

Package ‘a4Reporting’

March 25, 2024

Type Package
Title Automated Affymetrix Array Analysis Reporting Package
Version 1.50.0
Date 2020-10-15
Description Utility functions to facilitate the reporting of the Automated Affymetrix Array Analysis Reporting set of packages.
Imports methods, xtable
Suggests knitr, rmarkdown
biocViews Microarray
License GPL-3
VignetteBuilder knitr
RoxygenNote 7.1.1
git_url <https://git.bioconductor.org/packages/a4Reporting>
git_branch RELEASE_3_18
git_last_commit 5facc73
git_last_commit_date 2023-10-24
Repository Bioconductor 3.18
Date/Publication 2024-03-25
Author Tobias Verbeke [aut],
Laure Cougnaud [cre]
Maintainer Laure Cougnaud <laure.cougnaud@openanalytics.eu>

R topics documented:

annotationTable	2
annotationTable-class	3
generateEntrezIdLinks	4
generateGOIdLinks	5
print.xtableAnnotationTable	5
xtable,annotationTable,missing,missing,missing,missing,missing-method	6
Index	10

annotationTable	<i>Function to Create an annotationTable</i>
-----------------	----------------------------------------------

Description

This function takes data to be displayed as well as data containing hyperlinks corresponding to displayed data and constructs an object of class `annotationTable`

Usage

```
annotationTable(displayData, displayCols = NULL, hrefData = NULL)
```

Arguments

<code>displayData</code>	data frame containing data that is meant to be displayed in a LaTeX table
<code>displayCols</code>	list of named character vectors (of length one) that function as key-value pairs; the names (keys) correspond to columns for which the hyperlinks should be generated whereas the strings (values) indicate what kind of link should be produced based on the corresponding column in the <code>displayData</code> . The values should be one of "EntrezId" or "GOId".
<code>hrefData</code>	data frame containing hyperlink information for the columns of the same name in the <code>displayData</code> data frame

Details

If `hrefData` is given, the `displayCols` are not taken into account. If no `hrefData` is given, the information in `displayCols` allows to automatically create the `hrefData`.

Value

object of class 'annotationTable'

Author(s)

Tobias Verbeke

Examples

```
## some dummy data
dData <- data.frame(someSymbol = LETTERS[1:5],
  accessionNumber = c("X83928", "V00540", "U21090", "L38487", "M34057"))
at <- annotationTable(displayData = dData,
  displayCols = list(accessionNumber = "EntrezId"))
```

annotationTable-class *Class 'annotationTable'*

Description

Class to represent both displayed information and hyperlink information to prepare tabular output for LaTeX (with hyperlinks)

Usage

```
## S4 method for signature 'annotationTable'
show(object)
```

Arguments

object annotationTable object

Objects from the Class

Objects can be created by calls of the form `new("annotationTable", ...)` or using the wrapper function `annotationTable`

Slots

displayData: Object of class "data.frame" containing the columns to be displayed in the table

displayCols: Object of class "list" giving key-value pairs that allow to automatically generate the hyperlinks for the corresponding columns of the displayData

hrefData: Object of class "data.frame" giving the hyperlink information for the corresponding columns of the displayData

Methods

show signature(object = "annotationTable"): print an annotationTable (without displaying the hyperlink information)

Author(s)

Tobias Verbeke

Examples

```
showClass("annotationTable")
```

generateEntrezIdLinks *Transform an ENTREZ ID into a hyperlink*

Description

Utility function to transform an ENTREZ ID into a hyperlink on the NCBI Entrez page for the given gene

Usage

```
generateEntrezIdLinks(x)
```

Arguments

x vector of Entrez IDs

Value

vector of hyperlinks for the corresponding Entrez IDs

Note

Snippet taken from the annaffy package

Author(s)

Tobias Verbeke

See Also

[generateGOIdLinks](#)

Examples

```
generateEntrezIdLinks(c("5230", "18655"))
```

generateGOIdLinks	<i>Transform a GO ID into a hyperlink</i>
-------------------	-------------------------------------------

Description

Utility function to transform a GO ID into a hyperlink to the corresponding page on the gene ontology website

Usage

```
generateGOIdLinks(x)
```

Arguments

x	vector of GO IDs
---	------------------

Value

vector of hyperlinks

Note

Snippet taken from the annaffy package

Author(s)

Tobias Verbeke

See Also

[generateEntrezIdLinks](#)

print.xtableAnnotationTable	<i>Print method for 'xtableAnnotationTable' objects</i>
-----------------------------	---------------------------------------------------------

Description

Print method for 'xtableAnnotationTable' objects

Usage

```
## S3 method for class 'xtableAnnotationTable'  
print(x, ...)
```

Arguments

`x` Object of class 'xtableAnnotationTable'
`...` Further arguments passed to `print.xtable`

Details

Wrapper to be able to use a specific `sanitize.text` function in the `print.xtable` call

Value

No returned value, the object is printed.

Author(s)

Tobias Verbeke

See Also

[print.xtable](#)

xtable, annotationTable, missing, missing, missing, missing, missing-method
Methods for Function xtable in Package 'annotationTable'

Description

`xtable` methods for several `a4` objects, such as `annotationTable` objects, `topTable` objects etc.

