Package ‘BiocPkgTools’

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Type Package
Title Collection of simple tools for learning about Bioconductor Packages
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Description Bioconductor has a rich ecosystem of metadata around packages, usage, and build status. This package is a simple collection of functions to access that metadata from R. The goal is to expose metadata for data mining and value-added functionality such as package searching, text mining, and analytics on packages.
Depends htmlwidgets
Imports BiocFileCache, BiocManager, biocViews, tibble, magrittr, methods, rlang, stringr, rvest, dplyr, xml2, readr, httr, htmltools, DT, tools, utils, igraph, jsonlite, gh, RBGL, graph, rorcid
VignetteBuilder knitr
Suggests BiocStyle, knitr, rmarkdown, testthat, tm, lubridate, visNetwork, clipr, blastula, kableExtra, DiagrammeR, SummarizedExperiment
License MIT + file LICENSE
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Description

Calculate the 'dependency gain' from excluding one or more direct dependencies

Usage

.getDepGain(g, pkg, depsToRemove)

Arguments

g Package dependency graph
pkg Character string representing the package of interest
depsToRemove Character vector representing the dependencies to remove

Value

The 'dependency gain' that would be achieved by excluding the indicated direct dependencies

Author(s)

Charlotte Soneson
.get_cre_orcid  
get the ORCID id from cre field of Authors@R in packageDescription result

Description
get the ORCID id from cre field of Authors@R in packageDescription result

Usage
.get_cre_orcid(pkgname)

Arguments
pkgname character(1)

---

.get_orcid_rec  
process employment data from ORCID

Description
process employment data from ORCID

Usage
.get_orcid_rec(orcid, rename = TRUE)

Arguments
orcid character(1)
rename logical(1) if TRUE use short names
activitySince

What are the issues, pulls, commits created since a date?

Description

This function uses the gh package to get a list of either issues, pull requests, or GitHub commits since the specified date for a particular GitHub repository. The repository must have both the username/organization and the name, e.g., "Bioconductor/S4Vectors".

Usage

activitySince(
  gh_repo,
  activity = c("issues", "pulls", "commits"),
  status = c("closed", "open", "all"),
  Date,
  issue_metadata = c("created_at", "number", "title"),
  token = NULL
)

Arguments

gh_repo character(1) The GitHub repository location including the username/organization and the repository name, e.g., "Bioconductor/S4Vectors"
activity character(1) The type of repository activity to pull from the GitHub API. It can be one of "issues" (default), "pulls", or "commits".
status character(1) One of 'closed', 'open', or 'all' corresponding to the issue state desired from the GitHub API (Default: "closed"). This argument is ignored for the "commits" activity report.
Date character(1) The date cutoff from which to analyze closed issues in the YYYY-MM-DD or YYYY-MM-DDTHH:MM:SSZ format (ISO 8601).
issue_metadata character() The metadata labels to extract from the gh::gh response. See ?gh::gh for more details. Defaults to 'created_at', 'number', and 'title'. This argument is ignored for the "commits" activity report.
token character(1) For big requests, e.g., commit history, you may be prompted to use a GitHub Personal Access Token. Enter the token as plain text.

Details

The tibble returned by the commits activity report contains five columns:

• 'committer_date'
• 'commit' - hash
• 'parents' - hash of parent for merge commits
• 'author'
• 'message'

For information on other columns, refer to the GitHub API under repository issues or pulls (e.g., /repos/:repo/issues).

Value

A tibble with three columns corresponding to issue metadata (i.e., "created_at", "number", "title")

Examples

if (interactive()) {
  activitySince("Bioconductor/S4Vectors", "issues", "closed", "2021-05-01")
  activitySince("Bioconductor/S4Vectors", "issues", "open", "2022-05-01")
  activitySince("Bioconductor/S4Vectors", "commits", Date = "2022-05-01")
}

anacondaDownloadStats Get download statistics for Bioconductor packages distributed via Anaconda.

Description

Get download statistics for Bioconductor packages distributed via Anaconda.

Usage

anacondaDownloadStats()

Details

Anaconda provide daily download counts for all software packages they distribute. These are summarised into monthly tables of counts and made available from https://github.com/grimbough/anaconda-download-stats This function provides a mechanism to download these monthly counts for Bioconductor packages distributed through Anaconda.

Value

A data.frame of download statistics for all Bioconductor packages distributed by Anaconda, in tidy format. Note: Anaconda do not provide counts for unique IP addresses. This column is listed as NA for all packages to provide continuity with data from Bioconductor.org obtained by biocDownloadStats. The counts are updated monthly, so do not expect to see counts for the current month.

Author(s)

Mike L. Smith
Examples

```r
anacondaDownloadStats()
```

---

**biocBuildEmail**

Create and copy e-mail package notification template to clipboard

---

**Description**

The `biocBuildEmail` function provides a template for notifying maintainers of errors in the Bioconductor Build System (BBS). This convenience function returns the body of the email from a template within the package and provides a copy in the clipboard.

