Package ‘GlobalAncova’

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Title  Global test for groups of variables via model comparisons
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Description  The association between a variable of interest (e.g. two groups) and the global pattern
            of a group of variables (e.g. a gene set) is tested via a global F-test. We give the following
            arguments in support of the GlobalAncova approach: After appropriate normalisation, gene-
            expression-data appear rather symmetrical and outliers are no real problem, so least squares
            should be rather robust. ANCOVA with interaction yields saturated data modelling e.g. different
            means per group and gene. Covariate adjustment can help to correct for possible selection bias.
            Variance homogeneity and uncorrelated residuals cannot be expected. Application of ordinary
            least squares gives unbiased, but no longer optimal estimates (Gauss-Markov-Aitken).
            Therefore, using the classical F-test is inappropriate, due to correlation. The test statistic
            however mirrors deviations from the null hypothesis. In combination with a permutation
            approach, empirical significance levels can be approximated. Alternatively, an approximation
            yields asymptotic p-values. The framework is generalized to groups of categorical variables
            or even mixed data by a likelihood ratio approach. Closed and hierarchical testing procedures
            are supported. This work was supported by the NGFN grant 01 GR 0459, BMBF, Germany
            and BMBF grant 01ZX1309B, Germany.
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Depends  methods, corpcor, globaltest
Imports  annotate, AnnotationDbi, Biobase, dendextend, GSEABase, VGAM
Suggests  GO.db, golubEsets, hu6800.db, vsn, Rgraphviz
License  GPL (>= 2)
biocViews  Microarray, OneChannel, DifferentialExpression, Pathways,
            Regression
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bindata  Simulated binary data

Description

Simulated data consisting of 24 binary variables and a binary outcome Y with 100 observations. Names of variables associated with the outcome start with true, names of other variables start with zero.

Usage

data(bindata)

See Also

gGlobalAncova
**Gene expression data**

Normalized gene expression data of 12 patients with colorectal cancer. Samples are taken from inside the tumours. Additionally, from same patients samples are taken from normal tissue, see `colon.normal`. The expression matrix is only an exemplary subset of 1747 probe sets associated with cell proliferation.

**Usage**

```r
data(colon.normal)
```

**Format**

The format is:

```r
num [1:1747, 1:12] 8.74 10.53 8.48 12.69 8.55 ...
- attr(*, "dimnames")=List of 2
 ..$ : chr [1:1747] "200808_s_at" "215706_x_at" "217185_s_at" "202136_at" ...
```

**References**


**Examples**

```r
data(colon.normal)
#str(colon.normal)
```
Covariate information for the colon data

Description

Covariate data for the colon data example:

- **sex**: Sex of the patient.
- **age**: Age of the patient.
- **location**: Location of the tumour.
- **grade**: Histologic tumour grade.
- **UICC.stage**: UICC stage of colorectal carcinoma.

Usage

```r
data(colon.pheno)
```

Format

The format is:

- **'data.frame'**: 12 obs. of 5 variables:
  - **$sex**: Factor w/ 2 levels "0","1": 2 2 1 2 2 1 2 1 2 1 ...
  - **$age**: int 71 76 63 73 58 66 66 66 86 76 ...
  - **$location**: Factor w/ 2 levels "distal","proximal": 1 1 1 1 1 1 1 1 2 1 ...
  - **$grade**: Factor w/ 2 levels "2","3": 1 1 2 2 1 2 2 2 ...
  - **$UICC.stage**: Factor w/ 2 levels "2","3": 2 1 2 1 2 1 1 2 1 ...

References


Examples

```r
data(colon.pheno)
#str(colon.pheno)
```
**colon.tumour**

---

**Gene expression data**

---

**Description**

Normalized gene expression data of 12 patients with colorectal cancer. Samples are taken from inside the tumours. Additionally, from same patients samples are taken from normal tissue, see colon.normal. The expression matrix is only an exemplary subset of 1747 probe sets associated with cell proliferation.

**Usage**

data(colon.tumour)

**Format**

The format is:

```r
num [1:1747, 1:12] 8.77 10.40 8.52 12.86 8.28 ...  
- attr(*, "dimnames")=List of 2  
..$ : chr [1:1747] "200808_s_at" "215706_x_at" "217185_s_at" "202136_at" ...  
```

**References**


**Examples**

data(colon.tumour)  
#str(colon.tumour)

---

**GAhier class**

**Class "GAhier"**

---

**Description**

Class for storing results of hierarchical testing procedure performed by *gGlobalAncova.hierarchical*
GAhier class

Usage

```r
## S4 method for signature 'GAhier'
show(object)
## S4 method for signature 'GAhier'
results(object)
## S4 method for signature 'GAhier'
sigEndnodes(object, onlySingleton=FALSE)
## S4 method for signature 'GAhier'
Plot.hierarchy(object, dend, col=1:2, lwd=1:2, collab, returnend=FALSE, cex.labels=1.5, ...)
```

Arguments

- `object`: object of class `GAhier`
- `onlySingleton`: if TRUE, only names of singleton variables within the significant nodes are returned
- `dend`: dendrogram object specifying the hierarchy of the variables
- `col`: colors for significant and non-significant nodes and branches, respectively
- `lwd`: line width for branches to non-significant and significant nodes, respectively
- `collab`: vector of colors for coloring dendrogram leave labels (can be independent of significant/non-significant nodes); has to be named according to variable names; if missing, significant and non-significant variables are colored using colors defined in `col`
- `returnend`: if TRUE, updated dendrogram object is returned (e.g. for use in further plots)
- `cex.labels`: size of leave labels
- `...`: further graphical parameters, passed to `plot.dendrogram`

Slots

- `clustervariables`: Object of class "list" containing names of variables in each tested cluster
- `p.values`: Object of class "list" containing p-values for each tested cluster
- `alpha`: Object of class "numeric"; chosen global significance level; if `K` had been specified, this additionally contains the adjusted significance levels for the `K` sub-hierarchies
- `n.variables`: Object of class "numeric"; number of variables in total
- `permstats`: Object of class "matrixOrNULL"; if returnPermstats had been set to TRUE, this is a matrix containing individual statistics for all variables for all permutations, otherwise NULL

Methods

- `show` signature(object = "GAhier"): Show general information and significant end end nodes
- `results` signature(object = "GAhier"): Get a data.frame with significant end nodes, number and names of variables included in each node and corresponding p-value
- `sigEndnodes` signature(object = "GAhier"): Get names of significant end nodes
- `Plot.hierarchy` signature(object = "GAhier"): Plot hierarchy dendrogram, where significant nodes (and branches to those nodes) are highlighted
Note
Coloring the dendrogram in `Plot.hierarchy` is based on functionality from the `globaltest` package.

