# Package ‘annaffy’

April 3, 2024

**Version** 1.74.0  
**Date** 2021-06-04  
**Title** Annotation tools for Affymetrix biological metadata  
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**Depends** R (>= 2.5.0), methods, Biobase, BiocManager, GO.db  
**Imports** AnnotationDbi (>= 0.1.15), DBI  
**Suggests** hgu95av2.db, multtest, tcltk  
**Description** Functions for handling data from Bioconductor Affymetrix annotation data packages. Produces compact HTML and text reports including experimental data and URL links to many online databases. Allows searching biological metadata using various criteria.  
**License** LGPL  
**LazyLoad** yes  
**biocViews** OneChannel, Microarray, Annotation, GO, Pathways, ReportWriting  
**git_url** https://git.bioconductor.org/packages/annaffy  
**git_branch** RELEASE_3_18  
**git_last_commit** 15d4c6a  
**git_last_commit_date** 2023-10-24  
**Repository** Bioconductor 3.18  
**Date/Publication** Bioconductor 3.18

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Generic constructor for classes extending character

Description
Retrieve annotation from a character data source.

Usage
.aaf.character(probeids, chip, type, class)

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>probeids</td>
<td>character vector containing probe ids</td>
</tr>
<tr>
<td>chip</td>
<td>name of chip</td>
</tr>
<tr>
<td>type</td>
<td>type of annotation</td>
</tr>
<tr>
<td>class</td>
<td>class of object to be created</td>
</tr>
</tbody>
</table>

Value
A list of objects of class class containing the annotation data of from the type dataset for the given probeids. NA values are returned as empty objects.

Note
Written at the NASA Center for Computational Astrobiology
http://cca.arc.nasa.gov/

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

Fetch Gene Ontology term information

Description
Given a Gene Ontology number, return its type and name.

Usage
.aaf.goterm(num)

Arguments
<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>num</td>
<td>Gene Ontology number - should be formatted GO:XXXXXXX</td>
</tr>
</tbody>
</table>
.aaf.integer

**Value**

A list with components

- **type** Type of GO record, either Biological Process, Cellular Component, or Molecular Function.
- **name** A character vector containing the GO name.

**Note**

Written at the NASA Center for Computational Astrobiology
[http://cca.arc.nasa.gov/](http://cca.arc.nasa.gov/)

**Author(s)**

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

---

Generic constructor for classes extending integer

**Description**

Retrieve annotation from an integer data source.

**Usage**

```r
.aaf.integer(probeids, chip, type, class)
```

**Arguments**

- **probeids** character vector containing probe ids
- **chip** name of chip
- **type** type of annotation
- **class** class of object to be created

**Value**

A list of objects of class `class` containing the annotation data of from the `type` dataset for the given `probeids`. NA values are returned as empty objects.

**Note**

Written at the NASA Center for Computational Astrobiology
[http://cca.arc.nasa.gov/](http://cca.arc.nasa.gov/)

**Author(s)**

Colin A. Smith, <annaffy@colinsmith.org>
Fetch raw annotation data

Description

Retrieve annotation data from a data package, loading the library if necessary.

Usage

.aaf.raw(probeids, chip, type)

Arguments

- `probeids`: character vector containing probe ids
- `chip`: name of chip, see details
- `type`: type of annotation, see details

Details

The core workings of this function depend on an (informal) protocol used in creating the BioCondutor Affymetrix annotation data packages. Based on currently published (and unpublished) data packages, the current protocol includes the following features:

- The package is named after the chip, `<chip name>`
- The package contains datasets named `<chip name><data type>`

Value

A list of annotation data for the given probeids. Each list contains a sub-list containing the actual data.

Note

Written at the NASA Center for Computational Astrobiology
http://cca.arc.nasa.gov/

Author(s)

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>probeids</td>
<td>character vector containing probe ids</td>
</tr>
<tr>
<td>chip</td>
<td>name of chip</td>
</tr>
<tr>
<td>name</td>
<td>name of the column of data to return</td>
</tr>
</tbody>
</table>

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
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])
}
```

---

**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

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

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

Class aafChromosome, a class for gene chromosome assignments

Description
An abstraction for gene 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
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`. 
aafDescription

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

See Also
aafCytoband

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
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

---

**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.
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
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)
aafGO-class

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 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

---

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.
**aafIntensity-class**  

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

**See Also**  
  aafGO-class, aafGO

---

**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  

Constructor for *aafLocusLink* objects

**Description**

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

**Usage**

`aafLocusLink(probeids, chip)`
**aafLocusLink-class**

**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 aafLocus, 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*

---

**aafPathway**  *Constructor for aafPathway objects*

---

### Description

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

### Usage

```r
aafPathway(probeids, chip)
```

### Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td><code>probeids</code></td>
<td>character vector containing probe ids</td>
</tr>
<tr>
<td><code>chip</code></td>
<td>name of the chip data package</td>
</tr>
</tbody>
</table>

### 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])
}

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)).

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
**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 (no longer supported)
- `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`
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
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

---

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

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>
aafPubMed-class

See Also

aafPubMed-class

Examples

```r
if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  pmids <- aafPubMed(probes, "hgu95av2.db")
  show(pmids[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>

**See Also**

aafPubMed
### 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.

cgetCSS (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

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])
}

---

**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/column names.

`[` 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`
aafTableAnn  

Constructor for `aafTable` objects from annotation data

Description

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

Usage

```
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  

Constructor for `aafTable` objects from data frames

Description

Constructs an `aafTable` object given a data frame.

Usage

```
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>
A Function to Check for and Install Missing Annotation Packages

Description

This is a wrapper function that calls all the necessary functions to detect missing annotation packages, ensure all versions are compatible with the current version of annaffy, and download required packages. This is an internal function and should not be called by the end user.

Usage

chkPkgs(pkg)

Arguments

pkg The chip-level annotation package

Details

This function checks for the correct chip-level package, and if it is not installed will download and install. In the case that there are two versions of the same package installed, the function will return the library location of the package with the correct version.

Value

This function doesn’t return anything; it is only called for its side effect of loading or installing a chip-level annotation package.

Author(s)

James W. MacDonald <jmacdon@med.umich.edu> and Jeff Gentry <jgentry@jimmy.harvard.edu>
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**

- **object = ANY** Returns `<td>` tag containing HTML representation of `object`. Sets class attribute to `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`
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))))
```

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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