

# Package ‘ArrayTools’

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**Type** Package

**Title** geneChip Analysis Package

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**Author** Xiwei Wu, Arthur Li

**Depends** R (>= 2.7.0), affy (>= 1.23.4), Biobase (>= 2.5.5), methods

**Imports** affy, Biobase, graphics, grDevices, limma, methods, stats,utils, xtable

**Suggests** simpleaffy, R2HTML, affydata, affyPLM, genefilter, an-naffy,gcRMA, hugene10sttranscriptcluster.db

**Collate** Generic.R designMatrix-class.R contrastMatrix-class.R  
regressResult-class.R interactionResult-class.R  
preProcess3prime.R preProcessGeneST.R createExpressionSet.R  
regress.R selectSigGene.R postInteraction.R selectSigGeneInt.R  
createGSEAFiles.R createIndex.R createIngenuityFile.R  
geneFilter.R intensityPlot.R output.cls.R output.gct.R  
output.ing.R plotCluster.R qa3prime.R qaGeneST.R

**Maintainer** Arthur Li <xueli@coh.org>

**Description** This package is designed to provide solutions for quality assessment and to detect differentially expressed genes for the Affymetrix GeneChips, including both 3' -arrays and gene 1.0-ST arrays. The package generates comprehensive analysis reports in HTML format. Hyperlinks on the report page will lead to a series of QC plots, processed data, and differentially expressed gene lists. Differentially expressed genes are reported in tabular format with annotations hyperlinked to online biological databases.

**biocViews** Microarray, OneChannel, QualityControl, Preprocessing,Statistics, DifferentialExpression, Annotation, ReportWriting,Visualization

**License** LGPL (>= 2.0)

**LazyLoad** yes

**R topics documented:**

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<i>adjustment</i>	<i>Access the multiple comparison adjustment method from the regressResult or interactionResult class</i>
-------------------	---

**Description**

Access the multiple comparison adjustment method from the regressResult class or interactionResult class

**Usage**

`adjustment(object)`

**Arguments**

`object`            a regressResult or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

<i>contrastMatrix</i>	<i>Class to Contain the Contrast Matrix that Used for Linear Regression</i>
-----------------------	---

**Description**

Class to Contain the Contrast Matrix that Used for Linear Regression, inherited from the designMatrix class

**Creating Objects**

```
new("contrastMatrix", ..., design.matrix=[designMatrix],compare1=[character],compare2=[character],level=)
```

This creates a contrast matrix class. `design.matrix` is a `designMatrix` class. `compare1` the first value of the main covariate, and `compare2` is the second value of the main covariate. For example, suppose that the main covariate is "drug", and there are three unique values: "drug1", "drug2", and "placebo". You would like to compare "drug1" to "drug2". Then you would use "drug1" as `compare1` and "drug2" as `compare2`. If `interaction==TRUE`, do not specify `compare1` and `compare2`. You only specify `level` when the design matrix contains an interaction term. Suppose that you would like to compare "drug1" to "drug2" only when estrogen is "present", where "present"

is one of the values of the estrogen variable. You will use "present" as level. If `interaction==TRUE`, do not specify this value as well. You only specify `interaction==TRUE` when you would like to detect the interaction effect between two covariates. In this case, do not provide values for `compare1`, `compare2`, and `level`

### Slots

**contrast:** Object of class "matrix" contains the contrast matrix

**compare1:** Object of class "character" contains `compare1`

**compare2:** Object of class "character" contains `compare2`

**level:** Object of class "character" contains `level`

**interaction:** Object of class "logical" contains `interaction`

**design:** Object of class "matrix" contain the design matrix

**target:** Object of class "data.frame" contains `target`

**covariates:** Object of class "character" contains `covariates`

**intIndex:** Object of class "numeric" contains `intIndex`

### Extends

Class "[designMatrix](#)", directly.

### Methods

**getCompare1** signature(object = "contrastMatrix"): access the `compare1` slot

**getCompare2** signature(object = "contrastMatrix"): access the `compare2` slot

**getContrast** signature(object = "contrastMatrix"): access the contrast slot

**getInteraction** signature(object = "contrastMatrix"): access the `interaction` slot

**getLevel** signature(object = "contrastMatrix"): access the `level` slot

**initialize** signature(.Object = "contrastMatrix"): create a new contrast matrix class

**show** signature(object = "contrastMatrix"): print the contrast matrix

### Author(s)

Xiwei Wu, Arthur Li

### See Also

[designMatrix](#)

### Examples

```
data(eSetExample)
## One-way Anova
(design1<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment"))
(contrast1<- new("contrastMatrix", design.matrix = design1,
  compare1 = "Treated", compare2 = "Control"))

## Randomized block design
(design2<- new("designMatrix", target=pData(eSetExample),
  covariates = c("Treatment", "Group")))
```

```
(contrast2<- new("contrastMatrix", design.matrix = design2,
  compare1 = "Treated", compare2 = "Control"))

## Interaction design
(design3<- new("designMatrix", target=pData(eSetExample),
  covariates = c("Treatment", "Group"), intIndex=c(1,2)))
# Test for interaction:
(contrast.int<- new("contrastMatrix", design.matrix = design3,
  interaction=TRUE))
# Compare Treated vs Control among group A
(contrast.a<- new("contrastMatrix", design.matrix = design3,
  compare1 = "Treated", compare2 = "Control", level="A"))
```

