Package 'SMVar'

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Type Package

Title Structural Model for Variances

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Depends R (>= 2.6.0)

Description Implementation of the structural model for variances in order to detect differentially expressed genes from gene expression data.

License GPL

NeedsCompilation no

Repository CRAN

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Contents

`SMVar-package` *Structural Model for Variances*

Description

Package containing moderated t-tests to detect differentially expressed genes for paired and unpaired data

Details

Package:	SMVar
Type:	Package
Version:	1.3.3
Date:	2011-08-03
License:	GPL

SMVar.unpaired and SMVar.paired are the most important functions.

Author(s)

Guillemette Marot <guillemette.marot@inria.fr>

References

F. Jaffrezic, Marot, G., Degrelle, S., Hue, I. and Foulley, J. L. (2007) A structural mixed model for variances in differential gene expression studies. Genetical Research (89) 19:25

Examples

```
library(SMVar)
data(ApoAIdata)
attach(ApoAIdata)
SMVar.unpaired(ApoAIGeneId,list(ApoAICond1,ApoAICond2))
```

`ApoAIdata` *ApoAIdata*

Description

Example dataset for unpaired data

Usage

```
data(ApoAIdata)
```

Format

ApoAIdata is a list with 3 elements

ApoAIGeneId vector of fictive gene names)

ApoAICond1 matrix with 6226 rows and 8 columns with normalized normal mice measurements

ApoAICond2 matrix with 6226 rows and 8 columns with normalized KO mice measurements

Source

Similar to the example dataset used in the package Varmixt

References

M.J. Callow, S. Dudoit, E.L. Gong, T.P. Speed, and E.M. Rubin. Microarray expression profiling identifies genes with altered expression in hdl-deficien mice. Genome Res., 10(12) : 2022-9, 2000

Examples

```
data(ApoAIdata)
attach(ApoAIdata)
```

`SMVar.paired` *Structural model for variances with paired data*

Description

Function to detect differentially expressed genes when data are paired

Usage

```
SMVar.paired(geneNumbers, logratio, fileexport = NULL,
            minrep = 2, method = "BH", threshold = 0.05)
```

Arguments

`geneNumbers`	Vector with gene names or dataframe which contains all information about spots on the chip
`logratio`	matrix with one row by gene and one column by replicate giving the logratio
`fileexport`	file to export the list of differentially expressed genes
`minrep`	minimum number of replicates to take a gene into account, `minrep` must be higher than 2
`method`	method of multiple tests adjustment for p.values
`threshold`	threshold of False Discovery Rate

Details

This function implements the structural model for variances described in (Jaffrezic et al., 2007). Data must be normalized before calling the function. Matrix `geneNumbers` must have one of the following formats: "matrix","data.frame","vector","character","numeric","integer".

Value

Only the number of differentially expressed genes is printed. If asked, the file giving the list of differentially expressed genes is created

If the user creates an object when calling the function (for example "Stat=SMVar.paired(...)") then Stat contains the information for all genes, is sorted by ascending p-values and

`Stat$TestStat` gives the test statistics as described in the paper

`Stat$StudentPValue`
gives the raw p-values

`Stat$DegOfFreedom`
gives the number of degrees of freedom for the Student distribution for the test statistics

`Stat$LogRatio` gives the logratios

`Stat$AdjPValue` gives the adjusted p-values

Note

If the first column of the file geneNumbers contains identical names for two different spots, these two spots are only counted once if they are both differentially expressed. By default, the correction for multiple testing is Benjamini Hochberg with a threshold of False Discovery Rate (FDR) of 5%. The FDR threshold can be changed, and it is also possible to choose the multiple test correction method ("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"). To see the references for these methods, use the R-help ?p.adjust.

Author(s)

Guillemette Marot with contributions from Anne de la Foye

References

F. Jaffrezic, Marot, G., Degrelle, S., Hue, I. and Foulley, J. L. (2007) A structural mixed model for variances in differential gene expression studies. Genetical Research (89) 19:25

Examples

```
library(SMVar)
data(Spleendata)
attach(Spleendata)
SMVar.paired(SpleenGeneId,SpleenLogRatio)
```

SMVar.unpaired *Structural model for variances with unpaired data*

Description

Function to detect differentially expressed genes when data are unpaired

Usage

```
SMVar.unpaired(geneNumbers, listcond, fileexport = NULL,
               minrep = 2, method = "BH", threshold = 0.05)
```

Arguments

geneNumbers	Vector with gene names or dataframe which contains all information about spots on the chip
listcond	list of the different conditions to be compared
fileexport	file to export the list of differentially expressed genes
minrep	minimum number of replicates to take a gene into account, minrep must be higher than 2
method	method of multiple tests adjustment for p.values
threshold	threshold of False Discovery Rate

Details

This function implements the structural model for variances described in (Jaffrezic et al., 2007). Data must be normalized before calling the function. Matrix geneNumbers must have one of the following formats: "matrix","data.frame","vector","character","numeric","integer".

Value

Only the number of differentially expressed genes is printed. If asked, the file giving the list of differentially expressed genes is created.

If the user creates an object when calling the function (for example "Stat=SMVar.paired(...)") then Stat contains the information for all genes, is sorted by ascending p-values and

Stat$TestStat	gives the test statistics as described in the paper
Stat$StudentPValue	gives the raw p-values
Stat$DegOfFreedom	gives the number of degrees of freedom for the Student distribution for the test statistics
Stat$Cond1	gives the first condition considered in the log-ratio
Stat$Cond2	gives the second condition considered in the log-ratio
Stat$LogRatio	gives the logratios (listcond[[Cond2]]-listcond[[Cond1]])
Stat$AdjPValue	gives the adjusted p-values

Note

If the first column of the file geneNumbers contains identical names for two different spots, these two spots are only counted once if they are both differentially expressed. By default, the correction for multiple testing is Benjamini Hochberg with a threshold of False Discovery Rate (FDR) of 5%. The FDR threshold can be changed, and it is also possible to choose the multiple test correction method ("holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"). To see the references for these methods, use the R-help ?p.adjust.

Author(s)

Guillemette Marot with contributions from Anne de la Foye

References

F. Jaffrezic, Marot, G., Degrelle, S., Hue, I. and Foulley, J. L. (2007) A structural mixed model for variances in differential gene expression studies. Genetical Research (89) 19:25

Examples

```
library(SMVar)
data(ApoAIdata)
attach(ApoAIdata)
SMVar.unpaired(ApoAIGeneId,list(ApoAICond1,ApoAICond2))
```

`Spleendata` *Spleendata*

Description

Example dataset for paired data

Usage

```
data(Spleendata)
```

Format

Spleendata is a list with 2 elements

SpleenGeneId Gene names)

SpleenLogRatio Matrix with 4360 rows and 6 columns with normalized log-ratio

Source

Similar to the example dataset used in the package Varmixt

References

P. Delmar, Robin, S., Tronik-Le Roux S. and Daudin J.-J. (2005) Mixture model on the variance for the differential analysis of gene expression data, JRSS series C, 54(1), 31:50

Examples

```
data(Spleendata)
attach(Spleendata)
```

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