**Usage**

```r
biocBuildEmail(
  pkg,
  version = c("release", "devel"),
  PS = character(1L),
  dry.run = TRUE,
  to = NULL,
  cc = NULL,
  bcc = NULL,
  emailTemplate = templatePath(),
  core.name = NULL,
  core.email = NULL,
  core.id = NULL,
  textOnly = FALSE,
  resend = FALSE,
  verbose = FALSE,
  credFile = "~/.blastula_creds"
)
```

```
sentHistory()
```

**Arguments**

- `pkg` character(1) The name of the package in trouble
- `version` character() A vector indicating which version of Bioconductor the package is failing in (either 'release' or 'devel'; defaults to both)
- `PS` character(1) Postscript, an additional note to the recipient of the email (i.e., the package maintainer)
- `dry.run` logical(1) Display the email without sending to the recipient. It only works for HTML email reports and ignored when `textOnly=TRUE`
- `to` character() A vector of email addresses serving as primary recipients for the message. For secondary recipients, use the `cc` and `bcc` arguments.
cc, bcc character() A vector of email addresses for sending the message as a carbon copy or blind carbon copy.

emailTemplate character(1) The path to the email template Rmd file as obtained by templatePath(). A custom template can be provided as file path.

core.name character(1) The full name of the core team member

core.email character(1) The Roswell Park email of the core team member

core.id character(1) The internal identifier for the Roswell employee. This ID usually matches ^[A-Z][2][0-9]{5} for more recent identifiers.

textOnly logical(1) Whether to return the text of the email only. This avoids the use of the 'blastula' package and adds the text to the system clipboard if the clipr package is installed (default: FALSE)

resend logical(1) Whether to force a resend of the email

verbose logical(1) Whether to output full email information from 'smtp_send' (when dry.run is FALSE and 'blastula' is installed)

credFile character(1) An optional file generated by the blastula::create_smtp_creds_file function containing email authentication information (default: "/.blastula_creds"). See ?biocBuildEmail details.

Details

The credFile argument is a convenience for avoiding password entry at every instance an email is sent. If the default file "/.blastula_creds" does not exist, the user will be prompted for authorization information. Currently it is configured to emails for the core-team:

blastula::create_smtp_creds_file(
    file = "~/blastula_creds",
    user = "user.email@domain.org",
    host = "smtp.office365.com",
    port = 587,
    use_ssl = TRUE
)

Value

A character string of the email

sentHistory

Check the history of emails sent
biocBuildReport  

**Tidy Bioconductor build report results**

**Description**

The online Bioconductor build reports are great for humans to look at, but they are not easily computable. This function scrapes HTML and text files available from the build report online pages to generate a tidy data frame version of the build report.

**Usage**

```r
biocBuildReport(version = BiocManager::version(), stage.timings = FALSE)
```

**Arguments**

- **version** character(1) the character version number as used to access the online build report. For example, "3.14". The default is the "current version" as given by BiocManager::version(). Note that this is a character vector of length one and not a number.
- **stage.timings** logical(1) Whether to include the start, end, and elapsed time for each build, check, install stage from each building in the result (default: FALSE)

**Value**

A tbl_df object with columns pkg, version, author, commit, date, node, stage, and result.

**Examples**

```r
# Set the stage--what version of Bioconductor am I using?
BiocManager::version()

latest_build <- biocBuildReport()
head(latest_build)
```

---

biocDownloadStats  

**Get Bioconductor download statistics**

**Description**

Get Bioconductor download statistics

**Usage**

```r
biocDownloadStats(
  pkgType = c("software", "data-experiment", "workflows", "data-annotation")
)
```
Arguments

pkgType character(1) All or one of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to all types)

Details

Note that Bioconductor package download stats are not version-specific.

Value

A tibble of download statistics for all Bioconductor packages

Examples

biocDownloadStats()

biocExplore Explore Bioconductor packages interactively

Description

Explore Bioconductor packages through an interactive bubble plot. Click on bubbles to bring up additional information about the package. Size and proximity to center of a bubble is based on the downloads the package has in the past month.

Usage

biocExplore(top = 500L, ...)

Arguments

top maximum number of packages displayed in any biocView

... parameters passed to htmlwidgets::createWidget()

Value

A bubble plot of Bioconductor packages
**Description**

List all the packages associated with a maintainer. By default, it will return all packages associated with the maintainer@bioconductor.org email.

**Usage**

```r
biocMaintained(
  main = "maintainer@bioconductor\.org",
  version = BiocManager::version(),
  pkgType = c("software", "data-experiment", "workflows", "data-annotation")
)
```

**Arguments**

- `main` character(1) The regex for searching through the Maintainer column as obtained from `biocPkgList()`.
- `version` character(1) the character version number as used to access the online build report. For example, "3.14". The default is the "current version" as given by `BiocManager::version()`. Note that this is a character vector of length one and not a number.
- `pkgType` character(1) All or one of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to all types)

**Examples**

```r
biocMaintained()
```

---

**biocPkgList**

*Get full Bioconductor software package listing, with details*

**Description**

The BiocViews-generated VIEWS file is available for Bioconductor release and devel repositories. It contains quite a bit more information from the package DESCRIPTION files than the PACKAGES file. In particular, it contains biocViews annotations and URLs for vignettes and developer URLs.
Usage

```r
biocPkgList(
    version = BiocManager::version(),
    repo = "BioCsoft",
    addBiocViewParents = TRUE
)
```

Arguments

- **version**: The requested Bioconductor version. Will default to use the BiocManager defaults (i.e., `version()`).
- **repo**: The requested Bioconductor repository. The default will be the Bioconductor software repository: BioCsoft. Available repos include: "BioCsoft", "BioCann", "BioCexp", "BioCworkflows", and "CRAN". Note that not all repos are available for all versions, particularly older versions (but who would use those, right?).
- **addBiocViewParents**: logical(), whether to add all biocViews parents to biocViews annotations.

