

Package ‘deepdep’

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Title Visualise and Explore the Deep Dependencies of R Packages

Version 0.4.1

Description Provides tools for exploration of R package dependencies.

The main `deepdep()` function allows to acquire deep dependencies of any package and plot them in an elegant way.

It also adds some popularity measures for the packages e.g. in the form of download count through the 'cranlogs' package.

Uses the CRAN metadata database <<http://crandb.r-pkg.org>>

and Bioconductor metadata <<http://bioconductor.org>>.

Other data acquire functions are: `get_dependencies()`, `get_downloads()` and `get_description()`.

The `deepdep_shiny()` function runs shiny application that helps to produce a nice 'deepdep' plot.

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Encoding UTF-8

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Depends R (>= 3.2.0)

Imports cranlogs, httr, jsonlite

Suggests BiocManager, covr, devtools, ggplot2, ggraph, graphlayouts, igraph, knitr, miniCRAN, plyr, rmarkdown, scales, shiny, shinycssloaders, spelling, stringi, testthat (>= 2.1.0), vcr

VignetteBuilder knitr

URL <https://dominikrafacz.github.io/deepdep/>,

<https://github.com/DominikRafacz/deepdep>

BugReports <https://github.com/DominikRafacz/deepdep/issues>

Language en-GB

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deepdep	<i>Acquire the dependencies of the package on any depth level</i>
---------	---

Description

This function is an ultimate wrapper for [get_dependencies](#). It inherits all of the arguments and allows to recursively search for the dependencies at the higher level of depth.

Usage

```
deepdep(
  package,
  depth = 1,
  downloads = FALSE,
  bioc = FALSE,
  local = FALSE,
  dependency_type = "strong"
)
```

Arguments

package	A character. Name of the package that is on CRAN, Bioconductor repository or locally installed. See <code>bioc</code> and <code>local</code> arguments.
depth	An integer. Maximum depth level of the dependency. By default it's 1.
downloads	A logical. If TRUE add dependency downloads data. By default it's FALSE.
bioc	A logical value. If TRUE the Bioconductor dependencies data will be taken from the Bioconductor repository. For this option to work properly, <code>BiocManager</code> package needs to be installed.
local	A logical value. If TRUE only data of locally installed packages will be used (without API usage).
dependency_type	A character vector. Types of the dependencies that should be sought, a subset of <code>c("Imports", "Depends", "LinkingTo", "Suggests", "Enhances")</code> . Other possibilities are: character string "all", a shorthand for the whole vector; character string "most" for the same vector without "Enhances"; character string "strong" (default) for the first three elements of that vector. Works analogously to package_dependencies .

Value

An object of `deepdep` class.

See Also

[get_dependencies](#)

Examples

```
library(deepdep)

dd_downloads <- deepdep("ggplot2")
head(dd_downloads)

dd_2 <- deepdep("ggplot2", depth = 2, downloads = TRUE)
plot_dependencies(dd_2, "circular")

dd_local <- deepdep("deepdep", local = TRUE)
plot_dependencies(dd_local)
```

deepdep_shiny *Run Shiny app*

Description

This function runs shiny app that helps to produce nice deepdep plot.

Usage

```
deepdep_shiny()
```

get_available_packages
 Get the list of available packages

Description

Get names of packages that you have locally installed or that are available to be installed.

Usage

```
get_available_packages(bioc = FALSE, local = FALSE, reset_cache = FALSE)
```

Arguments

bioc	A logical value. If TRUE the Bioconductor dependencies data will be taken from the Bioconductor repository. For this option to work properly, BiocManager package needs to be installed.
local	A logical value. If TRUE only data of locally installed packages will be used (without API usage).
reset_cache	A logical value. If TRUE the cache will be cleared before obtaining the list of packages.

Details

Function uses caching - only the first usage scraps information from servers. Those objects are then saved locally in temporary file and further usages loads needed data from the file.

Arguments bioc and local cannot be TRUE simultaneously. If neither local nor bioc are TRUE, vector contains all packages available currently on CRAN. If bioc is TRUE, vector contains all packages available currently on CRAN and via Bioconductor. If local is TRUE, vector contains all of the packages that are currently installed.

Value

A character vector.