---

createExpressionSet      *Creating an ExpressionSet*

---

## Description

Create an ExpressionSet based on phenotype data and expression data

## Usage

```
createExpressionSet(pData, exprs, ...)
```

## Arguments

pData	a data frame contains the phenotype data
exprs	a data frame contains the expression data
...	additional arguments passed to new("ExpressionSet", exprs, phenoData, ...) if needed

## Value

an ExpressionSet

## Author(s)

Xiwei Wu, Arthur Li

## References

Bioconductor: Open software development for computational biology and bioinformatics R. Gentleman, V. J. Carey, D. M. Bates, B. Bolstad, M. Dettling, S. Dudoit, B. Ellis, L. Gautier, Y. Ge, and others 2004, Genome Biology, Vol. 5, R80

## See Also

[ExpressionSet](#)

**Examples**

```
data(pDataExample)
data(exprsExample)
eSet <- createExpressionSet (pDataExample, exprsExample,
  annotation = "hugene10sttranscriptcluster")
```

---

createGSEAFiles      *A Wrapper Function to create \*.GCT and \*.CLS for GSEA analysis*

---

**Description**

A Wrapper Function to create \*.GCT and \*.CLS for GSEA analysis

**Usage**

```
createGSEAFiles(mydir = getwd(), eSet, catVar)
```

**Arguments**

mydir	directory where you would like to store the files
eSet	an ExpressionSet
catVar	variable of interest

**Value**

Creating \*.GCT and \*.CLS for GSEA

**Author(s)**

Xiwei Wu, Arthur Li

**References**

<http://www.broad.mit.edu/gsea/>

**See Also**

[output.cls](#), [output.gct](#)

**Examples**

```
data(eSetExample)
## Not run: createGSEAFiles (mydir, eSetExample, "Treatment")
```

---

 createIndex

*Creating an HTML index file*


---

### Description

This HTML index file will link all the outputted result, including Quality Assessment Report, differentially expressed genes, etc...

### Usage

```
createIndex(..., mydir = getwd(), index.file = "index.html", createHeader = NULL)
```

### Arguments

...	regressionResults or interactionResult
mydir	the directory to contain the index file
index.file	name of the index file
createHeader	If want to want to create an Header, such as your name, company names, etc...

### Value

creating an HTML index-file in your directory

### Author(s)

Xiwei Wu, Arthur Li

### Examples

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
sigResult<- selectSigGene(result, fc.value=log2(2))
## Not run: Output2HTML(sigResult)

design.int<- new("designMatrix", target=pData(eSetExample), covariates = c("Treatment", "Group"),
  intIndex = c(1, 2))
contrast.int<- new("contrastMatrix", design.matrix = design.int, interaction=TRUE)
result.int<- regress(eSetExample, contrast.int)
sigResult.int <- selectSigGene(result.int)
intResult <- postInteraction(eSetExample, sigResult.int, mainVar = "Treatment",
  compare1 = "Treated", compare2 = "Control")
sigResultInt <- selectSigGeneInt(intResult)
## Not run: Output2HTML(sigResultInt)

## Not run: createIndex(sigResult, sigResultInt, createHeader = c("Arthur Li", "COH"))
```

---

createIngenuityFile      *A Wrapper Function to Create Files for Ingenuity Analysis*

---

### Description

A Wrapper Function to Create Files for Ingenuity Analysis

### Usage

```
createIngenuityFile(..., mydir = getwd(), eSet, filename = "IngenuityFile")
```

### Arguments

...	a list of regressResult class
mydir	the directory where you would like to store the file
eSet	an ExpressionSet
filename	file name

### Details

This function enable to create the ingenuity upload file based on a list of regressResult

### Value

create an Ingenuity upload file

### Author(s)

Xiwei Wu, Arthur Li

### References

<http://www.ingenuity.com/>

### Examples

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
## Not run: createIngenuityFile(result, eSet = eSetExample)
```



designMatrix

*Class to Contain the Design Matrix that Used for Linear Regression***Description**

Class to Contain the Design Matrix that Used for Linear Regression

**Creating Objects**

```
new("designMatrix", ..., target, covariates, intIndex=0)
```

This create as design matrix class. target is a data frame that contains chip and covaraite information, or experimental phenotypes recorded in eSet and ExpressionSet-derived classes. covariates is a list of 1-n covariates. If intIndex=0, the interaction effect is not considered; otherwise, use two integers to indicate which covariates are considered for interaction effect. For example, if covariates <- c("estrogen", "drug", "time") and you are considering the interaction between "estrogen" and "time", then you would write intIndex=c(1,3)

**Slots**

**design:** contains the design matrix

**target:** contains the target data

**covariates:** contains the covariates

**intIndex:** contains the intIndex

**Methods**

**getCovariates** signature(object = "designMatrix"): access the covariates slot

**getDesign** signature(object = "designMatrix"): access the design slot

**getIntIndex** signature(object = "designMatrix"): access the intIndex slot

**getTarget** signature(object = "designMatrix"): access the target slot

**initialize** signature(.Object = "designMatrix"): create a new designMatrix class

**show** signature(object = "designMatrix"): print the designMatrix class

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[contrastMatrix](#)

