Package ‘annaffy’

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aaf.handler

Handle fetching annotation data columns

Description

Dispatches requests for annotation data to the correct function. Alternatively returns a list of all the columns it supports.

Usage

aaf.handler(probeids, chip, name)

Arguments

- **probeids**: character vector containing probe ids
- **chip**: name of chip
- **name**: name of the column of data to return
**Value**

An aafList containing objects of the proper class.

If no arguments are passed, it will return a character vector of the columns currently supported.

**Note**

Written at the NASA Center for Computational Astrobiology

http://cca.arc.nasa.gov/

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

---

**aafChromLoc**

*Constructor for aafChromLoc objects*

**Description**

For the given probeids, constructs an aafList of aafChromLoc objects containing annotation data from the chip data package.

**Usage**

```r
aafChromLoc(probeids, chip)
```

**Arguments**

- `probeids` character vector containing probe ids
- `chip` name of the chip data package

**Value**

An aafList of aafChromLoc objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

- `aafChromLoc-class`

**Examples**

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  locations <- aafChromLoc(probes, "hgu95av2.db")
  show(locations[6:10])
}
```
Class aafChromLoc, a class for gene chromosome locations

Description
An abstraction for gene chromosome locations from Bioconductor data packages.

Objects from the Class
Objects are generally created by the aafChromLoc constructor. Objects can also be created manually by calls of the form new("aafChromLoc", description).

Slots
.Data: Object of class integer

Extends
Class integer, from data part.

Methods
No methods defined with class "aafChromLoc" in the signature. See generic implementations of getText, getURL, getHTML, getTD, and getCSS.

Author(s)
Colin A. Smith, <annaffy@colinsmith.org>

See Also
aafChromLoc

Constructor for aafChromosome objects

Description
For the given probeids, constructs an aafList of aafChromosome objects containing annotation data from the chip data package.

Usage
aafChromosome(probeids, chip)

Arguments
probeids character vector containing probe ids
chip name of the chip data package
Value

An aafList of aafChromosome objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafChromosome-class

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  chromosomes <- aafChromosome(probes, "hgu95av2.db")
  show(chromosomes[6:10])
}
```

Description

An abstraction for gene chromosome assignments from Bioconductor data packages.

Objects from the Class

Objects are generally created by the `aafChromosome` constructor. Objects can also be created manually by calls of the form `new("aafChromosome", description)`.

Slots

.Data: Object of class character

Extends

Class character, from data part.

Methods

No methods defined with class "aafChromosome" in the signature. See generic implementations of `getText`, `getURL`, `getHTML`, `getTD`, and `getCSS`.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafChromosome
**aafCytoband**  Constructor for *aafCytoband* objects

**Description**
For the given probeids, constructs an *aafList* of *aafCytoband* objects containing annotation data from the chip data package.

**Usage**

```r
aafCytoband(probeids, chip)
```

**Arguments**

- `probeids` character vector containing probe ids
- `chip` name of the chip data package

**Value**
An *aafList* of *aafCytoband* objects. NA values are returned as empty objects.

**Author(s)**
Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

- `aafCytoband-class`

**Examples**

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  bands <- aafCytoband(probes, "hgu95av2.db")
  show(bands[6:10])
}
```

---

**aafCytoband-class**  Class *aafCytoband*, a class for cytoband data

**Description**
An abstraction for cytoband data from Bioconductor data packages.

**Objects from the Class**
Objects are generally created by the `aafCytoband` constructor. Objects can also be created manually by calls of the form `new("aafCytoband", band, genbank)`. 
Slots

band: Object of class character containing genomic cytoband
gene: Object of class character containing containing Gene ID

Methods

getText (aafCytoband): Returns text of band.
getUrl (aafCytoband): Returns a URL corresponding entry in NCBI’s cytoband map viewer.
See generic implementations of getHTML, getTD, and getCSS.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafCytoband

---

aafDescription Constructor for aafDescription objects

Description

For the given probeids, constructs an aafList of aafDescription objects containing annotation data from the chip data package.

Usage

aafDescription(probeids, chip)

Arguments

probeids character vector containing probe ids
chip name of the chip data package

Value

An aafList of aafDescription objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafDescription-class
Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  descriptions <- aafDescription(probes, "hgu95av2.db")
  show(descriptions[6:10])
}
```

