Package ‘BiocManager’

May 4, 2024

Title Access the Bioconductor Project Package Repository

Description A convenient tool to install and update Bioconductor packages.

Version 1.30.23

Imports utils

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

URL https://bioconductor.github.io/BiocManager/

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

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

RoxygenNote 7.3.1

NeedsCompilation no

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Repository CRAN

Date/Publication 2024-05-04 06:20:02 UTC

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BiocManager-package  

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.

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_repository input to repositories(). See ?repositories.
**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")
}
```

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](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()`).
- **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`).
install

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

## 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

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

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.

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**

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

c-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**

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

```r
## 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.

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)

Martin Morgan <martin.morgan@roswellpark.org>

See Also

BiocManager::install() to update installed packages.

Examples

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

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.

Examples

BiocManager::version()
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