Usage

```
## S4 method for signature
## 'annotationTable,missing,missing,missing,missing,missing'
xtable(x, caption, label, align, digits, display)

## S4 method for signature 'annotationTable,ANY,ANY,ANY,ANY,ANY'
xtable(x, caption, label, align, digits, display)

## S4 method for signature 'annotationTable,ANY,ANY,ANY,numeric,ANY'
xtable(x, caption, label, align, digits, display)

## S3 method for class 'topTableGlmnet'
xtable(
  x,
  caption = NULL,
  label = NULL,
  align = NULL,
  digits = NULL,
```

```
        display = NULL,
        ...
    )

## S3 method for class 'topTableLognet'
xtable(
  x,
  caption = NULL,
  label = NULL,
  align = NULL,
  digits = NULL,
  display = NULL,
  ...
)

## S3 method for class 'topTableElnet'
xtable(
  x,
  caption = NULL,
  label = NULL,
  align = NULL,
  digits = NULL,
  display = NULL,
  ...
)

## S3 method for class 'pamClassConfusionTable'
xtable(
  x,
  caption = NULL,
  label = NULL,
  align = NULL,
  digits = NULL,
  display = NULL,
  ...
)

## S3 method for class 'topTablePam'
xtable(x, ...)

## S3 method for class 'topTableRfClass'
xtable(
  x,
  caption = NULL,
  label = NULL,
  align = NULL,
  digits = NULL,
  display = NULL,
```

...
)

Arguments

<code>x</code>	annotationTable object
<code>caption</code>	Character vector of length 1 or 2 containing the table's caption or title. If length is 2, the second item is the "short caption" used when LaTeX generates a "List of Tables". Set to NULL to suppress the caption. Default value is NULL.
<code>label</code>	Character vector of length 1 containing the LaTeX label or HTML anchor. Set to NULL to suppress the label. Default value is NULL.
<code>align</code>	Character vector of length equal to the number of columns of the resulting table, indicating the alignment of the corresponding columns. Also, " " may be used to produce vertical lines between columns in LaTeX tables, but these are effectively ignored when considering the required length of the supplied vector. If a character vector of length one is supplied, it is split as <code>strsplit(align, "")[[1]]</code> before processing. Since the row names are printed in the first column, the length of <code>align</code> is one greater than <code>ncol(x)</code> if <code>x</code> is a data.frame. Use "l", "r", and "c" to denote left, right, and center alignment, respectively. Use "p{3cm}" etc. for a LaTeX column of the specified width. For HTML output the "p" alignment is interpreted as "l", ignoring the width request. Default depends on the class of <code>x</code> .
<code>digits</code>	Numeric vector of length equal to one (in which case it will be replicated as necessary) or to the number of columns of the resulting table or matrix of the same size as the resulting table, indicating the number of digits to display in the corresponding columns. Since the row names are printed in the first column, the length of the vector <code>digits</code> or the number of columns of the matrix <code>digits</code> is one greater than <code>ncol(x)</code> if <code>x</code> is a data.frame. Default depends on the class of <code>x</code> . If values of <code>digits</code> are negative, the corresponding values of <code>x</code> are displayed in scientific format with <code>abs(digits)</code> digits.
<code>display</code>	Character vector of length equal to the number of columns of the resulting table, indicating the format for the corresponding columns. Since the row names are printed in the first column, the length of <code>display</code> is one greater than <code>ncol(x)</code> if <code>x</code> is a data.frame. These values are passed to the <code>formatC</code> function. Use "d" (for integers), "f", "e", "E", "g", "G", "fg" (for reals), or "s" (for strings). "f" gives numbers in the usual xxx.xxx format; "e" and "E" give n.ddde+nn or n.dddE+nn (scientific format); "g" and "G" put <code>x[i]</code> into scientific format only if it saves space to do so. "fg" uses fixed format as "f", but <code>digits</code> as number of <i>significant</i> digits. Note that this can lead to quite long result strings. Default depends on the class of <code>x</code> .
...	Additional arguments. (Currently ignored.)

Methods

`x = "annotationTable", caption = "missing", label = "missing", align = "missing", digits = "missing", display = "missing"`
generates a LaTeX representation for the given annotationTable

x = "annotationTable", caption = "ANY", label = "ANY", align = "ANY", digits = "ANY", display = "ANY"
generates a LaTeX representation for the given annotationTable

x = "annotationTable", caption = "ANY", label = "ANY", align = "ANY", digits = "numeric", display = "ANY"
generates a LaTeX representation for the given annotationTable

Examples

```
## some dummy data
dData <- data.frame(someSymbol = LETTERS[1:5], accessionNumber = c("X83928", "V00540", "U21090", "L38487", "M3405"))
at <- annotationTable(displayData = dData, displayCols = list(accessionNumber = "EntrezId"))
xat <- xtable(at)
print(xat, include.rownames = FALSE)
```

Index

- * **classes**
 - annotationTable-class, 3
- * **manip**
 - annotationTable, 2
 - generateEntrezIdLinks, 4
 - generateGOIdLinks, 5
 - print.xtableAnnotationTable, 5
 - xtable, annotationTable, missing, missing, missing, missing, missing-method, 6
- * **methods**
 - xtable, annotationTable, missing, missing, missing, missing, missing-method, 6
- annotationTable, 2
- annotationTable-class, 3
- generateEntrezIdLinks, 4, 5
- generateGOIdLinks, 4, 5
- print.xtable, 6
- print.xtableAnnotationTable, 5
- show, annotationTable-method
 - (annotationTable-class), 3
- xtable, annotationTable, ANY, ANY, ANY, ANY, ANY-method
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable, annotationTable, ANY, ANY, ANY, numeric, ANY-method
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable, annotationTable, missing, missing, missing, missing, missing-method, 6
- xtable-methods
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.pamClassConfusionTable
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.topTableElNet
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.topTableGlmnet
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.topTableLognet
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.topTablePam
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6
- xtable.topTableRfClass
 - (xtable, annotationTable, missing, missing, missing, missing, missing-method), 6