Author(s)
Manuela Hummel <m.hummel@dkfz.de>

See Also
`gGlobalAncova.hierarchical`

Examples
```r
class"GAhier")
# see examples in documentation of gGlobalAncova.hierarchical
```

Description
Computation of a permutation test for the association between sets of variables (e.g., genes, SNPs, ...) and clinical entities. The variables can be continuous, binary, categorical, ordinal, or of mixed types. The test is carried out by comparing the deviances of the full generalized linear model and the reduced model lacking the design parameters of interest. The variable-wise models are summarized to a global test statistic for the complete set.

Usage
```r
gGlobalAncova(data, formula.full, formula.red=~1, model.dat, Sets, sumstat=sum, perm=10000)
```

Arguments
- `data` data.frame of variables to be tested in sets (columns=variables); (multi-) categorical variables should be factors, ordinal variables should be ordered factors
- `formula.full` model formula for the full model
- `formula.red` model formula for the reduced model (that does not contain the terms of interest)
- `model.dat` data.frame of regressors, containing variables specified in `formula.full` and `formula.red`
- `Sets` vector of names or indices of variables or list of those, defining sets of variables
- `sumstat` function for summarizing univariate test statistics; default is `sum`
- `perm` number of permutations

Value
A data.frame with test statistic and p-value for each tested set.
Note
The test is fast for categorical data and categorical design variable. For other types of variables and more complex designs it is rather slow.

This work was supported by BMBF grant 01ZX1309B, Germany.

Author(s)
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See Also
GlobalAncova

Examples
\[
data\text{(bindata)}
g\text{GlobalAncova}\text{(bindata[,}-1\text{], formula.full = }\sim\text{group, model.dat = bindata, perm = 1000)}
\]

Description
Hierarchical testing procedure according to Meinshausen (2008) screening for groups of related variables within a hierarchy instead of screening individual variables independently. Groups are tested by the generalized GlobalAncova approach. The family-wise error rate is simultaneously controlled over all levels of the hierarchy. In order to reduce computational complexity for large hierarchies, a "short cut" is implemented, where the testing procedure is applied separately to K sub-hierarchies. The p-values are adjusted such that they are identical to the ones obtained when testing the complete hierarchy.

Usage
\[
g\text{GlobalAncova.hierarchical}(data, H, formula.full, formula.red=\sim 1, model.dat, sumstat=sum, alpha=0.05, K, perm=10000, returnPermstats=FALSE, permstats)
\]

Arguments
data
  data.frame of variables (columns=variables) to be tested hierarchically; (multi-
  ) categorical variables should be factors, ordinal variables should be ordered factors
H
  dendrogram object specifying the hierarchy of the variables; labels(H) has to coincide with colnames(data)
formula.full
  model formula for the full model
The hierarchical procedure starts with testing the global null hypothesis that all variables are not associated with the design of interest, and then moves down the given hierarchy testing subclusters of variables. A subcluster is only tested if the null hypothesis corresponding to its ancestor cluster could be rejected. The p-values are adjusted for multiple testing according to cluster size $p_{C,adj} = p_C m/|C|$, where $m$ is the total number of variables and $|C|$ is the number of variables in cluster $C$.

If $K$ is specified and the procedure is split to $K$ sub-hierarchies containing $m_1, \ldots, m_K$ variables, p-values are additionally adjusted by $\tau = m/m_k, k = 1, \ldots, K$, such that resulting p-values are identical to the ones obtained when testing the complete hierarchy

$$p_{C,adj,k} \cdot \tau = p_{Cm_k}/|C| \cdot m/m_k = p_{C,adj}$$

Value

an object of class GAhier

Author(s)

Manuela Hummel <m.hummel@dkfz.de>

References


See Also

gGlobalAncova, GAhier, Plot.hierarchy
Examples

data(bindata)
X <- as.matrix(bindata[,-1])

# get a hierarchy for variables
dend <- as.dendrogram(hclust(dist(t(X))))

# hierarchical test
set.seed(555)
res <- gGlobalAncova.hierarchical(X, H = dend, formula.full = ~group, model.dat = bindata, alpha = 0.05, perm = 1000)
results(res)

# get names of significant clusters
sigEndnodes(res)

# visualize results
Plot.hierarchy(res, dend)

# starting with 3 sub-hierarchies
set.seed(555)
res2 <- gGlobalAncova.hierarchical(X, H = dend, K = 3, formula.full = ~group, model.dat = bindata, alpha = 0.05, perm = 1000)
results(res2)

GlobalAncova

Global test for differential gene expression

Description

Computation of a F-test for the association between expression values and clinical entities. In many cases a two way layout with gene and a dichotomous group as factors will be considered. However, adjustment for other covariates and the analysis of arbitrary clinical variables, interactions, gene co-expression, time series data and so on is also possible. The test is carried out by comparison of corresponding linear models via the extra sum of squares principle. Corresponding p-values, permutation p-values and/or asymptotic p-values are given.

There are three possible ways of using GlobalAncova. The general way is to define formulas for the full and reduced model, respectively, where the formula terms correspond to variables in model.dat. An alternative is to specify the full model and the name of the model terms that shall be tested regarding differential expression. In order to make this layout compatible with the function call in the first version of the package there is also a method where simply a group variable (and possibly covariate information) has to be given. This is maybe the easiest usage in cases where no 'special' effects like e.g. interactions are of interest.

