biocViews

October 25, 2011

`BiocView-class` *Class "BiocView"*

Description

Representation of of Bioconductor "view".

Objects from the Class

Objects can be created by calls of the form `new("BiocView", ...)`.

Slots

`name`: Object of class `"character"` giving the name of the view.

`subViews`: Object of class `"character"` giving the names of the subviews of this view.

`parentViews`: Object of class `"character"` giving the names of the views that are this view's parents.

`Title`: Object of class `"character"` giving longer description of view?

`reposRoot`: Object of class `"character"` URL for repository

`homeUrl`: Object of class `"character"` ?

`htmlDir`: Object of class `"character"` ?

`packageList`: Object of class `"list"` consisting of `PackageDetail-class` objects

Extends

Class `"RepositoryDetail"`, directly. Class `"Htmlized"`, directly.

Methods

coerce `signature(from = "BiocView", to = "rdPackageTable")`: ...

htmlDoc `signature(object = "BiocView")`: ...

htmlFilename `signature(object = "BiocView")`: ...

htmlValue `signature(object = "BiocView")`: ...

show `signature(object = "BiocView")`: ...

Author(s)

Seth Falcon

Htmlized-class *Class "Htmlized"*

Description

A virtual class for HTML serialization method dispatch.

Objects from the Class

A virtual Class: No objects may be created from it.

Methods

htmlDoc `signature(object = "Htmlized")`: Return the html-ized representation of `object` as a complete HTML document.

Author(s)

Seth Falcon

PackageDetail-class *Class "PackageDetail"*

Description

Representation of R package metadata. Most slots correspond to fields in a package's DESCRIPTION file.

Objects from the Class

Objects can be created by calls of the form `new("PackageDetail", ...)`.

Slots

`Package`: Object of class `"character"` see DESCRIPTION

`Version`: Object of class `"character"` see DESCRIPTION

`Title`: Object of class `"character"` see DESCRIPTION

`Description`: Object of class `"character"` see DESCRIPTION

`Author`: Object of class `"character"` see DESCRIPTION

`Maintainer`: Object of class `"character"` see DESCRIPTION

`Depends`: Object of class `"character"` see DESCRIPTION

`Imports`: Object of class `"character"` see DESCRIPTION

`Suggests`: Object of class `"character"` see DESCRIPTION

`SystemRequirements`: Object of class `"character"` see DESCRIPTION

`License`: Object of class `"character"` see DESCRIPTION

`URL`: Object of class `"character"` see DESCRIPTION

`biocViews`: Object of class `"character"` see DESCRIPTION

`vignettes`: Object of class `"character"` giving paths to vignette pdf files in the repository

`vignetteScripts`: Object of class `"character"` giving paths to vignette Stangled R files in the repository

`vignetteTitles`: Object of class `"character"` giving the titles of the vignette files in the repository

`source.ver`: Object of class `"character"` version string for the source package

`win.binary.ver`: Object of class `"character"` version string for the 32-bit Windows binary package

`win64.binary.ver`: Object of class `"character"` version string for the 64-bit Windows binary package

`mac.binary.leopard.ver`: Object of class `"character"` version string for the OS X Leopard binary package

`downloadStatsUrl`: Object of class `"character"` An optional URL for the download history statistics.

`manuals`: Object of class `"character"` giving paths to reference manual pdf files in the repository

`dependsOnMe`: Object of class `"character"` giving packages found in the repository that depend on this package

`importsMe`: Object of class `"character"` giving packages found in the repository that imports this package

`suggestsMe`: Object of class `"character"` giving packages found in the repository that suggest this package

`functionIndex`: Object of class `"character"` Not used. Intended to hold function index data.

`reposFullUrl`: Object of class `"character"` The URL for the full URL of the root of the repository.

`reposRoot`: Object of class `"character"` The URL for the root of the repository.

`viewRoot`: Object of class `"character"` The URL for the view of the repository.

`devHistoryUrl`: Object of class `"character"` The URL for the development changelog.

Extends

Class `"Htmlized"`, directly.