Details

Since packages are annotated with the most specific views, the default functionality here is to add parent terms for all views for each package. For example, in the bioCsoft repository, all packages will have at least "Software" added to their biocViews. If one wants to stick to only the most specific terms, set `addBiocViewParents` to `FALSE`.

Value

An object of class `tbl_df`.

Examples

```r
bpkgl = biocPkgList()
unlist(bpkgl[1, 'Depends'])

# Get a list of all packages that
# import "GEOquery"
library(dplyr)
bpkgl %>%
  filter(Package == 'GEOquery') %>%
pull(c('importsMe'))
```
biocPkgRanges

Grab build report results from BUILD_STATUS_DB for a particular package range

Description

Grab build report results from BUILD_STATUS_DB for a particular package range

Usage

biocPkgRanges(
  start,
  end,
  condition = c("ERROR", "WARNINGS"),
  phase = "buildsrc",
  version = c("devel", "release")
)

Arguments

start character(1) alphabetically first package name in range
end character(1) alphabetically last package name in range
condition character(1) condition string, typically 'ERROR' or 'WARNING'
phase character(1) string for phase of event: 'install', 'checksrc', or 'buildsrc' (default)
version character(1) string indication Bioconductor version, either 'devel' (default) or 'release'

Author(s)

Vincent J. Carey

Examples

## Not run:
biocPkgRanges(
  start = "a4", end = "CMA",
  condition = "ERROR", version = "devel"
)
## End(Not run)
BiocPkgTools

Description

Bioconductor has a rich ecosystem of metadata around packages, usage, and build status. This package is a simple collection of functions to access that metadata from R. The goal is to expose metadata for data mining and value-added functionality such as package searching, text mining, and analytics on packages.

For developers

The `biocBuildReport` function returns a computable form of the Bioconductor Build Report.

For users

The `biocDownloadStats` function gets Bioconductor download stats, allowing users to quickly find commonly used packages. The `biocPkgList` is useful for getting a complete listing of all Bioconductor packages.

Infrastructure

Bioconductor packages all have Digital Object Identifiers (DOIs). This package contains basic infrastructure for creating, updating, and de-referencing DOIs.

BiocPkgTools-cache

Description

Managing user data is important to allow use of email functions such as `biocBuildEmail` and made easy with `BiocFileCache`.

Usage

```r
setCache(
    directory = tools::R_user_dir("BiocPkgTools", "cache"),
    verbose = TRUE,
    ask = interactive()
)

pkgToolsCache(...)```
Arguments

directory  The file location where the cache is located. Once set future downloads will go
to this folder.
verbose  Whether to print descriptive messages
ask  logical (default TRUE when interactive session) Confirm the file location of the
cache directory
...  For pkgToolsCache, arguments are passed to setCache

pkgToolsCache

Get the directory location of the cache. It will prompt the user to create a cache if not already
created. A specific directory can be used via setCache.

setCache

Specify the directory location of the data cache. By default, it will got to the user’s home/.cache/R
and "appname" directory as specified by tools::R_user_dir (with package="BiocPkgTools" and
which="cache").

Description

Currently, biocLastBuildDate is DEFUNCT. See functionality in BiocArchive.

Usage

biocLastBuildDate(version)

Arguments

erturn  character(1) Indicates the Bioconductor version for which the last build date is
sought.

Details

The function facilitates the discovery of last build dates useful for selecting a fixed date. Currently,
it looks at https://bioconductor.org/checkResults/ and parses the dates listed.

See Also

https://github.com/LiNk-NY/BiocArchive
The `biocRevDepEmail` function collects all the emails of the reverse dependencies and sends a notification that upstream package(s) have been deprecated or removed. It uses a template found in `inst/resources` with the `templatePath()` function.