Usage

## S4 method for signature 'matrix,formula,formula,ANY,missing,missing,missing'
GlobalAncova(xx, formula.full, formula.red, model.dat,
GlobalAncova

test.genes, method = c("permutation","approx","both","Fstat"), perm = 10000, max.group.size = 2500

## S4 method for signature
## 'matrix,formula,missing,ANY,missing,missing,character'
GlobalAncova(xx, formula.full, model.dat,test.terms,
        test.genes, method = c("permutation","approx","both","Fstat"), perm = 10000, max.group.size = 2500)

## S4 method for signature 'matrix,missing,missing,missing,ANY,ANY,missing'
GlobalAncova(xx, group, covars = NULL,
        test.genes, method = c("permutation","approx","both","Fstat"), perm = 10000, max.group.size = 2500)

Arguments

xx          Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of xx.

formula.full Model formula for the full model.

formula.red Model formula for the reduced model (that does not contain the terms of interest.)

model.dat   Data frame that contains all the variable information for each sample.

group       Vector with the group membership information.

covars      Vector or matrix which contains the covariate information for each sample.

test.terms  Character vector that contains names of the terms of interest.

test.genes  Vector of gene names or a list where each element is a vector of gene names.

method      p-values can be calculated permutation-based ("permutation") or by means of an approximation for a mixture of chi-square distributions ("approx"). Both p-values are provided when specifying method = "both". With option "Fstat" only the global F-statistics are returned without p-values or further information.

perm        Number of permutations to be used for the permutation approach. The default is 10,000.

max.group.size Maximum size of a gene set for which the asymptotic p-value is calculated. For bigger gene sets the permutation approach is used.

eps         Resolution of the asymptotic p-value.

acc         Accuracy parameter needed for the approximation. Higher values indicate higher accuracy.

Value

If test.genes = NULL a list with components

effect      Name(s) of the tested effect(s)

ANOVA       ANOVA table

test.result F-value, theoretical p-value, permutation-based and/or asymptotic p-value

terms       Names of all model terms
If a collection of gene sets is provided in `test.genes` a matrix is returned whose columns show the number of genes, value of the F-statistic, theoretical p-value, permutation-based and/or asymptotic p-value for each of the gene sets.

**Methods**

- \( xx = \text{"matrix"}, \) \( \text{formula.full} = \text{"formula"}, \) \( \text{formula.red} = \text{"formula"}, \) \( \text{model.dat} = \text{"ANY"}, \) \( \text{group} = \text{"missing"}, \) \( \text{covars} = \text{"missing"} \)

  In this method, besides the expression matrix \( xx \), model formulas for the full and reduced model and a data frame \( \text{model.dat} \) specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments \( \text{group} \), \( \text{covars} \) and \( \text{test.terms} \) are "missing" since they are not needed for this method.

- \( xx = \text{"matrix"}, \) \( \text{formula.full} = \text{"formula"}, \) \( \text{formula.red} = \text{"missing"}, \) \( \text{model.dat} = \text{"ANY"}, \) \( \text{group} = \text{"missing"}, \) \( \text{covars} = \text{"missing"} \)

  In this method, besides the expression matrix \( xx \), a model formula for the full model and a data frame \( \text{model.dat} \) specifying corresponding model terms are required. The character argument \( \text{test.terms} \) names the terms of interest whose association with differential expression will be tested. The basic idea behind this method is that one can select single terms, possibly from the list of terms provided by previous \texttt{GlobalAncova} output, and test them without having to specify each time a model formula for the reduced model. The arguments \( \text{formula.red} \), \( \text{group} \) and \( \text{covars} \) are "missing" since they are not needed for this method.

- \( xx = \text{"matrix"}, \) \( \text{formula.full} = \text{"missing"}, \) \( \text{formula.red} = \text{"missing"}, \) \( \text{model.dat} = \text{"missing"}, \) \( \text{group} = \text{"ANY"}, \) \( \text{covars} = \text{"ANY"} \)

  Besides the expression matrix \( xx \) a clinical variable \( \text{group} \) is required. Covariate adjustment is possible via the argument \( \text{covars} \) but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments \( \text{formula.full}, \text{formula.red}, \text{model.dat} \) and \( \text{test.terms} \) are "missing" since they are not needed for this method.

**Note**

This work was supported by the NGFN project 01 GR 0459, BMBF, Germany.

**Author(s)**

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with contributions from Sven Knueppel

**References**


**See Also**

\texttt{Plot.genes, Plot.subjects, GlobalAncova.closed, GAGO, GlobalAncova.decomp}
GlobalAncova gene set testing methods

Examples

```r
data(vantVeer)
data(phenodata)
data(pathways)

GlobalAncova(xx = vantVeer, formula.full = ~metastases + ERstatus, formula.red = ~ERstatus, model.dat = phenodata, test.genes = pathways[1], method = "both", perm = 100)
GlobalAncova(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metastases", model.dat = phenodata, test.genes = pathways[1], method = "both", perm = 100)
GlobalAncova(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, test.genes = pathways[1], method = "both", perm = 100)
```

GlobalAncova gene set testing methods

*Gene set testing of gene set databases using GlobalAncova*

Description

Three functions adapted from package `globaltest` to test gene sets from databases for association of the gene expression profile with a response variable. Three function are provided for Gene Ontology and for the Broad Institute’s gene sets.

