Package 'BiocInstaller'

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Title Install/Update Bioconductor, CRAN, and github Packages

Description This package is used to install and update Bioconductor, CRAN, and (some) github packages.

Version 1.32.1

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biocViews Infrastructure

Depends R (>= 3.5.0), R (< 3.6.0)

Suggests remotes, RUnit, BiocGenerics

License Artistic-2.0

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R topics documented:

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biocinstallRepos   *Display current Bioconductor and CRAN repositories.*

Description

Displays the URLs of the repositories used by biocLite to install Bioconductor and CRAN packages.

Usage

```
biocinstallRepos(siteRepos=character(), version=biocVersion())
```

Arguments

siteRepos   (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., "3.1") for which repositories are required.

Value

Named `character()` of repositories.

See Also

biocLite Installs/updates Bioconductor/CRAN packages.

install.packages installs the packages themselves.

chooseBioCmirror lets you choose from a list of all public Bioconductor mirror URLs.

chooseCRANmirror lets you choose from a list of all public CRAN mirror URLs.

Examples

```
biocinstallRepos()

## Choose mirrors
## Not run:
chooseCRANmirror()
chooseBioCmirror()

## End(Not run)
```

biocLite	*Install or update Bioconductor and CRAN packages*

Description

`biocLite` installs or updates Bioconductor and CRAN packages in a Bioconductor release. Upgrading to a new Bioconductor release requires additional steps; see `https://bioconductor.org/install`.

`BIOCINSTALLER_ONLINE_DCF` is an environment variable or global `options()` which, when set to `FALSE`, uses configuration information from a local archive rather than consulting the current online version.

Usage

```
biocLite(pkgs=c("Biobase", "IRanges", "AnnotationDbi"),
    suppressUpdates=FALSE,
    suppressAutoUpdate=FALSE,
    siteRepos=character(),
    ask=TRUE, ...)
```

Arguments

pkgs
: `character()` of package names to install or update. A missing value and `suppressUpdates=FALSE` updates installed packages, perhaps also installing `Biobase`, `IRanges`, and `AnnotationDbi` if they are not already installed. Package names containing a '/' are treated as github repositories and installed using the `install_github()` function of the `remotes` package.

suppressUpdates
: `logical(1)` or `character()`. When `FALSE`, biocLite asks the user whether old packages should be update. When `TRUE`, the user is not prompted to update old packages. When `character()` a vector specifying which packages to NOT update.

suppressAutoUpdate
: `logical(1)` indicating whether the `BiocInstaller` package updates itself.

siteRepos
: `character()` 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 `biocinstallRepos`).

ask
: `logical(1)` indicating whether to prompt user before installed packages are updated, or the character string 'graphics', which brings up a widget for choosing which packages to update. If TRUE, user can choose whether to update all outdated packages without further prompting, to pick and choose packages to update, or to cancel updating (in a non-interactive session, no packages will be updated). Otherwise, the value is passed to `update.packages`.

...
: Additional arguments.

  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 install (internally). A typical use is to build vignettes, via dependencies=TRUE, build_vignettes=TRUE.

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 install_github() function from the remotes package. For this reason it usually makes sense, when complicated installation options are needed, to invoke biocLite() separately for Bioconductor / CRAN packages and for github packages.

Setting BIOCINSTALLER_ONLINE_DCF 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

biocLite() returns the pkgs argument, invisibly.

See Also

[biocinstallRepos](#) returns the Bioconductor and CRAN repositories used by biocLite.

[install.packages](#) installs the packages themselves.

[update.packages](#) updates all installed packages.

[chooseBioCmirror](#) lets you choose from a list of all public Bioconductor mirror URLs.

[chooseCRANmirror](#) lets you choose from a list of all public CRAN mirror URLs.

[monograph_group](#), [RBioinf_group](#) and [biocases_group](#) return package names associated with Bioconductor publications.

[all_group](#) returns the names of all Bioconductor software packages.