**Examples**

```
data(eSetExample)
## One-way Anova
(design1<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment"))

## Randomized block design
(design2<- new("designMatrix", target=pData(eSetExample),
  covariates = c("Treatment", "Group")))
```

```
## Interaction design
(design3<- new("designMatrix", target=pData(eSetExample),
  covariates = c("Treatment", "Group"), intIndex=c(1,2)))
```

---

eSetExample

*An ExpressionSet example*


---

### Description

An ExpressionSet example

### Usage

```
data(eSetExample)
```

### Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 6 slots

### Examples

```
data(eSetExample)
```

---

exprsExample

*a data.frame contains expression data*


---

### Description

a data.frame contains expression data

### Usage

```
data(exprsExample)
```

### Format

A data frame with 1000 observations on the following 17 variables.

probeset\_id a numeric vector

H1.CEL a numeric vector

H2.CEL a numeric vector

H3.CEL a numeric vector

H4.CEL a numeric vector

H5.CEL a numeric vector

H6.CEL a numeric vector

H7.CEL a numeric vector

H8.CEL a numeric vector  
 H9.CEL a numeric vector  
 H10.CEL a numeric vector  
 H11.CEL a numeric vector  
 H12.CEL a numeric vector  
 H13.CEL a numeric vector  
 H14.CEL a numeric vector  
 H15.CEL a numeric vector  
 H16.CEL a numeric vector

### Examples

```
data(exprsExample)
```

---

geneFilter	<i>filter an ExpressionSet using different methods</i>
------------	--

---

### Description

Create a filtered 'ExpressionSet' based on background, range, or interquartile range

### Usage

```
geneFilter(object, pct = 0.1, numChip = ceiling(ncol(exprs(object)) * pct), bg = 4, range = 0, iqrPct = 0, output
```

### Arguments

object	an ExpressionSet
pct	percentage
numChip	number of chips. If you would like to filter the ExpressionSet based on at least 3 chips greater than 1 (bg=1), then set numChip = 3
bg	background value. If you would like to filter the ExpressionSet based on at least 3 chips greater than 1, then set bg=1
range	range = max value - min value of each gene
iqrPct	interquartile percentage
output	if output = TRUE, output filtered data in the sepecified directory
mydir	the directory containing the filtered data

### Details

There are three filtering methods. The User can use either one, two, or three. 1). At least a certain number of chips (numChip) are greater than a given background (bg) 2). The range of the gene have to be greater than a given value (range) 3). Calculating the interquartile range (IQR) of each gene to create an IQR vector. Based on the given percentage (e.g. iqrPct=0.2), find the corresponding percentile. If IQR is less than percentile, the gene will be filtered

**Value**

a filtered ExpressionSet

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
filtered <- geneFilter(eSetExample)
```

---

getAdjP

*access the adjPVal slot from regressResult or interactionResult class*

---

**Description**

access the adjPVal slot from regressResult or interactionResult class

**Usage**

```
getAdjP(object)
```

**Arguments**

object            a regressResult class or interactionResult class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getAnnotation	<i>access the annotation slot from the regressResult or interactionResult slot</i>
---------------	--

---

**Description**

access the annotation slot from the regressResult or interactionResult slot

**Usage**

```
getAnnotation(object)
```

**Arguments**

object            a regressResult class or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getCompare1	<i>Access the Compare1 slot from the contrastMatrix</i>
-------------	---

---

**Description**

Access the Compare1 slot from the contrastMatrix

**Usage**

```
getCompare1(object)
```

**Arguments**

object            a contrastMatrix class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**[contrastMatrix](#)

---

getCompare2	<i>Access the compare2 slot from the contrastMatrix class</i>
-------------	---

---

**Description**

Access the compare2 slot from the contrastMatrix class

**Usage**

```
getCompare2(object)
```

**Arguments**

object            a contrastMatrix class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**[contrastMatrix](#)

---

getContrast	<i>Access the contrast matrix from the contrastMatrix class</i>
-------------	---

---

**Description**

Access the contrast matrix from the contrastMatrix class

**Usage**

```
getContrast(object)
```

**Arguments**

object            a contrastMatrix class

**Value**

a numeric matrix

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[contrastMatrix](#)

---

getCovariates

*Accessing the covariates from the designMatrix class*

---

**Description**

Accessing the covariates from the designMatrix class

**Usage**

```
getCovariates(object)
```

**Arguments**

object            a designMatrix class

**Value**

a character vector containing covariates

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[designMatrix](#)

---

getDesign

*Access the design matrix from the designMatrix class*

---

**Description**

Access the design matrix from the designMatrix class

**Usage**

```
getDesign(object)
```

**Arguments**

object            a designMatrix class

**Value**

a matrix containing the designMatrix

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[designMatrix](#)

---

getF	<i>access the foldChange slot from regressionResult or interactionResult class</i>
------	--

---

**Description**

access the foldChange slot from regressionResult or interactionResult class

**Usage**

