Package 'ArrayTools'

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Type Package

Title geneChip Analysis Package

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

Suggests simpleaffy, R2HTML, affydata, affyPLM, genefilter, annaffy, 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.

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LazyLoad yes

biocViews Microarray, OneChannel, QualityControl, Preprocessing, StatisticalMethod, DifferentialExpression, Annotation, ReportWriting, Visualization

NeedsCompilation no

R topics documented:

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

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`

contrastMatrix *Class to Contain the Contrast Matrix that Used for Linear Regression*

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]`

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
...	addtional 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 ouputted 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 *filter an ExpressionSet using different methods*

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 =
```

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). Calulating the interquatile 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 *access the annotation slot from the regressResult or interactionResult slot*

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 *Access the Compare1 slot from the contrastMatrix*

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 *Access the compare2 slot from the contrastMatrix class*

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 *Access the contrast matrix from the contrastMatrix class*

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 *access the foldChange slot from regressionResult or interactionResult class*

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` *Access the foldChange slot from the regressResult or interactionResult class*

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` *Access the significantFCCutoff slot from the regressResult or interactionResult class*

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` *Access the filterMethod slot from the regressResult or interactionResult class*

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 *access the ID slot from the regressResult or interactionResult class*

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 mumeric vector

Author(s)

Xiwei Wu, Arthur Li

See Also

designMatrix

getLength *Calculate the Length of interactionResult class*

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 *Access the level slot from the contrastMatrix class*

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 interaction-Result 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 *Access the significantPvalueCutoff slot from regressResult or interactionResult class*

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 *Access the target slots from the designMatrix class*

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 refering 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 reggressResult 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 sigificant 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 tne orignal data, an ExpressionSetinto 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(regressOb
```

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 follwoing 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 direcotry from the mydir argument
mydir	specifed 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 *Proprocess genechip ST array*

Description

Proprocess genechip ST array by taking the log2 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 log2(0) = -Inf.
rmControl	Setting rmControl = TRUE to remove control probes.
output	If output = TRUE, it will output the preprocessed data in the specified direcotry from the mydir argument.
mydir	specifed directory to contain the output

Value

an ExpressionSet

Author(s)

Xiwei Wu, Arthur Li

Examples

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

---

qa3prime *Creating Quality Assessment Report for 3 Prime Array*

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 consistant across the samples. The signal for BioB should be the lowest, follows by BioC, BioD, and CreX (the highest).

Figure4: POLYA SPIKE plot. The mean signal of each group should be consistant across the samples. The signal for Lys should be the lowest, follows 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

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.tim
```

Arguments

object	an ExpressionSet
contrast	a contrastMatrix
method	choose the follwoing 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.
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 *Access the regressionMethod slot from the regressResult or interactionResult class*

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` *Class to Contain the Regression Result*

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 sigificant 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 sigificant 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 *select differentially expressed genes from the regressResult class*

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` *select differentially expressed genes from the interactionResult class*

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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