---

**aafDescription-class**  
*Class aafDescription, a class for gene descriptions*

**Description**

An abstraction for gene description from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafDescription` constructor. Objects can also be created manually by calls of the form `new("aafDescription", description)`.

**Slots**

`.Data`: Object of class character

**Extends**

Class character, from data part.

**Methods**

No methods defined with class "aafDescription" in the signature. See generic implementations of `getText`, `getURL`, `getHTML`, and `getTD`.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

`aafDescription`
Sample ExpressionSet used for demonstration purposes

Description

Contains expression values for 250 probe ids with 8 samples. Two covariates are provided. Expression comes from the hgu95av2 chip.

Details

The data is real but anonymized. 250 genes expression values were chosen at random from an existing ExpressionSet. Another 250 probe ids were selected at random and were assigned to the expression values. That way, expression values do not correspond to the true probe ids.

Post-processing was done with rma() in affy 1.2.23.

Constructor for aafGenBank objects

Description

For the given probeids, constructs an aafList of aafGenBank objects containing annotation data from the chip data package.

Usage

aafGenBank(probeids, chip)

Arguments

probeids character vector containing probe ids
chip name of the chip data package

Value

An aafList of aafGenBank objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafGenBank-class

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  gbs <- aafGenBank(probes, "hgu95av2.db")
  show(gbs[6:10])
}
```
**aafGenBank-class**

*Class aafGenBank, a class for GenBank accession numbers*

**Description**

An abstraction for GenBank accession numbers from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafGenBank` constructor. Objects can also be created manually by calls of the form `new("aafGenBank", accnum)`.

**Slots**

`.Data`: Object of class `character`

**Extends**

Class `character`, from data part.

**Methods**

- `getURL` (aafGenBank): Returns a URL to the corresponding entry in NCBI’s GenBank database. See generic implementations of `getText`, `getHTML`, and `getTD`.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

`aafGenBank`

---

**aafGO**

*Constructor for aafGO objects*

**Description**

For the given `probeids`, constructs an `aafList` of `aafGO` objects containing annotation data from the chip data package.

**Usage**

`aafGO(probeids, chip)`

**Arguments**

- `probeids`: character vector containing probe ids
- `chip`: name of the chip data package
Value

An aafList of aafGO objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafGO-class

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  gos <- aafGO(probes, "hgu95av2.db")
  show(gos[6:10])
}
```

---

**aafGO-class**

*Class aafGO, a class for gene ontology ids*

Description

An abstraction for gene ontology ids from Bioconductor data packages. This class is actually extends aafList and holds aafGOItem objects which have the actual annotation data.

Objects from the Class

Objects are generally created by the aafGO constructor. Objects can also be created manually by calls of the form `new("aafGO", list(goitems))`.

Slots

.Data: Object of class list

Extends

Class aafList, from data part.

Methods

*getText* (aafGO): Returns a comma delimeted list of the individual aafGOItem objects.

*getURL* (aafGO): Returns a single URL to an AmiGO page which displays all the gene ontology identifiers in an hierarchical listing.

*getHTML* (aafGO): Returns an HTML representation of each of the individual aafGOItem objects, concatenated together.

*getTD* (aafGO): Returns an HTML table cell representation with the class set to "aafGO".

*getCSS* (aafGOItem): Returns a line of CSS that indents GOItem paragraphs.
Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafGO, aafGOItem, aafList

aafGOItem-class

Class aafGOItem, a class for gene ontology id elements

Description

An abstraction for gene ontology id elements from Bioconductor data packages. Multiple instances of this class are held by the wrapper class aafGO.

