Package ‘pacs’

October 14, 2022

Title  Supplementary Tools for R Packages Developers
Version  0.4.8
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Description  Supplementary utils for CRAN maintainers and R packages developers.
  Validating the library, packages and lock files.
  Exploring a complexity of a specific package like evaluating its size in bytes with all dependencies.
  The shiny app complexity could be explored too.
  Assessing the life duration of a specific package version.
  Checking a CRAN package check page status for any errors and warnings.
  Retrieving a DESCRIPTION or NAMESPACE file for any package version.
  Comparing DESCRIPTION or NAMESPACE files between different package versions.
  Getting a list of all releases for a specific package.
  The Bioconductor is partly supported.
License  GPL (>= 3)
BugReports  https://github.com/Polkas/pacs/issues
Encoding  UTF-8
RoxygenNote  7.2.0
Depends  R (>= 3.5.0)
Imports  curl, memoise, jsonlite, xml2, stringi
Suggests  remotes, renv, withr, pkgsearch, mockery, testthat (>= 3.0.0), knitr, rmarkdown
Config/testthat/edition  3
VignetteBuilder  knitr
NeedsCompilation  no
Author  Maciej Nasinski [aut, cre]
Repository  CRAN
Date/Publication  2022-06-28 19:30:05 UTC
The shiny app dependencies

Description

the shiny app dependencies packages are checked recursively. The c("Depends", "Imports", "LinkingTo") DESCRIPTION files fields are checked recursively. The required dependencies have to be installed in the local repository. The default arguments setup is recommended.
Usage

\begin{verbatim}
app_deps(
    path = ".",
    fields = c("Depends", "Imports", "LinkingTo"),
    lib.loc = .libPaths(),
    local = TRUE,
    base = FALSE,
    description_v = FALSE,
    recursive = TRUE,
    repos = biocran_repos()
)
\end{verbatim}

Arguments

- **path** character path to the shiny app. Default: "."
- **fields** 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. Default: c("Depends", "Imports", "LinkingTo")
- **lib.loc** character vector of search paths with local packages. Default: .libPaths()
- **local** logical if to use local repository (or newest remote packages). Default: TRUE
- **base** logical if to add base packages too. If TRUE then pacs::pacs_base() are taken into account. Default: FALSE
- **description_v** logical if the dependencies version should be taken from description files, minimal required. By default installed versions are taken. Default: FALSE
- **recursive** logical if to assess the dependencies recursively. Default: TRUE
- **repos** character vector base URLs of the repositories to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value

character vector with dependency packages or data.frame when checking recursively.

Note

renv package has to be installed.

Examples

\begin{verbatim}
## Not run:
library(renv)
# Please update the path to the custom shiny app
app_path <- system.file("examples/04_mpg", package = "shiny")
pacs::app_deps(app_path)
pacs::app_deps(app_path, recursive = FALSE)
## End(Not run)
\end{verbatim}
app_size

Size of the shiny app

Description

The size of shiny app is a sum of dependencies packages and the app directory. The app dependencies packages are checked recursively, and only in local repository. The default arguments setup is recommended.

Usage

```r
app_size(
  path = ".",
  fields = c("Depends", "Imports", "LinkingTo"),
  lib.loc = .libPaths(),
  recursive = TRUE
)
```

Arguments

- **path** character path to the shiny app. Default: "."
- **fields** 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. Default: c("Depends", "Imports", "LinkingTo")
- **lib.loc** character vector of search paths with local packages. Default: .libPaths()
- **recursive** logical if to assess the dependencies recursively. Default: TRUE

Value

numeric size in bytes, to get MB ten divide by 10**6.

Note

renv package has to be installed. base packages (pacs::pacs_base()) are not taken into account.

Examples

```r
## Not run:
library(renv)
# Please update the path to the shiny app
cat(pacs::app_size(system.file("examples/04_mpg", package = "shiny")) / 10**6, "MB")
```

## End(Not run)
biocran_repos  

CRAN and Bioconductor repositories

Description

CRAN and Bioconductor repositories. The newest Bioconductor release for the specific R version is assumed.

Usage

```r
biocran_repos(version = NULL)
```

Arguments

- `version` character
  - the Bioconductor release. By default the newest Bioconductor release for the specific R version is assumed, if not available only CRAN repository is returned. Available Bioconductor versions for your R version could be checked with `pacs::bio_releases()`. Default NULL

Value

- named character
  - vector of repositories.

Note

- The Internet connection is needed to get Bioconductor repositories.

Examples

```r
## Not run:
pacs::biocran_repos()
## End(Not run)
```

bio_releases  

Retrieving all Bioconductor releases

Description

Retrieving all Bioconductor releases. The data is downloaded from https://www.bioconductor.org/about/release-announcements/.

Usage

```r
bio_releases()
```
checked_packages

Value
data.frame with the same structure as the html table on https://www.bioconductor.org/about/release-announcement/

Note
Results are cached for 30 minutes with memoise package.