```r
biocRevDepEmail(
    packages,
    which = c("strong", "most", "all"),
    PS = character(1L),
    version = BiocManager::version(),
    dry.run = TRUE,
    cc = NULL,
    emailTemplate = templatePath("revdeprenote"),
    core.name = NULL,
    core.email = NULL,
    core.id = NULL,
    textOnly = FALSE,
    verbose = FALSE,
    credFile = "~/blastula_creds",
    ..., 
    pkg
)
```

**Arguments**

- `packages` character() A vector of CRAN and/or Bioconductor packages for whose reverse dependencies are to be checked and notified.
- `which` a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
- `PS` character(1) Postscript, an additional note to the recipient of the email (i.e., the package maintainer)
- `version` character() A vector indicating which version of Bioconductor the package is failing in (either 'release' or 'devel'; defaults to both)
- `dry.run` logical(1) Display the email without sending to the recipient. It only works for HTML email reports and ignored when textOnly=TRUE
- `cc` character() A vector of email addresses for sending the message as a carbon copy.
emailTemplate character(1) The path to the email template Rmd file as obtained by templatePath().
A custom template can be provided as file path.
core.name character(1) The full name of the core team member
core.email character(1) The Roswell Park email of the core team member
core.id character(1) The internal identifier for the Roswell employee. This ID usually matches ^[A-Z]{2}[0-9]{5}$ for more recent identifiers.
textOnly logical(1) Whether to return the text of the email only. This avoids the use of the 'blastula' package and adds the text to the system clipboard if the clipr package is installed (default: FALSE)
verbose logical(1) Whether to output full email information from 'smtp_send' (when dry.run is FALSE and 'blastula' is installed)
credFile character(1) An optional file generated by the blastula::create_smtp_creds_file function containing email authentication information (default: "~/.blastula_creds"). See ?biocBuildEmail details.
pkg character(1) DEPRECATED. The name of a single package whose reverse dependencies are to be checked and notified.
... Additional inputs to internal functions (not used).

Examples

biocRevDepEmail(
  "FindMyFriends", version = "3.13", dry.run = TRUE, textOnly = TRUE
)

buildPkgDependencyDataFrame

Work with Bioconductor package dependencies

Description

Bioconductor is built using an extensive set of core capabilities and data structures. This leads to package developers depending on other packages for interoperability and functionality. This function extracts package dependency information from biocPkgList and returns a tidy data.frame that can be used for analysis and to build graph structures of package dependencies.

Usage

buildPkgDependencyDataFrame(dependencies = c("strong", "most", "all"), ...)

Arguments

dependencies character() a vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
... parameters passed along to biocPkgList
buildPkgDependencyIgraph

Value

A data.frame (also a tbl_df) of S3 class "biocDepDF" including columns "Package", "dependency", and "edgetype".

Note

This function requires network access.

See Also

See buildPkgDependencyIgraph, biocPkgList.

Examples

# performs a network call, so must be online.
library(BiocPkgTools)
depdf <- buildPkgDependencyDataFrame()
head(depdf)
library(dplyr)
# filter to include only "Imports" type
# dependencies
imports_only <- depdf |> filter(edgetype=="Imports")

# top ten most imported packages
imports_only |> select(dependency) |> 
             group_by(dependency) |> tally() |> 
             arrange(desc(n))

# The Bioconductor packages with the
# largest number of imports
largest_importers <- imports_only |> 
                    select(Package) |> 
                    group_by(Package) |> tally() |> 
                    arrange(desc(n))

# not sure what these packages do. Join
# to their descriptions
biocPkgList() |> select(Package, Description) |> 
              left_join(largest_importers) |> arrange(desc(n)) |> 
              head()
Description

Package dependencies represent a directed graph (though Bioconductor dependencies are not an acyclic graph). This function simply returns an igraph graph from the package dependency data frame from a call to `buildPkgDependencyDataFrame` or any tidy data frame with rows of (Package, dependency) pairs. Additional columns are added as igraph edge attributes (see `graph_from_data_frame`).

Usage

`buildPkgDependencyIgraph(pkgDepDF)`

Arguments

- `pkgDepDF`: a tidy data frame. See description for details.

Value

An igraph directed graph. See the igraph package for details of what can be done.

See Also

See `buildPkgDependencyDataFrame`, `graph_from_data_frame`, `inducedSubgraphByPkgs`, `subgraphByDegree`, `igraph-es-indexing`, `igraph-vs-indexing`

Examples

```r
library(igraph)

pkg_dep_df = buildPkgDependencyDataFrame()