Objects from the Class

Objects are generally created by the aafGO constructor. Objects can also be created manually by calls of the form new(“aafGOItem”, id, name, type).

Slots

id: Object of class character containing GO id
name: Object of class character containing textual name
type: Object of class character containing GO subtype
evid: Object of class character containing GO evidence code

Methods

getText (aafGOItem): Returns textual representation formatted “id: name”.

getURL (aafGOItem): Returns a URL to the corresponding gene ontology entry on AmiGO.

getHTML (aafGOItem): Returns an HTML representation including the URL link, gene ontology name, and rollover subtype.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafGO-class, aafGO
Class `aafIntensity`, a class for gene expression values

**Description**
A class for displaying gene expression values with a green background of differing intensities.

**Objects from the Class**
Objects are generally created by the `aafTableInt` constructor. Objects can also be created manually by calls of the form `new("aafIntensity", intensity)`.

**Slots**
- `.Data`: Object of class `numeric`

**Extends**
Class `numeric`, from data part.

**Methods**
- `getTD` (`aafIntensity`): Returns an HTML table cell with background varying from white to green depending on intensity. Scaling is controlled by two options, `minIntensity` (fully white) and `maxIntensity` (fully green), usually set by `writeHTML`.

see generic implementations of `getText`, `getURL`, `getHTML`, and `getCSS`.

**Author(s)**
Colin A. Smith, <annaffy@colinsmith.org>

**See Also**
- `aafTableInt`

Class `aafList`, a specialized subclass of `list`

**Description**
A class for lists of annotation data objects.

**Objects from the Class**
Objects are generally created by any of the annotation data constructors that are also part of this package. Objects can also be created manually by calls of the form `new("aafList", list)`.

**Slots**
- `.Data`: Object of class `list`
Extends

Class list, from data part.

Methods

- **getText** (aafList): Returns a character vector containing textual representations of every item.
- **getURL** (aafList): Returns a character vector containing single URLs (if possible) of every item.
- **getHTML** (aafList): Returns a character vector containing HTML representations of every item.
- **getTD** (aafList): Returns a character vector containing HTML table cell representations of every item.
- **getCSS** (aafList): Returns getCSS() of the first item in the list.
- **[** (aafList): Returns a subset of aafList as another aafList object.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

---

### aafLocusLink

Constructor for aafLocusLink objects

**Description**

For the given probeids, constructs an aafList of aafLocusLink objects containing annotation data from the chip data package.

**Usage**

```r
aafLocusLink(probeids, chip)
```

**Arguments**

- **probeids** character vector containing probe ids
- **chip** name of the chip data package

**Value**

An aafList of aafLocusLink objects. NA values are returned as empty objects.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

