Package ‘pkgndep’

August 9, 2023

Type Package

Title Analyze Dependency Heaviness of R Packages

Version 1.99.2

Date 2023-08-08

Depends R (>= 4.0.0)

Imports ComplexHeatmap (>= 2.6.0), GetoptLong, GlobalOptions, utils, grid, hash, methods, BiocManager, brew, BiocVersion

Suggests knitr, rmarkdown, svglite, callr, rjson, Rook, igraph, ggplot2, ggrepel, base64, testthat, cowplot

Description A new metric named 'dependency heaviness' is proposed that measures the number of additional dependency packages that a parent package brings to its child package and are unique to the dependency packages imported by all other parents. The dependency heaviness analysis is visualized by a customized heatmap. The package is described in [doi:10.1093/bioinformatics/btac449]. We have also performed the dependency heaviness analysis on the CRAN/Bioconductor package ecosystem and the results are implemented as a web-based database which provides comprehensive tools for querying dependencies of individual R packages. The systematic analysis on the CRAN/Bioconductor ecosystem is described in [doi:10.1016/j.jss.2023.111610]. From 'pkgndep' version 2.0.0, the heaviness database includes snapshots of the CRAN/Bioconductor ecosystems for many old R versions.

URL https://github.com/jokergoo/pkgndep

VignetteBuilder knitr

License MIT + file LICENSE

NeedsCompilation no

Author Zuguang Gu [aut, cre] (https://orcid.org/0000-0002-7395-8709)

Maintainer Zuguang Gu <z.gu@dkfz.de>

Repository CRAN

Date/Publication 2023-08-08 23:00:15 UTC
R topics documented:

- ALL_BIOC_RELEASES ........................................... 3
- all_pkg_stat_snapshot ....................................... 3
- check_pkg ....................................................... 4
- child_dependency .............................................. 4
- co_heaviness ................................................... 5
- dependency_database .......................................... 6
- dependency_heatmap .......................................... 6
- dependency_report ............................................ 7
- dependency_website .......................................... 8
- downstream_dependency ...................................... 8
- get_all_functions_imported_to_children .................. 9
- gini_index ..................................................... 10
- heaviness ...................................................... 10
- heaviness_database ......................................... 11
- heaviness_from_upstream .................................... 12
- heaviness_on_children ...................................... 12
- heaviness_on_downstream .................................... 13
- heaviness_report ............................................. 14
- is_parent ....................................................... 15
- is_upstream .................................................... 15
- loaded_packages ............................................. 16
- load_all_pkg_dep ............................................. 17
- load_from_heaviness_db ..................................... 17
- load_heaviness_timeline .................................... 18
- load_pkg_db ................................................... 19
- load_pkg_description ........................................ 20
- load_pkg_downstream_dependency_path_snapshot ............ 20
- load_pkg_namespace ......................................... 21
- load_pkg_stat_snapshot ..................................... 21
- parent_dependency ........................................... 22
- pkgndep ....................................................... 23
- pkgndep_opt .................................................. 24
- plot.pkgndep ................................................. 24
- print.pkgndep ................................................ 25
- reformat_db ................................................... 26
- required_dependency_packages ............................... 27
- upstream_dependency ........................................ 27

Index 29
ALL_BIOC_RELEASES

All Bioconductor releases

Description

All Bioconductor releases

Usage

ALL_BIOCRELEASES

Value

A data frame

Examples

ALL_BIOCRELEASES

all_pkg_stat_snapshot

The complete table of dependency heaviness for all CRAN/Bioconductor packages

Description

The complete table of dependency heaviness for all CRAN/Bioconductor packages

Usage

all_pkg_stat_snapshot()

Value

The returned data frame is directly from load_pkg_stat_snapshot, but with only a subset of columns of heaviness metrics.

Examples

# There is no example
NULL
**check_pkg**  
*Check whether a package is available*

**Description**

Check whether a package is available

**Usage**

```r
check_pkg(pkg, bioc = FALSE)
```

**Arguments**

- `pkg`: The name of the package.
- `bioc`: Whether it is a Bioconductor package.