Examples

## Not run:
pacs::bio_releases()
## End(Not run)

---

checked_packages  Retrieving all R CRAN packages check pages statuses.

Description
Retrieving all R CRAN packages check pages statuses. The data is downloaded from https://cran.r-project.org/web/checks/check_summary_by_package.html.

Usage
checked_packages()

Value
data.frame with the same structure as the html table on https://cran.r-project.org/web/checks/check_summary_by_package.html.

Note
Results are cached for 30 minutes with memoise package. Some packages could be duplicated as not all tests are performed for a new version so two versions still coexists. Checks with asterisks (*) indicate that checking was not fully performed, this is a case for less than 1% of all packages.

Examples

## Not run:
pacs::checked_packages()
## End(Not run)
compareVersionsMax

Maximum version across the vector

Description
Reduce function over the utils::compareVersion

Usage
compareVersionsMax(vec, na.rm = TRUE)

Arguments

vec character vector.
na.rm logical if to remove NA values.

Value
character maximum version

Examples
compareVersionsMax(c("1.1.1", "0.2.0"))

compareVersionsMin
Minimum version across the vector

Description
Reduce function over the utils::compareVersion

Usage
compareVersionsMin(vec, na.rm = TRUE)

Arguments

vec character vector.
na.rm logical if to remove NA values.

Value
character minimal version

Examples
compareVersionsMin(c("1.1.1", "0.2.0"))
### cran_flavors

**Description**

Retrieving all R CRAN servers flavors. The data is downloaded from [https://cran.r-project.org/web/checks/check_flavors.html](https://cran.r-project.org/web/checks/check_flavors.html).

**Usage**

```r
cran_flavors()
```

**Value**

data.frame with the same structure as the html table on [https://cran.r-project.org/web/checks/check_flavors.html](https://cran.r-project.org/web/checks/check_flavors.html).

**Note**

Results are cached for 30 minutes with memoise package.

**Examples**

```r
## Not run:
pacs::cran_flavors()
## End(Not run)
```

### dir_size

**Description**

size of package.

**Usage**

```r
dir_size(path = ".", recursive = TRUE)
```

**Arguments**

- `path` character path to the shiny app. Default: "."
- `recursive` logical if to assess the dependencies recursively. Default: TRUE

**Value**

numeric size in bytes, to get MB ten divide by 10**6.
Examples

```r
## Not run:
cat(pacs::dir_size(system.file(package = "stats")) / 10**6, "MB")
```

## End(Not run)

```
lib_validate

Validate the local library

Description

Checking if installed packages have correct versions taking into account all DESCRIPTION files requirements. Moreover identifying which packages are newest releases. Optionally we could add life duration and CRAN check page status for each package.

Usage

```
lib_validate(
  lib.loc = .libPaths(),
  fields = c("Depends", "Imports", "LinkingTo"),
  lifeduration = FALSE,
  checkred = list(scope = character(0), flavors = NULL),
  built = FALSE,
  repos = biocran_repos()
)
```

Arguments

```
lib.loc character vector of search paths with local packages. Default: .libPaths()
fields 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. Default: c("Depends", "Imports", "LinkingTo")
lifeduration logical if to assess life duration for each package in the library. For installed newest releases of packages, a local evaluation is used. MEATCRAN CRANDB is used for libraries with less than 500 packages. Otherwise the direct web page download from CRAN is used. Default: ‘FALSE’
checkred list with two named fields, scope and flavor. scope of R CRAN check pages statuses to consider, any of c("ERROR", "FAIL", "WARN", "NOTE"). flavor is a vector of CRAN machines to consider, which might be retrieved with pacs::cran_flavors()$Flavor. By default an empty scope field deactivated assessment for checkred column, and NULL flavor will results in checking all machines. Default: list(scope = character(0), flavor = NULL)
```
lib_validate

built logical if to add an R version under which each package was installed. Useful mainly for a local usage. Packages installed with a previous version of R could not work correctly with the new version of R. Default: FALSE

repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value
data.frame with 4/6/8/9/10 columns.

Package character a package name.

Version.expected.min character expected by DESCRIPTION files minimal version. "" means not specified so the newest version.

Version.have character installed package version.

version_status numeric -1/0/1 which comes from utils::compareVersion function. 0 means that we have the same version as required by DESCRIPTION files. -1 means we have too low version installed, this is an error. 1 means we have higher version.

built character package was built under this R version

built_status integer if the package was built under the current R version, then 1 (good) and for older R versions 0 (possibly bad). A package built under older R version or mix of packages built under different versions could bring possible failures.

newest logical (Internet needed) if the installed version is the newest one. For Bioconductor if is the newest one per R version.

cran logical (Internet needed) if the package is on CRAN, version is not taken into account here.

checkred (Optional) (Internet needed) logical if the NEWEST package contains any specified statuses on CRAN check page. pacs::checked_packages is used to quickly retrieve all statuses at once.

lifeduration (Optional) (Internet needed) integer number of days a package was released.

Note
Version.expected.min column not count packages which are not a dependency for any package, so could not be find in DESCRIPTION files. When turn on the lifeduration options, calculations might be time consuming for libraries bigger than 500 packages. Results are cached for 30 minutes with memoise package. BioConductor packages are tested only in available scope, checkred is not assessed for them. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/.

Examples