Examples

```
library(deepdep)

av <- get_available_packages()
head(av)
```

get_dependencies	<i>Acquire the dependencies of the package</i>
------------------	--

Description

This function uses [get_description](#) and [get_downloads](#) to acquire the dependencies of the package (with their downloads).

Usage

```
get_dependencies(
  package,
  downloads = TRUE,
  bioc = FALSE,
  local = FALSE,
  dependency_type = "strong"
)
```

Arguments

package	A character. Name of the package that is on CRAN, Bioconductor repository or locally installed. See <code>bioc</code> and <code>local</code> arguments.
downloads	A logical. If TRUE add package downloads data. By default it's TRUE.
bioc	A logical value. If TRUE the Bioconductor dependencies data will be taken from the Bioconductor repository. For this option to work properly, <code>BiocManager</code> package needs to be installed.
local	A logical value. If TRUE only data of locally installed packages will be used (without API usage).
dependency_type	A character vector. Types of the dependencies that should be sought, a subset of <code>c("Imports", "Depends", "LinkingTo", "Suggests", "Enhances")</code> . Other possibilities are: character string "all", a shorthand for the whole vector; character string "most" for the same vector without "Enhances"; character string "strong" (default) for the first three elements of that vector. Works analogously to package_dependencies .

Value

An object of package_dependencies class.

See Also

[get_description](#) [get_downloads](#)

Examples

```
library(deepdep)
```

```
dependencies <- get_dependencies("htmltools", downloads = FALSE)
dependencies
```

```
dependencies_local <- get_dependencies("deepdep", downloads = FALSE, local = TRUE)
dependencies_local
```

get_description

Scrap the DESCRIPTION file and CRAN metadata of the package

Description

This function uses api of **CRAN Data Base** to scrap the DESCRIPTION file and CRAN metadata of the package. It caches the results to speed the computation process.

Usage

```
get_description(package, bioc = FALSE, local = FALSE, reset_cache = FALSE)
```

Arguments

package	A character. Name of the package that is on CRAN, Bioconductor repository or locally installed. See bioc and local arguments.
bioc	A logical value. If TRUE the Bioconductor dependencies data will be taken from the Bioconductor repository. For this option to work properly, BiocManager package needs to be installed.
local	A logical value. If TRUE only data of locally installed packages will be used (without API usage).
reset_cache	A logical value. If TRUE the cache will be cleared before obtaining the list of packages.

Value

An object of package_description class.

Examples

```
library(deepdep)

description <- get_description("ggplot2")
description

description_local <- get_description("deepdep", local = TRUE)
description_local
```

get_downloads	<i>Scrap the download data of the package</i>
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Description

This function uses **API** of **CRAN Logs** to scrap the download logs of the package.

Usage

```
get_downloads(package)
```

Arguments

package A character. Name of the package that is on CRAN.

Value

An object of package_downloads class.

Examples

```
library(deepdep)

downloads <- get_downloads("ggplot2")
downloads
```

plot_dependencies *Main plot function for a deepdep object*

Description

Visualize dependency data from a deepdep object using ggplot2 and ggraph packages. Several tree-like layouts are available.

Usage

```
plot_dependencies(  
  x,  
  type = "circular",  
  same_level = FALSE,  
  reverse = FALSE,  
  label_percentage = 1,  
  show_version = FALSE,  
  show_downloads = FALSE,  
  show_stamp = TRUE,  
  declutter = FALSE,  
  ...  
)  
  
## Default S3 method:  
plot_dependencies(  
  x,  
  type = "circular",  
  same_level = FALSE,  
  reverse = FALSE,  
  label_percentage = 1,  
  show_version = FALSE,  
  show_downloads = FALSE,  
  show_stamp = TRUE,  
  declutter = FALSE,  
  ...  
)  
  
## S3 method for class 'character'  
plot_dependencies(  
  x,  
  type = "circular",  
  same_level = FALSE,  
  reverse = FALSE,  
  label_percentage = 1,  
  show_version = FALSE,  
  show_downloads = FALSE,  
  show_stamp = TRUE,  
  ...  
)
```



```

    declutter = FALSE,
    ...
)

## S3 method for class 'deepdep'
plot_dependencies(
  x,
  type = "circular",
  same_level = FALSE,
  reverse = FALSE,
  label_percentage = 1,
  show_version = FALSE,
  show_downloads = FALSE,
  show_stamp = TRUE,
  declutter = FALSE,
  ...
)