Methods

htmlDoc `signature(object = "PackageDetail")`: Return an `XMLNode` instance containg a complete HTML document representation of the package.

htmlFilename `signature(object = "PackageDetail")`: Return a filename appropriate for the HTML document representation.

htmlValue `signature(object = "PackageDetail")`: Return `XMLNode` instance containing an HTML representation of the package.

Details

pdAuthorMaintainerInfo-class pdVignetteInfo-class pdDownloadInfo-class pdDetailsInfo-class pdDescriptionInfo-class pdVigsAndDownloads-class

Dummy classes for HTML generation. Each dummy class is a simple extension (it does not add any slots). The purpose of each dummy class is to allow for method dispatch to generate HTML via the htmlValue method.

You can convert convert a PackageDetail instance to one of the dummy classes like this: descInfo <- as(pdObj, "pdDescriptionInfo")

Author(s)

Seth Falcon

Examples

```
pd <- new("PackageDetail",
          Package="MyFancyPackage",
          Version="1.2.3",
          Title="A Fancy Package",
          Description="This package does fancy things",
          Author="A. Coder",
          Maintainer="A. Coder <acoder@foo.bar.net>",
          Depends="methods",
          Imports="ASimplePackage",
          Suggests="MyDataPackage",
          biocViews="Infrastructure",
          vignettes="vignettes/MyFancyPackage/inst/doc/MFP1.pdf,\nvignettes/MyFancyPackag
          vignetteScripts="vignettes/MyFancyPackage/inst/doc/MFP1.R\nvignettes/MyFancyPac
          vignetteTitles="MFP1 Document,\nMFP2 Document",
          source.ver="src/contrib/MyFancyPackage_1.2.3.tar.gz",
          win.binary.ver="bin/windows/contrib/2.6/MyFancyPackage_1.2.2.zip",
          win64.binary.ver="bin/windows64/contrib/2.6/MyFancyPackage_1.2.2.zip",
          mac.binary.leopard.ver="bin/macosx/leopard/contrib/2.6/MyFancyPackage_1.2.3.tgz
          dependsOnMe=c("PackageThatExposesMe"),
          importsMe=c("AnEvenFancierPackage","AMuchFancierPackage"),
          suggestsMe="PackageThatUsesMeInVignette",
          reposRoot="http://foo.bar.org")

html <- htmlValue(pd)
pd
```

RepositoryDetail-class

Class "RepositoryDetail"

Description

Representation of R package repository index

Objects from the Class

Objects can be created by calls of the form new("RepositoryDetail", ...).

Slots

`Title`: Object of class `"character"` giving the title for the repository.

`reposRoot`: Object of class `"character"` giving the root URL of the repository

`homeUrl`: Object of class `"character"` ?

`htmlDir`: Object of class `"character"` ?

`packageList`: Object of class `"list"` consisting of objects of class `PackageDetail-class`

Extends

Class `"Htmlized"`, directly.

Methods

htmlDoc `signature(object = "RepositoryDetail")`: ...

htmlFilename `signature(object = "RepositoryDetail")`: ...

htmlValue `signature(object = "RepositoryDetail")`: ...

Author(s)

Seth Falcon

`biocViews-package` *Categorized views of R package repositories*

Description

Structures for vocabularies and narratives of views. This can be used to create HTML views of the package structure in a Bioconductor repository.

Details

Package:	biocViews
Version:	1.11.4
Depends:	R (>= 2.4.0), methods, utils
Imports:	tools, Biobase, graph (>= 1.9.26), RBGL (>= 1.13.5), XML
Suggests:	Biobase
License:	Artistic-2.0
URL:	http://www.bioconductor.org/packages/release/BiocViews.html
biocViews:	Infrastructure

Index:

biocViewsVocab	Bioconductor Task Views Vocabulary Data
extractVignettes	Extract pdf vignettes from local package repository
genReposControlFiles	Generate CRAN-style repository control files
getBiocSubViews	Build a list of BiocView objects from a package repository
getBiocViews	Build a list of BiocView objects from a package repository
getPacksAndViews	Parse VIEWS file for views and packages
getSubTerms	Retrieve a term and its children from a vocab DAG
htmlDoc	Create a complete HTML document representation of an object
htmlFilename	Return a filename for an object's HTML representation
htmlValue	HTML Representation of an Object
writeBiocViews	Write a list of BiocView objects to HTML
writeHtmlDoc	Write an XML DOM containing HTML to a file
writePackageDetailHtml	Write HTML files for packages in a CRAN-style repository
writeRepositoryHtml	Write package descriptions and a repository index as HTML
writeTopLevelView	Write the view for the root of a vocabulary to disk
write_REPOSITORY	Write a REPOSITORY control file for a CRAN-style package repository
write_SYMBOLS	Write a SYMBOLS file
write_VIEWS	Write a VIEWS control file for a CRAN-style package repository