Usage

```r
GAGO(xx, ..., id, annotation, probe2entrez,
ontology = c("BP", "CC", "MF"), minsize=1, maxsize=Inf,
multtest = c("holm", "focuslevel", "BH", "BY"),
focuslevel = 10, sort = TRUE)

GABroad(xx, ..., id, annotation, probe2entrez, collection,
category = c("c1", "c2", "c3", "c4", "c5"),
multtest = c("holm", "BH", "BY"), sort = TRUE)
```

Arguments

- **xx**: Matrix of gene expression data, where columns correspond to samples and rows to genes. Gene names have to be included as the row names of `xx`
- **...**: Arguments describing the tests to be performed are passed on to `GlobalAncova`. Note that only the approximative version of `GlobalAncova` is used here and hence the parameter `method` is not available. Even though the number of permutations (`perm`) may be specified since very large gene sets (with more genes than `max.group.size`) are treated with the permutation test.
- **id**: The identifier(s) of gene sets to be tested (character vector). If omitted, tests all gene sets in the database.
- **annotation**: The name of the probe annotation package for the microarray that was used, or the name of the genome wide annotation package for the species (e.g. `org.Hs.eg.db` for human). If an organism package is given, the argument `probe2entrez` must be supplied.
GlobalAncova gene set testing methods

probe2entrez  Use only if no probe annotation package is available. A mapping from probe identifiers to entrez gene ids. May be an environment, named list or named vector.

multtest  The method of multiple testing correction. Choose from: Benjamini and Hochberg FDR control (BH); Benjamini and Yekutieli FDR control (BY) or Holm familywise error control (holm). For GAGO also the focus level method is available. See focusLevel.

sort  If TRUE, sorts the results to increasing p-values.

ontology  The ontology or ontologies to be used. Default is to use all three ontologies.

minsize  The minimum number of probes that may be annotated to a gene set. Gene sets with fewer annotated probes are discarded.

maxsize  The maximum number of probes that may be annotated to a gene set. Gene sets with more annotated probes are discarded.

focuslevel  The focus level to be used for the focus level method. Either a vector of gene set ids, or a numerical level. In the latter case, findFocus is called with maxsize at the specified level to find a focus level.

collection  The Broad gene set collection, created by a call to getBroadSets.

category  The subcategory of the Broad collection to be tested. The default is to test all sets.

Details

These are utility functions to make it easier to do gene set testing of gene sets available in gene set databases. The functions automatically retrieve the gene sets, preprocess and select them, perform global test, do multiple testing correction, and sort the results on the basis of their p-values. All functions require that annotate and the appropriate annotation packages are installed. GAGO requires the GO.db package; GABroad requires the user to download the XML file "msigdb_v2.5.xml" from \http://www.broad.mit.edu/gsea/downloads.jsp, and to preprocess that file using the getBroadSets function.

Value

The function returns a data frame with raw and multiplicity-adjusted p-values for each gene set.

Note

Functions GAGOand GABroad correspond to functions gtGO, and gtBroad in package globaltest. The difference is in the use of the GlobalAncova test instead of gt within the procedures.

Author(s)

Jelle Goeman: <j.j.goeman@lumc.nl>; Jan Oosting; Manuela Hummel

References

GlobalAncova-methods

See Also
gtGO, gtKEGG, gtBroad, GlobalAncova, gt.

Examples

# see vignettes of packages GlobalAncova and globaltest and help of gtGO

GlobalAncova-methods  Methods for Function GlobalAncova

Description

There are three possible ways of using GlobalAncova. The general way is to define formulas for the full and reduced model, respectively, where the formula terms correspond to variables in model.dat. An alternative is to specify the full model and the name of the model terms that shall be tested regarding differential expression. In order to make this layout compatible with the function call in the first version of the package there is also a method where simply a group variable (and possibly covariate information) has to be given. This is maybe the easiest usage in cases where no 'special' effects like e.g. interactions are of interest.

Methods

\[
\text{xx = "matrix", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing", covars = "missing"}
\]

In this method, besides the expression matrix \( xx \), model formulas for the full and reduced model and a data frame \( \text{model.dat} \) specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments \( \text{group, covars and test.terms} \) are "missing" since they are not needed for this method.

\[
\text{xx = "matrix", formula.full = "formula", formula.red = "missing", model.dat = "ANY", group = "missing", covars = "missing"}
\]

In this method, besides the expression matrix \( xx \), a model formula for the full model and a data frame \( \text{model.dat} \) specifying corresponding model terms are required. The character argument \( \text{test.terms} \) names the terms of interest whose association with differential expression will be tested. The basic idea behind this method is that one can select single terms, possibly from the list of terms provided by previous GlobalAncova output, and test them without having to specify each time a model formula for the reduced model. The arguments \( \text{formula.red, group and covars} \) are "missing" since they are not needed for this method.

\[
\text{xx = "matrix", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "ANY", covars = "ANY"}
\]

Besides the expression matrix \( xx \) a clinical variable \( \text{group} \) is required. Covariate adjustment is possible via the argument \( \text{covars} \) but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments \( \text{formula.full, formula.red, model.dat and test.terms} \) are "missing" since they are not needed for this method.
GlobalAncova.closed  

Closed testing procedure for testing several groups of genes using GlobalAncova

Description

Computation of a closed testing procedure for several groups of genes, e.g. pathways, as an alternative of correcting for multiple testing. Starting from the pathways of interest a family of null hypotheses is created that is closed under intersection. Each null hypothesis can be rejected at a given level if it is rejected along with all hypotheses included in it.

There are three possible ways of using GlobalAncova. Also GlobalAncova.closed can be invoked with these three alternatives.

