Package ‘BiocManager’

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available  

**Description**

The function lists all packages available from `repositories()` when no pattern is provided. This usually includes CRAN and Bioconductor packages. The function can also be used to check for package name availability. Common use cases include annotation package lookups by organism short name (e.g., "hsapiens").

**Usage**

```r
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
if (interactive()) {
  avail <- BiocManager::available()
  length(avail)

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

---

**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.

Options influencing package behavior (see ?options, ?getOption) include:

- "repos", "BiocManager.check_repositories": URLs of additional repositories for use by `BiocManager::install()`. See ?repositories.
- "pkgType": The default type of packages to be downloaded and installed; see ?install.packages.
- "timeout": The maximum time allowed for download of a single package, in seconds. BiocManager increases this to 300 seconds to accommodate download of large BSgenome and other packages.

System environment variables influencing package behavior include:

- BIOCONDUCTOR_ONLINE VERSION_DIAGNOSIS advanced configuration to avoid Bioconductor version checks. See ?install.
- BIOCONDUCTOR_CONFIG_FILE for offline use of BiocManager versioning functionality. See ?install.
- BIOCONDUCTOR_USE_CONTAINER_REPOSITORY opt out of binary package installations. See ?containerRepository.
- BIOCMANAGER_CHECK_REPOSITORIES silence messages regarding non-standard CRAN or Bioconductor repositories. See ?repositories.
- BIOCMANAGER_SITE_REPOSITORY configure a more permanent site_repositories input to `repositories()`. See ?repositories.

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install

See Also

Useful links:

- https://bioconductor.github.io/BiocManager/
- Report bugs at https://github.com/Bioconductor/BiocManager/issues

Examples

```r
R.version.string
packageVersion("BiocManager")
if (requireNamespace("BiocVersion", quietly = TRUE))
  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

```r
install(
  pkgs = character(),
  ..., 
  site_repository = character(),
  update = TRUE,
  ask = TRUE,
  checkBuilt = FALSE,
  force = 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()`).
install

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.

force logical(1). If TRUE re-download a package that is currently up-to-date.

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`.

See `repositories` for additional detail on customizing where BiocManager searches for package installation.

`BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS` is an environment variable or global options() which, when set to FALSE, allows organizations and its users to use offline repositories with BiocManager while enforcing appropriate version checks between `Bioconductor` and R. 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 regarding the current release and development versions of `Bioconductor`. In addition, offline organizations and its users should set the `BIOCONDUCTOR_CONFIG_FILE` environment variable or option to a .yaml file similar to https://bioconductor.org/config.yaml for full offline use and version validation.

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")
```

## 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.

`containerRepository()` reports the location of the repository of binary packages for fast installation within containerized versions of Bioconductor, if available.

**Usage**

```r
repositories(
  site_repository = character(),
  version = BiocManager::version(),
  ..., 
  type = "both"
)
```

```r
containerRepository(version = BiocManager::version(), type = "binary")
```

**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.
repositories

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

... Additional parameters passed to lower level functions, not used.

type (Optional) character(1) indicating the type of package repository to retrieve (default: "both"). Setting type to "source" will disable any Bioconductor binary packages specifically built for the containers.

Details

repositories() returns the appropriate software package repositories for your version of Bioconductor.

Bioconductor has a 'release' and a 'devel' semi-annual release cycle. Packages within a release have been tested against each other and the current version of packages on CRAN. Bioconductor best practice is to use packages from the same release, and from the appropriate CRAN repository.

To install binary packages on containerized versions of Bioconductor, a default binary package location URL is set as a package constant, see BiocManager:::BINARY_BASE_URL. Binary package installations are enabled by default for Bioconductor Docker containers. Anyone wishing to opt out of the binary package installation can set either the variable or the option, BIOCONDUCTOR_USE_CONTAINER_REPOSITORY, to FALSE. Note that the availability of Bioconductor package binaries is experimental and binary installations are intended to be used with bioconductor/bioconductor_docker images where such installations correspond to specific versions of Linux / Ubuntu.

If alternative default repositories are known to provide appropriate versions of CRAN or Bioconductor packages, the message may be silenced by setting either the option or the variable to FALSE, i.e., options(BiocManager.check_repositories = FALSE) or BIOCMANAGER_CHECK_REPOSITORIES=FALSE. Alternative default repositories are not guaranteed to work without issues related to incompatible package installations and are used at the user's own risk.

The intended use of site_repository = is to enable installation of packages not available in the default repositories, e.g., packages internal to an organization and not yet publicly available. A secondary use might provide alternative versions (e.g., compiled binaries) of packages available in the default repositories. Note that R's standard rules of package selection apply, so the most recent version of candidate packages is selected independent of the location of the repository in the vector returned by repositories(). To set a more permanent site repository, one can use either the BIOCMANAGER_SITE_REPOSITORY environment variable or the options(BiocManager.site_repository = ...) option.

For greater flexibility in installing packages while still adhering as much as possible to Bioconductor best practices, use repositories() as a basis for constructing the repos = argument to install.packages() and related functions.

The unexported URL to the base repository is available with BiocManager:::BINARY_BASE_URL. BIOCONDUCTOR_USE_CONTAINER_REPOSITORY is an environment variable or global options() which, when set to FALSE, avoids the fast installation of binary packages within containerized versions of Bioconductor.

Value

repositories(): named character() of repositories.

containerRepository(): character(1) location of binary repository, if available, or character(0) if not.
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)

containerRepository() # character(0) if not within a Bioconductor container

---

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().
valid

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.

sITERepository 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. When internet access is unavailable, an empty `biocValid` list is returned. If all packages ("pkgs") are up to date, then TRUE is returned.

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

Author(s)

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See Also

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

Examples

```r
if (interactive()) {
  BiocManager::valid()
}
```
Description

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

Usage

```r
version()
```

```r
## 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.

Examples

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