

# biocViews

February 9, 2012

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BiocView-class      *Class "BiocView"*

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## 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"*

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### 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

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PackageDetail-class  
*Class "PackageDetail"*

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### 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 containing 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 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
```

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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

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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:**

BiocView-class	Class "BiocView"
Htmlized-class	Class "Htmlized"
PackageDetail-class	Class "PackageDetail"
RepositoryDetail-class	Class "RepositoryDetail"

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

<code>HOWTO-BCV</code>	Basic package usage
<code>createReposHtml</code>	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")
```

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biocViewsVocab	<i>Bioconductor Task Views Vocabulary Data</i>
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### 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)
```

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<code>extractManually</code>	<i>Extract Rd man pages and build pdf reference manuals from local package repository</i>
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### 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

```
extractManually(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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extractReadmes      *Extract README files from source package tarballs*

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**Description**

Extracts README files from source tarballs of packages.

**Usage**

```
extractReadmes(reposRoot, srcContrib, destDir)
```

**Arguments**

reposRoot	Top level path for CRAN-style repos
srcContrib	Location of source packages
destDir	where to extract

---

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**

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

**Author(s)**

Seth Falcon

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`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**

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

**Author(s)**

Seth Falcon

**See Also**[write\\_PACKAGES](#), [extractVignettes](#), [write\\_REPOSITORY](#), [write\\_VIEWS](#)

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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 decedents.

### Usage

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

### Arguments

<code>reposUrl</code>	URL for a CRAN-style repository that hosts a VIEWS file at the top-level.
<code>vocab</code>	A <code>graph-class</code> object representing the ontology of views. This graph should be a directed acyclic graph (DAG).
<code>topTerm</code>	A string giving the name of the subview DAG. This view and all of its decedents will be included in the result.
<code>local</code>	logical indicating whether to assume a local package repository. The default is <code>FALSE</code> in which case absolute links to package detail pages are created.
<code>htmlDir</code>	if the <code>local</code> argument is <code>TRUE</code> , 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	<i>Build a list of BiocView objects from a package repository</i>
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**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 <a href="#">graph-class</a> 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 <code>biocViews</code> 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 <code>local</code> 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])
```

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getPackageNEWS      *Retrieve and print package NEWS*

---

### Description

These functions visit two repository PACKAGE files, identifying packages that are present in the ‘current’ repository and have NEWS since the base version of the same package in the ‘previous’ repository. All NEWS is reported for packages only in the current repository.

### Usage

```
getPackageNEWS (prevRepos="http://www.bioconductor.org/packages/2.8/bioc",
                currRepos="http://www.bioconductor.org/packages/2.9/bioc",
                srcDir, tarred = TRUE)
printNEWS (dbs, destfile, overwrite = FALSE, width = 68, ...)
```

### Arguments

prevRepos	character (1) repository from which NEWS starts.
currRepos	character (1) repository of current packages.
srcDir	character (1) directory containing the source all current packages
tarred	logical (1) indicating whether the source packages are in tar.gz (e.g., repository src/), or source (e.g., svn root)
dbs	A list of news_db elements, as returned by getPackageNEWS.
destfile	character (1) file path to the location where NEWS will be printed.
overwrite	logical (1) indicating whether destfile can be over-written, if it exists.
width	numeric (1) number of characters news items are to be wrapped to, excluding indent.
...	additional arguments, unused.

### Value

A list of news\_db files, as returned by `utils::news`, for each package for which relevant NEWS is available.

### Author(s)

Martin Morgan [mtmorgan@fhcrc.org](mailto:mtmorgan@fhcrc.org)

---

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 <code>graph-class</code> 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 <code>biocViews</code> field in the 'DESCRIPTION' file.
local	logical indicating whether certain links should be absolute (using <code>reposURL</code> ) 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 <code>graphNEL</code> representing a DAG
term	A string giving a term in the vocabulary (a node in <code>dag</code> )

**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**

<code>object</code>	An object
<code>...</code>	Not currently used.

**Value**

An instance of `XMLNode` from the XML package.

**Author(s)**

Seth Falcon

**See Also**

[htmlValue](#), [htmlFilename](#)

---

htmlFilename	<i>Return a filename for an object's HTML representation</i>
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**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](#)

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htmlValue	<i>HTML Representation of an Object</i>
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**Description**

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

**Usage**

```
htmlValue(object)
```

**Arguments**

object	An object
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**Value**

An instance of `XMLNode` from the `XML` package.

**Author(s)**

Seth Falcon

**See Also**[htmlDoc](#), [htmlFilename](#)

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<code>writeBiocViews</code>	<i>Write a list of BiocView objects to HTML</i>
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**Description**

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

**Usage**

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

**Arguments**

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

**Author(s)**

Seth Falcon

**See Also**[getBiocViews](#), [genReposControlFiles](#), [write\\_VIEWS](#)

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<code>writeHtmlDoc</code>	<i>Write an XML DOM containing HTML to a file</i>
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---

**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**

<code>html</code>	A DOM object from the XML package
<code>file</code>	A string giving the filename



**Arguments**

reposRoot	Root directory of a CRAN-style repository
reposUrl	URL of repository
viewUrl	url of VIEWS file
reposFullUrl	Full URL of VIEWS file
downloadStatsUrl	URL to download stats page
devHistoryUrl	Dev history URL

---

```
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 <code>".."</code> which works well if the package description HTML files are written to an <code>html</code> subdirectory under the root of the repository.
viewUrl	string giving the prefix for the URL in links to the view pages. The <code>biocViews</code> 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 <code>reposUrl</code> .
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 <code>TRUE</code> . If you are generating HTML for a remote repository, you will want to set this to <code>FALSE</code> .
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**

<code>dir</code>	A string giving a directory in which to write the HTML file
<code>vocab</code>	A <code>graphNEL</code> 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](#)

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<code>write_SYMBOLS</code>	<i>Write a SYMBOLS file</i>
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**Description**

Writes a DCF formatted file, `SYMBOLS`, containing the symbols exported by each package in a directory containing 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](#)

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write_VIEWS	<i>Write a VIEWS control file for a CRAN-style package repository</i>
-------------	---

---

### 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 <code>source</code> , <code>win.binary</code> , <code>win64.binary</code> , <code>mac.binary</code> , or <code>mac.binary.leopard</code> 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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