```

Arguments

x	A deepdep object or a character package name.
type	A character. Possible values are circular and tree.
same_level	A logical. If TRUE links between dependencies on the same level will be added. By default it's FALSE.
reverse	A logical. If TRUE links between dependencies pointing from deeper level to more shallow level will be added. By default it's FALSE.
label_percentage	A numeric value between 0 and 1. A fraction of labels to be displayed. By default it's 1 (all labels displayed).
show_version	A logical. If TRUE required version of package will be displayed below package name. Defaults to FALSE.
show_downloads	A logical. If TRUE total number of downloads of packages will be displayed below package names. Defaults to FALSE.
show_stamp	A logical. If TRUE (the default) the package version and plot creation time will be added
declutter	A logical. If TRUE then all layers beyond the first one ignore non-strong dependencies (i.e. "Suggests" and "Enhances"). This visualizes the so-called "hard costs of weak suggests".
...	Other arguments passed to the <code>deepdep</code> function.

Value

A `ggplot2`, `gg`, `ggraph`, `deepdep_plot` class object.

Examples

```
library(deepdep)

#:# use local packages
plot_dependencies("deepdep", depth = 2, local = TRUE)

dd <- deepdep("ggplot2")
plot_dependencies(dd, "tree")

dd2 <- deepdep("ggplot2", depth = 2)
plot_dependencies(dd2, "circular")

#:# show grand_total download count
plot_dependencies("shiny", show_downloads = TRUE)
```

plot_downloads

Plot download count of CRAN packages.

Description

This function uses **API of CRAN Logs** to scrap the download logs of the packages and then plots the data. It works on objects of class character (vector), deepdep, package_dependencies and package_downloads.

Usage

```
plot_downloads(x, ...)

## Default S3 method:
plot_downloads(x, ...)

## S3 method for class 'deepdep'
plot_downloads(x, from = Sys.Date() - 365, to = Sys.Date(), ...)

## S3 method for class 'package_dependencies'
plot_downloads(x, from = Sys.Date() - 365, to = Sys.Date(), ...)

## S3 method for class 'package_downloads'
plot_downloads(x, from = Sys.Date() - 365, to = Sys.Date(), ...)

## S3 method for class 'character'
plot_downloads(x, from = Sys.Date() - 365, to = Sys.Date(), ...)
```

Arguments

- x A character vector. Names of the packages that are on CRAN.
- ... Ignored.
- from A Date class object. From which date plot the data. By default it's one year back.
- to A Date class object. To which date plot the data. By default it's now.

Value

A ggplot2 class object.

Examples

```
library(deepdep)

plot_downloads("htmltools")

dd <- deepdep("ggplot2")
plot_downloads(dd)
```

`print.available_packages`
Print function for an object of available_packages class

Description

Print function for an object of available_packages class

Usage

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

Arguments

- x An object of available_packages class.
- ... other

Examples

```
library(deepdep)

av <- get_available_packages()
head(av)
```

print.deepdep	<i>Print function for an object of deepdep class</i>
---------------	--

Description

Print function for an object of deepdep class

Usage

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

Arguments

x	An object of deepdep class.
...	other

Examples

```
library(deepdep)

dd <- deepdep("stringr")
dd
```

print.package_dependencies	<i>Print function for an object of package_dependencies class</i>
----------------------------	---

Description

Print function for an object of package_dependencies class

Usage

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

Arguments

x An object of package_dependencies class.
... other

Examples

```
library(deepdep)  
  
get_dependencies("htmltools", downloads = TRUE)
```

print.package_description
Print function for an object of package_description class

Description

Print function for an object of package_description class

Usage

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

Arguments

x An object of package_description class.
... other

Examples

```
library(deepdep)  
  
description <- get_description("ggplot2")  
description
```

```
print.package_downloads
```

Print function for an object of package_downloads class

Description

Print function for an object of package_downloads class

Usage

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

Arguments

x	An object of package_downloads class.
...	other

Examples

```
library(deepdep)  
  
desc <- get_downloads("stringr")  
desc
```

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