The terms of the vocabulary are stored in a DAG, which can be loaded as the serialized data object `biocViewsVocab`. For listing of available terms use function `getSubTerms`.

Further information is available in the following two vignettes:

HOWTO-BCV	Basic package usage
createReposHtml	Further information for repository admins

Author(s)

VJ Carey <stvjc@channing.harvard.edu>, BJ Harshfield <rebjh@channing.harvard.edu>, S Falcon <sfalcon@fhcrc.org>

Maintainer: Biocore Team c/o BioC user list <bioconductor@stat.math.ethz.ch>

Examples

```
data(biocViewsVocab)
getSubTerms(biocViewsVocab, "AssayTechnologies")
```

biocViewsVocab *Bioconductor Task Views Vocabulary Data*

Description

A graphNEL-class instance representing the Bioconductor Task Views as a directed graph.

Usage

```
data(biocViewsVocab)
```

Format

The format is: graphNEL instance

Details

The source for the vocabulary data is in the dot directory of the package in file biocViewsVocab.dot. This is transformed to GXL using the dot2gxl command line utility from the graphviz package. Then the fromGXL function from the graph package is used to convert to graphNEL-class.

Examples

```
data(biocViewsVocab)
biocViewsVocab
## If you have Rgraphviz available, you can
## plot the vocabulary with plot(biocViewsVocab)
```

extractManuals *Extract Rd man pages and build pdf reference manuals from local package*

Description

This function extracts Rd man pages and builds pdf reference manuals from the man subdirectory of R source packages archives (.tar.gz) found in a local package repository.

All Rd files found in man will be extracted and used during the pdf construction process. Only source package archives will be processed. The constructed pdf files will be extracted under destDir and will be found in PKGNAME/man/*.pdf.

Prior to extraction, all Rd and pdf files in destDir/PKGNAME/man will be removed.

Usage

```
extractManuals(reposRoot, srcContrib, destDir)
```

Arguments

reposRoot	character vector giving the path to the root of the local CRAN-style package repository
srcContrib	character vector giving the relative path from the reposRoot to the source packages. In a standard CRAN-style repository, this will be src/contrib.
destDir	character vector specifying the directory in which the extracted files will be written. If missing, files will be written to <reposRoot>/manuals.

Author(s)

Patrick Aboyoun

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extractVignettes *Extract pdf vignettes from local package repository*

Description

This function extracts pdf files from the inst/doc subdirectory of R source packages archives (.tar.gz) found in a local package repository.

All pdf files found in inst/doc will be extracted. Only source package archives will be processed. The extracted pdf files will be extracted under destDir and will be found in PKGNAME/inst/doc/*.pdf.

Prior to extraction, all pdf files in destDir/PKGNAME/inst/doc will be removed.

Usage

```
extractVignettes(reposRoot, srcContrib, destDir)
```

Arguments

reposRoot	character vector giving the path to the root of the local CRAN-style package repository
srcContrib	character vector giving the relative path from the reposRoot to the source packages. In a standard CRAN-style repository, this will be src/contrib.
destDir	character vector specifying the directory in which the extracted files will be written. If missing, files will be written to <reposRoot>/vignettes.

Author(s)

Seth Falcon

genReposControlFiles *Generate CRAN-style repository control files*

Description

This function generates control files for CRAN-style repositories. For each path specified in `contribPaths` a `PACKAGES` file is written. In addition, two top-level control files are created:

`REPOSITORY` contains information about the specified contrib paths.

`VIEWS` contains metadata for all packages in the repository including the paths to any extracted vignettes, if found. This file is useful for generating HTML views of the repository.

