

Package: BiocArchive (via r-universe)

August 22, 2024

Title Access the Bioconductor archives and install packages from previous releases

Version 1.0.1

Description Install older versions of Bioconductor based on the R version currently installed in the system. The package relies on BiocManager to install packages but makes sure that CRAN package versions are downloaded from P3M snapshots. These snapshots will coincide with the last published built date of the requested Bioconductor version.

Imports BiocManager, methods, memoise, RCurl, rvest, utils, xml2, yaml

Suggests BiocStyle, knitr, lubridate, rmarkdown, tinytest

VignetteBuilder knitr

License Artistic-2.0

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.1

Date 2024-05-23

Repository <https://link-ny.r-universe.dev>

RemoteUrl <https://github.com/Bioconductor/BiocArchive>

RemoteRef HEAD

RemoteSha f8d8b0117717a64d6c816a248a6602e0319f62fc

Contents

checkBioCmirror	2
CRANinstall	3
install	4
lastBuilt	5
repositories	6
valid	7

Index	9
--------------	----------

checkBioCmirror	<i>Check whether a Bioconductor mirror is configured</i>
-----------------	--

Description

The function checks the PACKAGES file with `RCurl::url.exists`.

Usage

```
checkBioCmirror(
  mirror = getOption("BioC_mirror"),
  version = BiocManager::version(),
  repoType = c("BioCsoft", "BioCann", "BioCexp", "BioCworkflows", "BioCbooks"),
  type = getOption("pkgType")
)
```

Arguments

mirror	character(1) The Bioconductor mirror to be tested resolves from <code>getOption("BioC_mirror")</code> . If one is not selected, <code>chooseBioCmirror()</code> will be run and the user will be able to select a mirror interactively.
version	character(1) The Bioconductor version to be checked.
repoType	character(1) One of the Bioconductor package types, including <code>BioCsoft</code> (default), <code>BioCann</code> , <code>BioCexp</code> , <code>BioCworkflows</code> , and <code>BioCbooks</code> .
type	character(1) The package type whether "source", "binary", "mac.binary", or "win.binary" as given by <code>getOption("pkgType")</code> . See <code>install.packages</code> for details.

Value

A logical value indicating availability of the mirror indicated in the name.

Examples

```
bioc_url <- "https://bioconductor.org"
bioc_mirror <- c(`0-Bioconductor (World-wide) [https]` = bioc_url)
checkBioCmirror(mirror = bioc_mirror)
```

 CRANinstall

Install packages from the CRAN archive

Description

The function looks through the CRAN archive for each package and finds the package versions that are compatible with the archived Bioconductor version using the release date of that Bioconductor version as reported by `lastBuilt`.

Usage

```
CRANinstall(
  pkgs,
  version = BiocManager::version(),
  dry.run = FALSE,
  ...,
  last_built = lastBuilt(version = version)
)
```

Arguments

<code>pkgs</code>	<code>character()</code> A vector of package names whose versions are sought to be compatible with the archived version of Bioconductor.
<code>version</code>	<code>character(1)</code> The desired version to reproduce. This is largely dictated by the current R / Bioconductor version installed and is indicated by <code>BiocManager::version</code> by default.
<code>dry.run</code>	<code>logical(1)</code> Whether to show only the time machine repository and forgo the package installation.
<code>...</code>	Additional parameters for the <code>BiocManager::install()</code> function
<code>last_built</code>	named <code>character(1)</code> A character scalar of the date of the Bioconductor versions last build. The name corresponds to the Bioconductor version, e.g., <code>c('3.14' = "2022-04-13")</code> . By default, the <code>lastBuilt()</code> function reports the date from the value of the <code>version</code> argument.

Value

Mostly called for its side effect of installing the package from the CRAN archives that corresponds to the given Bioconductor version.

Examples

```
CRANinstall(c("dplyr", "ggplot2"), version = "3.14", dry.run = TRUE)
```

install	<i>Install packages from a previous release of Bioconductor for reproducibility</i>
---------	---

Description

This function allows users to install packages from a previously released Bioconductor version.

Usage

```
install(
  pkgs = character(),
  version = BiocManager::version(),
  snapshot = getOption("BiocArchive.snapshot", "P3M"),
  dry.run = FALSE,
  ...,
  last_built = lastBuilt(version = 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> .
version	character(1) The desired version to reproduce. This is largely dictated by the current R/Bioconductor version installed and is indicated by <code>BiocManager::version</code> by default.
snapshot	character(1) The snapshot CRAN repository to use for reproducibility. This defaults to the value of <code>getOption("BiocArchive.snapshot", "P3M")</code> .
dry.run	logical(1) Whether to show only the time machine repository and forgo the package installation.
...	Additional parameters for the <code>BiocManager::install()</code> function
last_built	named character(1) A character scalar of the date of the Bioconductor versions last build. The name corresponds to the Bioconductor version, e.g., <code>c('3.14' = "2022-04-13")</code> . By default, the <code>lastBuilt()</code> function reports the date from the value of the <code>version</code> argument.

Details

CRAN packages for out-of-date *Bioconductor* installations can be installed from historical 'snapshots' consistent with the last date the Bioconductor version was current. This behavior is largely dictated by the actual R/Bioconductor installation, e.g., Bioconductor 3.11. For example, *Bioconductor* version 3.11 was current until October 28, 2020; CRAN packages are therefore installed from a snapshot created on 2020-10-28. By default, the snapshots are from 'P3M', the **Posit Public Package Manager**. Use `options(BiocArchive.snapshot = "CRAN")` to use the current CRAN repository (i.e., disabling the snapshot feature).

Note that the function will temporarily change the `getOption('repos')` setting for CRAN to allow installation of CRAN packages from either the **P3M** time machines. The function will also modify the `BIOCONDUCTOR_USE_CONTAINER_REPOSITORY` environment variable to temporarily disable binary package installations. This is due to the possibility of CRAN packages in the Bioconductor binary repositories that are not fixed to a certain release date. Note that `BiocArchive.snapshot` has replaced `BiocManager.snapshot`.

It may be desirable to specify different default repositories, especially CRAN, for intentionally out-of-date *Bioconductor* releases (e.g., to support reproducible research). Our approach automatically provides an alteration to the `repos` option, e.g., `options(repos = c(CRAN = "https://packagemanager.posit.co/cran/2022-04-13/"))`.

Value

Mostly called for the side-effects of copying and modifying the `config.yaml` and `.Renv` files to reproduce an R / Bioconductor package environment from a previous Bioconductor release.

Examples

