	observation weights; 1 by default.

**Details**

The algorithm will turn a non-increasing into a non-decreasing one. pava is an internal function used to force monotonicity, e.g. of p1 in function Zfreq

**Value**

A non-decreasing sequence

**Author(s)**

R.F. Raubertas, code from S list

**Examples**

```
pava(c(1, 2, 4, 3, 5))
# [1] 1.0 2.0 3.5 3.5 5.0
```

---

rank.genes *Rank genes with respect to multiple criteria*

---

**Description**

It is assumed that genes come in rows and the criteria in columns. Furthermore, high values should be good. After ranking the genes with respect to each criterion, the function does a PCA on the ranks, uses the first PC to obtain the final ranks. In principle it could happen that genes are ranked in the opposite direction to the one intended, but that should be evident from a quick glance at the results.

**Usage**

```
rank.genes(data = indats)
```

**Arguments**

`data` A matrix with the criteria in columns.

**Value**

The total ranks of the genes.

**Author(s)**

Per Broberg

---

`rank.trend` *Trend analysis based on ranks*

---

**Description**

Ranks are used to score genes with respect to degree of agreement to a given trend or pattern, Lehmann (1974) p.294.

**Usage**

```
rank.trend(data = x, pattern = c(1:ncol(data)), har = FALSE)
```

**Arguments**

`data` A data frame with one array in each column  
`pattern` A permutation of the integers 1:ncol(data)  
`har` logical parameter indicating whether or not a score based on Hardy's theorem shall be calculated.

**Details**

The rank scores gives a higher weight to a deviation from trend in more distant observations than a deviation between neighbouring observations. The p-values are calculated through a normal approximation.

**Value**

A list with the components

`score` the rank score for each gene  
`hardy` if `har = TRUE` the hardy score, NULL otherwise  
`pvals` the p-values for the null hypothesis of no trend

**Author(s)**

Per Broberg

**References**

Lehmann, E.L. (1975) Nonparametrics: Statistical Methods Based on Ranks, Holden-Day

**Examples**

```
# not run
D <- c(123, 334, 578, 762, 755, 890)
rank.trend(data = t(as.matrix(D)), har = TRUE)
#      Trend score Hardy score p-value for no trend
# [1,]          2          90          0.01750284
```

---

rsd.test	<i>Compare two groups with respect to their RSD (CV)</i>
----------	--

---

**Description**

A by row comparison of the Relative Standard Deviation (RSD), aka Coefficient of Variation (CV), is done using a bootstrap

**Usage**

```
rsd.test(data1 = x, data2= y, B = NULL)
```

**Arguments**

data1	A matrix with the samples for group 1 in columns.
data2	A matrix with the samples for group 2 in columns.
B	the number of bootstrap iterations. If NULL no bootstrap is performed.

**Value**

A list with the components

cv1	A vector of the RSD's for sample 1
cv2	A vector of the RSD's for sample 2
t.stat	the test statistic
p.vals	A vector of p-values for the comparison between <i>cv1</i> and <i>cv2</i>

**Author(s)**

Per Broberg

**References**

Broberg P, Estimation of Relative Standard Deviation,(1999) in *Drug Development and Industrial Pharmacy*, Vol 25 no 1 37-43

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`samroc.result-class`*Class "samroc.result" for results of the function samrocN*

---

## Description

The class `samroc.result` is the output of a call to `samrocN` and the input of various other functions.

## Slots

`d`: Object of class "numeric". Observed test statistic.  
`diff`: Object of class "numeric". Estimate of effect, e.g. difference between group means.  
`se`: Object of class "numeric". Standard error of `diff`.  
`d0`: Object of class "matrix". Permutation test statistics.  
`p0`: Object of class "numeric". The estimated proportion unaffected genes.  
`s0`: Object of class "numeric". The fudge factor.  
`pvalues`: Object of class "numeric". The p-values.  
`N.list`: Object of class "integer". The optimal top list size among the sizes suggested.  
`errors`: Object of class "numeric". The sum of false positives and false negatives given a list that includes the current gene.  
`formula`: Object of class "formula". The linear model formula used.  
`contrast`: Object of class "numeric". The contrast estimated.  
`annotation`: Object of class "character". Annotation or comments regarding the analysis. By default the date.  
`N.sample`: Object of class "integer". The number of samples.  
`B`: Object of class "integer". The number of permutations.  
`call`: Object of class "character". The call to the function.  
`id`: Object of class "character". The probeset ids.  
`error.df`: Object of class "integer". The error degrees of freedom.  
`design`: Object of class "matrix". The design matrix.

## Methods

**show** (`samroc.result`): Summarizes the test result.

**plot** (`samroc.result`): Plots the density of the observed test statistic and that of the corresponding null distribution

## Author(s)

Per Broberg

## See Also

[samrocN](#)



samrocN

Calculate ROC curve based SAM statistic

**Description**

Calculation of the regularised t-statistic which minimises the false positive and false negative rates.

**Usage**

```

samrocN(data=M, formula=~as.factor(g), contrast=c(0,1), N = c(50, 100, 200, 300),
smooth = FALSE, w = 1, measure = "euclid", p0 = NULL, probeset = NULL)

```

**Arguments**

data	The data matrix, or ExpressionSet
formula	a linear model formula
contrast	the contrast to be estimated
N	the size of top lists under consideration
B	the number of bootstrap iterations
perc	the largest eligible percentile of SE to be used as fudge factor
smooth	if TRUE, the std will be estimated as a smooth function of expression level
w	the relative weight of false positives
measure	the goodness criterion
p0	the proportion unchanged probesets; if NULL p0 will be estimated
probeset	probeset ids;if NULL then "probeset 1", "probeset 2", ... are used.