# at this point, filter or join to manipulate
# dependency data frame as you see fit.

g = buildPkgDependencyIgraph(pkg_dep_df)
g

# Look at nodes and edges
head(V(g)) # vertices
head(E(g)) # edges

# subset graph by attributes

head(sort(degree(g, mode='in'), decreasing=TRUE))
head(sort(degree(g, mode='out'), decreasing=TRUE))
```
class-dependencies  Retrieve Class relationships

Description
As the title says it should do something with class relationships

Usage

buildClassDepGraph(class, includeUnions = FALSE)
buildClassDepData(class, includeUnions = FALSE)
buildClassDepFromPackage(pkg, includeUnions = FALSE)
plotClassDep(class, includeUnions = FALSE)
plotClassDepData(data)
plotClassDepGraph(g)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>class</td>
<td>a single character value defining a ‘S4’ class name</td>
</tr>
<tr>
<td>includeUnions</td>
<td>TRUE or FALSE: Should union definitions included in the result? (default: FALSE)</td>
</tr>
<tr>
<td>pkg</td>
<td>a single character value defining a package name</td>
</tr>
<tr>
<td>data</td>
<td>a data.frame with compatible columns. See output of buildClassDepData</td>
</tr>
<tr>
<td>g</td>
<td>an igraph object with compatible edge attributes. See output of buildClassDepGraph</td>
</tr>
</tbody>
</table>

Examples

library("SummarizedExperiment")
depData <- buildClassDepData("RangedSummarizedExperiment")
depData
g <- buildClassDepGraph("RangedSummarizedExperiment")
plotClassDepGraph(g)

CRANstatus  Check the CRAN build report page and email a notification

Description
The CRANstatus function allows users to check the status of a package and send an email report of any failures.
Usage

CRANstatus(
  pkg,
  core.name = NULL,
  core.email = NULL,
  core.id = NULL,
  to.mail = "maintainer@bioconductor.org",
  dry.run = TRUE,
  emailTemplate = templatePath(\"cranreport\")
)

Arguments

pkg character(1) The name of the package in trouble
core.name character(1) The full name of the core team member
core.email character(1) The Roswell Park email of the core team member
core.id character(1) The internal identifier for the Roswell employee. This ID usually matches ^[A-Z][2][0-9]{5}$ for more recent identifiers.
to.mail The email of the CRAN report recipient
dry.run logical(1) Display the email without sending to the recipient. It only works for HTML email reports and ignored when textOnly=TRUE
eemailTemplate character(1) The path to the email template Rmd file as obtained by templatePath(). A custom template can be provided as file path.

Description

This function is used internally to generate XML elements from the datacite.org website for incoming Bioconductor packages.

Usage

dataciteXMLGenerate(pkg)

Arguments

pkg The name of a Bioconductor package

Value

An xml_document object from the xml2 package.

See Also

?xml2::\'xml_document-class'
firstInBioc  

**When did a package enter Bioconductor?**

**Description**
This function uses the `biocDownloadStats` data to approximate when a package entered Bioconductor. Note that the download stats go back only to 2009.

**Usage**
```
firstInBioc(download_stats)
```

**Arguments**
- `download_stats`: a data frame from `biocDownloadStats`

**Examples**
```
dls <- biocDownloadStats()
tail(firstInBioc(dls))
```

generateBiocPkgDOI  

**Generate a DOI for a Bioconductor package**

**Description**
This function makes calls out to the DataCite REST API described here: [https://support.datacite.org/docs/api-create-dois](https://support.datacite.org/docs/api-create-dois). The function creates a new DOI for a Bioconductor package (cannot already exist). The target URL for the DOI is the short Bioconductor package URL.

**Usage**
```
generateBiocPkgDOI(pkg, authors, pubyear, event = "publish", testing = TRUE)
```

**Arguments**
- `pkg`: character(1) package name
- `authors`: character vector of authors (will be “pasted” together)
- `pubyear`: integer(1) publication year
- `event`: Either "hide", "register", or publish". Typically, we use "publish" to make the DOI findable.
- `testing`: logical(1) If true, will use the apitest user with the password apitest. These DOIs will expire. The same apitest:apitest combination can be used to login to the website for doing things using the web interface. If false, the Bioconductor-specific user credentials should be in the correct environment variables.
Details

The login information for the "real" Bioconductor account should be stored in the environment variables "DATACITE_USERNAME" and "DATACITE_PASSWORD"

The GUI is available here: https://doi.datacite.org/.

Value

The DOI as a character(1) vector.

Examples

```R
## Not run:
x = generateBiocPkgDOI('RANDOM_TEST_PACKAGE','Sean Davis',1972)

## End(Not run)
```

---

**getBiocVignette**  
*Download a Bioconductor vignette*

Description

The actual vignette path is available using `biocPkgList`.

Usage

```R
getBiocVignette(
  vignettePath,
  destfile = tempfile(),
  version = BiocManager::version()
)
```

Arguments

- `vignettePath` character(1) the additional path information to get to the vignette
- `destfile` character(1) the file location to store the vignette
- `version` character(1) such as "3.7", defaults to user version

Value

character(1) The filename of the downloaded vignette
getPackageInfo

Generate needed information to create DOI from a package directory.

Description

Generate needed information to create DOI from a package directory.

Usage

getPackageInfo(dir)

Arguments

dir character(1) Path to package

Value

A data.frame
**get_bioc_data**

*Get data from Bioconductor*

**Description**

Get data from Bioconductor

**Usage**

```r
get_bioc_data()
```

**Value**

A JSON string containing Bioconductor package details

**Examples**

```r
bioc_data <- get_bioc_data()
```

---

**get_cre_orcids**

*get ORCID ids from cre fields of Authors@R in packageDescription results*

**Description**

get ORCID ids from cre fields of Authors@R in packageDescription results

**Usage**

```r
get_cre_orcids(pkgnames)
```

**Arguments**

- `pkgnames`: character() must be installed

**Note**

returns NA if no ORCID provided in Authors@R for package description

**Examples**

