Package ‘BiocManager’

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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

```r
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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Authors:

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See Also

Useful links:

- Report bugs at [https://github.com/Bioconductor/BiocManager/issues](https://github.com/Bioconductor/BiocManager/issues)

Examples

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

pkgs character() vector of package names to install or update. A missing value updates installed packages according to update = and ask =. Package names containing a '/' are treated as GitHub repositories and installed using remotes::install_github().

... Additional arguments used by install.packages().

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 BiocManager::repositories()).

update logical(1). When FALSE, BiocManager::install() does not attempt to update old packages. When TRUE, update old packages according to ask.

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 ask = FALSE).

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.

version character(1) Bioconductor version to install, e.g., version = "3.8". The special symbol version = "devel" 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 online 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

```r
## 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")
```

---

`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 BiocManager::install() when fix=TRUE.
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 ?install.
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
'BiocManager::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()

<table>
<thead>
<tr>
<th>version</th>
<th>Version of Bioconductor currently in use.</th>
</tr>
</thead>
</table>

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

Examples

BiocManager::version()
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