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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
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)
Class \textit{aafChromLoc}, a class for gene chromosome locations

\textbf{Description}

An abstraction for gene chromosome locations from Bioconductor data packages.

\textbf{Objects from the Class}

Objects are generally created by the \texttt{aafChromLoc} constructor. Objects can also be created manually by calls of the form \texttt{new("aafChromLoc", description)}.

\textbf{Slots}

\texttt{.Data:} Object of class \texttt{integer}

\textbf{Extends}

Class \texttt{integer}, from data part.

\textbf{Methods}

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

\textbf{Author(s)}

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

\textbf{See Also}

\texttt{aafChromLoc}

\texttt{aafChromLoc} \hspace{1cm} \textit{Constructor for aafChromLoc objects}

\textbf{Description}

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

\textbf{Usage}

\texttt{aafChromLoc(probeids, chip)}

\textbf{Arguments}

\begin{itemize}
  \item \texttt{probeids} character vector containing probe ids
  \item \texttt{chip} name of the chip data package
\end{itemize}
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])
}
```

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

```r
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`. 

---
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

aafGenBank-class

Constructor for aafGenBank objects

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

Usage
aafGenBank(probeids, chip)

Arguments

<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 the chip data package</td>
</tr>
</tbody>
</table>
aafGO-class

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])
}
```

---

**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.
aafGOItem-class

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
**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**

```r
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])
}
```

---

**.aaf.goterm**  
*Fetch Gene Ontology term information*

**Description**

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

**Usage**

```r
.aaf.goterm(num)
```
**aaf.handler**

**Arguments**

- **num** Gene Ontology number - should be formatted `GO:XXXXXXX`

**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](mailto: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**

- **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/](http://cca.arc.nasa.gov/)

**Author(s)**

Colin A. Smith, [annaffy@colinsmith.org](mailto:annaffy@colinsmith.org)
.aaf.integer  

*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)

---

**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⟩
Class aafLocusLink, a class for LocusLink ids

Description
An abstraction for LocusLink ids from Bioconductor data packages.

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

Slots
.Data: Object of class integer

Extends
Class integer, from data part.

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

See generic implementations of getText, getHTML, and getTD.

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

See Also
aafLocusLink

Constructor for 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

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)).

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

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
**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**

- `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])
}
```

---

**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

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⟩

#### 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])
}
```

.aaf.raw

Fetch raw annotation data

Description

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

Usage

```r
.aaf.raw(probeids, chip, type)
```
**aafSearchGO**

**Arguments**

- **probesid** 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 probesid. 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⟩

---

**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")
}
```
Class aafSigned, a class for signed numerical data

Description

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

Objects from the Class

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

Slots

.Data: Object of class numeric

Extends

Class numeric, from data part.

Methods

getTD (aafSigned): Returns an HTML table cell with class differentially set based on sign. aafSignedPos is used for positive values. aafSignedNeg is used for negative values. aafSignedZero is used for zero values.

getCSS (aafSigned): Returns two lines of CSS that set the cell background of positive values light blue and negative values light red.

See generic implementations of getText, getURL, and getHTML.

Author(s)

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

See Also

aafTable

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

.D ata: 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

---

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])
}
```

---

**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`
Class aafTable, a tabular microarray data class

Description

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

Objects from the Class

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

Slots

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

Methods

- **probeids** (aafTable): Returns a character vector containing the probe ids for each row of the table.
- **probeids<-** (aafTable): Sets the probe ids for the table rows. Can be set to `character(0)` if unknown or not applicable.
- **colnames** (aafTable): Returns a character vector containing the names of the columns stored in the table.
- **colnames<-** (aafTable): Set the column names for the table. Each must be unique.
- **dim** (aafTable): Returns the dimensions of the table.
- **merge** (aafTable, aafTable, all = FALSE, all.x = all, all.y = all, suffixes = c(".x",".y")): Merges two tables together, aligning common probe ids if possible. Duplicate column names are given suffixes to make them unique. Returns the merged table.
- **rbind** (aafTable, aafTable, ...): Vertically combines tables by row. Requires that column names be identical and that all tables either have probe ids defined or not.
- [ Returns a subset of the table based on [row, column]. Indices may be passed as integers or probe ids/column names.
- [[ Returns the given table column. This also supports recursive subsetting to address columns, then cells, then sub-cells (if applicable). See `Extract` for more information.
- $ 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.
**aafTableFrame**

Author(s)

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

See Also

aafTable, aafTableFrame, aafTableAnn, aafTableInt

---

**aafTableFrame**  
*Constructor for aafTable objects from data frames*

**Description**

Constructs an aafTable object given a data frame.

**Usage**

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

**Arguments**

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

**Value**

An aafTable object.

**Author(s)**

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

See Also

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

**Description**

Constructs an aafTable object containing expression values given an ExpressionSet.

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

**Usage**

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

**Arguments**

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

**Value**

An aafTable object.

**Author(s)**

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

**See Also**

- `aafTable-class`, `aafIntensity`

---

**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)
```
**aafUniGene-class**

**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`

---

**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

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

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

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)
getCSS-methods

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
**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`
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
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
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
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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