**Details**

One of the suggestions to avoid heavy dependencies is to put parent packages that are not frequently used to 'Suggests' and to load them when the corresponding functions are used. Here the `check_pkg` function helps to check whether these parent packages are available and if not, it prints messages to guide users to install the corresponding packages.

**Examples**

```r
# There is no example
NULL
```

---

**child_dependency**  
*Get child dependency for a package*

**Description**

Get child dependency for a package

**Usage**

```r
child_dependency(package, fields = NULL, online = FALSE)
```

**Arguments**

- `package`: Package name.
- `fields`: Which fields in DESCRIPTION? Values should be in `Depends`, `Imports`, `LinkingTo`, `Suggests` and `Enhances`. The value can also be set to `strong` or `weak`.
- `online`: Whether use the newest package database directly from CRAN/Bioconductor or the pre-computed package database? The version of the pre-computed package database can be set via `pkgndep_opt$heaviness_db_version`. 
**co_heaviness**

**Value**

A data frame with child packages as well as its heaviness on its child packages. If `snapshot` is set to `FALSE`, heaviness on child packages is set to `NA`.

**Examples**

```
## Not run:
child_dependency("ComplexHeatmap")
## End(Not run)
```

---

**co_heaviness**

Co-heaviness for pairs of parent packages

**Description**

Co-heaviness for pairs of parent packages

**Usage**

```
co_heaviness(x, rel = FALSE, a = 10, jaccard = FALSE)
```

**Arguments**

- `x`: An object returned by `pkgndep`.
- `rel`: Whether to return the absolute measure or the relative measure.
- `a`: A constant added for calculating the relative measure.
- `jaccard`: Whether to return Jaccard coefficient?

**Details**

Denote a package as P and its two strong parent packages as A and B, i.e., parent packages in "Depends", "Imports" and "LinkingTo", the co-heaviness for A and B is calculated as follows.

Denote S_A as the set of reduced dependency packages when only moving A to "Suggests" of P, and denote S_B as the set of reduced dependency packages when only moving B to "Suggests" of P, denote S_AB as the set of reduced dependency packages when moving A and B together to "Suggests" of P, the co-heaviness of A, B on P is calculated as

\[
\text{length}(\text{setdiff}(S_{AB}, \text{union}(S_A, S_B)))
\]

which is the number of reduced package only caused by co-action of A and B.

Note the co-heaviness is only calculated for parent packages in "Depends", "Imports" and "LinkingTo".

When `jaccard` is set to `TRUE`, the function returns jaccard coefficient. \(\text{setdiff}(S_{AB}, \text{union}(S_A, S_B))\) is actually the set of dependencies imported by and only by two parent packages A and B. Thus the jaccard coefficient is calculated as

\[
\frac{\text{length}(\text{setdiff}(S_{AB}, \text{union}(S_A, S_B)))}{\text{length}(S_{AB})}
\]
### Examples

```r
## Not run:
# DESeq version 1.36.0, the dependencies have been changed in later versions.
x = readRDS(system.file("extdata", "DESeq2_dep.rds", package = "pkgndep"))
hm = co_heaviness(x)
ComplexHeatmap::Heatmap(hm)
co_heaviness(x, jaccard = TRUE)

## End(Not run)
```

---

**dependency_database**

*Database of package dependency heaviness of all R packages*

**Description**

Database of package dependency heaviness of all R packages

**Usage**

```r
dependency_database(version = pkgndep_opt$heaviness_db_version)
```

**Arguments**

- `version` Version of the heaviness database. See `pkgndep_opt$heaviness_db_version`.

