

Package ‘BiocManager’

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Title Access the Bioconductor Project Package Repository

Description A convenient tool to install and update Bioconductor packages.

Version 1.30.9

Imports utils

Suggests BiocStyle, BiocVersion, remotes, testthat, withr, curl, knitr

BugReports <https://github.com/Bioconductor/BiocManager/issues>

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available *Discover packages available for installation.*

Description

Discover packages available for installation.

Usage

```
available(pattern = "", include_installed = TRUE)
```

Arguments

pattern character(1) pattern to filter (via `grep(pattern=...)`) available packages; the filter is not case sensitive.

include_installed logical(1) When TRUE, include installed packages in list of available packages; when FALSE, exclude installed packages.

Value

character() vector of package names available for installation.

Examples

```
avail <- BiocManager::available()
length(avail)

BiocManager::available("bs.*hsapiens")
```

BiocManager-pkg *Install or update Bioconductor, CRAN, or GitHub packages*

Description

This package provides tools for managing *Bioconductor* and other packages in a manner consistent with *Bioconductor*'s package versioning and release system.

Details

Main functions are as follows; additional help is available for each function, e.g., `?BiocManager::version`.

`BiocManager::install()` Install or update packages from *Bioconductor*, CRAN, and GitHub.

`BiocManager::version()` Report the version of *Bioconductor* in use.

`BiocManager::available()` Return a character() vector of package names available (at `BiocManager::repositories()` for installation.

`BiocManager::valid()` Determine whether installed packages are from the same version of *Bioconductor*.

`BiocManager::repositories()` *Bioconductor* and other repository URLs to discover packages for installation.

The version of `_Bioconductor_` in use is determined by the installed version of a second package, `BiocVersion`. `BiocVersion` is installed automatically during first use of ``BiocManager::install()``. If `BiocVersion` has not yet been installed, the version is determined by code in base R.

Author(s)

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See Also

Useful links:

- Report bugs at <https://github.com/Bioconductor/BiocManager/issues>

Examples

```
R.version.string
packageVersion("BiocManager")
if ("BiocVersion" %in% rownames(installed.packages()))
  packageVersion("BiocVersion")
BiocManager::version()
```

install

*Install or update Bioconductor, CRAN, and GitHub packages***Description**

The `BiocManager::install()` function installs or updates *Bioconductor* and CRAN packages in a *Bioconductor* release. Upgrading to a new *Bioconductor* release may require additional steps; see <https://bioconductor.org/install>.

Usage

```
install(pkgs = character(), ..., site_repository = character(),
        update = TRUE, ask = TRUE, checkBuilt = FALSE,
        version = BiocManager::version())
```

Arguments

<code>pkgs</code>	<code>character()</code> vector of package names to install or update. A missing value updates installed packages according to <code>update =</code> and <code>ask =</code> . Package names containing a <code>'/</code> are treated as GitHub repositories and installed using <code>remotes::install_github()</code> .
<code>...</code>	Additional arguments used by <code>install.packages()</code> .
<code>site_repository</code>	(Optional) <code>character(1)</code> vector representing an additional repository in which to look for packages to install. This repository will be prepended to the default repositories (which you can see with <code>BiocManager::repositories()</code>).
<code>update</code>	<code>logical(1)</code> . When <code>FALSE</code> , <code>BiocManager::install()</code> does not attempt to update old packages. When <code>TRUE</code> , update old packages according to <code>ask</code> .
<code>ask</code>	<code>logical(1)</code> indicating whether to prompt user before installed packages are updated. If <code>TRUE</code> , user can choose whether to update all outdated packages without further prompting, to pick packages to update, or to cancel updating (in a non-interactive session, no packages will be updated unless <code>ask = FALSE</code>).
<code>checkBuilt</code>	<code>logical(1)</code> . If <code>TRUE</code> a package built under an earlier major.minor version of R (e.g., 3.4) is considered to be old.
<code>version</code>	<code>character(1)</code> <i>Bioconductor</i> version to install, e.g., <code>version = "3.8"</code> . The special symbol <code>version = "devel"</code> installs the current 'development' version.

Details

Installation of *Bioconductor* and CRAN packages use R's standard functions for library management – `install.packages()`, `available.packages()`, `update.packages()`. Installation of GitHub packages uses the `remotes::install_github()`.

When installing CRAN or *Bioconductor* packages, typical arguments include: `lib.loc`, passed to `old.packages()` and used to determine the library location of installed packages to be updated; and `lib`, passed to `install.packages()` to determine the library location where `pkgs` are to be installed.

When installing GitHub packages, `...` is passed to the **remotes** package functions `install_github()` and `remotes::install()`. A typical use is to build vignettes, via `dependencies=TRUE, build_vignettes=TRUE`. `BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS` is an environment variable or `global options()` which, when set to `FALSE`, avoids the R and *Bioconductor* version checks that are done by querying an on-line configuration file. Setting `BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS` to `FALSE` can speed package loading when internet access is slow or non-existent, but may result in out-of-date information about the current release and development versions of *Bioconductor*.