Examples

```
## Not run:
## Change default Bioconductor and CRAN mirrors
chooseBioCmirror()
chooseCRANmirror()

## If you don't have the BiocInstaller package installed, you can
## quickly install and load it as follows:
source("https://bioconductor.org/biocLite.R")  # 'http' if 'https' unavailable

## The most recent version of the BiocInstaller package is now loaded.
## No need to load it with library().

## installs default packages (if not already installed) and updates
## previously installed packages
biocLite()

## Now install a CRAN package:
biocLite("survival")

## install a Bioconductor package, but don't update all installed
## packages as well:
```

```
biocLite("GenomicRanges", suppressUpdates=TRUE)

## Install default packages, but do not update any package whose name
## starts with "org." or "BSgenome."
biocLite(suppressUpdates=c("^org\.", "^BSgenome\."))

## install a package from source:
biocLite("IRanges", type="source")

## install all Bioconductor software packages
biocLite(all_group())


## End(Not run)
## Show the Bioconductor and CRAN repositories that will be used to
## install/update packages.
biocinstallRepos()

## Use local archive rather than current online configuration
## information. Set this prior to loading the BiocInstaller package.
options(BIOCINSTALLER_ONLINE_DCF = FALSE)
```

---

biocUpdatePackages	*Update previously installed Bioconductor or CRAN packages and their dependencies.*

Description

Update previously installed Bioconductor and CRAN packages and their dependencies. Use `biocLite` to install new packages or to update all out-of-date packages. Upgrading to a new Bioconductor release requires additional steps; see <https://bioconductor.org/install>.

Usage

```
biocUpdatePackages(pkgs, dependencies = NA, repos=biocinstallRepos(), ...)
```

Arguments

pkgs	character() of package names to install or update.
dependencies	character() describing out-of-date dependencies that are also updated. Defaults to c("Depends", "Imports", "LinkingTo") but can be a subset of c("Depends", "Imports", "LinkingTo", "Suggests", "Enhances").
repos	character() of named repositories in which to look for package updates, in the style of biocinstallRepos().
...	Additional arguments, passed to `update.packages`. For example, ask=FALSE to avoid prompts to update individual packages.

Value

'NULL', invisibly.

Author(s)

Martin Morgan mtmorgan@fhcrc.org

See Also

biocLite

Examples

```
## Not run:
biocUpdatePackages("GenomicRanges", ask=FALSE)

## End(Not run)
```

BiocUpgrade	*Upgrade Bioconductor to the latest version available for this version of R*

Description

Downloads the latest version of the BiocInstaller package, and upgrades all currently installed packages to the latest repositories **for this version of R**.

To upgrade, use:

```
## 'http' if 'https' unavailable
source("https://bioconductor.org/biocLite.R")
biocLite("BiocUpgrade")
```

See Also

biocLite Installs/updates Bioconductor/CRAN packages.

chooseBioCmirror lets you choose from a list of all public Bioconductor mirror URLs.

chooseCRANmirror lets you choose from a list of all public CRAN mirror URLs.

biocinstallRepos returns the Bioconductor and CRAN repositories used by biocLite.

install.packages installs the packages themselves.

Examples

```
## Not run:
source("https://bioconductor.org/biocLite.R")
biocLite("BiocUpgrade")

## End(Not run)
```

biocValid	*Validate installed package versions against biocLite versions.*

Description

Check that installed packages are consistent (neither out-of-date nor too new) with the version of R and Bioconductor in use, using `biocLite` for validation.

Usage

```
biocValid(pkgs = installed.packages(lib.loc, priority = priority),
    lib.loc = NULL, priority = "NA", type = getOption("pkgType"),
    filters = NULL, silent = FALSE, ..., fix=FALSE)
```

Arguments

pkgs	A character list of package names for checking, or a matrix as returned by `installed.packages`.
lib.loc	The library location(s) of packages to be validated; see `installed.packages`.
priority	check validity of all, "base", or "recommended" packages; see `installed.packages`.
type	The type of available package (e.g., binary, source) to check validity against; see `available.packages`.
filters	Filter available packages to check validity against; see `available.packages`.
silent	Report how packages are invalid (silent=FALSE, default) and abort execution, or return a logical(1) (silent=TRUE) indicating the overall validity of installed packages.
...	Additional arguments, passed to `biocLite` when fix=TRUE.
fix	When `TRUE`, invoke `biocLite` to reinstall (update or downgrade, as appropriate) invalid packages.

Details

This function compares the version of installed packages to the version of packages associated with the version of R and Bioconductor appropriate for the BiocInstaller package currently in use.

Packages are reported as 'out-of-date' if a more recent version is available at the repositories specified by `biocinstallRepos()`. Usually, `biocLite()` 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 `biocinstallRepos()` repositories. It is possible to down-grade by re-installing a too new package "PkgA" with `biocLite("PkgA")`. It is important for the user to understand how their installation became too new, and to avoid this in the future.