**Examples**

```r
if(interactive()) {
  dependency_database()
}
```

---

**dependency_heatmap**

*Make the dependency heatmap*

**Description**

Make the dependency heatmap

**Usage**

```r
dependency_heatmap(x, pkg_fontsize = 10*cex, title_fontsize = 12*cex,
legend_fontsize = 10*cex, fix_size = !dev.interactive(), cex = 1,
help = TRUE, file = NULL, res = 144)
```
dependency_report

Arguments

- **x**: An object from `pkgndep`.
- **pkg_fontsize**: Font size for the package names.
- **title_fontsize**: Font size for the title.
- **legend_fontsize**: Font size for the legends.
- **fix_size**: Should the rows and columns in the heatmap have fixed size?
- **cex**: A factor multiplicated to all font sizes.
- **help**: Whether to print help message?
- **file**: A path of the figure. The size of the figure is automatically calculated.
- **res**: Resolution of the figure (only for png and jpeg).

Details

If `fix_size` is set to TRUE. The size of the whole plot can be obtained by:

```
size = dependency_heatmap(x, fix_size = TRUE)
```

where `size` is a numeric vector of length two which are the width and height of the whole heatmap.

If `file` argument is set, the size of the figure is automatically calculated.

If there are no dependency packages stored in `x`, NULL is returned.

Value

A vector of two numeric values (in inches) that correspond to the width and height of the plot.

Examples

```r
# See examples in `pkgndep()`.
```

```
dependency_report HTML report for package dependency heaviness analysis

Description

HTML report for package dependency heaviness analysis

Usage

dependency_report(...) 

Arguments

... Pass to `heaviness_report`.
**Details**

It is the same as `heaviness_report`.

**Examples**

```r
# There is no example
NULL
```

dependency_website  
*Database of package dependency heaviness of all R packages*

**Description**

Database of package dependency heaviness of all R packages

**Usage**

```r
dependency_website(version = pkgndep_opt$heaviness_db_version)
```

**Arguments**

- `version`  
  Version of the heaviness database. See `pkgndep_opt$heaviness_db_version`.

**Examples**

```r
if(interactive()) {
  dependency_website()
}
```

downstream_dependency  
*Get downstream dependency for a package*

**Description**

Get downstream dependency for a package

**Usage**

```r
downstream_dependency(package, online = FALSE)
```

**Arguments**

- `package`  
  Package name.
- `online`  
  Whether use the newest package database directly from CRAN/Bioconductor or the pre-computated package database? The version of the pre-computated package database can be set via `pkgndep_opt$heaviness_db_version`.
get_all_functions_imported_to_children

Details
Downstream packages with relations of Depends, Imports and LinkingTo are retrieved.

Value
A data frame with all downstream packages.

Examples
```r
## Not run:
downstream_dependency("ComplexHeatmap")
## End(Not run)
```
gini_index \hspace{1cm} Gini index

**Description**

Gini index

**Usage**

\[ \text{gini\_index}(v) \]

**Arguments**

- \(v\): A numeric vector.

**Examples**

```r
x = readRDS(system.file("extdata", "ComplexHeatmap\_dep.rds", package = "pkgndep"))
gini\_index(x\$heaviness[x\$which\_required])
```

heaviness \hspace{1cm} Heaviness from parent packages

**Description**

Heaviness from parent packages

**Usage**

\[ \text{heaviness}(x, \text{rel} = \text{FALSE}, a = 10, \text{only\_strong\_dep} = \text{FALSE}) \]

**Arguments**

- \(x\): An object returned by \texttt{pkgndep}.
- \(\text{rel}\): Whether to return the absolute measure or the relative measure.
- \(a\): A constant added for calculating the relative measure.
- \(\text{only\_strong\_dep}\): Whether to only return the heaviness for strong parents.
The heaviness from a parent package is calculated as follows: If package B is in the Depends/Imports/LinkingTo fields of package A, which means, package B is necessary for package A, denote $v_1$ as the total numbers of packages required for package A, and $v_2$ as the total number of required packages if moving package B to Suggests (which means, now B is not necessary for A). The absolute measure is simply $v_1 - v_2$ and relative measure is $(v_1 + a)/(v_2 + a)$.

In the second scenario, if B is in the Suggests/Enhances fields of package A, now $v_2$ is the total number of required packages if moving B to Imports, the absolute measure is $v_2 - v_1$ and relative measure is $(v_2 + a)/(v_1 + a)$.

Value

A numeric vector.

Examples