aafLocusLink-class
Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  lls <- aafLocusLink(probes, "hgu95av2.db")
  show(lls[6:10])
}
```

---

**aafLocusLink-class**  
*Class aafLocusLink, a class for LocusLink ids*

**Description**

An abstraction for LocusLink ids from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafLocusLink` constructor. Objects can also be created manually by calls of the form `new("aafLocusLink", id)`.

**Slots**

- `.Data`: Object of class integer

**Extends**

Class integer, from data part.

**Methods**

- `getURL` (aafLocusLink): Returns a URL to the corresponding entry in NCBI’s LocusLink database. On the rare chance that more than one id is defined, more than one URL will be returned.

See generic implementations of `getText`, `getHTML`, and `getTD`.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

`aafLocusLink`
Constructor for aafPathway objects

Description
For the given probeids, constructs an aafList of aafPathway objects containing annotation data from the chip data package.

Usage
aafPathway(probeids, chip)

Arguments
probeids character vector containing probe ids
chip name of the chip data package

Value
An aafList of aafPathway objects. NA values are returned as empty objects.

Author(s)
Colin A. Smith, <annaffy@colinsmith.org>

See Also
aafPathway-class

Examples
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  pathways <- aafPathway(probes, "hgu95av2.db")
  show(pathways[6:10])
}

Class aafPathway, a class for KEGG pathway ids

Description
An abstraction for KEGG pathway ids from Bioconductor data packages. This class is actually extends aafList and holds aafPathwayItem objects which have the actual annotation data.

Objects from the Class
Objects are generally created by the aafPathway constructor. Objects can also be created manually by calls of the form new("aafPathway", list(pathwayitems)).
**Slots**

.Data: Object of class list

**Extends**

Class aafList, from data part.

**Methods**

getText (aafGO): Returns a comma delimitated list of the individual aafPathwayItem objects.

getURL (aafGO): Returns zero length character vector because this method is not valid for this class.

getHTML (aafGO): Returns an HTML representation of each of the individual aafPathwayItem objects, concatenated together.

getTD (aafGO): Returns an HTML table cell representation with the class set to "aafPathway".

getCSS (aafGO): Returns a line of CSS which intends PathwayItem paragraphs.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

aafPathway, aafPathwayItem, aafList

---

**Description**

An abstraction for KEGG pathway id elements from Bioconductor data packages. Multiple instances of this class are held by the wrapper class aafPathway.

**Objects from the Class**

Objects are generally created by the aafPathway constructor. Objects can also be created manually by calls of the form new("aafPathwayItem", id, name, enzyme).

**Slots**

id: Object of class character containing KEGG pathway id

name: Object of class character containing textual name

enzyme: Object of class character containing the Enzyme Commission number if applicable

**Methods**

getText (aafPathwayItem): Returns textual representation formatted "id: name".

getURL (aafPathwayItem): Returns a URL to the corresponding entry in the Kyoto Encyclopedia of Genes and Genomes database. If there is a corresponding EC number, it will be highlighted in red.

getHTML (aafPathwayItem): Returns an HTML representation including the URL link and pathway name.
**aafProbe**

**Constructor for aafProbe objects**

**Description**

For the given probeids, constructs an aafList of aafProbe objects.

**Usage**

```r
aafProbe(probeids)
```

**Arguments**

- `probeids` character vector containing probe ids

**Value**

An aafList of aafProbe objects.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

`aafProbe-class`

**Examples**

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  probesets <- aafProbe(probes)
  getURL(probesets[6:10])
}
```
Description
An abstraction for Affymetrix ProbeSet ids.

Objects from the Class
Objects are generally created by the aafProbe constructor. Objects can also be created manually by calls of the form new("aafProbe", id).

Slots
.Data: Object of class character

Extends
Class character, from data part.

Methods
getURL(aafProbe): Returns a URL to the annotation found in the Affymetrix NetAffx Analysis Center.
See generic implementations of getText, getHTML, and getTD.

Author(s)
Colin A. Smith, <annaffy@colinsmith.org>

See Also
aafProbe

Constructor for aafPubMed objects

Description
For the given probeids, constructs a list of aafPubMed objects containing annotation data from the chip data package.

Usage
aafPubMed(probeids, chip)

Arguments
probeids character vector containing probe ids
chip name of the chip data package
Value

An `aafList` of `aafPubMed` objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