```
## Not run:
pacs::lib_validate()
pacs::lib_validate(checkred = list(scope = c("ERROR", "FAIL", "WARN")))
pacs::lib_validate(checkred = list(  
    scope = c("ERROR", "FAIL"),  
    flavors = pacs::match_flavors())
```
lock_validate

Validate a specific renv lock file

Description

This function will be especially useful when renv lock file is built manually. Checking if packages in the lock file have correct versions taking into account their DESCRIPTION files requirements (c("Depends", "Imports", "LinkingTo")). Moreover identifying which packages are newest releases. Optionally we could add life duration and CRAN check page status for each dependency.

Usage

lock_validate(
  path,
  lifeduration = FALSE,
  checkred = list(scope = character(0), flavors = NULL),
  lib.loc = .libPaths(),
  repos = biocran_repos()
)

Arguments

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>path</td>
<td>character path to the shiny app. Default: &quot;.&quot;</td>
</tr>
<tr>
<td>lifeduration</td>
<td>logical if to assess life duration for each package in the library. For installed newest releases of packages, a local evaluation is used. MEATCRAN CRANDB is used for libraries with less than 500 packages. Otherwise the direct web page download from CRAN is used. Default: ‘FALSE’</td>
</tr>
<tr>
<td>checkred</td>
<td>list with two named fields, scope and flavor. scope of R CRAN check pages statuses to consider, any of c(&quot;ERROR&quot;, &quot;FAIL&quot;, &quot;WARN&quot;, &quot;NOTE&quot;). flavor is a vector of CRAN machines to consider, which might be retrieved with pacs::cran_flavors()$flavor. By default an empty scope field deactivated assessment for checkred column, and NULL flavor will results in checking all machines. Default: list(scope = character(0), flavor = NULL)</td>
</tr>
<tr>
<td>lib.loc</td>
<td>character vector of search paths with local packages. Default: .libPaths()</td>
</tr>
<tr>
<td>repos</td>
<td>character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()</td>
</tr>
</tbody>
</table>
lock_validate

Value

data.frame with 2/6/7/8 columns.

Package character a package name.

Version.expected.min (conditional) (Internet needed) character expected by DESCRIPTION files minimal version. "" means not specified so the newest version.

Version.expected character package version in the renv lock file.

version_status (conditional) numeric -1/0/1 which comes from utils::compareVersion function. 0 means that we have the same version as required by DESCRIPTION files. -1 means we have too low version installed, this is an error. 1 means we have higher version.

newest logical (Internet needed) if the installed version is the newest one.

cran logical (Internet needed) if the package is on CRAN, version is not taken into account here.

checkred (Optional) (Internet needed) logical if the NEWEST package contains any specified statuses on CRAN check page.

lifeduration (Optional) (Internet needed) integer number of days a package was released.

Note

Version.expected.min column not count packages which are not a dependency for any package, so could not be find in DESCRIPTION files. Version.expected.min and version_status are assessed only if there are less than 500 packages in the lock file. When turn on the lifeduration option, calculations might be time consuming when there is more than 500 packages. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/

Examples

```r
## Not run:
# path or url
url <- "https://raw.githubusercontent.com/Polkas/pacs/master/tests/testthat/files/renv_test.lock"
pacs::lock_validate(url)

pacs::lock_validate(
  url,
  checkred = list(scope = c("ERROR", "FAIL"), flavors = pacs::match_flavors())
)

pacs::lock_validate(
  url,
  lifeduration = TRUE,
  checkred = list(scope = c("ERROR", "FAIL"), flavors = NULL)
)

## End(Not run)
```
match_flavors

Get all matched CRAN servers to the local OS

Description
CRAN servers matched to the local OS.

Usage
match_flavors()

Value
character vector matched server names.

Note
The Internet connection is needed to use the function.

Examples
## Not run:
pacs::match_flavors()
## End(Not run)

pacs_base
Get base R packages

Description
get base packages, all or only startup.

Usage
pacs_base(startup = FALSE)

Arguments
startup logical include only startup packages. Default: FALSE

Value
character vector
Examples

```r
## Not run:
pacs_base()
pacs_base(startup = TRUE)
## End(Not run)
```

`pacs_lifeduration` Packages life duration for a specific version

Description

packages life duration for certain versions.

Usage

```r
pacs_lifeduration(
  pacs,
  versions,
  source = c("crandb", "loop_crandb", "loop_cran"),
  lib.loc = .libPaths(),
  repos = biocran_repos()
)
```

Arguments

- `pacs` character vector of packages names.
- `versions` character vector of packages versions.
- `source` character one of c("crandb", "loop_crandb", "loop_cran"). The "crandb" works if less than `getOption("pacs.crandb_limit")` (currently 500) packages are looked for. Default: "crandb"
- `lib.loc` character vector of search paths with local packages. Default: `.libPaths()`
- `repos` character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default `pacs::biocran_repos()`

Value

data.frame with two columns package name and life duration.

Note

Results are cached for 30 minutes with memoise package. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/. For `source = "loop_cran"` the function will scrap two CRAN URLs. Works only with CRAN packages. Please as a courtesy to the R CRAN, don’t overload their servers by constantly using this function.
Examples