```r
x = readRDS(system.file("extdata", "ComplexHeatmap dep.rds", package = "pkgdep"))
heaviness(x)
heaviness(x, rel = TRUE)
```

heaviness_database

Database of package dependency heaviness of all R packages

Description

Database of package dependency heaviness of all R packages

Usage

```r
heaviness_database(version = pkndep_opt$heaviness_db_version)
```

Arguments

version Version of the heaviness database. See pkndep_opt$heaviness_db_version.

Examples

```r
if(interactive()) {
  heaviness_database()
}
```
heaviness_from_upstream

Heaviness from all upstream packages

Description

Heaviness from all upstream packages

Usage

heaviness_from_upstream(package)

Arguments

package A package name.

Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via pkgndep_opt$heaviness_db_version.

Value

A named vector.

Examples

# There is no example
NULL

heaviness_on_children Heaviness on all child packages

Description

Heaviness on all child packages

Usage

heaviness_on_children(package, add_values_attr = FALSE, total = FALSE)

Arguments

package A package name.
add_values_attr Whether to include "values" attribute? Internally used.
total Whether to return the total heaviness?
heaviness_on_downstream

Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via `pkgndep_opt$heaviness_db_version`.

Value

The value is the mean heaviness of the package on all its child packages.

Examples

```r
## Not run:
heaviness_on_children("ComplexHeatmap")
## End(Not run)
```

heaviness_on_downstream

Heaviness on all downstream packages

Description

Heaviness on all downstream packages

Usage

```r
heaviness_on_downstream(package, add_values_attr = FALSE, via = NULL,
                         total = FALSE, internal = FALSE)
```

Arguments

- `package`: A package name.
- `add_values_attr`: Whether to include "values" attribute? Internally used.
- `via`: Whether to only consider downstream packages via a intermediate package?
- `total`: Whether to return the total heaviness?
- `internal`: Whether to use internally calculated heaviness?

Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via `pkgndep_opt$heaviness_db_version`. 
Value

The value is the mean heaviness of the package on all its downstream packages. Denote \( n \) as the number of all its downstream packages, \( k_i \) as the number of required packages for package \( i \), \( v_1 \) as the total number of required packages for all downstream packages, i.e. \( v_1 = \sum_i^n k_i \). Denote \( p_i \) as the number of required packages if moving package to Suggests, and \( v_2 \) as the total number of required packages, i.e. \( v_2 = \sum_i^n p_i \). The final heaviness on downstream packages is \( (v_1 - v_2)/n \).

Note since the interaction from package to its downstream packages may go through several intermediate packages, which means, the reduction of required packages for a downstream package might be joint effects from all its upstream packages, thus, to properly calculate the heaviness of a package to its downstream packages, we first make a copy of the package database and move package to Suggests for all packages which depends on package. Then for all downstream packages of package, dependency analysis by \pkg{pkgndep} is redone with the modified package database. Finally, the heaviness on downstream packages is collected and the mean heaviness is calculated.

Examples

```r
## Not run:
heaviness_on_downstream("ComplexHeatmap")
## End(Not run)
```

Description

HTML report for package dependency heaviness analysis

Usage

```r
heaviness_report(pkg, file = NULL)
```

Arguments

- `pkg`: An object from \pkg{pkgndep}.
- `file`: The path of the html file. If it is not specified, the report will be automatically opened in the web browser.

Value

The path of the HTML file of the report.

Examples

