

# GlobalAncova

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colon.normal	<i>Gene expression data</i>
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### 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.normal)
```

**Format**

The format is:

```
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"
...
..$ : chr [1:12] "Co10.N.E.84.F.CEL" "Co14.N.E.89.F.CEL" "Co17.N.E.1037.F.CEL"
"Co1.N.E.31.F.CEL" ...
```

**References**

Groene, J. et al., 2006, Transcriptional census of 36 microdissected colorectal cancers yields a gene signature to distinguish UICC II and III, *Int J Cancer* 119(8):1829–36.

**Examples**

```
data(colon.normal)
#str(colon.normal)
```

---

colon.pheno

*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**

```
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 60 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 1 2 2 2 ...

**\$UICC.stage:** Factor w/ 2 levels "2","3": 2 1 2 1 2 1 1 1 2 1 ...

## References

Groene, J. et al., 2006, Transcriptional census of 36 microdissected colorectal cancers yields a gene signature to distinguish UICC II and III, *Int J Cancer* 119(8):1829–36.

## Examples

```
data(colon.pheno)
#str(colon.pheno)
```

---

colon.tumour	<i>Gene expression data</i>
--------------	-----------------------------

---

## 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:

```
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"
...
..$ : chr [1:12] "Co10.T.IT.83.F.CEL" "Co14.T.IT.88.F.CEL" "Co17.T.IT.563.F.CEL"
"Co1.T.IT.30.F.CEL" ...
```

## References

Groene, J. et al., 2006, Transcriptional census of 36 microdissected colorectal cancers yields a gene signature to distinguish UICC II and III, *Int J Cancer* 119(8):1829–36.

## Examples

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

---

Multiple testing on the GO graph

*Multiple testing on the GO graph*

---

### Description

Three functions adapted from package **globaltest** to test (part of) the GO graph for association of the gene expression profile of GO terms with a response variable. Used together, these functions return multiplicity-adjusted p-values calculated using the Focus Level procedure that preserves the structure of the GO graph.

### Usage

```
GAGO(..., GO, focus, maxalpha = 0.05, stopafter = 100, verbose = FALSE)
```

### Arguments

...	Arguments describing the tests to be performed are passed on to <a href="#">GlobalAncova</a> . Note that only the approximative version of <a href="#">GlobalAncova</a> is used here and hence the parameter <code>method</code> is not available. Even though the number of permutations ( <code>perm</code> ) may be specified since very large gene sets (with more genes than <code>max.group.size</code> ) are treated with the permutation test.
GO	An object of class <a href="#">GOstructure</a> describing the structure of the GO graph. This object should be created using <a href="#">makeGOstructure</a> .
focus	A vector of GO ids to describe the focus level. Typically made using <a href="#">getFocus</a> .
maxalpha	The maximum multiplicity-adjusted p-value. The algorithm will stop when this value is exceeded.
stopafter	The maximum number of significant GO terms to be found. The algorithm will stop when this value is exceeded.
verbose	If set to <code>TRUE</code> , prints much more extensive progress information.

### Details

Previous to a call to `GAGO`, first use [makeGOstructure](#) to make a GO graph tailored to a specific data set. Then [getFocus](#) can be used to choose a focus level. Finally `GAGO` performs the focus level procedure.

### Value

The function returns a named vector of multiplicity-adjusted p-values. Adjusted p-values of GO terms not appearing in this vector are larger than the chosen value of `maxalpha`.

### Note

Function `GAGO` corresponds to function `gtGO` in package **globaltest**. The difference is in the use of the `GlobalAncova` test instead of `globaltest` within the focus level procedure.

### Author(s)

Jelle Goeman: [j.j.goeman@lumc.nl](mailto:j.j.goeman@lumc.nl); Jan Oosting; Manuela Hummel

## References

Goeman, J.J. and Mansmann, U., Family-wise error rate on the directed acyclic graph of Gene Ontology, submitted.

## See Also

[gtGO](#), [GlobalAncova](#), [globaltest](#), [GOstructure](#), [makeGOstructure](#), [getFocus](#)

## Examples

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

---

GlobalAncova.closed

*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 = "matrix", test.genes="list", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group`**

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`**

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`**

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.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,
                    previous.test, level, formula.full, formula.red, model.dat, method = c(
                    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,
                    previous.test, level, formula.full, test.terms, model.dat, method = c(
                    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,
                    previous.test, level, group, covars = NULL, method = c("permutation", "
                    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).