Usage

## S4 method for signature
## 'matrix,list,formula,formula,ANY,missing,missing,missing'
GlobalAncova.closed(xx, test.genes,
formula.full, formula.red, model.dat, previous.test, level, method = c("permutation","approx"),
max.group.size = 2500, eps = 1e-16, acc = 50)

## S4 method for signature
## 'matrix,list,formula,missing,ANY,missing,missing,character'
GlobalAncova.closed(xx, test.genes,
formula.full, model.dat, test.terms, previous.test, level, method = c("permutation","approx"),
max.group.size = 2500, eps = 1e-16, acc = 50)

## S4 method for signature
## 'matrix,list,missing,missing,missing,ANY,ANY,missing'
GlobalAncova.closed(xx, test.genes,
group, covars = NULL, previous.test, level, method = c("permutation","approx"), perm = 10000,
max.group.size = 2500, eps = 1e-16, acc = 50)

Arguments

xx  Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of xx.

test.genes  A list of named pathways that shall be tested, each containing vectors of gene names.

previous.test  The output of a call to GlobalAncova with specified option test.genes according to the pathways of interest (optional).

level  The global level of significance of the testing procedure.

formula.full  Model formula for the full model.
formula.red  | Model formula for the reduced model (that does not contain the terms of interest).
model.dat    | Data frame that contains all the variable information for each sample.
group        | Vector with the group membership information.
covars       | Vector or matrix which contains the covariate information for each sample.
test.terms   | Character vector that contains names of the terms of interest.
method       | Raw p-values can be calculated permutation-based ("permutation") or by means of an approximation ("approx").
perm          | Number of permutations to be used for the permutation approach. The default is 10,000.
max.group.size | Maximum size of a gene set for which the asymptotic p-value is calculated. For bigger gene sets the permutation approach is used.
eps           | Resolution of the asymptotic p-value.
acc           | Accuracy parameter needed for the approximation. Higher values indicate higher accuracy.

Value
A list with components

new.data  | Family of null hypotheses (vectors of genes to be tested simultaneously with GlobalAncova).
test.results | Test results for each pathway of interest and all hypotheses included in it.
significant | Names of the significant pathways.
not.significant | Names of the non significant pathways.

Methods

xx = "matrix", test.genes="list", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing"
In this method, besides the expression matrix xx and the list of gene groups test.genes, model formulas for the full and reduced model and a data frame model.dat specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments group, covars and test.terms are "missing" since they are not needed for this method.

xx = "matrix", test.genes="list", formula.full = "formula", formula.red = "missing", model.dat = "ANY", group = "missing"
In this method, besides the expression matrix xx and the list of gene groups test.genes, a model formula for the full model and a data frame model.dat specifying corresponding model terms are required. The character argument test.terms names the terms of interest whose association with differential expression will be tested. The arguments formula.red, group and covars are "missing" since they are not needed for this method.

xx = "matrix", test.genes="list", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "missing"
Besides the expression matrix xx and the list of gene groups test.genes a clinical variable
group is required. Covariate adjustment is possible via the argument covars but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments formula.full, formula.red, model.dat and test.terms are "missing" since they are not needed for this method.

Note
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References

See Also
GlobalAncova, Plot.genes, Plot.subjects

GlobalAncova.closed-methods
Methods for Function GlobalAncova.closed

Description
There are three possible ways of using GlobalAncova, use methods ?GlobalAncova for getting more information. Also GlobalAncova.closed can be invoked with these three alternatives.

Methods

\[ xx = \text{"matrix"}, \text{test.genes}="\text{list"}, \text{formula.full} = \text{"formula"}, \text{formula.red} = \text{"formula"}, \text{model.dat} = \text{"ANY"}, \text{group} = \text{"missing"} \]

In this method, besides the expression matrix \( xx \) and the list of gene groups \( \text{test.genes} \), model formulas for the full and reduced model and a data frame \( \text{model.dat} \) specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments \( \text{group} \), \( \text{covars} \) and \( \text{test.terms} \) are "missing" since they are not needed for this method.

\[ xx = \text{"matrix"}, \text{test.genes}="\text{list"}, \text{formula.full} = \text{"formula"}, \text{formula.red} = \text{"missing"}, \text{model.dat} = \text{"ANY"}, \text{group} = \text{"missing"} \]

In this method, besides the expression matrix \( xx \) and the list of gene groups \( \text{test.genes} \), a model formula for the full model and a data frame \( \text{model.dat} \) specifying corresponding model terms are required. The character argument \( \text{test.terms} \) names the terms of interest whose association with differential expression will be tested. The arguments \( \text{formula.red} \), \( \text{group} \) and \( \text{covars} \) are "missing" since they are not needed for this method.
xx = "matrix", test.genes="list", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "ANY", covars = "ANY", test.terms = "missing"

Besides the expression matrix xx and the list of gene groups test.genes a clinical variable group is required. Covariate adjustment is possible via the argument covars but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments formula.full, formula.red, model.dat and test.terms are "missing" since they are not needed for this method.

GlobalAncova.decomp

GlobalAncova with sequential and type III sum of squares decomposition and adjustment for global covariates

Description

Computation of a F-test for the association between expression values and clinical entities. The test is carried out by comparison of corresponding linear models via the extra sum of squares principle. In models with various influencing factors extra sums of squares can be treated with sequential and type III decomposition. Adjustment for global covariates, e.g. gene expression values in normal tissue as compared to tumour tissue, can be applied. Given theoretical p-values may not be appropriate due to correlations and non-normality. The functions are hence seen more as a descriptive tool.

Usage

GlobalAncova.decomp(xx, formula, model.dat = NULL, method = c("sequential", "type3", "all"), test.genes = NULL, genewise = FALSE, zz = NULL, zz.per.gene = FALSE)

Arguments

xx
Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of xx.

formula
Model formula for the linear model.

model.dat
Data frame that contains all the variable information for each sample.

method
Whether sequential or type III decomposition or both should be calculated.

test.genes
Vector of gene names or a list where each element is a vector of gene names.

genewise
Shall the sequential decomposition be displayed for each single gene in a (small) gene set?

zz
Global covariate, i.e. matrix of same dimensions as xx.

zz.per.gene
If set to TRUE the adjustment for the global covariate is applied on a gene-wise basis.

Value

Depending on parameters test.genes, method and genewise ANOVA tables, or lists of ANOVA tables for each decomposition and/or gene set, or lists with components of ANOVA tables for each gene are returned.
Note

This work was supported by the NGFN project 01 GR 0459, BMBF, Germany.