```
getF(object)
```

**Arguments**

object            a regressResult or interactionResult class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)



---

getFC	<i>Access the foldChange slot from the regressResult or interactionResult class</i>
-------	---

---

**Description**

Access the foldChange slot from the regressResult or interactionResult class

**Usage**

```
getFC(object)
```

**Arguments**

object            a regressResult class or interactionResult class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getFCCutoff	<i>Access the significantFCCutoff slot from the regressResult or interactionResult class</i>
-------------	--

---

**Description**

Access the significantFCCutoff slot from the regressResult or interactionResult class

**Usage**

```
getFCCutoff(object)
```

**Arguments**

object            a regressResult or interactionResult class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getFilterMethod	<i>Access the filterMethod slot from the regressResult or interactionResult class</i>
-----------------	---

---

**Description**

Access the filterMethod slot from the regressResult or interactionResult class

**Usage**

```
getFilterMethod(object)
```

**Arguments**

object            a regressResult or interactionResult class

**Value**

a list

**Author(s)**

Xiwei Wu, Arthur Li

**References**

~put references to the literature/web site here ~

**See Also**

[regressResult](#) [interactionResult](#)

---

getID	<i>access the ID slot from the regressResult or interactionResult class</i>
-------	---

---

**Description**

access the ID slot from the regressResult or interactionResult class

**Usage**

```
getID(object)
```

**Arguments**

object            a regressResult class or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getIndex

*Access the SignificantIndex slot from the regressResult or interaction-Result class*

---

**Description**

Access the SignificantIndex slot from the regressResult or interactionResult class

**Usage**

getIndex(object)

**Arguments**

object            a regressResult or interactionResult class

**Value**

a logical vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

getInteraction                      *Access the interaction slot from the contrastMatrix class*

---

**Description**

Access the interaction slot from the contrastMatrix class

**Usage**

```
getInteraction(object)
```

**Arguments**

object                      a contrastMatrix class

**Value**

a logical vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[contrastMatrix](#)

---

getIntIndex                      *Access the IntIndex slot from the designMatrix class*

---

**Description**

Access the IntIndex slot from the designMatrix class

**Usage**

```
getIntIndex(object)
```

**Arguments**

object                      an designMatrix class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[designMatrix](#)

---

getLength	<i>Calculate the Length of interactionResult class</i>
-----------	--

---

**Description**

Calculate the Length of interactionResult class

**Usage**

```
getLength(object)
```

**Arguments**

object            an interactionResult class

**Value**

a numeric value

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[interactionResult](#)

---

getLevel	<i>Access the level slot from the contrastMatrix class</i>
----------	--

---

**Description**

Access the level slot from the contrastMatrix class

**Usage**

```
getLevel(object)
```

**Arguments**

object            a contrastMatrix class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[contrastMatrix](#)

---

getNormalizationMethod

*Access the significantIndex slot from the regressResult or interactionResult class*

---

**Description**

Access the significantIndex slot from the regressResult or interactionResult class

**Usage**

getNormalizationMethod(object)

**Arguments**

object                    a regressResult or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getP

*Access the pValue slot from regressResult or interactionResult class*

---

**Description**

Access the pValue slot from regressResult or interactionResult class

**Usage**

getP(object)

**Arguments**

object                    a regressResult or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getPCutoff	<i>Access the significantPvalueCutoff slot from regressResult or interactionResult class</i>
------------	--

---

**Description**

Access the significantPvalueCutoff slot from regressResult or interactionResult class

**Usage**

```
getPCutoff(object)
```

**Arguments**

object            a regressResult or interactionResult class

**Value**

a numeric vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

getTarget	<i>Access the target slots from the designMatrix class</i>
-----------	--

---

**Description**

Access the target slots from the designMatrix class

**Usage**

```
getTarget(object)
```

**Arguments**

object            a designMatrix class

**Value**

a data frame contains the target file

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[designMatrix](#)

---

hugene10stCONTROL    *hugene10stCONTROL*

---

**Description**

It is used to remove "normgene" and "control" genes for hugene10st array in the preProcessGeneST function. It is not intended to be used by the user.

**Usage**