```r
get_cre_orcids(c("BiocPkgTools", "utils"))
```
githubDetails

Get package details from GitHub

Description

For packages that live on GitHub, we can mine further details. This function returns the GitHub details for the listed packages.

Usage

githubDetails(pkgs, sleep = 0)

Arguments

pkgs  
a character() vector of username/repo for one or more GitHub repos, such as seandavi/GEOquery.

sleep  
numeric() denoting the number of seconds to sleep between GitHub API calls. Since GitHub rate limits its APIs, it might be necessary to either use small chunks of packages iteratively or to supply a non-zero argument here. See the details section for a better solution using GitHub tokens.

Details

The gh function is used to do the fetching. If the number of packages supplied to this function is large (>40 or so), it is possible to run into problems with API rate limits. The gh package uses the environment variable "GITHUB_PAT" (for personal access token) to authenticate and then provide higher rate limits. If you run into problems with rate limits, set sleep to some small positive number to slow queries. Alternatively, create a Personal Access Token on GitHub and register it. See the gh package for details.

Examples

pkglist = biocPkgList()

# example of "pkgs" format.
head(pkglist$URL)

gh_list = githubURLParts(pkglist$URL)
gh_list = gh_list[!is.null(gh_list$user_repo),]

head(gh_list$user_repo)

ghd = githubDetails(gh_list$user_repo[1:5])
lapply(ghd, '[[', 'stargazers')
githubURLParts

Extract GitHub user and repo name from GitHub URL

Description
Extract GitHub user and repo name from GitHub URL

Usage
githubURLParts(urls)

Arguments
urls A character() vector of URLs

Value
A data.frame with four columns:
• url The original GitHub URL
• user_repo The GitHub "username/repo", combined
• user The GitHub username
• repo The GitHub repo name

Examples
# find GitHub URL details for
# Bioconductor packages
bpkgl = biocPkgList()
urldetails = githubURLParts(bpkgl$URL)
urldetails = urldetails[!is.na(urldetails$urldetails$uri),]
head(urldetails)

inducedSubgraphByPkgs
Return a minimal subgraph based on package name(s)

Description
Find the subgraph induced by including specific packages. The induced subgraph is the graph that includes the named packages and all edges connecting them. This is useful for a developer, for example, to examine her packages and their intervening dependencies.

Usage
inducedSubgraphByPkgs(g, pkgs, pkg_color = "red")
Arguments

- **g**: an igraph graph, typically created by `buildPkgDependencyIgraph`.
- **pkgs**: character() vector of packages to include. Package names not included in the graph are ignored.
- **pkg_color**: character(1) giving color of named packages. Other packages in the graph that fall in connecting paths will be colored as the igraph default.

Examples

```r
library(igraph)
g = buildPkgDependencyIgraph(buildPkgDependencyDataFrame())
g2 = inducedSubgraphByPkgs(g, pkgs=c('GenomicFeatures', 'TCGAbiolinksGUI', 'BiocGenerics', 'org.Hs.eg.db', 'minfi', 'limma'))
g2
V(g2)
plot(g2)
```

latestPkgStats | Summary of the latest package statistics

Description

The `latestPkgStats` function combines outputs from several functions to generate a table of relevant statistics for a given package.

Usage

```r
latestPkgStats(
  gh_repo,
  Date,
  pkgType = c("software", "data-experiment", "workflows", "data-annotation")
)
```

Arguments

- **gh_repo**: character(1) The GitHub repository location including the username / organization and the repository name, e.g., "Bioconductor/S4Vectors".
- **Date**: character(1) The date cutoff from which to analyze closed issues in the YYYY-MM-DD or YYYY-MM-DDTHH:MM:SSZ format (ISO 8601).
- **pkgType**: character(1) One of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to 'software')
Examples

```r
if (interactive()) {
  latestPkgStats("Bioconductor/BiocGenerics", "2021-05-05")
}
```

**orcid_table**

get data.frame of employment info from orcid

**Description**

get data.frame of employment info from orcid

**Usage**

```r
orcid_table(orcids)
```

**Arguments**

- **orcids** character()

**Examples**

```r
if (interactive()) {  # need a token?
  oids <- c("0000-0003-4046-0063", "0000-0003-4046-0063")
  print(orcid_table(oids))
  oids <- c(oids, NA)
  print(orcid_table(oids))
  print(orcid_table(oids[1]))
}
```

**pkgBiocDeps**

Look up a package's Bioconductor dependencies

**Description**

The function uses the pkgType argument to restrict the look up to only the relevant Bioconductor repository. It works for multiple packages of the same type.

**Usage**