```r
if(interactive()) {
  x = readRDS(system.file("extdata", "ComplexHeatmap_dep.rds", package = "pkgndep"))
  heaviness_report(x)
}
```
is_parent

Test the parent-child relationship

Description
Test the parent-child relationship

Usage

is_parent(parent, child, ...)

Arguments

parent
A vector of package names.

child
A single package name.

... Pass to parent_dependency.

Value
A logical vector.

Examples

# There is no example
NULL

is_upstream

Test upstream-downstream relationship

Description
Test upstream-downstream relationship

Usage

is_upstream(upstream, package, ...)

Arguments

upstream
A vector of package names.

package
A single package name.

... Pass to upstream_dependency.
Value

A logical vector.

Examples

# There is no example
NULL

loaded_packages

Description

Loaded packages

Usage

loaded_packages(pkg, verbose = TRUE)

Arguments

pkg           A package name.
verbose       Whether to print messages.

Details

It loads pkg into a new R session and collects which other packages are loaded by parsing the output from sessionInfo.

Value

A data frame.

Examples

loaded_packages("ComplexHeatmap")
load_all_pkg_dep

Load dependency analysis results of all packages

Description

Load dependency analysis results of all packages

Usage

load_all_pkg_dep(hash = TRUE)

Arguments

hash

Whether to convert the named list to a hash table by hash.

Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via pkgndep_opt$heaviness_db_version.

Value

A list (as a hash table) of pkgndep objects where each element corresponds to the analysis on one package.

Examples

## Not run:
lt = load_all_pkg_dep()
length(lt)
head(names(lt))
lt[['ggplot2']]

## End(Not run)

load_from_heaviness_db

Load pre-computed objects

Description

Load pre-computed objects

Usage

load_from_heaviness_db(file)
Arguments

file File name.

Details

The pathway of the file can be set via pkgndep_opt$db_file_template.
Internally used.

Examples

# There is no example
NULL

load_heaviness_timeline

Load heaviness statistics at all time points

Description

Load heaviness statistics at all time points

Usage

load_heaviness_timeline()

Details

Used internally.

Value

A list of data frames.

Examples

# There is no example
NULL
Description

Load package database

Usage

load_pkg_db(lib = NULL, online = TRUE, db = NULL, verbose = TRUE)

Arguments

lib       Local library path. If the value is NA, only remote package database is used.

online    If the value is TRUE, it will directly use the newest package database file from
           CRAN/Bioconductor. If the value is FALSE, it uses the pre-computed package
           database on a specific CRAN/Bioconductor snapshot. The version of the pre-
           computed package database can be set via pkgndep_opt$heaviness_db_version.

db        A pre-computed pkg_db object.

verbose   Whether to print messages.

Details

It loads the package database from CRAN/Bioconductor and locally installed packages.

The database object internally is cached for repeated use of other functions in this package.

Value

A pkg_db class object. See reformat_db for how to use the pkg_db object.

Examples

## Not run:
pkg_db = load_pkg_db(lib = NA)
pkg_db

## End(Not run)
load_pkg_description  Load DESCRIPTION files of all packages

Description
Load DESCRIPTION files of all packages

Usage
load_pkg_description()

Details
It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via pkgndep_opt$heaviness_db_version.

Value
A list of character vectors.

Examples
```r
## Not run:
ltd = load_pkg_description()
ltd[1:2]
## End(Not run)
```

load_pkg_downstream_dependency_path_snapshot

Load downstream dependency paths for all packages

Description
Load downstream dependency paths for all packages

Usage
load_pkg_downstream_dependency_path_snapshot()

Details
It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via pkgndep_opt$heaviness_db_version.

Value
A list.
Examples

```r
## Not run:
downstream_path_list = load_pkg_downstream_dependency_path_snapshot()
downstream_path_list[["ComplexHeatmap"]]
## End(Not run)
```

# load_pkg_namespace

Load NAMESPACE files of all packages

## Description

Load NAMESPACE files of all packages

## Usage

```r
load_pkg_namespace()
```

## Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via `pkgndep_opt$heaviness_db_version`.

## Value

A list of character vectors.

## Examples

```r
## Not run:
lt = load_pkg_namespace()
lt[1:2]
## End(Not run)
```

# load_pkg_stat_snapshot

Load all package dependency statistics

## Description

Load all package dependency statistics

## Usage