```r
## Not run:
pacs::pacs_lifeduration(c("dplyr", "tidyr"), c("1.0.0", "1.2.0"))
pacs::pacs_lifeduration(c("dplyr", "tidyr"), c("1.0.0", "1.2.0"), source = "loop_cran")
# last versions
pacs::pacs_lifeduration(c("dplyr", "tidyr"), sapply(c("dplyr", "tidyr"), pacs::pac_last))
## End(Not run)
```

---

pac_checkpage

**Retrieving the R CRAN package check page**

Description

Retrieving the R CRAN package check page.

Usage

```r
pac_checkpage(pac)
```

Arguments

- `pac`: character a package name.

Value

- data.frame.

Note

Results are cached for 30 minutes with `memoise` package. If you need to check many packages at once then is recommended usage of `pacs::checked_packages`. Please as a courtesy to the R CRAN, don’t overload their server by constantly using this function.

Examples

```r
## Not run:
pacs::pac_checkpage("dplyr")
## End(Not run)
```
pac_checkred

Checking the R CRAN package check page status

Description

using package R CRAN check page to validate if there are ANY errors and/or fails and/or warnings and/or notes.

Usage

pac_checkred(pac, scope = c("ERROR", "FAIL"), flavors = NULL)

Arguments

pac character a package name.
scope character vector scope of the check, accepted values c("ERROR", "FAIL", "WARN", "NOTE"). Default: c("ERROR", "FAIL")
flavors character vector of CRAN server names to consider, possible names could be get with pacs::cran_flavors()$flavor. The pacs::match_flavors() function could be used to get CRAN server names matched for your local OS. By default all CRAN machines are considered NULL value. Default: NULL

Value

logical if the package fail under specified criteria.

Note

Results are cached for 30 minutes with memoise package. If you need to check many packages at once then is recommended usage of pacs::checked_packages. The used repository https://cran.rstudio.com/. Please as a courtesy to the R CRAN, don’t overload their server by constantly using this function.

Examples

## Not run:
pacs::pac_checkred("dplyr")
pacs::pac_checkred("dplyr", scope = c("ERROR"))
pacs::pac_checkred("dplyr",
  scope = c("ERROR", "FAIL", "WARN"),
  flavors = pacs::match_flavors()
)

## End(Not run)
pac_compare_namespace

Compare NAMESPACE exports between specific CRAN packages versions

Description

using the remote github CRAN mirror to compare NAMESPACE exports between specific packages versions.

Usage

pac_compare_namespace(
  pac,
  old = NULL,
  new = NULL,
  lib.loc = .libPaths(),
  repos = "https://cran.rstudio.com/"
)

Arguments

pac character a package name.
old character an old version of package, default local version. Default: NULL
new character a new version of package, default newest version. Default: NULL
lib.loc character vector of search paths with local packages. Default: .libPaths()
repos character vector repositories URLs to use. Used only for the validation. Default: https://cran.rstudio.com/

Value

list with `c("imports", "exports", "exportPatterns", "importClasses", "importMethods", "exportClasses", "exportMethods", "exportClassPatterns", "dynlib", "S3methods")` slots, and added and removed ones for each of them.

Examples

```r
## Not run:
pacs::pac_compare_namespace("shiny", "1.0.0", "1.6.0")
pacs::pac_compare_namespace("shiny", "1.0.0", "1.6.0")$exports
# local version to newest one
pacs::pac_compare_namespace("shiny")
## End(Not run)
```
pac_compare_versions

Compare DESCRIPTION files dependencies between specific CRAN packages versions

Description
using the remote github CRAN mirror to compare DESCRIPTION files dependencies between specific packages versions.

Usage
pac_compare_versions(
  pac,
  old = NULL,
  new = NULL,
  fields = c("Imports", "Depends", "LinkingTo"),
  lib.loc = .libPaths(),
  repos = "https://cran.rstudio.com/")

Arguments
  pac character a package name.
  old character an old version of package, default local version. Default: NULL
  new character a new version of package, default newest version. Default: NULL
  fields 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. Default: c("Depends", "Imports", "LinkingTo")
  lib.loc character vector of search paths with local packages. Default: .libPaths()
  repos character vector repositories URLs to use. Used only for the validation. Default https://cran.rstudio.com/

Value
data.frame with 4 columns.

Package character package names.
Version.OLD character versions of dependencies required by an old package version.
Version.NEW character versions of dependencies required by a new package version.
version_status numeric -1/0/1 which comes from utils::compareVersion function. 0 means that both versions have the same requirement. -1 means that the new version remove this requirement. 1 means that the new version added a new requirement.
Examples