`aafPubMed-class`

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  pmids <- aafPubMed(probes, "hgu95av2.db")
  show(pmids[6:10])
}
```

---

**Description**

An abstraction for LocusLink ids from Bioconductor data packages.

**Objects from the Class**

Objects are generally created by the `aafPubMed` constructor. Objects can also be created manually by calls of the form `new("aafPubMed", id)`.

**Slots**

- `.Data`: Object of class `integer`

**Extends**

Class `integer`, from data part.

**Methods**

- `getHTML` (aafPubMed): Returns an HTML link along with the number of abstracts.
- `getTD` (aafPubMed): Returns an HTML table cell representation with the class set to "aafPubMed".
- `getCSS` (aafPubMed): Returns a line of CSS which centers the PubMed link.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>
**aafSearchGO**

*Find probe ids corresponding to GO ids*

**Description**
Searches Gene Ontology ids for corresponding probe ids in a given chip, optionally including descendants.

**Usage**
```r
aafSearchGO(chip, ids, descendents = TRUE, logic = "OR")
```

**Arguments**
- `chip`: name of the chip data package
- `ids`: numeric or character vector of GO ids
- `descendents`: logical, include GO descendents?
- `logic`: type of logic to use, "AND" or "OR"

**Value**
A character vector of probe ids matching the search criteria.

**Author(s)**
Colin A. Smith, <annaffy@colinsmith.org>

**See Also**
- `aafSearchText`

---

**aafSearchText**

*Search metadata annotation text*

**Description**
Searches Bioconductor metadata annotation package text for specific strings or Perl compatible regular expressions.

**Usage**
```r
aafSearchText(chip, colnames, text, logic = "OR")
```
Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>chip</td>
<td>name of the chip data package</td>
</tr>
<tr>
<td>colnames</td>
<td>character vector of metadata column names to search</td>
</tr>
<tr>
<td>text</td>
<td>character vector of strings/regular expressions to match</td>
</tr>
<tr>
<td>logic</td>
<td>type of logic to use, &quot;AND&quot; or &quot;OR&quot;</td>
</tr>
</tbody>
</table>

Value

A character vector of probe ids matching the search criteria.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafSearchGO

Examples

```r
if (require(hgu95av2.db)) {
  aafSearchText("hgu95av2.db", "Description", c("kinase", "interferon"))
  # aafSearchText("hgu95av2.db", c("Gene Ontology", "Pathway"), "ribosome")
}
```

aafSigned-class

Class aafSigned, a class for signed numerical data

Description

A class for displaying signed numerical data with different styles depending on the sign.

Objects from the Class

Objects are generally created by the aafTable constructor. Objects can also be created manually by calls of the form new("aafSigned", signedval).

Slots

.Data: Object of class numeric

Extends

Class numeric, from data part.

Methods

- **getTD** (aafSigned): Returns an HTML table cell with class differentially set based on sign. aafSignedPos is used for positive values. aafSignedNeg is used for negative values. aafSignedZero is used for zero values.
- **getCSS** (aafSigned): Returns two lines of CSS that set the cell background of positive values light blue and negative values light red.

See generic implementations of getText, getURL, and getHTML.
Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafTable

---

**aafSymbol**  
*Constructor for aafSymbol objects*

### Description

For the given probeids, constructs a list of aafSymbol objects containing annotation data from the chip data package.

### Usage

```r
aafSymbol(probeids, chip)
```

### Arguments

- `probeids`: character vector containing probe ids
- `chip`: name of the chip data package

### Value

An aafList of aafSymbol objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafSymbol-class

### Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  symbols <- aafSymbol(probes, "hgu95av2.db")
  show(symbols[6:10])
}
```
aafSymbol-class

Class aafSymbol, a class for gene symbols

Description

An abstraction for gene symbol from Bioconductor data packages.

Objects from the Class

Objects are generally created by the aafSymbol constructor. Objects can also be created manually by calls of the form new("aafSymbol", description).

Slots

.data: Object of class character with gene symbol

Extends

Class character, from data part.

Methods

No methods defined with class "aafSymbol" in the signature. See generic implementations of getText, getUrl, getHTML, and getTD.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafSymbol

aafTable

Constructor for aafTable objects

Description

Constructs an aafTable object given vectors, lists, or aafList objects.