```r
load_pkg_stat_snapshot()
```
Details

It is calculated based on a specific CRAN/Bioconductor snapshot. The version is set via `pkgndep_opt$heaviness_db_version`.

Value

A data frame.

Examples

```r
## Not run:
df = load_pkg_stat_snapshot()
head(df)

## End(Not run)
```

---

**parent_dependency**

Get parent dependency for a package

Description

Get parent dependency for a package

Usage

```r
parent_dependency(package, fields = NULL, online = FALSE)
```

Arguments

- `package`: Package name.
- `fields`: Which fields in DESCRIPTION? Values should be in Depends, Imports, LinkingTo, Suggests and Enhances. The value can also be set to strong or weak.
- `online`: Whether use the newest package database directly from CRAN/Bioconductor or the pre-computed package database? The version of the pre-computed package database can be set via `pkgndep_opt$heaviness_db_version`.

Value

A data frame with parent packages as well as their heaviness on package. If snapshot is set to FALSE, heaviness on child packages is set to NA.

Examples

```r
## Not run:
parent_dependency("ComplexHeatmap")

## End(Not run)
```
pkgndep

Package dependency analysis

Description
Package dependency analysis

Usage
pkgndep(package, verbose = TRUE, online = TRUE, load = FALSE, parse_namespace = TRUE)

Arguments

- **package**: Package name. The value can be 1. a CRAN/Bioconductor package, 2. an installed package, 3. a path of a local package, 4. URL of a GitHub repository.
- **verbose**: Whether to show messages.
- **online**: If the value is TRUE, it will directly use the newest package database file from CRAN/Bioconductor. Note the default Bioconductor version is the one corresponding to the current R version. If you want to use a higher bioc version, you need to set the global option pkgndep_opt$bioc_version. If the value of online is FALSE, a snapshot of the CRAN/Bioconductor package database will be used. The version of the package database snapshot can be via the global option pkgndep_opt$heaviness_db_version.
- **load**: If the value is TRUE, the package is loaded into a fresh new R session and the function will check which upstream packages are also loaded into the R session. Note it is possible that an "Imports" package is not loaded or a "Suggests" package is loaded in the R session when loading package.
- **parse_namespace**: Whether to also parse the NAMESPACE file. It is only used internally.

Value
A pkgndep object.

Examples

```r
## Not run:
x = pkgndep("ComplexHeatmap")

## End(Not run)
# The 'x' variable generated by 'pkgndep()' is already saved in this package.
x = readRDS(system.file("extdata", "ComplexHeatmap_dep.rds", package = "pkgndep"))
x
dependency_heatmap(x)
```
Description

Global parameters for pkgndep

Usage

pkgndep_opt(..., RESET = FALSE, READ.ONLY = NULL, LOCAL = FALSE, ADD = FALSE)

Arguments

...  Arguments for the parameters, see "details" section
RESET  Reset to default values.
READ.ONLY  Please ignore.
LOCAL  Please ignore.
ADD  Please ignore.

Details

There are following parameters:

bioc_version  The bioconductor version. By default it is the version corresponding to the R version under use. Please note this option is only for switching between bioc release version and development version, while not for switching to very old bioc versions.

heaviness.db_version  The version of the heaviness database. The value can be the corresponding bioc version, the R version or the corresponding date for the bioc release. All supported values are in the object ALL_BIOCRELEASES.

Examples

pkgndep_opt

Description

Make the dependency heatmap

Usage

## S3 method for class 'pkgndep'
plot(x, ...)

plot.pkgndep  Make the dependency heatmap
print.pkgndep

**Arguments**

- **x**  
  An object from `pkgndep`.

- **...**  
  Other arguments.

**Details**

Please use `dependency_heatmap` instead.

**Examples**

```r
# There is no example
NULL
```

---

**Description**

Print method

**Usage**

```r
## S3 method for class 'pkgndep'
print(x, ...)
```

**Arguments**

- **x**  
  An object from `pkgndep`.

- **...**  
  Other arguments.

**Value**

No value is returned.

**Examples**