```r
pkgBiocDeps(
  pkg,
  pkgType = c("software", "data-experiment", "workflows", "data-annotation"),
  which = "strong",
  only.bioc = TRUE,
  version = BiocManager::version()
)
```
pkgBiocRevDeps

Obtain all the reverse dependencies for a Bioconductor package

Description

The function returns a slightly upgraded list with dependency types as elements and package names in each of those elements, if any. The types of dependencies can be seen in the which argument documentation.

Usage

pkgBiocRevDeps(
  pkg,
  pkgType = c("software", "data-experiment", "workflows", "data-annotation"),
  which = "all",
  only.bioc = TRUE,
  version = BiocManager::version()
)

## S3 method for class 'biocrevdeeps'
summary(object, ...)
pkgCombDependencyGain

Arguments

pkg character(1) The name of a Bioconductor package
pkgType character(1) One of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to 'software')
which a character vector listing the types of dependencies, a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances"). Character string "all" is shorthand for that vector, character string "most" for the same vector without "Enhances", character string "strong" (default) for the first three elements of that vector.
only.bioc logical(1) Whether to only return Bioconductor dependencies in the list (default TRUE)
version (Optional) character(1) or package_version indicating the Bioconductor version (e.g., "3.8") for which repositories are required.
object an object for which a summary is desired.
... additional arguments affecting the summary produced.

Details

The summary method of the biocrevdeps class given by pkgBiocRevDeps provides a tally in each dependency field.

Value

A biocrevdeps list class object

Examples

rdeps <- pkgBiocRevDeps("MultiAssayExperiment", which = "all")
rdeps
summary(rdeps)

pkgCombDependencyGain

Calculate dependency gain achieved by excluding combinations of packages

Description

Calculate dependency gain achieved by excluding combinations of packages

Usage

pkgCombDependencyGain(pkg, depdf, maxNbr = 3L)
pkgDepImports

Arguments

pkg character, the name of the package for which we want to estimate the dependency gain

depdf a tidy data frame with package dependency information obtained through the function buildPkgDependencyDataFrame

maxNbr numeric, the maximal number of direct dependencies to leave out simultaneously

Value

A data frame with three columns: ExclPackages (the excluded direct dependencies), NbrExcl (the number of excluded direct dependencies), DepGain (the dependency gain from excluding these direct dependencies)

Author(s)

Charlotte Soneson

Examples

depdf <- buildPkgDependencyDataFrame(
  dependencies=c("Depends", "Imports"),
  repo=c("BioCsoft", "CRAN")
)

pcd <- pkgCombDependencyGain('GEOquery', depdf, maxNbr = 3L)

head(pcd[order(pcd$DepGain, decreasing = TRUE), ])

pkgDepImports

Report package imported functionality

Description

Function adapted from 'itdepends::dep_usage_pkg' at https://github.com/r-lib/itdepends to obtain the functionality imported and used by a given package.

Usage

pkgDepImports(pkg)

Arguments

pkg character() name of the package for which we want to obtain the functionality calls imported from its dependencies and used within the package.
**pkgDepMetrics**

**Details**
Certain imported elements, such as built-in constants, will not be identified as imported functionality by this function.

**Value**
A tidy data frame with two columns:
- pkg: name of the package dependency.
- fun: name of the functionality call imported from the dependency in the column pkg and used within the analyzed package.

**Author(s)**
Robert Castelo

**Examples**
```r
cpkgDepImports('BiocPkgTools')
```

---

**pkgDepMetrics**
*Report package dependency burden*

**Description**
Elaborate a report on the dependency burden of a given package.

**Usage**
```r
tpkgDepMetrics(pkg, depdf)
```

**Arguments**
- **pkg** character() name of the package for which we want to obtain metrics on its dependency burden.
- **depdf** a tidy data frame with package dependency information obtained through the function `buildPkgDependencyDataFrame`.

**Value**
A tidy data frame with different metrics on the package dependency burden. More concretely, the following columns:
- ImportedAndUsed: number of functionality calls imported and used in the package.
- Exported: number of functionality calls exported by the dependency.
- **Usage**: \((\text{ImportedAndUsed} \times 100) / \text{Exported}\). This value provides an estimate of what fraction of the functionality of the dependency is actually used in the given package.

- **DepOverlap**: Similarity between the dependency graph structure of the given package and the one of the dependency in the corresponding row, estimated as the Jaccard index between the two sets of vertices of the corresponding graphs. Its values goes between 0 and 1, where 0 indicates that no dependency is shared, while 1 indicates that the given package and the corresponding dependency depend on an identical subset of packages.

- **DepGainIfExcluded**: The 'dependency gain' (decrease in the total number of dependencies) that would be obtained if this package was excluded from the list of direct dependencies. The reported information is ordered by the Usage column to facilitate the identification of dependencies for which the analyzed package is using a small fraction of their functionality and therefore, it could be easier remove them. To aid in that decision, the column DepOverlap reports the overlap of the dependency graph of each dependency with the one of the analyzed package. Here a value above, e.g., 0.5, could, albeit not necessarily, imply that removing that dependency could substantially lighten the dependency burden of the analyzed package.

An NA value in the ImportedAndUsed column indicates that the function pkgDepMetrics() could not identify what functionality calls in the analyzed package are made to the dependency.

**Author(s)**

Robert Castelo
Charlotte Soneson

**Examples**

depdf <- buildPkgDependencyDataFrame(
  dependencies=c("Depends", "Imports"),
  repo=c("BioCsoft", "CRAN")
)
pkgDepMetrics('BiocPkgTools', depdf)

---

**pkgDownloadRank**

What is a package's download rank?

**Description**

This function uses available.packages to calculate the download rank percentile of a given package. It approximates what is observed in the Bioconductor landing page.

**Usage**

```r
pkgDownloadRank(
  pkg,
  pkgType = c("software", "data-experiment", "workflows", "data-annotation"),
  version = BiocManager::version()
)`
Arguments

pkg character(1) The name of a Bioconductor package
pkgType character(1) One of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to 'software')
version (Optional) character(1) or package_version indicating the Bioconductor version (e.g., "3.8") for which repositories are required.