```
data(hugene10stCONTROL)
```

**Format**

A data frame with 4201 observations on the following 2 variables.

---

interactionResult-class    *Class to Contain the Regression Result Based on An Interaction Model*

---

**Description**

Class to Contain the Regression Result Based on An Interaction Model. Interaction is a statistical term referring to a situation when the relationship between the outcome and the variable of the main interest differs at different levels of the extraneous variable

**Creating Objects**

interactionResult object is generally created from the postInteraction function See [postInteraction](#)

**Object Components**

A list of four or more components. Each component is a regressResult class. The first component contains all the genes. The second component contains genes with the interaction effect The rest components contains genes with the interaction effect across different levels. Each component contains the result for each level.

**Extends**

Class "[list](#)", from data part. Class "[vector](#)", by class "list", distance 2.



**Methods**

**adjustment** signature(object = "regressResult"): access the adjustment slot

**getAdjP** signature(object = "regressResult"): access the adjPVal slot

**getAnnotation** signature(object = "regressResult"): access the annotation slot

**getContrast** signature(object = "regressResult"): access the contrast slot

**getF** signature(object = "regressResult"): access the FValue slot

**getFC** signature(object = "regressResult"): access the foldChange slot

**getFCCutoff** signature(object = "regressResult"): access the significantFCCutoff slot

**getFileName** signature(object = "regressResult"): access the fileName slot

**getFilterMethod** signature(object = "regressResult"): access the filterMethod slot

**getID** signature(object = "regressResult"): access the ID slot

**getIndex** signature(object = "regressResult"): access the significantIndex slot

**getNormalizationMethod** signature(object = "regressResult"): access the normalizationMethod slot

**getP** signature(object = "regressResult"): access the pValue slot

**getPCutoff** signature(object = "regressResult"): access the significantPvalueCutoff slot

**Output2HTML** signature(object = "regressResult"): create HTML file for significant genes in regressionResult

**regressionMethod** signature(object = "regressResult"): access the regressionMethod slot

**selectSigGene** signature(object = "regressResult"): select significant genes for regressionResult class

**show** signature(object = "regressResult"): print regressResult

**Sort** signature(x = "regressResult"): sort regressResult

**summary** signature(object = "regressResult"): print the summary for regressResult

**getLength** signature(object = "interactionResult"): calculate the length of the interactionResult class

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#)

**Examples**

```
## Creating the interactionREsult takes a few steps:
data(eSetExample)
design.int<- new("designMatrix", target=pData(eSetExample), covariates = c("Treatment", "Group"),
  intIndex = c(1, 2))
contrast.int<- new("contrastMatrix", design.matrix = design.int, interaction=TRUE)
result.int<- regress(eSetExample, contrast.int)
sigResult.int <- selectSigGene(result.int)
intResult <- postInteraction(eSetExample, sigResult.int, mainVar ="Treatment",
  compare1 = "Treated", compare2 = "Control")
```

---

mogene10stCONTROL    *mogene10stCONTROL*

---

### Description

It is used to remove "normgene" and "control" genes for mogene10st array in the preProcessGeneST function. It is not intended to be used by the user.

### Usage

```
data(mogene10stCONTROL)
```

### Format

A data frame with 6613 observations on the following 2 variables.

---

output.cls                      *Create \*.CLS file for GSEA analysis*

---

### Description

Create \*.CLS file for GSEA analysis

### Usage

```
output.cls(target, variable, filename = "phenotype")
```

### Arguments

target	pheno Data file
variable	variable of interest
filename	file name

### Value

create a \*.CLS file

### Author(s)

Xiwei, Wu, Arthur Li

### References

<http://www.broad.mit.edu/gsea/>

### See Also

[output.gct](#), [createGSEAFiles](#)

---

output.gct

*Create an \*.GCT file for GSEA analysis*

---

**Description**

Create an \*.GCT file for GSEA analysis

**Usage**

```
output.gct(normal, filename = "probe")
```

**Arguments**

normal	an ExpressionSet
filename	file name

**Value**

create an \*.GCT file

**Author(s)**

Xiwei Wu, Arthur Li

**References**

<http://www.broad.mit.edu/gsea/>

**See Also**

[output.cls](#), [createGSEAFiles](#)

---

output.ing

*Create an Ingenuity File for Ingenuity Analysis*

---

**Description**

Create an Ingenuity File for Ingenuity Analysis

**Usage**

```
output.ing(allfile, eSet, filename = "IngenuityFile")
```

**Arguments**

allfile	a list of regressResult class
eSet	an ExpressionSet
filename	file name

**Value**

create an txt file for Ingenuity Analysis

**Author(s)**

Xiwei Wu, Arthur Li

**References**

<http://www.ingenuity.com/>

**See Also**

[createIngenuityFile](#)

---

Output2HTML

*Creating HTML file for regressResult or interactionResult class*

---

**Description**

Creating HTML file for regressResult or interactionResult class

**Usage**

```
Output2HTML(object, ...)
```

**Arguments**

object	an regressResult or interactionResult class
...	you can specify the directory to store the result by using the mydir argument. The default value of mydir is the current working directory

**Value**

creating an HTML file

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
sigResult<- selectSigGene(result, fc.value=log2(2))
### Not run: Output2HTML(sigResult)
```

---

pDataExample                      *a phenoData example*

---

**Description**

a data frame contains the phenotype data

**Usage**

```
data(pDataExample)
```

**Format**

A data frame with 16 observations on the following 2 variables.

Treatment a character vector

Group a character vector

**Examples**

```
data(pDataExample)
```

---

postInteraction                      *Create an Object of InteractionResult Class for Testing Interaction*

---

**Description**

Based on the result from the interaction test by looking at the result from the regressResult object, this function partitions the original data, an ExpressionSet into groups, one contains the genes without the interaction and others contains the genes with the interaction across different level of covariates.