```
install("DESeq2", version = "3.14", snapshot = "P3M", dry.run = TRUE)
```

lastBuilt

Obtain the last build date for a particular Bioconductor version

Description

The function facilitates the discovery of last build dates useful for selecting a fixed date to be used in conjunction with `options("BiocArchive.snapshot")`. Currently, it looks at <https://bioconductor.org/checkResults/> and parses the dates listed.

Usage

```
lastBuilt(version = "all")
```

Arguments

`version` character(1) Indicates the Bioconductor version for which the last build date is sought. By default, 'all' versions will be returned.

Value

character(1) The last build date for the specified Bioconductor version.

Examples

```
lastBuilt(version = "3.14")
```

 repositories

Display Bioconductor and CRAN snapshot repositories

Description

`repositories()` reports the URLs from which to install *Bioconductor* and CRAN packages. There repositories are based on the data of the last build of the archived Bioconductor release.

Usage

```
repositories(
  site_repository = character(),
  version = BiocManager::version(),
  snapshot = getOption("BiocArchive.snapshot", "P3M"),
  last_built = lastBuilt(version = version)
)
```

Arguments

<code>site_repository</code>	(Optional) <code>character(1)</code> 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.
<code>version</code>	(Optional) <code>character(1)</code> or <code>package_version</code> indicating the <i>Bioconductor</i> version (e.g., "3.8") for which repositories are required.
<code>snapshot</code>	<code>character(1)</code> The snapshot CRAN repository to use for reproducibility. This defaults to the value of <code>getOption("BiocArchive.snapshot", "P3M")</code> .
<code>last_built</code>	<code>named character(1)</code> A character scalar of the date of the Bioconductor versions last build. The name corresponds to the Bioconductor version, e.g., <code>c('3.14' = "2022-04-13")</code> . By default, the <code>lastBuilt()</code> function reports the date from the value of the <code>version</code> argument.

Details

The CRAN repository reflects the snapshot arguments, which can be either P3M, or CRAN. The CRAN option will default to the established repository. For installation of archived packages on CRAN, see the [CRANinstall](#) function.

When binary installations are enabled via `BIOCONDUCTOR_USE_CONTAINER_REPOSITORY`, the function will temporarily disable binary installation of packages. Bioconductor binary repositories may include CRAN packages that are not fixed to the release date.

Value

A character vector of Bioconductor and CRAN repositories accounting for previous releases

See Also

[CRANinstall](#)

Examples

```
if (interactive()) {  
  # run within the Bioconductor 3.14 Docker container  
  repositories(version = "3.14", snapshot = "P3M")  
}
```

valid

Validate installed packages versions against archive constraints

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 = utils::installed.packages(lib.loc, priority = priority),  
  lib.loc = NULL,  
  priority = "NA",  
  type = getOption("pkgType"),  
  filters = NULL,  
  ...,  
  checkBuilt = FALSE,  
  site_repository = character(),  
  version = BiocManager::version(),  
  last_built = lastBuilt(version = version),  
  snapshot = getOption("BiocArchive.snapshot", "P3M")  
)
```

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> .

<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>site_repository</code>	<code>character(1)</code> . See <code>?install</code> .
<code>version</code>	<code>character(1)</code> The desired version to reproduce. This is largely dictated by the current R / Bioconductor version installed and is indicated by <code>BiocManager::version</code> by default.
<code>last_built</code>	<code>named character(1)</code> A character scalar of the date of the Bioconductor versions last build. The name corresponds to the Bioconductor version, e.g., <code>c('3.14' = "2022-04-13")</code> . By default, the <code>lastBuilt()</code> function reports the date from the value of the <code>version</code> argument.
<code>snapshot</code>	<code>character(1)</code> The snapshot CRAN repository to use for reproducibility. This defaults to the value of <code>getOption("BiocArchive.snapshot", "P3M")</code> .

Details

The function mainly works with the CRAN repositories location given by the `repositories()` function. There is no reliable way to verify `CRANinstall` installations other than by running the function with the `dry.run = TRUE` parameter and manually comparing versions.

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 archived 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.

Examples

```
if (interactive()) {  
  valid()  
}
```


Index

`available.packages`, [7](#)

`BiocArchive.snapshot (install)`, [4](#)

`BiocManager.snapshot (install)`, [4](#)

`checkBioCmirror`, [2](#)

`CRANinstall`, [3](#), [6](#), [7](#)

`install`, [4](#), [7](#)

`installed.packages`, [7](#)

`lastBuilt`, [5](#)

`repositories`, [6](#)

`valid`, [7](#)