<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>group</code>	Vector with the group membership information.
<code>covars</code>	Vector or matrix which contains the covariate information for each sample.
<code>test.terms</code>	Character vector that contains names of the terms of interest.
<code>method</code>	Raw p-values can be calculated permutation-based (" <code>permutation</code> ") or by means of an approximation (" <code>approx</code> ").
<code>perm</code>	Number of permutations to be used for the permutation approach. The default is 10,000.
<code>max.group.size</code>	Maximum size of a gene set for which the asymptotic p-value is calculated. For bigger gene sets the permutation approach is used.
<code>eps</code>	Resolution of the asymptotic p-value.
<code>acc</code>	Accuracy parameter needed for the approximation. Higher values indicate higher accuracy.

### Value

A list with components

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

### Methods

**`xx = "matrix", test.genes="list", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group`**

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`**

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`**

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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**Author(s)**

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**References**

Marcus, R., Peritz, E. and Gabriel, K.R., 1976, On closed testing procedures with special reference to ordered analysis of variance, *Biometrika* 63 (3): 655–660.

**See Also**

[GlobalAncova](#), [Plot.genes](#), [Plot.subjects](#)

---

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", "typ
```

**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.

**Author(s)**

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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 =
GlobalAncova.decomp(xx = vantVeer, formula = ~ grade + metastases + ERstatus, model.dat =

# 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 =
```

---

GlobalAncova

*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

**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.

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

---

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,
             test.genes, method = c("permutation", "approx", "both", "Fstat"), perm =
```

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

## 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 =
```

## Arguments

<code>xx</code>	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 <code>xx</code> .
<code>formula.full</code>	Model formula for the full model.
<code>formula.red</code>	Model formula for the reduced model (that does not contain the terms of interest.)
<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>group</code>	Vector with the group membership information.
<code>covars</code>	Vector or matrix which contains the covariate information for each sample.
<code>test.terms</code>	Character vector that contains names of the terms of interest.
<code>test.genes</code>	Vector of gene names or a list where each element is a vector of gene names.
<code>method</code>	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 <code>method = "both"</code> . With option "Fstat" only the global F-statistics are returned without p-values or further information.
<code>perm</code>	Number of permutations to be used for the permutation approach. The default is 10,000.
<code>max.group.size</code>	Maximum size of a gene set for which the asymptotic p-value is calculated. For bigger gene sets the permutation approach is used.
<code>eps</code>	Resolution of the asymptotic p-value.
<code>acc</code>	Accuracy parameter needed for the approximation. Higher values indicate higher accuracy.

## Value

If `test.genes = NULL` a list with components

<code>effect</code>	Name(s) of the tested effect(s)
<code>ANOVA</code>	ANOVA table
<code>test.result</code>	F-value, theoretical p-value, permutation-based and/or asymptotic p-value
<code>terms</code>	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 = "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.

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

## 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

Mansmann, U. and Meister, R., 2005, Testing differential gene expression in functional groups, *Methods Inf Med* 44 (3).

## See Also

[Plot.genes](#), [Plot.subjects](#), [GlobalAncova.closed](#), [GAGO](#), [GlobalAncova.decomp](#)

## Examples

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

```
GlobalAncova(xx = vantVeer, formula.full = ~metastases + ERstatus, formula.red = ~ERstatus)
GlobalAncova(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metastases")
GlobalAncova(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, test.terms = "metastases")
```

---

<code>pair.compare</code>	<i>Pairwise comparisons of factor levels within GlobalAncova</i>
---------------------------	--

---

**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)
```

**Arguments**

<code>xx</code>	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 <code>xx</code> .
<code>formula</code>	Model formula for the linear model.
<code>group</code>	Factor for which pairwise comparisons shall be calculated.
<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>test.genes</code>	Vector of gene names or a list where each element is a vector of gene names.
<code>perm</code>	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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 Ulrich Mansmann <mansmann@ibe.med.uni-muenchen.de>

**See Also**

[GlobalAncova](#), [GlobalAncova.decomp](#)

**Examples**

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

```
pair.compare(xx = vantVeer, formula = ~ grade, group = "grade", model.dat = phenodata, te
```

---

 pathways

*Cancer related pathways*


---

### 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" "AF018081"
"NM_003005" ...
$ wnt_signaling : chr [1:176] "AB033058" "AB033087" "NM_003012" "NM_003014"
...
```

### Examples

```
data(pathways)
#str(pathways)
```

---

 phenodata

*Covariate information for the van t'Veer data*


---

### Description

Covariate 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 ordered levels).

