

Package ‘BiocManager’

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Title Access the Bioconductor Project Package Repository

Description A convenient tool to install and update Bioconductor packages.

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Depends R (>= 3.5.0)

Imports utils

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

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.

Author(s)

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See Also

Useful links:

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

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, version = BiocManager::version())
```

Arguments

pkgs	character() 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> .
...	Additional arguments used by <code>install.packages()</code> .
site_repository	(Optional) character(1) 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>).
update	logical(1). When FALSE, <code>BiocManager::install()</code> does not attempt to update old packages. When TRUE, update old packages according to <code>ask</code> .
ask	logical(1) indicating whether to prompt user before installed packages are updated. If TRUE, 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>).
version	character(1) <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, ..., site_repository = character())

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

Arguments

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

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 'unknown_version'  
print(x, ...)
```

Arguments

x	An <code>unknown_version</code> 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.

Examples

```
BiocManager::version()
```


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