```r
## Not run:
pacs::pac_compare_versions("memoise", "0.2.1", "2.0.0")
pacs::pac_compare_versions("memoise", "0.2.1")
# local version to newest one
pacs::pac_compare_versions("memoise")
## End(Not run)
```

### Description

Package dependencies from DESCRIPTION files with installed or expected versions or newest released.

### Usage

```r
pac_deps(
  pac,         # character a package name.
  fields = c("Depends", "Imports", "LinkingTo"),
  lib.loc = .libPaths(),
  base = FALSE,
  local = TRUE,
  description_v = FALSE,
  attr = TRUE,
  recursive = TRUE,
  repos = biocran_repos()
)
```

### Arguments

- `pac` 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. Default: c("Depends", "Imports", "LinkingTo")

- `fields` character vector of search paths with local packages. Default: .libPaths()

- `base` logical if to add base packages too. If TRUE then pacs::pacs_base() are taken into account. Default: FALSE

- `local` logical if to use local repository (or newest remote packages). Default: TRUE

- `description_v` logical if the dependencies version should be taken from description files, minimal required. By default installed versions are taken. Default: FALSE
attr logical if a package and its version should be added as an attribute of data.frame or for FALSE as an additional record. Default: TRUE
recursive logical if to assess the dependencies recursively. Default: TRUE
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default `pacs::biocran_repos()`

Value
data.frame with packages and their versions. Versions are taken from `installed.packages` or newest released.

Note
When function is invoked in the loop afterwards results could be aggregated like, `stats::aggregate(results[, c("Version"), drop = FALSE], list(Package = results$Package), pacs::compareVersionsMax)`.

Examples

```r
## Not run:
pacs::pac_deps("stats", base = TRUE)$Package
pacs::pac_deps("memoise")$Package
pacs::pac_deps("memoise", description_v = FALSE)
# raw dependencies from DESCRIPTION file
pacs::pac_deps("memoise", description_v = TRUE, recursive = FALSE)
# raw dependencies from DESCRIPTION file - last release
pacs::pac_deps("memoise", description_v = TRUE, local = FALSE, recursive = FALSE)
```

## End(Not run)

### pac_deps_dev

**Package dependencies - developer perspective**

Description
A higher-level function, build from `pacs::pacs_deps`. Package dependencies installed when e.g. R CMD check a package. "Depends", "Imports", "LinkingTo", "Suggests" fields from the DESCRIPTION file and their recursive dependencies taken from "Depends", "Imports", "LinkingTo" fields. Dependencies are taken remotely for the newest version.

Usage

```r
pac_deps_dev(
  pac,
  base = FALSE,
  local = FALSE,
  attr = TRUE,
  repos = pacs::biocran_repos()
)
```
pac_deps_heavy

Arguments

pac character a package name.

base logical if to add base packages too. If TRUE then pacs::pacs_base() are taken into account. Default: FALSE

local logical if to use local repository (or newest remote packages). Default: FALSE

attr logical if a package and its version should be added as an attribute of data.frame or for FALSE as an additional record. Default: TRUE

repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value

data.frame with packages and their versions. Versions are taken from installed.packages or newest released.

Examples

## Not run:
pacs::pac_deps_dev("dplyr")
pacs::pac_deps_dev("pacs")
# with the main package in the list
pacs::pac_deps_dev("pacs", attr = FALSE)

## End(Not run)

---

pac_deps_heavy Package direct dependencies and number of dependencies for each of them

Description

A higher-level function, build from pacs::pacs_deps and tools::package_dependencies. A tool to identify a main sources of dependencies, which direct dependencies are the heaviest one.

Usage

pac_deps_heavy(
pac,
fields = c("Depends", "Imports", "LinkingTo"),
lib.loc = .libPaths(),
base = FALSE,
local = FALSE,
repos = pacs::biocran_repos()
)
Arguments

pac character a package name.
fields 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. Default: c("Depends", "Imports", "LinkingTo")
lib.loc character vector of search paths with local packages. Default: .libPaths()
base logical if to add base packages too. If TRUE then pacs::pacs_base() are taken into account. Default: FALSE
local logical if to use local repository (or newest remote packages). Default: FALSE
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value
data.frame with three columns c("Package", "NrDeps", "NrUniqueDeps"): package name, number of dependencies and number of unique dependencies (not shared by other direct dependencies).

Note
Please take into account that the sum of the dependencies is not equal to the number of dependencies of the main package, because some dependencies are overlapping.

Examples