Usage

aafTable(..., items = list(...), colnames = names(items),
probeids = character(0), signed = FALSE)
arguments

... named arguments, one for each column
items alternatively a named list of the items to be put in the table
colnames character vector of column names
probeids character vector of probe ids associated with each row
signed boolean, should each column be colored based on the sign?

value

An aafTable object.

author(s)

Colin A. Smith, <annaffy@colinsmith.org>

see also

aafTable-class

---

aafTable-class Class aafTable, a tabular microarray data class

description

A class for storing and flexible output of microarray data to HTML and text formats.

objects from the class

Objects are generally created by any of the annotation table constructors that are also part of this package. Objects can also be created manually by calls of the form new("aafList", probeids, table).

slots

probeids: Object of class character containing the probe ids for each row of the table.
table: Object of class list containing aafList objects all of the same length, representing the columns of the table. Each item in the list must have a unique name.

methods

probeids (aafTable): Returns a character vector containing the probe ids for each row of the table.
probeids<- (aafTable): Sets the probe ids for the table rows. Can be set to character(0) if unknown or not applicable.
colnames (aafTable): Returns a character vector containing the names of the columns stored in the table.
colnames<- (aafTable): Set the column names for the table. Each must be unique.
dim (aafTable): Returns the dimensions of the table.
merge (aafTable, aafTable, all = FALSE, all.x = all, all.y = all, suffixes = c(".x", ".y")): Merges two tables together, aligning common probe ids if possible. Duplicate column names are given suffixes to make them unique. Returns the merged table.
`rbind` (aafTable, aafTable, ...): Vertically combines tables by row. Requires that column names be identical and that all tables either have probe ids defined or not.

Returns a subset of the table based on [row, column]. Indices may be passed as integers or probe ids/column names.

`\$` Returns the given table column. This also supports recursive subsetting to address columns, then cells, then sub-cells (if applicable). See Extract for more information.

`savetableHTML` (aafTable, filename, title = "Bioconductor Affymetrix Probe Listing", colnames = colnames(aafTable), range = 1:dim(aafTable)[1], open = FALSE, widget = FALSE): Saves the table to HTML with the specified filename and title. Both the columns and the range of table rows can be specified. Range can either be specified as a character vector of probe ids or an integer vector of row positions. One can also specify whether to open the resulting file in the browser and whether to use a widget for column selection.

`savetableText` (aafTable, filename, header = TRUE, colnames = colnames(aafTable), range = 1:dim(aafTable)[1], widget = FALSE): Saves the table to tab delimited text with specified filename and optional header. Both the columns and the range of table rows can be specified. Range can either be specified as a character vector of probe ids or an integer vector of row positions. One can also specify whether to use a widget for column selection.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

aafTable, aafTableFrame, aafTableAnn, aafTableInt
Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafTable-class

---

**aafTableFrame**

*Constructor for aafTable objects from data frames*

**Description**

Constructs an aafTable object given a data frame.

**Usage**

```r
aafTableFrame(frame, colnames = names(frame), probeids = row.names(frame),
               signed = FALSE)
```

**Arguments**

- `frame`: data frame to be converted to the table
- `colnames`: character vector of column names
- `probeids`: character vector of probe ids associated with each row
- `signed`: boolean, should each column be colored based on the sign?

**Value**

An aafTable object.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafTable-class
**aafTableInt**  
*Constructor for aafTable objects from ExpressionSets*

**Description**

Constructs an aafTable object containing expression values given an ExpressionSet. In the resulting HTML table, the expression values will have backgrounds with varying intensities of green depending on the expression measure.

**Usage**

```r
aafTableInt(exprSet, colnames = sampleNames(exprSet), 
             probeids = featureNames(exprSet))
```

**Arguments**

- `exprSet`: object of class ExpressionSet
- `colnames`: character vector of column names
- `probeids`: character vector of probe ids associated with each row

**Value**

An aafTable object.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>

**See Also**

aafTable-class, aafIntensity

---

**aafUniGene**  
*Constructor for aafUniGene objects*

**Description**

For the given probeids, constructs a list of aafUniGene objects containing annotation data from the chip data package.

