

# Package ‘SMVar’

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**Type** Package

**Title** Structural Model for Variances

**Version** 1.3.4

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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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SMVar-package	<i>Structural Model for Variances</i>
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## 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))
```

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ApoAIdata

*ApoAIdata*

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### 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-deficient mice. *Genome Res.*, 10(12) : 2022-9, 2000

## Examples

```
data(ApoAIData)
attach(ApoAIData)
```

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SMVar.paired	<i>Structural model for variances with paired data</i>
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## 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)
```

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SMVar.unpaired	<i>Structural model for variances with unpaired data</i>
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**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))
```

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Spleendata

*Spleendata*

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**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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