```r
## Not run:
pacs::pac_deps_heavy("caret")
pacs::pac_deps_heavy("dplyr")
## End(Not run)
```

Description

Package dependencies from DESCRIPTION files retrieved recursively for certain version or time point.
Usage

pac_deps_timemachine(
  pac,
  version = NULL,
  at = NULL,
  fields = c("Depends", "Imports", "LinkingTo"),
  recursive = TRUE
)

Arguments

pac character a package name.
version character version of a package. Default: NULL
at Date from which to take the version. Default: NULL
fields 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. Default: c("Depends", "Imports", "LinkingTo")
recursive logical if to assess the dependencies recursively. Default: TRUE

Value
	named vector package dependencies and their versions at the release date of main package plus one day.

Note

Longer lived version is taken if 2 is available at the same date (switch time).

Examples

## Not run:
pacs::pac_deps_timemachine("memoise", "0.2.1")
pacs::pac_deps_timemachine("memoise", at = as.Date("2019-01-01"))
pacs::pac_deps_timemachine("dplyr", at = as.Date("2015-01-01"))

## End(Not run)

Description

A higher-level function, build from pacs::pacs_deps. Package dependencies installed when run installed.packages. "Depends", "Imports", "LinkingTo" fields from the DESCRIPTION file and their recursive dependencies taken from the same fields. Dependencies are taken remotely for the newest version.
Usage

```r
pac_deps_user(
  pac,
  base = FALSE,
  local = FALSE,
  attr = TRUE,
  repos = pacs::biocran_repos()
)
```

Arguments

- **pac**: character a package name.
- **base**: logical if to add base packages too. If TRUE then `pacs::pacs_base()` are taken into account. Default: FALSE
- **local**: logical if to use local repository (or newest remote packages). Default: FALSE
- **attr**: logical if a package and its version should be added as an attribute of data.frame or for FALSE as an additional record. Default: TRUE
- **repos**: character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default `pacs::biocran_repos()`

Value

data.frame with packages and their versions. Versions are taken from `installed.packages` or newest released.

Examples