**ERstatus** Estrogen receptor status (pos-positive/neg-negative).

**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 3 2 1 3 3 2 ...
```

```
$ERstatus: Factor w/ 2 levels "neg","pos": 2 2 1 2 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**

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

**Author(s)**

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**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
```

---

Plot.genes

*Methods for Function Plot.genes*

---

**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**

**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.

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

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

```
## S4 method for signature 'matrix, formula, formula, ANY,
##   missing, missing, missing':
Plot.genes(xx, formula.full, formula.red, model.dat, test.genes, Colorgroup = NU

## S4 method for signature 'matrix, formula, missing, ANY,
##   missing, missing, character':
Plot.genes(xx, formula.full, test.terms, model.dat, test.genes, Colorgroup = NUL

## S4 method for signature 'matrix, missing, missing,
##   missing, ANY, ANY, missing':
Plot.genes(xx, group, covars = NULL, test.genes, Colorgroup = NULL, legendpos =
```

**Arguments**

<code>xx</code>	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 <code>xx</code> .
<code>formula.full</code>	Model formula for the full model.
<code>formula.red</code>	Model formula for the reduced model (that does not contain the terms of interest.)
<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>group</code>	Vector with the group membership information.
<code>covars</code>	Vector or matrix which contains the covariate information for each sample.
<code>test.terms</code>	Character vector that contains names of the terms of interest.
<code>test.genes</code>	Vector of gene names or gene indices specifying the gene set. If missing, the plot refers to all genes in <code>xx</code> .
<code>Colorgroup</code>	Character variable giving the group that specifies coloring. If the function is called using the argument <code>group</code> then this variable is assumed to be relevant for coloring.
<code>legendpos</code>	Position of the legend (a single keyword from the list <code>"bottomright"</code> , <code>"bottom"</code> , <code>"bottomleft"</code> , <code>"left"</code> , <code>"topleft"</code> , <code>"top"</code> , <code>"topright"</code> , <code>"right"</code> and <code>"center"</code> ).
<code>returnValues</code>	Shall bar heights (gene-wise reduction in sum of squares) be returned?
<code>bar.names</code>	Vector of bar labels. If missing, gene names from <code>test.genes</code> or row names of <code>xx</code> are taken.
<code>...</code>	Graphical parameters for specifying colors, titles etc.

**Methods**

**xx = "matrix", formula.full = "formula", formula.red = "formula", model.dat = "ANY", group = "missing", covars = "missing", test.terms = "missing", test.genes = "missing", legendpos = "center", returnValues = FALSE, bar.names = NULL, ...**

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 = "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.

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

### Note

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

### Author(s)

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### See Also

[GlobalAncova](#), [Plot.subjects](#), [Plot.sequential](#)

### Examples

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

Plot.genes(xx = vantVeer, formula.full = ~metastases + ERstatus, formula.red = ~ERstatus,
Plot.genes(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metastases",
Plot.genes(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, test.terms = "metastases")
```

---

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

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

**Arguments**

<code>xx</code>	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 <code>xx</code> .
<code>formula</code>	Model formula for the linear model.
<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>test.genes</code>	Vector of gene names or gene indices specifying a gene set.
<code>name.geneset</code>	Name of the plotted geneset.

**Note**

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

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

**See Also**

[GlobalAncova.decomp](#), [Plot.genes](#), [GlobalAncova](#)

**Examples**

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

```
Plot.sequential(vantVeer, formula = ~ ERstatus + metastases + grade, model.dat = phenodat
```

---

Plot.subjects

*Methods for Function Plot.subjects*

---

**Description**

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

**Methods**

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

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 = "missing", test.terms = "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.

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

*Subjects Plot for GlobalAncova*

---

## 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, test.genes, Colorgroup = "missing", test.terms = "missing")

## S4 method for signature 'matrix, formula, missing, ANY,
##   missing, missing, character':
Plot.subjects(xx, formula.full, test.terms, model.dat, test.genes, Colorgroup = "missing", test.terms = "missing")

## S4 method for signature 'matrix, missing, missing,
##   missing, ANY, ANY, missing':
Plot.subjects(xx, group, covars = NULL, test.genes, Colorgroup = NULL, sort = FALSE)
```

## Arguments

<code>xx</code>	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 <code>xx</code> .
<code>formula.full</code>	Model formula for the full model.
<code>formula.red</code>	Model formula for the reduced model (that does not contain the terms of interest.)
<code>model.dat</code>	Data frame that contains all the variable information for each sample.
<code>group</code>	Vector with the group membership information.
<code>covars</code>	Vector or matrix which contains the covariate information for each sample.
<code>test.terms</code>	Character vector that contains names of the terms of interest.

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

## Methods

**`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.

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

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

## Note

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

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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 = ~ERstat
Plot.subjects(xx = vantVeer, formula.full = ~metastases + ERstatus, test.terms = "metasta
Plot.subjects(xx = vantVeer, group = phenodata$metastases, covars = phenodata$ERstatus, t

```

---

 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**

```

data(vantVeer)
#str(vantVeer)

```

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