Usage

```
genReposControlFiles(reposRoot, contribPaths)
```

Arguments

`reposRoot`	character vector containing the path to the CRAN-style repository root directory.
`contribPaths`	A named character vector. Valid names are `source`, `win.binary`, `win64.binary`, `mac.binary`, and `mac.binary.leopard`. Values indicate the paths to the package archives relative to the `reposRoot`.

Author(s)

Seth Falcon

See Also

`write_PACKAGES`, `extractVignettes`, `write_REPOSITORY`, `write_VIEWS`

getBiocSubViews *Build a list of BiocView objects from a package repository*

Description

This function returns a list of `BiocView-class` objects corresponding to the subgraph of the views DAG induced by `topTerm`. In short, this does the same thing as `getBiocViews`, but limits the vocabulary to `topTerm` and all of its decendents.

Usage

```
getBiocSubViews(reposUrl, vocab, topTerm, local = FALSE, htmlDir = "")
```

Arguments

reposUrl	URL for a CRAN-style repository that hosts a VIEWS file at the top-level.
vocab	A graph-class object representing the ontologyof views. This graph should be a directed acyclic graph (DAG).
topTerm	A string giving the name of the subview DAG. This view and all of its decendents will be included in the result.
local	logical indicating whether to assume a local package repository. The default is FALSE in which case absolute links to package detail pages are created.
htmlDir	if the local argument is TRUE, this will be used as the relative path for package HTML files.

Details

The root of the vocabulary DAG is implicitly included in the view creation process order to build views with a link back to the top. It is removed from the return list.

This function is tailored to generation of Bioconductor Task Views. With the current vocabulary, it probably only makes sense to call it with topView set to one of "Software", "AnnotationData", or "ExperimentData". This is a hack to allow the biocViews code to manage HTML views across more than one repository.

Value

A list of BiocView-class objects. The names of the list give the name of the corresponding view.

Author(s)

Seth Falcon

See Also

write_VIEWS, writeBiocViews

Examples

```
data(biocViewsVocab)
reposPath <- system.file("doc", package="biocViews")
reposUrl <- paste("file://", reposPath, sep="")
biocViews <- getBiocSubViews(reposUrl, biocViewsVocab, "Software")
print(biocViews[1:2])
```

---

getBiocViews *Build a list of BiocView objects from a package repository*

Description

Given the URL to a CRAN-style package repository containing a VIEWS file at the top-level and a graph-class object representing a DAG of views, this function returns a list of BiocView-class objects.

Usage

```
getBiocViews(reposUrl, vocab, defaultView, local = FALSE, htmlDir = "")
```

Arguments

reposUrl	URL for a CRAN-style repository that hosts a VIEWS file at the top-level.
vocab	A graph-class object representing the ontology of views. This graph should be a directed acyclic graph (DAG).
defaultView	A string giving the term to use for packages that do not list a term of their own via the biocViews field in the 'DESCRIPTION' file.
local	logical indicating whether to assume a local package repository. The default is FALSE in which case absolute links to package detail pages are created.
htmlDir	if the local argument is TRUE, this will be used as the relative path for package HTML files.

Value

A list of BiocView-class objects. The names of the list give the name of the corresponding view.

Author(s)

Seth Falcon

See Also

write_VIEWS, writeBiocViews

Examples

```
data(biocViewsVocab)
reposPath <- system.file("doc", package="biocViews")
reposUrl <- paste("file://", reposPath, sep="")
biocViews <- getBiocViews(reposUrl, biocViewsVocab, "NoViewProvided")
print(biocViews[1:2])
```

---

getPacksAndViews *Parse VIEWS file for views and packages*

Description

Given a repository URL, download and parse the VIEWS file.

Usage

```
getPacksAndViews(reposURL, vocab, defaultView, local=FALSE)
```

Arguments

reposURL	character vector giving the URL of a CRAN-style repository containing a VIEWS file at the top-level.
vocab	A graph-class object representing the ontologyof views. This graph should be a directed acyclic graph (DAG).
defaultView	A string giving the term to use for packages that do not list a term of their own via the biocViews field in the 'DESCRIPTION' file.
local	logical indicating whether certain links should be absolute (using reposURL) or relative.