Value

The package’s percentile rank, in terms of download statistics, and proportion in the name

Examples

## Percentile rank for BiocGenerics (top 1%)
pkgDownloadRank("BiocGenerics", "software")

pkgDownloadStats Get Bioconductor download statistics for a package

Description

Get Bioconductor download statistics for a package

Usage

pkgDownloadStats(
  pkg,
  pkgType = c("software", "data-experiment", "workflows", "data-annotation"),
  years = format(Sys.time(), "%Y")
)

Arguments

pkg character(1) The name of a Bioconductor package
pkgType character(1) One of 'software', 'data-experiment', 'workflows', or 'data-annotation' (defaults to 'software')
years numeric(), character() A vector of years from which to obtain download statistics (defaults to current year)

Value

A tibble of download statistics

Examples

pkgDownloadStats("GenomicRanges")
**ProblemPage**

generate hyperlinked HTML for build reports for Bioconductor packages

**Description**

This is a quick way to get an HTML report of packages maintained by a specific developer or which depend directly on a specified package. The function is keyed to filter based on either the maintainer name or by using the 'Depends', 'Suggests' and 'Imports' fields in package descriptions.

**Usage**

```r
problemPage(
  authorPattern = "V.*Carey",
  dependsOn, 
  ver = "devel",
  includeOK = FALSE
)
```

**Arguments**

- `authorPattern` character(1) regexp used with `grep()` to filter author field of package DESCRIPTION for listing
- `dependsOn` character(1) name of a Bioconductor package. The function will return the status of packages that directly depend on this package. Can only be used when 'authorPattern' is the empty string.
- `ver` character(1) version tag for Bioconductor
- `includeOK` logical(1) include entries from the build report that are listed as "OK". Default FALSE will result in only those entries that are in WARNING or ERROR state.

**Value**

DT::datatable call; if assigned to a variable, must evaluate to get the page to appear

**Author(s)**

Vince Carey, Mike L. Smith

**Examples**

```r
if (interactive()) {
  problemPage()
  problemPage(dependsOn = "limma")
}
```
**repositoryStats**  

Bioconductor Binary Repository Statistics

**Description**

Summarize binary packages compatible with the Bioconductor or Terra container in use.

**Usage**

```r
repositoryStats(
  version = BiocManager::version(),
  binary_repository = BiocManager::containerRepository(version)
)
```

## S3 method for class 'repositoryStats'

```r
print(x, ...)
```

**Arguments**

- **version** (Optional) character(1) or package_version indicating the *Bioconductor* version (e.g., "3.8") for which repositories are required.
- **binary_repository** character(1) location of binary repository as given by BiocManager::containerRepository (default)
- **x** the object returned by repositoryStats().
- **...** further arguments passed to or from other methods (not used).

**Value**

a list of class repositoryStats with the following fields:

- **container**: character(1) container label, e.g., bioconductor_docker, or NA if not evaluated on a supported container.
- **bioconductor_version**: package_version the Bioconductor version provided by the user.
- **repository_exists**: logical(1) TRUE if a binary repository exists for the container and Bioconductor_Version version.
- **bioconductor_binary_repository**: character(1) repository location, if available, or NA if the repository does not exist.
- **n_software_packages**: integer(1) number of software packages in the Bioconductor source repository.
- **n_binary_packages**: integer(1) number of binary packages available. When a binary repository exists, this number is likely to be larger than the number of source software packages, because it includes the binary version of the source software packages, as well as the (possibly CRAN) dependencies of the binary packages.
- `n_binary_software_packages`: integer(1) number of binary packages derived from Bioconductor source packages. This number is less than or equal to `n_software_packages`.

- `missing_binaries`: integer(1) the number of Bioconductor source software packages that are not present in the binary repository.

- `out_of_date_binaries`: integer(1) the number of Bioconductor source software packages that are newer than their binary counterpart. A newer source software package might occur when the main Bioconductor build system has updated a package after the most recent run of the binary build system.

### Methods (by generic)
- `print(repositoryStats)`: Print a summary of package availability in binary repositories.

### Examples

```r
stats <- repositoryStats()  # obtain statistics
stats                   # display a summary
stats$container        # access an element for further computation
```

---

**Subset graph by degree**

### Description

While the `inducedSubgraphByPkgs` returns the subgraph with the minimal connections between named packages, this function takes a vector of package names, a degree (1 or more) and returns the subgraph(s) that are within degree of the package named.

### Usage

```r
subgraphByDegree(g, pkg, degree = 1, ...)
```

### Arguments

- `g`  
  an igraph graph, typically created by `buildPkgDependencyIgraph`

- `pkg`  
  character(1) package name from which to measure degree.

- `degree`  
  integer(1) degree, limit search for adjacent vertices to this degree.

- `...`  
  passed on to `distances`

### Value

An igraph graph, with only nodes and their edges within degree of the named package.
Examples

g = buildPkgDependencyIgraph(buildPkgDependencyDataFrame())
g2 = subgraphByDegree(g, 'GEOquery')
g2

templatePath

Obtain the location of available email templates

Description

These templates are used with biocBuildEmail to notify maintainers regarding package errors and final deprecation warning.

Usage

templatePath(
  type = c("buildemail", "deprecation", "deprecguide", "cranreport", "revdepo note")
)

Arguments

type character(1) Either one of "buildemail", "deprecation", "deprecguide", "cranreport", or "revdepo note". See the templates in the resources folder.
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