```r
# See examples in `pkgndep()`.
```
reformat_db  Format the package database

Description

Format the package database

Usage

reformat_db(db, version = NULL)

Arguments

db  A data frame returned from available.packages or installed.packages.

version  Version of the database, a self-defined text.

Details

It reformats the data frame of the package database into a pkg_db class object.

Value

A pkg_db class object. There are the following methods:

pkg_db$get_meta(package, field=NULL)  field can take values in "Package", "Version" and "Repository".

pkg_db$get_dependency_table(package)  Get the dependency table.

pkg_db$get_rev_dependency_table(package)  Get the reverse dependency table.

pkg_db$package_dependencies(package, recursive=FALSE, reverse=FALSE, which="strong", simplify=FALSE)  All the arguments are the same as in package_dependencies. Argument simplify controls whether to return a data frame or a simplified vector.

Examples

## Not run:
db = available.packages()
db2 = reformat_db(db)

# a pkg_db object generated on 2021-10-28 can be loaded by load_pkg_db()
db2 = load_pkg_db(online = FALSE)
db2
db2$get_meta("ComplexHeatmap")
db2$get_dependency_table("ComplexHeatmap")
db2$get_rev_dependency_table("ComplexHeatmap")
db2$package_dependencies("ComplexHeatmap")
db2$package_dependencies("ComplexHeatmap", recursive = TRUE)

## End(Not run)
required_dependency_packages

Description

Required dependency packages

Usage

required_dependency_packages(x, all = FALSE)

Arguments

x An object from pkgndep.

all Whether to include the packages required if also including packages from "Suggests"/"Enhances" field.

Details

The function returns all upstream packages.

Value

A vector of package names.

Examples

## Not run:
x = readRDS(system.file("extdata", "ComplexHeatmap_dep.rds", package = "pkgndep"))
required_dependency_packages(x)
## End(Not run)

upstream_dependency

Get upstream dependency for a package

Description

Get upstream dependency for a package

Usage

upstream_dependency(package, online = FALSE)
upstream_dependency

Arguments

- **package**  
  Package name.

- **online**  
  Whether use the newest package database directly from CRAN/Bioconductor or the pre-computed package database? The version of the pre-computed package database can be set via `pkgndep_opt$heaviness_db_version`.

Details

Upstream packages with relations of "Depends", "Imports" and "LinkingTo" are retrieved.

Value

A data frame with all upstream packages.

Examples

```r
## Not run:
upstream_dependency("ComplexHeatmap")

## End(Not run)
```
Index

ALL_BIOC_RELEASES, 3, 24
all_pkg_stat_snapshot, 3
available.packages, 26

check_pkg, 4
child_dependency, 4
cohaviness, 5

dependency_database, 6
dependency_heatmap, 6, 25
dependency_report, 7
dependency_website, 8
downstream_dependency, 8

get_all_functions_imported_to_children, 9
gini_index, 10

hash, 17
heaviness, 10
heaviness_database, 11
heaviness_from_upstream, 12
heaviness_on_children, 12
heaviness_on_downstream, 13
heaviness_report, 7, 8, 14

installed.packages, 26
is_parent, 15
is_upstream, 15

load_all_pkg_dep, 17
load_from_heaviness_db, 17
load_heaviness_timeline, 18
load_pkg_db, 19
load_pkg_description, 20
load_pkg_downstream_dependency_path_snapshot,

load_pkg_namespace, 21
load_pkg_stat_snapshot, 3, 21
loaded_packages, 16

package_dependencies, 26
parent_dependency, 15, 22
pkgndep, 5, 7, 9, 10, 14, 23, 25, 27
pkgndep_opt, 4, 6, 8, 11–13, 17–23, 24, 28
plot.pkgndep, 24
print.pkgndep, 25
reformat_db, 19, 26
required_dependency_packages, 27

sessionInfo, 16

upstream_dependency, 15, 27