```r
## Not run:
pacs::pac_deps_user("dplyr")
pacs::pac_deps_user("pacs")
# with the main package in the list
pacs::pac_deps_user("pacs", attr = FALSE)
## End(Not run)
```

---

pac_description

---

Description

CRAN package DESCRIPTION file taken locally or remotely from GITHUB CRAN mirror or CRAN website. By default works for the newest package version.
pac_health

Usage

pac_description(
  pac,
  version = NULL,
  at = NULL,
  local = FALSE,
  lib.loc = .libPaths(),
  repos = "https://cran.rstudio.com/")

Arguments

  pac character a package name.
  version character version of a package. Default: NULL
  at Date from which to take the version. Default: NULL
  local logical if to use local repository (or newest remote packages). Default: FALSE
  lib.loc character vector of search paths with local packages. Default: .libPaths()
  repos character vector repositories URLs to use. Used only for the validation. Default: https://cran.rstudio.com/

Value

  list with names proper for DESCRIPTION file fields.

Note

  Results are cached for 30 minutes with memoise package.

Examples

  ## Not run:
  pacs::pac_description("dplyr", version = "0.8.0")
  pacs::pac_description("dplyr", at = as.Date("2019-02-01"))

  ## End(Not run)

---

pac_health  

CRAN package health state at a specific Date or for a specific version

Description

  a package health for a certain version or at a specific Date. By default works for the newest package version. A healthy package was published for more than x days, where default is 14 days. CRAN team gives around one/two week to resolved a package which gave errors under the check page. The newest release is checked for any warnings/errors on the R CRAN package check page.
pac_health

Usage

pac_health(
  pac,  
  version = NULL,  
  at = NULL,  
  limit = 14,  
  scope = c("ERROR", "FAIL"),  
  flavors = NULL,  
  lib.loc = .libPaths(),  
  repos = "https://cran.rstudio.com/",  
  source = c("crandb", "cran")
)

Arguments

pac character a package name.
version character version of a package. Default: NULL
at Date from which to take the version. Default: NULL
limit numeric at least days to treat as healthy, ">=limit". Default: 14
scope character vector scope of the check, accepted values c("ERROR", "FAIL", 
"WARN", "NOTE"). Default: c("ERROR", "FAIL")
flavors character vector of CRAN server names to consider, possible names could 
be get with pacs::cran_flavors()$Flavor. The pacs::match_flavors() 
function could be used to get CRAN server names matched for your local OS. 
By default all CRAN machines are considered NULL value. Default: NULL
lib.loc character vector of search paths with local packages. Default: .libPaths()
repos character vector repositories URLs to use. Default: https://cran.rstudio.com/
source character one of c("crandb", "cran"). Using the METACRAN CRANDB or the 
direct web page download from CRAN. Default: "crandb"

Value

 logical if a package is healthy.

Note

Results are cached for 30 minutes with memoise package. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch. https://r-hub.github.io/pkgsearch/. For source = "cran" the function will scrap two CRAN URLS. Works only with CRAN packages. Please as a courtesy to the R CRAN, don’t overload their servers by constantly using this function.

Examples

## Not run:
pacs::pac_health("memoise")
pacs::pac_health("dplyr", version = "0.8.0", limit = 14)
pac_isin

Checking if a package is in repositories

Description

using utils::available.packages to check if package is in repositories.

Usage

pac_isin(pac, repos = biocran_repos())

Arguments

pac character a package name.
repos character vector base URLs of the repositories to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value

logical if a package is inside repositories.

Note

Results are cached for 30 minutes with memoise package.

Examples

## Not run:
pac_isin("dplyr")
pac_isin("dplyr", repos = "https://cran.rstudio.com/")
pac_isin("dplyr", repos = biocran_repos()[grep("Bio", names(biocran_repos()))])

## End(Not run)
pac_islast  

Checking if a package version is the most recent one

Description

checking if a package version is the most recent one, by default the installed version is compared.

Usage

pac_islast(pac, version = NULL, lib.loc = .libPaths(), repos = biocran_repos())

Arguments

pac character a package name.
version character version of a package. Default: NULL
lib.loc character vector of search paths with local packages. Default: .libPaths()
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pac::biocran_repos()

Value

logical if a package is inside repositories.

Note

Results are cached for 30 minutes with memoise package.

Examples

## Not run:
pac_islast("memoise")
pac_islast("dplyr", version = "1.0.0")
pac_islast("S4Vectors")
pac_islast("S4Vectors", version = pac_last("S4Vectors"))

## End(Not run)
pac_last

Getting the most recent package version

Description

using utils::available.packages to get the newest package version.

Usage

pac_last(pac, repos = biocran_repos())

Arguments

pac character a package name.
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value

character most recent package version.

Note

Results are cached for 30 minutes with memoise package. For Bioconductor the newest one per R version.

Examples

## Not run:
pac_last("dplyr")
pac_last("S4Vectors")

## End(Not run)

pac_lifeduration

Package version life duration at specific Date or for a specific version

Description

a package life duration for a certain version or at a specific Date. By default works for the newest package version.
Usage

pac_lifeduration(
  pac,
  version = NULL,
  at = NULL,
  lib.loc = .libPaths(),
  repos = biocran_repos(),
  source = c("crandb", "cran")
)

Arguments

pac character a package name.
version character version of a package. Default: NULL
at Date from which to take the version. Default: NULL
lib.loc character vector of search paths with local packages. Default: .libPaths()
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pac::biocran_repos()
source character one of c("crandb", "cran"). Using the METACRAN CRANDB or the direct web page download from CRAN. Default: "crandb"

Value
difftime, number of days package version was the newest one.

Note

Results are cached for 30 minutes with memoise package. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/. For source = "cran" the function will scrap two CRAN URLs. Works only with CRAN packages. Please as a courtesy to the R CRAN, don’t overload their servers by constantly using this function.

Examples

## Not run:
pacs::pac_lifeduration("memoise")
pacs::pac_lifeduration("memoise", source = "cran")
pacs::pac_lifeduration("dplyr", version = "0.8.0")
pacs::pac_lifeduration("dplyr", at = as.Date("2019-02-14"))
# For Bioconductor packages it will work only for the newest per R version and installed ones.
pacs::pac_lifeduration("S4Vectors")

## End(Not run)
Description

CRAN package NAMESPACE file taken locally or remotely from GITHUB CRAN mirror or CRAN website. By default works for the newest package version.

Usage

pac_namespace(
  pac, version = NULL, at = NULL, local = FALSE,
  lib.loc = .libPaths(), repos = "https://cran.rstudio.com/"
)

Arguments

pac character a package name.
version character version of a package. Default: NULL
at Date from which to take the version. Default: NULL
local logical if to use local repository (or newest remote packages). Default: FALSE
lib.loc character vector of search paths with local packages. Default: .libPaths()
repos character vector repositories URLs to use. Used only for the validation. Default: https://cran.rstudio.com/

Value

list with names proper for NAMESPACE file, the same as format as returned by base::parseNamespaceFile.

Note

Results are cached for 30 minutes with memoise package. This function is mainly built under source code from base::parseNamespaceFile.

Examples

```r
## Not run:
pacs::pac_namespace("dplyr", version = "0.8.0")
pacs::pac_namespace("dplyr", at = as.Date("2019-02-01"))
pacs::pac_namespace("memoise", local = TRUE)

## End(Not run)
```
pac_size

Size of the package

Description

Size of package.

Usage

pac_size(pac, lib.loc = .libPaths())

Arguments

pac character a package name.
lib.loc character vector of search paths with local packages. Default: .libPaths()

Value

numeric size in bytes, to get MB ten divide by 10**6.

Examples

## Not run:
cat(pacs::pac_size("stats") / 10**6, "MB")

## End(Not run)

pac_timemachine

Package metadata for all releases

Description

Using CRAN website to get a package metadata used at a specific Date or a Date interval or for specific version.

Usage

pac_timemachine(
  pac,
  at = NULL,
  from = NULL,
  to = NULL,
  version = NULL,
  source = c("crandb", "cran")
)


Arguments

pac  character a package name.
at  Date from which to take the version. Default: NULL
from  Date the lower limit. Default: NULL
to  Date the upper limit. Default: NULL
version  character version of a package. Default: NULL
source  character one of c("crandb", "cran"). Using the METACRAN CRANDB or the direct web page download from CRAN. Default: "crandb"

Value
data.frame with 7 columns

Package  character package name.
Version  character package version.
Released  character release Date
Archived  character archived Date.
LifeDuration  difftime number of days the version was the newest one.
URL  character the suffix of the base URL to tar.gz file. The base part of URL in the result is https://cran.r-project.org/src/contrib/.
Size  character size of the tar.gz file.

Note
Results are cached for 30 minutes with memoise package. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/. For source = "cran" the function will scrap two CRAN URLs. Works only with CRAN packages. Please as a courtesy to the R CRAN, don’t overload their servers by constantly using this function.

Examples