**Usage**

```
postInteraction(eSet, regressObject, mainVar, compare1, compare2, method = regressionMethod(regressObject))
```

**Arguments**

eSet	an ExpressionSet
regressObject	a regressResult
mainVar	variable of main interest
compare1	the first value of the mainVar. For example, suppose that mainVar is "drug", and there are three unique values: "drug1", "drug2", and "placebo". You would like to compare "drug1" to "drug2". Then you would use "drug1" as compare1
compare2	Based on the example for compare1, "drug2" will be the compare2
method	It is used to run regression within each level of the effect modifier. choose the following three options: "limma" (LIMMA), "regression" (ordinary linear regression), "permutation" (permutation test)
adj	adjustment method for multiple comparison test, including "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". The default value is "none". Type help(p.adjust) for more detail.

**Value**

an interactionResult class. The first component contains all the result for all the genes. The second component contains the genes without the interaction effect. The rest of the components contains genes with the interactions.

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
design.int<- new("designMatrix", target=pData(eSetExample), covariates = c("Treatment", "Group"),
  intIndex = c(1, 2))
contrast.int<- new("contrastMatrix", design.matrix = design.int, interaction=TRUE)
result.int<- regress(eSetExample, contrast.int)
sigResult.int <- selectSigGene(result.int)
intResult <- postInteraction(eSetExample, sigResult.int, mainVar = "Treatment",
  compare1 = "Treated", compare2 = "Control")
```

---

```
preProcess3prime
```

*A wrapper function to normalize the the 3 prime array*

---

**Description**

A wrapper function to normalize the 3 prime array by using either RMA or GCRMA method

**Usage**

```
preProcess3prime(object, method = c("rma", "gcrma"), output = FALSE, mydir = getwd())
```

**Arguments**

object	an AffyBatch.
method	either rma or gcrma
output	If output = TRUE, it will output the preprocessed data in the specified directory from the mydir argument
mydir	specified directory to contain the output

**Value**

an ExpressionSet

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

~~objects to See Also as [help](#), ~~~

**Examples**

```
if (require(affydata)) {  
  data(Dilution)  
  eset <- preProcess3prime(Dilution)  
}
```

---

preProcessGeneST	<i>Proprocess genechip ST array</i>
------------------	-------------------------------------

---

**Description**

Proprocess genechip ST array by taking the log<sub>2</sub> of the expression value.

**Usage**

```
preProcessGeneST(object, offset = 1, rmControl = TRUE, output = FALSE, mydir = getwd())
```

**Arguments**

object	an ExpressionSet.
offset	The offset is added to the expression value to avoid $\log_2(0) = -\text{Inf}$ .
rmControl	Setting <code>rmControl = TRUE</code> to remove control probes.
output	If <code>output = TRUE</code> , it will output the preprocessed data in the specified directory from the <code>mydir</code> argument.
mydir	specified directory to contain the output

**Value**

an ExpressionSet

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)  
processedData <- preProcessGeneST(eSetExample)
```

**Description**

Creating Quality Assessment Report for 3 Prime Array in HTML file

**Usage**

```
qa3prime(object, parameters, outputFile = "QA.html", mydir = getwd())
```

**Arguments**

object	an AffyBatch object
parameters	The names of the variables to be included in the report
outputFile	The name of the outputfile. Make sure write ".html"
mydir	The name of the directory containing the report

**Details**

This function creates quality control report in an HTML file that contains a set of 9 assessment figures.

Figure1: The Raw Intensity Plot. The raw intensity should be similar across all chips

Figure2: The Average Background/Percentage Present Plot. The Average Background should be similar across all chips. The Percentage Present should be similar across all chips, except that in rare situations transcription is globally shut down or turned on under some conditions

Figure3: The Scaling Factor Plot. The scaling factor should be within 3-fold across all chips

Figure4: The Hybridization Controls Plot. BioB, BioC, BioD, CreX should be called present, except that it is acceptable if BioB is absent sometimes.

Figure5: The Housekeeping Controls Plot. The GAPDH ratio should be around 1 and the actin ratio should be less than 3. Note that if two-cycle amplification or NuGen amplification is used, this ratio could be much higher.

Figure6: The RNA Degradation Plot. On Affymetrix GeneChips, individual probes in a probeset are ordered by location relative to the 5' end of the targeted RNA molecule. On each chip, probe intensities are averaged by location in the probeset, with the average taken over probesets. In an RNA digestion plot, these means are plotted side-by-side, making it easy to notice any 5' to 3' trend. The trend can be due to RNA degradation or 3'-biased amplification. Since RNA degradation typically starts from the 5' end of the molecule and amplification starts at the 3' end, we would expect probe intensities to be systematically lowered at the 5' end of a probeset when compared to the 3' end.

Figure7: The Hierarchical Clustering of Samples. Samples will be grouped using hierarchical clustering and principal component analysis (PCA). If the sample preparation steps introduced bigger variation than biological variation, treatment groups will be mixed up in the plot. This could also happen when the samples between groups were mixed up accidentally when the samples were prepared. We acknowledge that clinical samples are harder to collect and sometimes impossible to control. Therefore, sample QC criteria will be much looser when dealing with clinical samples.

Figure8: The Pseudo-chip Images. A Pseudo-chip image plots the weights and residuals from the model fit. The image plot allows detection of artifacts on the chip.