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See Also

Plot.sequential, pair.compare, GlobalAncova

Examples

data(vantVeer)
data(phenodata)
data(pathways)

# sequential or type III decomposition
GlobalAncova.decomp(xx = vantVeer, formula = ~ grade + metastases + ERstatus, model.dat = phenodata, method = "sequential")
GlobalAncova.decomp(xx = vantVeer, formula = ~ grade + metastases + ERstatus, model.dat = phenodata, method = "type3")

# adjustment for global covariate
data(colon.tumour)
data(colon.normal)
data(colon.pheno)
GlobalAncova.decomp(xx = colon.tumour, formula = ~ UICC.stage + sex + location, model.dat = colon.pheno, method = "all")

pair.compare

Pairwise comparisons of factor levels within GlobalAncova

Description

Pairwise comparisons of gene expression in different levels of a factor by GlobalAncova tests. The method uses the reduction in residual sum of squares obtained when two respective factor levels are set to the same level. Holm-adjusted permutation-based p-values are given.

Usage

pair.compare(xx, formula, group, model.dat = NULL, test.genes = NULL, perm = 10000)
pair.compare

Arguments

\textit{xx} \hspace{1cm} \text{Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of \textit{xx}.}

\textit{formula} \hspace{1cm} \text{Model formula for the linear model.}

\textit{group} \hspace{1cm} \text{Factor for which pairwise comparisons shall be calculated.}

\textit{model.dat} \hspace{1cm} \text{Data frame that contains all the variable information for each sample.}

\textit{test.genes} \hspace{1cm} \text{Vector of gene names or a list where each element is a vector of gene names.}

\textit{perm} \hspace{1cm} \text{Number of permutations to be used for the permutation approach. The default is 10,000.}

Value

An ANOVA table, or list of ANOVA tables for each gene set, for the pairwise comparisons.

Note

This work was supported by the NGFN project 01 GR 0459, BMBF, Germany.

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See Also

\textit{GlobalAncova}, \textit{GlobalAncova.decomp}

Examples

\begin{verbatim}
data(vantVeer)
data(phenodata)
data(pathways)

pair.compare(xx = vantVeer, formula = ~ grade, group = "grade", model.dat = phenodata, test.genes = pathways[1:3], perm = 100)
\end{verbatim}
Description

A list of nine cancer related pathways corresponding to the van t’Veer data. Each element contains a vector gene names corresponding to those in the data set.

Usage

data(pathways)

Format

The format is:
List of 9
$ androgen_receptor_signaling: chr [1:72] "AW025529" "NM_001648" "NM_001753" "NM_003298"
... 
$ apoptosis: chr [1:187] "AB033060" "NM_002341" "NM_002342" "AI769763"
... 
$ cell_cycle_control: chr [1:31] "NM_001759" "NM_001760" "NM_001786" "NM_001789"
... 
$ notch_delta_signalling: chr [1:34] "NM_002405" "AL133036" "NM_003260" "NM_004316"
...
$ p53_signalling: chr [1:33] "NM_002307" "NM_002392" "NM_003352" "NM_002745"
... 
$ ras_signalling: chr [1:266] "D25274" "AI033397" "NM_003029" "NM_001626"
... 
$ tgf_beta_signaling: chr [1:82] "NM_003036" "AI090812" "AI697699" "AI760298"
... 
$ tight_junction_signaling: chr [1:326] "D25274" "AA604213" "AA604213" "NM_003005"
... 
$ wnt_signaling: chr [1:176] "AB033058" "AB033087" "NM_003012" "NM_003014"
...

Examples

data(pathways)
#str(pathways)

Description

Covariate information for the van t’Veer data

Sample data for the van t’Veer example:

Sample  Sample number.
metastases  Development of distant metastases within five years (0-no/1-yes).
grade  Tumor grade (three ordere levels).
ERstatus  Estrogen receptor status (pos-positive/neg-negative).
Plot.all

Usage

data(phenodata)

Format

The format is:

'data.frame': 96 obs. of 4 variables:
$Sample: int 1 2 3 4 5 6 7 8 9 10 ...
$metastases: int 0 0 0 0 0 0 0 0 0 ...
$grade: int 2 1 3 3 2 1 3 3 2 ...
$ERstatus: Factor w/ 2 levels "neg","pos": 2 2 1 2 2 2 1 2 2 ...

Examples

data(phenodata)
#str(phenodata)

Plot.all

Combined visualization of sequential decomposition and influence of single genes on the GlobalAncova statistic

Description

Plot that combines Plot.genes and Plot.sequential into one graphic.

Usage

Plot.all(xx, formula, model.dat = NULL, test.genes = NULL, name.geneset = "")

Arguments

xx Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of xx.

formula Model formula for the linear model.

model.dat Data frame that contains all the variable information for each sample.

test.genes Vector of gene names or gene indices specifying a gene set.

name.geneset Name of the plotted geneset.

Note

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Author(s)

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Urlich Mansmann <mansmann@ibe.med.uni-muenchen.de>

See Also

Plot.genes, Plot.sequential, GlobalAncova.decomp, GlobalAncova

Examples

data(vantVeer)
data(phenodata)
data(pathways)

Plot.all(vantVeer, formula = ~ ERstatus + metastases + grade, model.dat = phenodata, test.genes = pathways[[3]], name.geneset = "cell cycle pathway")

Plot.features

Features Plot for generalized Global Ancova

Description

Produces a plot to show the influence of individual variables on the test result produced by GlobalAncova. The variables can be continuous, binary, categorical, ordinal, or of mixed types.

Usage

Plot.features(data, formula.full, formula.red = ~1, model.dat, Set, returnValues = FALSE, ...)