```r
## Not run:
pacs::pac_timemachine("dplyr")
pacs::pac_timemachine("dplyr", at = as.Date("2017-02-02"))
pacs::pac_timemachine("dplyr", from = as.Date("2017-02-02"), to = as.Date("2018-04-02"))
pacs::pac_timemachine("dplyr", at = Sys.Date())
pacs::pac_timemachine("tidyr", from = as.Date("2020-06-01"), to = Sys.Date())
## End(Not run)
```
pac_true_size  True size of the package

Description

True size of the package as it takes into account its all dependencies, recursively.

Usage

pac_true_size(
  pac,
  fields = c("Depends", "Imports", "LinkingTo"),
  lib.loc = .libPaths(),
  exclude_joint = 0L
)

Arguments

pac character a package name.
fields 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. Default: c("Depends", "Imports", "LinkingTo")
lib.loc character vector of search paths with local packages. Default: .libPaths()
exclude_joint integer exclude packages which are dependencies of at least N other packages, not count main package dependencies. Default: 0

Value

numeric size in bytes, to get MB then divide by 10**6.

Note

R base packages are not counted. The default value of fields should be suited for almost all scenarios.

Examples

## Not run:
# size in MB, with all its dependencies
pacs::pac_true_size("memoise") / 10**6

## End(Not run)
pac_validate

Validate a specific local package

Description
Checking if installed package dependencies have correct versions taking into account their DESCRIPTION files requirements. Moreover identifying which packages are newest releases. Optionally we could add life duration and CRAN check page status for each dependency.

Usage
pac_validate(
  pac,
  lib.loc = .libPaths(),
  fields = c("Depends", "Imports", "LinkingTo"),
  lifeduration = FALSE,
  checkred = list(scope = character(0), flavors = NULL),
  repos = biocran_repos()
)

Arguments
pac character a package name.
lib.loc character vector of search paths with local packages. Default: .libPaths()
fields 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. Default: c("Depends", "Imports", "LinkingTo")
lifeduration logical if to assess life duration for each package in the library. For installed newest releases of packages, a local evaluation is used. MEATCRAN CRANDB is used for libraries with less than 500 packages. Otherwise the direct web page download from CRAN is used. Default: 'FALSE'
checkred list with two named fields, scope and flavor. scope of R CRAN check pages statuses to consider, any of c("ERROR", "FAIL", "WARN", "NOTE"). flavor is a vector of CRAN machines to consider, which might be retrieved with pacs::cran_flavors()$Flavor. By default an empty scope field deactivated assessment for checkred column, and NULL flavor will results in checking all machines. Default: list(scope = character(0), flavor = NULL)
repos character vector of repositories URLs to use. By default checking CRAN and newest Bioconductor per R version. Default pacs::biocran_repos()

Value
data.frame with 5/7/8/9 columns.
Package character a package name.

Version.expected.min character expected by DESCRIPTION files minimal version. "" means not specified so the newest version.

Version.have character installed package version.

version_status numeric -1/0/1 which comes from utils::compareVersion function. 0 means that we have the same version as required by DESCRIPTION files. -1 means we have too low version installed, this is an error. 1 means we have higher version.

direct logical if the package is in the first dependency layer, direct dependencies from DESCRIPTION file.

newest logical (Internet needed) if the installed version is the newest one.

cran logical (Internet needed) if the package is on CRAN, version is not taken into account here.

checkred (Optional) (Internet needed) logical if the NEWEST package contains any specified statuses on CRAN check page.

lifeduration (Optional) (Internet needed) integer number of days a package was released.

Note

Version.expected.min column not count packages which are not a dependency for any package, so could not be find in DESCRIPTION files. When turn on the lifeduration option, calculations might be time consuming when there is more than 500 packages. Please as a courtesy to the R CRAN, don’t overload their server by constantly using this function with lifeduration or checkred turned on. Results are cached with memoise package, memory cache. The crandb R packages database is a part of METACRAN project, source: Csárdi G, Salmon M (2022). pkgsearch: Search and Query CRAN R Packages. https://github.com/r-hub/pkgsearch, https://r-hub.github.io/pkgsearch/.

Examples

## Not run:
pacs::pac_validate("memoise")
pacs::pac_validate(
  "memoise",
  lifeduration = TRUE,
  checkred = list(scope = c("ERROR", "FAIL"), flavors = NULL)
)
pacs::pac_validate(  
  "memoise",
  lifeduration = TRUE,
  checkred = list(scope = c("ERROR", "FAIL"), flavors = pacs::match_flavors())
)

## End(Not run)
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