Figure9: The Normalized Unscaled Standard Error (NUSE) and Relative Log Expression (RLE) Plots. The NUSE is fitted robustly by iteratively reweighted least squares (IRLS) so that the standard error of the estimated log2 scale expression can be estimated. The boxplots of the NUSE show the differences in hybridization quality most clearly, in magnitude as well as variability. A high NUSE likely corresponds to a low signal. The RLE plot is a boxplot showing the distribution of Log2 ratio of each chip relative to a median chip. A discordant distribution infers a problem with the chip.

### Value

no value is returned

### Author(s)

Xiwei Wu, Arthur Li

### References

<http://www.affymetrix.com>

### Examples

```
## Not run: qa3prime(AffyBatchExample, c("var1", "var2"))
```

---

 qaGeneST

*Creating Quality Assessment Report for Gene ST Array*


---

### Description

Creating Quality Assessment Report for Gene ST Array in HTML file

### Usage

```
qaGeneST(object, parameters, QC, mydir = getwd(), outputFile = "QA.html")
```

### Arguments

object	an ExpressionSet
parameters	The names of the variables to be included in the report
QC	The QC report generated from Affymetrix Expression Console
mydir	The name of the directory containing the report
outputFile	The name of the outputfile. Make sure write ".html"

### Details

This function creates quality control report in an HTML file that contains a set of 8 assessment figures.

Figure1: The intensity distributio Plot. The raw intensity should be similar across all chips

Figure2: The Mean Signal Plot. The mean signal of each group should be consistant across the samples. The positive control should be higher than the negative controls.

Figure3: BAC SPIKE plot. The mean signal of each group should be constant across the samples. The signal for BioB should be the lowest, followed by BioC, BioD, and CreX (the highest).

Figure4: POLYA SPIKE plot. The mean signal of each group should be constant across the samples. The signal for Lys should be the lowest, followed by Thr, Phe, and Dap.

Figure5: POS VS NEG AUC plot. Pos vs neg auc is the area under the curve (AUC) for a receiver operating characteristic (ROC) plot comparing signal values for the positive controls to the negative controls. In practice the expected value for this metric is tissue type specific and may be sensitive to the quality of the RNA sample. Values between 0.80 and 0.90 are typical.

Figure6: MAD RESIDUAL MEAN plot. A measure of how well or poor all of the probes on a given chip fit the RMA or PLIER model. An unusually high mean absolute deviation of the residuals from the median suggests problematic data for that chip.

Figure7: RLE MEAN plot. This metric is generated by taking the signal estimate for a given probeset on a given chip and calculating the difference in log base 2 from the median signal value of that probeset over all the chips. When just the replicates are analyzed together the mean absolute RLE should be consistently low, reflecting the low biological variability of the replicates.

Figure8: Hierarchical Clustering of Samples . Samples will be grouped using hierarchical clustering and principal component analysis (PCA). If the sample preparation steps introduced bigger variation than biological variation, treatment groups will be mixed up in the plot. This could also happen when the samples between groups were mixed up accidentally when the samples were prepared. We acknowledge that clinical samples are harder to collect and sometimes impossible to control. Therefore, sample QC criteria will be much looser when dealing with clinical samples.

#### Value

no value is returned

#### Author(s)

Xiwei Wu, Arthur Li

#### References

[http://www.affymetrix.com/support/technical/whitepapers/exon\\_gene\\_arrays\\_qa\\_whitepaper.pdf](http://www.affymetrix.com/support/technical/whitepapers/exon_gene_arrays_qa_whitepaper.pdf)

#### Examples

```
data(eSetExample)
logdata <- preProcessGeneST(eSetExample)
data(QC)
## Not run: qaGeneST(logdata, c("Treatment", "Group"), QC)
```

---

QC

*sample QC result from Affy Expression Console*

---

#### Description

quality assessment result sample data generated from Affy Expression Console

**Usage**

```
data(QC)
```

**Examples**

```
data(QC)
```

---

```
regress
```

---

*Run regression to fit genewise linear model*

---

**Description**

Fit genewise linear model using LIMMA package, ordinary linear regression, or permutation method.

**Usage**

```
regress(object, contrast, method = c("limma", "regression", "permutation"), adj = "none", permute.time = 100)
```

**Arguments**

object	an ExpressionSet
contrast	a contrastMatrix
method	choose the following three options: "limma" (LIMMA), "regression" (ordinary linear regression), "permutation" (permutation test)
adj	adjustment method for multiple comparison test, including "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none". The default value is "none". Type <code>help(p.adjust)</code> for more detail.
permute.time	number of permutation times, only used for the "permutation" method

**Value**

an object of regressResult

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
```

---

regressionMethod	<i>Access the regressionMethod slot from the regressResult or interactionResult class</i>
------------------	---

---

**Description**

Access the regressionMethod slot from the regressResult or interactionResult class

**Usage**

