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-class**  
*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`

---

**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**  
`aafChromLoc(probeids, chip)`

**Arguments**  
- `probeids`: character vector containing probe ids
- `chip`: name of the chip data package
aafChromosome-class

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])
}
```

---

aafChromosome-class

*Class aafChromosome, a class for gene chromosome assignments*

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
aafChromosome  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
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  chromosomes <- aafChromosome(probes, "hgu95av2.db")
  show(chromosomes[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

---

**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

`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])
}
```

---

### 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`
**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])
}
```

**aafExpr**  
*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.
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 delimited 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
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])
}
```

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

---

**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⟩
aafGenBank

See Also

aafGenBank

---

**aafGenBank**  
*Constructor for aafGenBank objects*

**Description**

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

**Usage**

```r
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])
}
```
aafIntensity-class  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

aafList-class  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-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
**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])
}
```

---

**aafPathway-class**  
*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)).`
aafPathway

Slots

.Data: Object of class list

Extends

Class aafList, from data part.

Methods

getText (aafGO): Returns a comma delimited 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

aafPathway \quad Constructor \quad for \quad aafPathway \quad 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⟩
aafPathwayItem-class

See Also

aafPathway-class

Examples

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

---

aafPathwayItem-class

Class `aafPathwayItem`, a class for KEGG pathway id elements

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.

Author(s)

Colin A. Smith, ⟨annaffy@colinsmith.org⟩

See Also

aafPathway-class, aafPathway
Class *aafProbe*, a class for Probe ids

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 *aafProbe* objects

Description

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

Usage

*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])
}
```

---

**aafPubMed-class**  
*Class aafPubMed, a class for PubMed ids*

**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)
aafPubMed

**See Also**

aafPubMed

---

**aafPubMed**  
*Constructor for aafPubMed objects*

**Description**

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

**Usage**

```r
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])
}
```
**aafSearchGO**  
*Find probe ids corresponding to GO ids*

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

**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**  
- **chip**: name of the chip data package  
- **colnames**: character vector of metadata column names to search  
- **text**: character vector of strings/regular expressions to match  
- **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

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)
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

Constructor for aafSymbol objects

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

Usage
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

if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  symbols <- aafSymbol(probes, "hgu95av2.db")
  show(symbols[6:10])
}
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.
- **$** Returns the given table column.

**saveHTML** *(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.

**saveText** *(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`

---

**aafTable**  
*Constructor for aafTable objects*

**Description**

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

**Usage**

```r
aafTable(..., items = list(...), colnames = names(items),
          probeids = character(0), signed = FALSE)
```
**Description**

Constructs an `aafTable` object given a set of probe ids and desired annotation types.

**Usage**

```r
aafTableAnn(probeids, chip, colnames = aaf.handler(chip = chip), widget = FALSE)
```

**Arguments**

- `probeids` character vector of probe ids
- `chip` name of the data package in which the annotation data is stored
- `colnames` character vector of annotation types
- `widget` boolean, use widget to select columns?

**Value**

An `aafTable` object.

**Author(s)**

Colin A. Smith, ⟨annaffy@colinsmith.org⟩

**See Also**

`aafTable-class`
aafTableFrame \hspace{1cm} \textit{Constructor for aafTable objects from data frames}

\textbf{Description}

Constructs an \texttt{aafTable} object given a data frame.

\textbf{Usage}

\begin{verbatim}
aafTableFrame(frame, colnames = names(frame), probeids = row.names(frame), signed = FALSE)
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \texttt{frame} \hspace{0.5cm} data frame to be converted to the table
\item \texttt{colnames} \hspace{0.5cm} character vector of column names
\item \texttt{probeids} \hspace{0.5cm} character vector of probe ids associated with each row
\item \texttt{signed} \hspace{0.5cm} boolean, should each column be colored based on the sign?
\end{itemize}

\textbf{Value}

An \texttt{aafTable} object.

\textbf{Author(s)}

Colin A. Smith, \{annaffy@colinsmith.org\}

\textbf{See Also}

\texttt{aafTable-class}

\begin{verbatim}
aafTableInt(exprSet, colnames = sampleNames(exprSet), probeids = featureNames(exprSet))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \texttt{exprSet} \hspace{0.5cm} object of class \texttt{ExpressionSet}
\item \texttt{colnames} \hspace{0.5cm} character vector of column names
\item \texttt{probeids} \hspace{0.5cm} character vector of probe ids associated with each row
\end{itemize}

\textbf{Description}

Constructs an \texttt{aafTable} object containing expression values given an \texttt{ExpressionSet}.

In the resulting HTML table, the expression values will have backgrounds with varying intensities of green depending on the expression measure.

\textbf{Usage}

\begin{verbatim}
aafTableInt(exprSet, colnames = sampleNames(exprSet), probeids = featureNames(exprSet))
\end{verbatim}

\textbf{Arguments}

\begin{itemize}
\item \texttt{exprSet} \hspace{0.5cm} object of class \texttt{ExpressionSet}
\item \texttt{colnames} \hspace{0.5cm} character vector of column names
\item \texttt{probeids} \hspace{0.5cm} character vector of probe ids associated with each row
\end{itemize}
**Value**

An `aafTable` object.

**Author(s)**

Colin A. Smith, (annaffy@colinsmith.org)

**See Also**

`aafTable-class`, `aafIntensity`

---

### 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`
**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])
}
```

---

**getCSS-methods**  
*Methods for function getCSS*

**Description**

Methods to get relevant stylesheet lines for an object.

**Methods**

- `object = ANY` Returns an empty character vector.
getHTML-methods

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
object = ANY  Returns \texttt{<td>} tag containing HTML representation of 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
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**
object = ANY  Returns a comma delimited list of the elements in list.

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

**See Also**
aafList-class, aafCytoband-class, aafGO-class, aafGOItem-class, aafPathway-class, aafPathwayItem-class

---

**getURL-methods**  
*Methods for function getURL*

**Description**
Methods to get a URL link to a web resource 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, aafGenBank-class, aafLocusLink-class, aafCytoband-class, aafUniGene-class, aafPubMed-class, aafGO-class, aafGOItem-class, aafPathwayItem-class
is.annpkg  

**Determine if packages contain annotation**

**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.annpkg(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)))))
```
selectorWidget

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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