Arguments

data data.frame of variables to be tested in sets (columns=variables); (multi-) categorical variables should be factors, ordinal variables should be ordered factors
formula.full model formula for the full model
formula.red model formula for the reduced model (that does not contain the terms of interest)
model.dat data.frame of regressors, containing variables specified in formula.full and formula.red
Set optional vector of names or indices of variables, defining the set of variables to plot; if missing, all variables in data are shown
returnValues shall variable-wise statistics = bar heights be returned?
... graphical parameters passed to barplot

Value

If returnValues = TRUE, a vector with the bar heights is returned.
Plot.genes

Author(s)
Manuela Hummel <m.hummel@dkfz.de>

See Also
gGlobalAncova, Plot.genes

Examples

```r
data(bindata)
Plot.features(bindata[, -1], formula.full = ~group, model.dat = bindata)
```

---

Plot.genes

Genes Plot for Global Ancova

Description

Produces a plot to show the influence of individual genes on the test result produced by `GlobalAncova`. There are three possible ways of using `GlobalAncova`. Also `Plot.genes` can be invoked with these three alternatives.

Usage

```r
## S4 method for signature 'matrix,formula,formula,ANY,missing,missing,missing'
Plot.genes(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, legendpos = "topright", returnValues = FALSE, bar.names, ...)

## S4 method for signature 'matrix,formula,missing,ANY,missing,missing,character'
Plot.genes(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, legendpos = "topright", returnValues = FALSE, bar.names, ...)

## S4 method for signature 'matrix,missing,missing,missing,ANY,ANY,missing'
Plot.genes(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, legendpos = "topright", returnValues = FALSE, bar.names, ...)
```

Arguments

- **xx**: Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of `xx`.
- **formula.full**: Model formula for the full model.
- **formula.red**: Model formula for the reduced model (that does not contain the terms of interest).
- **model.dat**: Data frame that contains all the variable information for each sample.
- **group**: Vector with the group membership information.
- **covars**: Vector or matrix which contains the covariate information for each sample.
Plot.genes

test.terms Character vector that contains names of the terms of interest.
test.genes Vector of gene names or gene indices specifying the gene set. If missing, the plot refers to all genes in xx.
Colorgroup Character variable giving the group that specifies coloring. If the function is called using the argument group then this variable is assumed to be relevant for coloring.
legendpos Position of the legend (a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center").
returnValues Shall bar heights (gene-wise reduction in sum of squares) be returned?
bar.names Vector of bar labels. If missing, gene names from test.genes or row names of xx are taken.
... Graphical parameters for specifying colors, titles etc.

Methods

xx = "matrix", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing", covars = "ANY"

In this method, besides the expression matrix xx, model formulas for the full and reduced model and a data frame model.dat specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments group, covars and test.terms are "missing" since they are not needed for this method.

xx = "matrix", formula.full = "formula", formula.red = "missing", model.dat = "ANY", group = "missing", covars = "ANY"

In this method, besides the expression matrix xx, a model formula for the full model and a data frame model.dat specifying corresponding model terms are required. The character argument test.terms names the terms of interest whose association with differential expression will be tested. The arguments formula.red, group and covars are "missing" since they are not needed for this method.

xx = "matrix", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "ANY", covars = "ANY"

Besides the expression matrix xx a clinical variable group is required. Covariate adjustment is possible via the argument covars but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments formula.full, formula.red, model.dat and test.terms are "missing" since they are not needed for this method.

Note

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Manuela Hummel <m.hummel@dkfz.de>

See Also

GlobalAncova, Plot.subjects, Plot.sequential
Examples

```r
data(vantVeer)
data(phenodata)
data(pathways)

Plot.genes(xx = vantVeer, formula.full = ~metastases + ERstatus, formula.red = ~ERstatus, model.dat = phenodata, test.genes = pathways[[3]], colorgroup = "metastases")
Plot.genes(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metastases", model.dat = phenodata, test.genes = pathways[[3]])
Plot.genes(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, test.genes = pathways[[3]])
```

Description

There are three possible ways of using `GlobalAncova`, use methods ?GlobalAncova for getting more information. Also `Plot.genes` can be invoked with these three alternatives.

Methods

For `xx = "matrix", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing", covars = "missing", test.terms = "missing"`

In this method, besides the expression matrix `xx`, model formulas for the full and reduced model and a data frame `model.dat` specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments `group`, `covars` and `test.terms` are "missing" since they are not needed for this method.

For `xx = "matrix", formula.full = "formula", formula.red = "missing", model.dat = "ANY", group = "missing", covars = "missing", test.terms = "character"`

In this method, besides the expression matrix `xx`, a model formula for the full model and a data frame `model.dat` specifying corresponding model terms are required. The character argument `test.terms` names the terms of interest whose association with differential expression will be tested. The arguments `formula.red`, `group` and `covars` are "missing" since they are not needed for this method.

For `xx = "matrix", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "ANY", covars = "ANY", test.terms = "missing"`

Besides the expression matrix `xx` a clinical variable `group` is required. Covariate adjustment is possible via the argument `covars` but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments `formula.full`, `formula.red`, `model.dat` and `test.terms` are "missing" since they are not needed for this method.
**Plot.sequential**  

*Visualization of sequential decomposition*

**Description**

Plot to show the sum of squares decomposition for each gene into parts according to all variables.

**Usage**

```r
Plot.sequential(xx, formula, model.dat = NULL, test.genes = NULL, name.geneset = "")
```

**Arguments**

- `xx`: Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of `xx`.
- `formula`: Model formula for the linear model.
- `model.dat`: Data frame that contains all the variable information for each sample.
- `test.genes`: Vector of gene names or gene indices specifying a gene set.
- `name.geneset`: Name of the plotted geneset.

**Note**

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- Urlich Mansmann <mansmann@ibe.med.uni-muenchen.de>

**See Also**

- `GlobalAncova.decomp`, `Plot.genes`, `GlobalAncova`

**Examples**

```r
data(vantVeer)
data(phenodata)
data(pathways)

Plot.sequential(vantVeer, formula = ~ ERstatus + metastases + grade, model.dat = phenodata, test.genes = pathways[[3]])
```
Plot.subjects

Description

Produces a plot to show the influence of the samples on the test result produced by GlobalAncova.

There are three possible ways of using GlobalAncova. Also Plot.subjects can be invoked with these three alternatives.