Value

`BiocManager::install()` returns the `pkgs` argument, invisibly.

See Also

`BiocManager::repositories()` returns the *Bioconductor* and CRAN repositories used by `install()`.
[install.packages\(\)](#) installs the packages themselves (used by `BiocManager::install` internally).
[update.packages\(\)](#) updates all installed packages (used by `BiocManager::install` internally).
[chooseBioCmirror\(\)](#) allows choice of a mirror from all public *Bioconductor* mirrors.
[chooseCRANmirror\(\)](#) allows choice of a mirror from all public CRAN mirrors.

Examples

```
## Not run:
## update previously installed packages
BiocManager::install()

## install Bioconductor packages, and prompt to update all
## installed packages
BiocManager::install(c("GenomicRanges", "edgeR"))

## install a CRAN and Bioconductor packages:
BiocManager::install(c("survival", "SummarizedExperiment"))

## install a package from source:
BiocManager::install("IRanges", type="source")

## End(Not run)
```

repositories

Display current Bioconductor and CRAN repositories.

Description

`repositories()` reports the URLs from which to install *Bioconductor* and CRAN packages. It is used by `BiocManager::install()` and other functions.

Usage

```
repositories(site_repository = character(),  
            version = BiocManager::version())
```

Arguments

`site_repository` (Optional) character(1) representing an additional repository (e.g., a URL to an organization's internally maintained repository) in which to look for packages to install. This repository will be prepended to the default repositories returned by the function.

`version` (Optional) character(1) or `package_version` indicating the *Bioconductor* version (e.g., "3.8") for which repositories are required.

Value

Named character() of repositories.

See Also

`BiocManager::install()` Installs or updates Bioconductor, CRAN, and GitHub packages.
`chooseBioCmirror()` choose an alternative Bioconductor mirror; not usually necessary.
`chooseCRANmirror()` choose an alternative CRAN mirror; not usually necessary.
`setRepositories()` Select additional repositories for searching.

Examples

```
BiocManager::repositories()  
## Not run:  
BiocManager::repositories(version="3.8")  
  
## End(Not run)
```

valid

Validate installed package versions against correct versions.

Description

Check that installed packages are consistent (neither out-of-date nor too new) with the version of R and *Bioconductor* in use.

Usage

```
valid(pkgs = installed.packages(lib.loc, priority = priority),
      lib.loc = NULL, priority = "NA", type = getOption("pkgType"),
      filters = NULL, ..., checkBuilt = FALSE,
      site_repository = character())

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

Arguments

pkgs	A character() vector of package names for checking, or a matrix as returned by installed.packages .
lib.loc	A character() vector of library location(s) of packages to be validated; see installed.packages() .
priority	character(1) Check validity of all, "base", or "recommended" packages; see installed.packages() .
type	character(1) The type of available package (e.g., binary, source) to check validity against; see available.packages() .
filters	character(1) Filter available packages to check validity against; see available.packages() .
...	Additional arguments, passed to <code>BiocManager::install()</code> when <code>fix=TRUE</code> .
checkBuilt	logical(1). If TRUE a package built under an earlier major.minor version of R (e.g., 3.4) is considered to be old.
site_repository	character(1). See <code>?install</code> .
x	A 'biocValid' object returned by 'BiocManager::valid()'.

Details

This function compares the version of installed packages to the version of packages associated with the version of *R* and *Bioconductor* currently in use.

Packages are reported as 'out-of-date' if a more recent version is available at the repositories specified by ``BiocManager::repositories()``. Usually, ``BiocManager::install()`` is sufficient to update packages to their most recent version.

Packages are reported as 'too new' if the installed version is more recent than the most recent available in the ``BiocManager::repositories()``. It is possible to down-grade by re-installing a too new package "PkgA" with ``BiocManger::install("PkgA")``. It is important for the user to understand how their installation became too new, and to avoid this in the future.

Value

biocValid list object with elements `too_new` and `out_of_date` containing `data.frames` with packages and their installed locations that are too new or out-of-date for the current version of *Bioconductor*.

'`print()`' is invoked for its side effect.

Author(s)

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See Also

`BiocManager::install()` to update installed packages.

Examples

```
BiocManager::valid()
```

version

Version of Bioconductor currently in use.

Description

`version()` reports the version of *Bioconductor* appropriate for this version of R, or the version of *Bioconductor* requested by the user.

Usage

```
version()
```

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

Arguments

`x` An `unknown_version` instance used to represent the situation when the version of *Bioconductor* in use cannot be determined.

`...` Additional arguments, ignored.

Details

`version()` (and all functions requiring version information) fails when version cannot be validated e.g., because internet access is not available.

Value

A two-digit version, e.g., 3.8, of class `package_version` describing the version of *Bioconductor* in use.

version

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Examples

```
BiocManager::version()
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