**Usage**

```r
aafUniGene(probeids, chip)
```

**Arguments**

- `probeids`: character vector containing probe ids
- `chip`: name of the chip data package
Value

An aafList of aafUniGene objects. NA values are returned as empty objects.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafUniGene-class

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  ugs <- aafUniGene(probes, "hgu95av2.db")
  show(ugs[6:10])
}
```

aafUniGene-class

Class aafUniGene, a class for UniGene cluster ids

Description

An abstraction for UniGene cluster ids from Bioconductor data packages.

Objects from the Class

Objects are generally created by the `aafUniGene` constructor. Objects can also be created manually by calls of the form `new("aafUniGene", id)`.

Slots

.Data: Object of class character

Extends

Class character, from data part.

Methods

- `getURL` (aafUniGene): Returns a URLs to the corresponding entry in NCBI’s UniGene database. On the rare chance that more than one id is defined, more than one URL will be returned.

- `getHTML` (aafUniGene): Returns an HTML representation with a link to the UniGene database. On the rare chance that more than one id is defined, more than one link will be returned.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>

See Also

aafUniGene
getCSS-methods  
*Methods for function getCSS*

**Description**

Methods to get relevant stylesheet lines for an object.

**Methods**

object = ANY  
Returns an empty character vector.

**Note**

For information about other implementations of this method, see documentation of the respective class.

**See Also**

aafList-class, aafPubMed-class, aafGO-class, aafPathway-class, aafSigned-class

getHTML-methods  
*Methods for function getHTML*

**Description**

Methods to get an HTML representation of an object.

**Methods**

object = ANY  
Returns text of object along with URL link if applicable. If object is floating point, it displays a fixed number of significant digits as specified by the sigfigs option (default 6).

**Note**

For information about other implementations of this method, see documentation of the respective class.

**See Also**

aafList-class, aafPubMed-class, aafGO-class, aafGOItem-class, aafPathway-class, aafPathwayItem-class
getTD-methods

Methods for function getTD

Description
Methods to get an HTML table cell representation of an object.

Methods

\texttt{object = ANY}  Returns <td> tag containing HTML representation of \texttt{object}. Sets class attribute to \texttt{class(object)}.

Note
For information about other implementations of this method, see documentation of the respective class.

See Also
\texttt{aafList-class, aafGO-class, aafPathway-class, aafIntensity-class}

getText-methods

Methods for function getText

Description
Methods to get a textual representation of an object.

Methods

\texttt{object = ANY}  Returns a comma delimited list of the elements in \texttt{list}.

Note
For information about other implementations of this method, see documentation of the respective class.

See Also
\texttt{aafList-class, aafCytoband-class, aafGO-class, aafGOItem-class, aafPathway-class, aafPathwayItem-class}
is.annpkg

is.annpkg

**Description**

Checks to see that the given packages contain all the necessary annotation environments to be usable by annaffy.

**Usage**

```r
is.annpkg(packages, lib.loc = NULL)
```

**Arguments**

- `packages`: character vector containing package names to check
- `lib.loc`: a character vector with path names of R libraries, or NULL. The default value of NULL corresponds to all libraries currently known. If the default is used, the loaded packages are searched before the libraries.

**Value**

A logical vector indicating whether the packages contain annotation data.

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>
Examples

```r
pkgnames <- installed.packages()[,"Package"]
pkgnames <- pkgnames[1:5]
pkgnames[is.anmpkg(pkgnames)]
```

selectorWidget

**Dialog to select items from a list**

Description

Presents the user with a dialog box to select items from a list.

Usage

```r
selectorWidget(options, selected = character(0), title = "Selector",
 ordersel = FALSE, ordernsel = FALSE,
 height = max(10, min(20, length(options))))
```

Arguments

- **options**: vector, options to be selected from
- **selected**: vector, subset of options selected by default
- **title**: character scalar, window title
- **ordersel**: boolean, keep the selected items in order?
- **ordernsel**: boolean, keep the not selected items in order?
- **height**: scalar, height of the two listboxes

Value

A character vector containing the selected items. If a vector of a different class was initially provided, it must be manually coerced back to the correct type.

Author(s)

Colin A. Smith, <annaffy@colinsmith.org>
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