Usage

## S4 method for signature 'matrix,formula,formula,ANY,missing,missing,missing'
Plot.subjects(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, sort = FALSE, legendpos = "topright", returnValues = FALSE, bar.names, ...)

## S4 method for signature
## 'matrix,formula,missing,ANY,missing,missing,character'
Plot.subjects(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, sort = FALSE, legendpos = "topright", returnValues = FALSE, bar.names, ...)

## S4 method for signature 'matrix,missing,missing,missing,ANY,ANY,missing'
Plot.subjects(xx, formula.full, formula.red, model.dat, group, covars = NULL, test.terms, test.genes, Colorgroup = NULL, sort = FALSE, legendpos = "topright", returnValues = FALSE, bar.names, ...)

Arguments

xx Matrix of gene expression data, where columns correspond to samples and rows to genes. The data should be properly normalized beforehand (and log- or otherwise transformed). Missing values are not allowed. Gene and sample names can be included as the row and column names of xx.

formula.full Model formula for the full model.

formula.red Model formula for the reduced model (that does not contain the terms of interest.)

model.dat Data frame that contains all the variable information for each sample.

group Vector with the group membership information.

covars Vector or matrix which contains the covariate information for each sample.

test.terms Character vector that contains names of the terms of interest.

test.genes Vector of gene names or gene indices specifying the gene set. If missing, the plot refers to all genes in xx.

Colorgroup Character variable giving the group that specifies coloring. If the function is called using the argument group then this variable is assumed to be relevant for coloring.

sort Should the samples be ordered by colorgroup?

legendpos Position of the legend (a single keyword from the list "bottomright", "bottom", "bottomleft", "left", "topleft", "top", "topright", "right" and "center").
Plot(subjects)

returnValues  Shall bar heights (subject-wise reduction in sum of squares) be returned?
bar.names  Vector of bar labels. If missing, column names of xx are taken.
...  Graphical parameters for specifying colors, titles etc.

Methods

\[
\text{xx = "matrix", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing", covars = missing }
\]
In this method, besides the expression matrix xx, model formulas for the full and reduced model and a data frame model.dat specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments group, covars and test.terms are "missing" since they are not needed for this method.

\[
\text{xx = "matrix", formula.full = "formula", formula.red = "missing", model.dat = "ANY", group = "missing", covars = missing }
\]
In this method, besides the expression matrix xx, a model formula for the full model and a data frame model.dat specifying corresponding model terms are required. The character argument test.terms names the terms of interest whose association with differential expression will be tested. The arguments formula.red, group and covars are "missing" since they are not needed for this method.

\[
\text{xx = "matrix", formula.full = "missing", formula.red = "missing", model.dat = "missing", group = "ANY", covars = ANY }
\]
Besides the expression matrix xx a clinical variable group is required. Covariate adjustment is possible via the argument covars but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments formula.full, formula.red, model.dat and test.terms are "missing" since they are not needed for this method.

Note

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See Also

GlobalAncova, Plot.genes, Plot.sequential

Examples

data(vantVeer)
data(phenodata)
data(pathways)
Plot.subjects(xx = vantVeer, formula.full = ~metastases + ERstatus, formula.red = ~ERstatus, model.dat = phenodata)
Plot.subjects(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metastases", model.dat = phenodata)
Plot.subjects(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, test.genes = pathways[[3]]

Methods

\[
xx = \text{"matrix"}, \text{formula.full} = \text{"formula"}, \text{formula.red} = \text{"formula"}, \text{model.dat} = \text{"ANY"}, \text{group} = \text{"missing"}, \text{covars} = \text{"missing"}
\]

In this method, besides the expression matrix \(xx\), model formulas for the full and reduced model and a data frame \(\text{model.dat}\) specifying corresponding model terms have to be given. Terms that are included in the full but not in the reduced model are those whose association with differential expression will be tested. The arguments \(\text{group}\), \(\text{covars}\) and \(\text{test.terms}\) are "missing" since they are not needed for this method.

\[
xx = \text{"matrix"}, \text{formula.full} = \text{"formula"}, \text{formula.red} = \text{"missing"}, \text{model.dat} = \text{"ANY"}, \text{group} = \text{"missing"}, \text{covars} = \text{"missing"}
\]

In this method, besides the expression matrix \(xx\), a model formula for the full model and a data frame \(\text{model.dat}\) specifying corresponding model terms are required. The character argument \(\text{test.terms}\) names the terms of interest whose association with differential expression will be tested. The arguments \(\text{formula.red}\), \(\text{group}\) and \(\text{covars}\) are "missing" since they are not needed for this method.

\[
xx = \text{"matrix"}, \text{formula.full} = \text{"missing"}, \text{formula.red} = \text{"missing"}, \text{model.dat} = \text{"missing"}, \text{group} = \text{"ANY"}, \text{covars} = \text{"ANY"}
\]

Besides the expression matrix \(xx\) a clinical variable \(\text{group}\) is required. Covariate adjustment is possible via the argument \(\text{covars}\) but more complex models have to be specified with the methods described above. This method emulates the function call in the first version of the package. The arguments \(\text{formula.full}\), \(\text{formula.red}\), \(\text{model.dat}\) and \(\text{test.terms}\) are "missing" since they are not needed for this method.

 vantVeer  

Gene expression data

Description

Normalized gene expression data for the van t’Veer example: A subset of 96 samples without BRCA1 or BRCA2 mutations and 1113 genes associated with nine cancer related pathways (see also ?pathways) was chosen.

Usage

data(vantVeer)
Format

The format is:
num [1:1113, 1:96] 0.13 0.936 -0.087 0.118 0.168 -0.081 0.023 -0.086 -0.154 0.025 ...
- attr(*, "dimnames")=List of 2
  ..$ : chr [1:1113] "AW025529" "NM_001648" "NM_001753" "NM_003298" ...
  ..$: chr [1:96] "1" "2" "3" "4" ...

Examples

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#str(vantVeer)
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