**Details**

The test statistic is based on the one in Tusher et al (2001):

$$\frac{d = \mathit{diff}}{s_0 + s}$$

where  $\mathit{diff}$  is a the estimate of a constrast,  $s_0$  is the regularizing constant and  $s$  the standard error. At the heart of the method lies an estimate of the false negative and false positive rates. The test is calibrated so that these are minimised. For calculation of  $p$ -values a bootstrap procedure is invoked. Further details are given in Broberg (2003). Note that the definition of  $p$ -values follows that in Davison and Hinkley (1997), in order to avoid  $p$ -values that equal zero.

The  $p$ -values are calculated through permuting the residuals obtained from the null model, assuming that this corresponds to the full model except for the parameter being tested, corresponding to the contrast coefficient not equal to zero. This means that factors not tested are kept fixed. NB This may be adequate for testing a factor with two levels or a regression coefficient (correlation), but it is not adequate for all linear models.

**Value**

An object of class samroc.result.

**Author(s)**

Per Broberg

**References**

Tusher, V.G., Tibshirani, R., and Chu, G. (2001) Significance analysis of microarrays applied to the ionizing radiation response. *PNAS* Vol. 98, no.9, pp. 5116-5121

Broberg, P. (2002) Ranking genes with respect to differential expression , <http://genomebiology.com/2002/3/9/preprint/0007>

Broberg, P: Statistical methods for ranking differentially expressed genes. *Genome Biology* 2003, 4:R41 <http://genomebiology.com/2003/4/6/R41>

Davison A.C. and Hinkley D.V. (1997) *Bootstrap Methods and Their Application*. Cambridge University Press

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 samrocNboot

---

*Calculate ROC curve based SAM statistic*


---

**Description**

A c-code version of samrocN. Calculation of the regularised t-statistic which minimises the false positive and false negative rates.

**Usage**

```
samrocNboot (data=M, formula=~as.factor(g), contrast=c(0,1), N = c(50, 100, 200, 300),
smooth=FALSE, w = 1, measure = "euclid", probeset = NULL)
```

**Arguments**

data	The data matrix
formula	a linear model formula
contrast	the contrast to be estimated
N	the size of top lists under consideration
B	the number of bootstrap iterations
perc	the largest eligible percentile of SE to be used as fudge factor
smooth	if TRUE, the std will be estimated as a smooth function of expression level
w	the relative weight of false positives
measure	the goodness criterion
probeset	probeset ids;if NULL then "probeset 1", "probeset 2", ... are used.

## Details

The test statistic is based on the one in Tusher et al (2001):

$$\frac{d = \mathit{diff}}{s_0 + s}$$

where  $\mathit{diff}$  is a the estimate of a contrast,  $s_0$  is the regularizing constant and  $s$  the standard error. At the heart of the method lies an estimate of the false negative and false positive rates. The test is calibrated so that these are minimised. For calculation of  $p$ -values a bootstrap procedure is invoked. Further details are given in Broberg (2003).

The  $p$ -values are calculated through permuting the rows of the design matrix. NB This is not adequate for all linear models.

samrocNboot uses C-code to speed up the bootstrap loop.

## Value

An object of class samroc.result.

## Author(s)

Per Broberg and Freja Vamborg

## References

Tusher, V.G., Tibshirani, R., and Chu, G. (2001) Significance analysis of microarrays applied to the ionizing radiation response. *PNAS* Vol. 98, no.9, pp. 5116-5121

Broberg, P. (2002) Ranking genes with respect to differential expression , <http://genomebiology.com/2002/3/9/preprint/0007>

Broberg. P: Statistical methods for ranking differentially expressed genes. *Genome Biology* 2003, 4:R41 <http://genomebiology.com/2003/4/6/R41>

## Examples

```
library(multtest)
#Loading required package: genefilter
#Loading required package: survival
#Loading required package: splines
#Loading required package: reposTools
data(golub)
# This makes the expression data from Golub et al available
# in the matrix golub, and the sample labels in the vector golub.cl
set.seed(849867)
samroc.res <- samrocNboot(data = golub, formula = ~as.factor(golub.cl))
# The proportion of unchanged genes is estimated at
samroc.res@p0
# The fudge factor equals
samroc.res@s0
# A histogram of p-values
hist(samroc.res@pvalues)
# many genes appear changed
```

union.of.pways

*Create the union of two pathway lists*

---

**Description**

This function takes two lists where each component is a vector of probe sets ids and create a new such list that contains all probe sets and pathways from the two lists.

**Usage**

```
union.of.pways(x, y)
```

**Arguments**

x	the first list
y	the second list

**Details**

The function *merge.list* in package *RCurl* forms a basis for this function which adds the ability to add new probe sets to existing pathways.

**Value**

A list which is the union of the two input lists.

**Note**

Experimental function. Feedback appreciated.

**Author(s)**

Per Broberg

**Examples**

```
X = list(a=c(1,2),c=c(1,2));Y = list(a=c(3,4),d=c(12,2))
union.of.pways(X,Y)
```

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