Value

A list with named elements:

views: Vector of view memberships. Names are package names.

pkgList: A list of PackageDetail-class objects.

Author(s)

Seth Falcon

---

getSubTerms *Retrieve a term and its children from a vocab DAG*

Description

Given a Directed Acyclic Graph (DAG) represented as a graphNEL instance, return a character vector consisting of the specified term and all of its descendants. That is, give the list of terms for which a path exists starting at term.

Usage

```
getSubTerms(dag, term)
```

Arguments

dag	A graphNEL representing a DAG
term	A string giving a term in the vocabulary (a node in dag)

Value

A character vector of term names.

Author(s)

S. Falcon

Examples

```
data(biocViewsVocab)
getSubTerms(biocViewsVocab, "Software")
```

htmlDoc — *Create a complete HTML document representation of an object*

Description

This generic function should return an XMLNode instance representing the specified object in HTML as a complete HTML document.

Usage

```
htmlDoc(object, ...)
```

Arguments

object	An object
...	Not currently used.

Value

An instance of XMLNode from the XML package.

Author(s)

Seth Falcon

See Also

htmlValue, htmlFilename

htmlFilename — *Return a filename for an object's HTML representation*

Description

This function returns a string containing an appropriate filename for storing the object's HTML representation.

Usage

```
htmlFilename(object, ...)
```

Arguments

object	An object.
...	Not currently used

Value

A character vector of length one containing the filename.

Author(s)

Seth Falcon

See Also

htmlValue, htmlDoc

---

htmlValue *HTML Representation of an Object*

Description

This generic function should return an XMLNode instance representing the specified object in HTML

Usage

```
htmlValue(object)
```

Arguments

object	An object

Value

An instance of XMLNode from the XML package.

Author(s)

Seth Falcon

See Also

htmlDoc, htmlFilename

---

writeBiocViews *Write a list of BiocView objects to HTML*

Description

This function serializes a list of BiocView-class objects to a series of HTML files.

Usage

```
writeBiocViews(bvList, dir, backgroundColor="transparent")
```

Arguments

bvList	A list of BiocView-class objects
dir	A character vector giving the directory where the HTML files will be written.
backgroundColor	A character vector giving the background color for the body in the CSS file.

Author(s)

Seth Falcon

See Also

getBiocViews, genReposControlFiles, write_VIEWS

---

writeHtmlDoc *Write an XML DOM containing HTML to a file*

Description

Given a DOM tree from the XML package and a filename, write the DOM to disk creating an HTML file.

Usage

```
writeHtmlDoc(html, file)
```

Arguments

html	A DOM object from the XML package
file	A string giving the filename

Author(s)

S. Falcon

---

writePackageDetailHtml *Write HTML files for packages in a CRAN-style repository*

Description

This function creates package "homepages" that describe the package and provide links to download package artifacts in the repository.

Usage

```
writePackageDetailHtml(pkgList, htmlDir = "html", backgroundColor="transparent")
```

Arguments

pkgList	A list of PackageDescription objects.
htmlDir	The files will be written to this directory.
backgroundColor	A character vector giving the background color for the body in the CSS file.

Author(s)

Seth Falcon

See Also

writeRepositoryHtml

---

writeRepositoryHtml

Write package descriptions and a repository index as HTML

Description

This function generates an HTML file for each package in a repository and generates an index.html file that provides an alphabetized listing of the packages.

Usage

```
writeRepositoryHtml(reposRoot, title, reposUrl = "..", viewUrl = "../..",
                    reposFullUrl=reposUrl, downloadStatsUrl="",
                    devHistoryUrl="", link.rel = TRUE,
                    backgroundColor="transparent")
```

Arguments

reposRoot	string specifying the path to the root of the CRAN-style package repository.
title	string giving the title for the repository
reposUrl	string giving the prefix for URL in links generated on the package description pages. The default is "..." which works well if the package description HTML files are written to an html subdirectory under the root of the repository.
viewUrl	string giving the prefix for the URL in links to the view pages. The biocViews terms will be linked to views summary pages with this prefix.
reposFullUrl	string giving the full prefix for URL in links generated on the package description pages. The default is reposUrl.
downloadStatsUrl	string giving the prefix for the URL in links to the download history statistics pages.
devHistoryUrl	string giving the prefix for the URL in links to the development changelog.
link.rel	logical indicating whether the index page should generate relative URL links. The default is TRUE. If you are generating HTML for a remote repository, you will want to set this to FALSE.
backgroundColor	A character vector giving the background color for the body in the CSS file.