```
regressionMethod(object)
```

**Arguments**

object            a regressResult or interactionResult class

**Value**

a character vector

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

---

regressResult-class	<i>Class to Contain the Regression Result</i>
---------------------	---

---

**Description**

Class to Contain the Regression Result

**Creating Objects**

regressResult object is generally created from the regress function See [regress](#)

**Slots**

ID: contains probe ID/gene ID

foldChange: contains fold change value

FValue: contains F statistics

pValue: contains p value

adjPVal: contains adjusted p value

contrast: contains class "contrastMatrix"

regressionMethod: contains regression method: "limma", "regression", or "permutation"

**adjustment:** contains method for multiple comparison adjustment  
**significantIndex:** contains a logical index indicating significant genes  
**significantPvalueCutoff:** contains a cutoff p-value for choosing significant genes  
**significantFCCutoff:** contains a fold change cutoff value for choosing significant genes  
**fileName:** contains a file name for output purpose  
**annotation:** contains annotation  
**normalizationMethod:** contains normalization method - for output purpose  
**filterMethod:** contains filtered method - for output purpose

## Methods

**adjustment** signature(object = "regressResult"): access the adjustment slot  
**getAdjP** signature(object = "regressResult"): access the adjPVal slot  
**getAnnotation** signature(object = "regressResult"): access the annotation slot  
**getContrast** signature(object = "regressResult"): access the contrast slot  
**getF** signature(object = "regressResult"): access the FValue slot  
**getFC** signature(object = "regressResult"): access the foldChange slot  
**getFCCutoff** signature(object = "regressResult"): access the significantFCCutoff slot  
**getFileName** signature(object = "regressResult"): access the fileName slot  
**getFilterMethod** signature(object = "regressResult"): access the filterMethod slot  
**getID** signature(object = "regressResult"): access the ID slot  
**getIndex** signature(object = "regressResult"): access the significantIndex slot  
**getNormalizationMethod** signature(object = "regressResult"): access the normalizationMethod slot  
**getP** signature(object = "regressResult"): access the pValue slot  
**getPCutoff** signature(object = "regressResult"): access the significantPvalueCutoff slot  
**Output2HTML** signature(object = "regressResult"): create HTML file for significant genes in regressionResult  
**regressionMethod** signature(object = "regressResult"): access the regressionMethod slot  
**selectSigGene** signature(object = "regressResult"): select significant genes for regressionResult class  
**show** signature(object = "regressResult"): print regressResult  
**Sort** signature(x = "regressResult"): sort regressResult  
**summary** signature(object = "regressResult"): print the summary for regressResult

## Author(s)

Xiwei Wu, Arthur Li

## Examples

```

data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
  
```

---

selectSigGene	<i>select differentially expressed genes from the regressResult class</i>
---------------	---

---

**Description**

select differentially expressed genes based on p value and/or fold change from the regressResult class

**Usage**

```
selectSigGene(object, p.value = 0.05, fc.value = 0)
```

**Arguments**

object	an regressResult class
p.value	p value
fc.value	fold change cut-off value

**Value**

an regressResult

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
sigResult<- selectSigGene(result, fc.value=log2(2))
```

---

selectSigGeneInt	<i>select differentially expressed genes from the interactionResult class</i>
------------------	---

---

**Description**

select differentially expressed genes based on p value and/or fold change from the interactionResult class

**Usage**

```
selectSigGeneInt(object, pGroup = 0.05, fcGroup = 0, pMain = 0.05, fcMain = 0)
```

**Arguments**

object	an interactionResult class
pGroup	the p value that used to select significant genes at each level of the covariate
fcGroup	the fold change value that used to select significant genes at each level of the covariate
pMain	the p values that used to select significant genes among genes without any interaction effect
fcMain	the fold change values that used to select significant genes among genes without any interaction effect

**Value**

an interactionResult

**Author(s)**

Xiwei Wu, Arthur Li

**Examples**

```
data(eSetExample)
design.int<- new("designMatrix", target=pData(eSetExample), covariates = c("Treatment", "Group"),
  intIndex = c(1, 2))
contrast.int<- new("contrastMatrix", design.matrix = design.int, interaction=TRUE)
result.int<- regress(eSetExample, contrast.int)
sigResult.int <- selectSigGene(result.int)
intResult <- postInteraction(eSetExample, sigResult.int, mainVar ="Treatment",
  compare1 = "Treated", compare2 = "Control")
sigResultInt <- selectSigGeneInt(intResult)
```

---

Sort

*Sort a regressionResult or an interactionResult*

---

**Description**

Sort a regressionResult or an interactionResult based on p-value, fold-change, or F statistics

**Usage**

```
Sort(x, ...)
```

**Arguments**

x	a regressResult or an interactionResult class
...	any other arguments. See below...

**Value**

if sorting a regressResult, returned value is a data frame if sorting a interactionResult, returned value is a list of data frames

**Sort a regressResult or an interactionResult class**

```
Sort(x, sorted.by = c("pValue", "log2Ratio", "F"), top=20)
```

x is a regressResult class or an interactionResult class. sorted.by can be specified by using "pValue" (p value), "log2Ratio" (log2 of fold-change value) or "F" (F statistics). top is used to specified number of genes being printed

**Author(s)**

Xiwei Wu, Arthur Li

**See Also**

[regressResult](#) [interactionResult](#)

**Examples**

```
data(eSetExample)
design<- new("designMatrix", target=pData(eSetExample), covariates = "Treatment")
contrast<- new("contrastMatrix", design.matrix = design,
  compare1 = "Treated", compare2 = "Control")
result<- regress(eSetExample, contrast)
Sort(result)
```



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