Package ‘annaffy’

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**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

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.aaf.character

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>

.aaf.goterm

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>
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/

Author(s)

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

Generic constructor for classes extending integer

Description

Retrieve annotation from an integer data source.

Usage

.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/

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 BioConductor 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 feching 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)
aafChromLoc-class

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])
}
```
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

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

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

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.
Description
For the given probe ids, 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
aafCytoband

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.
**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])
}
```
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`

---

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.
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)
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`

---

**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

```
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

```r
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`: Returns a comma delimited list of the individual `aafPathwayItem` objects.
- `getURL`: Returns zero length character vector because this method is not valid for this class.
- `getHTML`: Returns an HTML representation of each of the individual `aafPathwayItem` objects, concatenated together.
- `getTD`: Returns an HTML table cell representation with the class set to "aafPathway".
- `getCSS`: Returns a line of CSS which intends `PathwayItem` paragraphs.

Author(s)

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

See Also

`aafPathway`, `aafPathwayItem`, `aafList`
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 (no longer supported)
enzyme: Object of class character containing the Enzyme Commision 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
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

if (require(hgu95av2.db)) {
  data(aafExpr)
  probes <- featureNames(aafExpr)
  probesets <- aafProbe(probes)
  getURL(probesets[6:10])
}

aafProbe-class

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

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>
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

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

aafSearchText(chip, colnames, text, logic = "OR")
aafSigned-class

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")
}
```

---

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

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**

```r
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
```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 | 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

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
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>
chkPks

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

chkPks(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>

See Also

aafTable-class, aafIntensity
**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
getURL-methods

Methods for function getURL

Description
Methods to get a URL link to a web resource for an object.

Methods

\texttt{object = ANY} Returns an empty character vector.

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

See Also
\texttt{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

\texttt{is.annpkg(packages, lib.loc = NULL)}

Arguments

\texttt{packages} character vector containing package names to check
\texttt{lib.loc} a character vector with path names of R libraries, or \texttt{NULL}. The default value of \texttt{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>
selectorWidget

**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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