Author(s)

Seth Falcon

`writeTopLevelView` *Write the view for the root of a vocabulary to disk*

Description

Given a directory and a vocabulary represented as a `graphNEL` containing a DAG of terms, write the top-level term to disk as HTML.

This assumes your vocabulary has a single term with no parents.

Usage

```
writeTopLevelView(dir, vocab)
```

Arguments

`dir`	A string giving a directory in which to write the HTML file
`vocab`	A `graphNEL` instance giving the DAG of terms. It should have a root node. That is, there should be exactly one node with no incoming edges.

Author(s)

S. Falcon

`write_REPOSITORY` *Write a REPOSITORY control file for a CRAN-style package repository*

Description

This function writes a `REPOSITORY` file at the top-level of a CRAN-style repository. This file is DCF formatted and describes the location of packages available in the repository. Here is an example for a repository containing only source and Windows binary packages:

```
source: src/contrib
win.binary: bin/windows/contrib/2.6
win64.binary: bin/windows64/contrib/2.6
mac.binary.leopard: bin/mac/leopard/contrib/2.6
provides: source, win.binary, win64.binary, mac.binary.leopard
```

Usage

```
write_REPOSITORY(reposRootPath, contribPaths)
```

Arguments

reposRootPath	character vector containing the path to the CRAN-style repository root directory.
contribPaths	A named character vector. Valid names are source, win.binary, win64.binary, mac.binary, and mac.binary.leopard. Values indicate the paths to the package archives relative to the reposRoot.

Author(s)

Seth Falcon

See Also

write_PACKAGES, extractVignettes, genReposControlFiles, write_VIEWS

---

write_SYMBOLS *Write a SYMBOLS file*

Description

Writes a DCF formatted file, SYMBOLS, containing the symbols exported by each package in a directory containg R package source directories.

Usage

```
write_SYMBOLS(dir, verbose = FALSE, source.dirs=FALSE)
```

Arguments

dir	The root of a CRAN-style package repository containing source packages. When source.dirs is TRUE, dir should be a directory containing R package source directories
verbose	Logical. When TRUE, progress is printed to the standard output.
source.dirs	Logical. When TRUE, interpret dir as a directory containing source package directories. When FALSE, the default, dir is assumed to be the root of a CRAN-style package repository and the function will operate on the source package tarballs in dir/src/contrib.

Value

Returns NULL. Called for the side-effect of creating a SYMBOLS file in dir.

Author(s)

S. Falcon

See Also

write_PACKAGES write_VIEWS

write_VIEWS *Write a VIEWS control file for a CRAN-style package repository*

Description

This function writes a VIEWS file to the top-level of a CRAN-style package repository. The VIEWS file is in DCF format and describes all packages found in the repository.

The VIEWS file contains the complete DESCRIPTION file for each source package in the repository. In addition, metadata for available binary packages and vignettes is centralized here.

Usage

```
write_VIEWS(reposRootPath, fields = NULL,
            type = c("source", "win.binary", "win64.binary",
                     "mac.binary", "mac.binary.leopard"),
            verbose = FALSE, vignette.dir = "vignettes")
```

Arguments

reposRootPath	character vector containing the path to the CRAN-style repository root directory.
fields	Any additional fields to include. You shouldn't need this, but if you have added fields to the DESCRIPTION files of the packages in the repository, you may want it.
type	One of source, win.binary, win64.binary, mac.binary, or mac.binary.leopard indicating which set of packages should be used to build up the "shared" information. Since a repository can contain different versions of the same package (source vs binary) the shared information may not be reliable.
verbose	logical, if TRUE, print progress messages.
vignette.dir	character specifying where to look for vignettes.

Warning

This function uses a private function from the tools package: tools:::.build_repository_package_db.

Author(s)

Seth Falcon

See Also

write_PACKAGES, extractVignettes, genReposControlFiles, write_REPOSITORY

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