Value

`logical(1)` indicating overall validity of installed packages.

Author(s)

Martin Morgan mtmorgan@fhcrc.org

See Also

biocLite to update installed packages.

Examples

```
try(biocValid())
```

---

biocVersion	*Bioconductor version*

Description

This function reports the Bioconductor version in use, as determined by the BiocInstaller package.

Usage

```
biocVersion()
```

Value

package_version representing the Bioconductor version in use.

See Also

biocLite Installs/updates Bioconductor/CRAN packages.

BiocUpgrade Upgrading to new versions.

Examples

```
biocVersion()
```

Package Groups	*Convenience functions to return package names associated with Bioconductor publications.*

Description

Returns character vectors of packages associated with Bioconductor publications, which can then be passed to biocLite()

Usage

```
monograph_group()
RBioinf_group()
biocases_group()
all_group()
```

Value

character() of package names.

See Also

biocLite Installs/updates Bioconductor/CRAN packages.

biocinstallRepos returns the Bioconductor and CRAN repositories used by biocLite.

install.packages installs the packages themselves.

chooseBioCmirror lets you choose from a list of all public Bioconductor mirror URLs.

chooseCRANmirror lets you choose from a list of all public CRAN mirror URLs.

Examples

```
## Get the names of packages used in the book
## "Bioconductor Case Studies":
biocases_group()

## Get the names of packages used in the book
## "R Programming for Bioinformatics":
RBioinf_group()

## Get the names of packages used in the monograph
## "Bioinformatics and Computational Biology Solutions
## Using R and Bioconductor":
monograph_group()

## Get the names of all Bioconductor software packages
all_group()
```

---

useDevel   *Get the 'devel' version of the BiocInstaller package.*

Description

Downloads the 'devel' version of the BiocInstaller package so that all subsequent invocations of biocLite and biocinstallRepos use the devel repositories.

Displays the URLs of the repositories used by biocLite to install Bioconductor and CRAN packages.

Should only be used with a release (or patched) version of R, freshly installed.

Usage

```
isDevel()
useDevel(devel=TRUE)
```

Arguments

devel   Whether to look in the devel (TRUE) or release (FALSE) repositories in subsequent invocations of biocLite and biocinstallRepos.

Details

Bioconductor has a 'release' branch and a 'devel' branch. The branch in use depends on the version of R and the version of the BiocInstaller.

useDevel() installs the correct version of the BiocInstaller package for use of the devel version of Bioconductor, provided it is supported by the version of R in use.

isDevel() returns TRUE when the version of BiocInstaller in use corresponds to the 'devel' version of Bioconductor.

In more detail, the version number of the BiocInstaller package determines whether to download packages from the release or devel repositories of Bioconductor. In keeping with Bioconductor versioning conventions, if the middle number (y in x.y.z) is even, the package is part of a release version; if odd, it's part of a devel version.

By default, when BiocInstaller is first installed and when the version of R supports the current release version of Bioconductor, BiocInstaller will use the release repository.

To change the version of BiocInstaller to support the 'devel' branch of Bioconductor, run useDevel(). With argument TRUE (the default), it will download the devel version of BiocInstaller and subsequently all packages downloaded with biocLite will be from the devel repository. You should run useDevel only once.

During release cycles where both the release and devel version of Bioconductor use the same version of R, it is possible to use release and devel versions of Bioconductor with the same installation of R. To do this, use the R_LIBS_USER environment variable. First, create two separate directories for your BioC release and devel packages. Suggested directory names are as follows:

Linux:

~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-release

~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-devel

Mac OS:

~/Library/R/3.2-bioc-release/library

~/Library/R/3.2-bioc-devel/library

Windows:

C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.2-bioc-release

C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.2-bioc-devel

(change YOUR_USER_NAME to your user name)

Invoke "R for bioc-devel" or "R for bioc-release" from the command line as follows:

Linux:

R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-release R

R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-devel R

Mac OS X:

R_LIBS_USER=~~/Library/R/3.2-bioc-release/library R R_LIBS_USER=~~/Library/R/3.2-bioc-devel/library R

Windows:

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.2-bioc-release && R"

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.2-bioc-devel && R"

(Note: this assumes that R.exe is in your PATH.)

If you launch R in this way and then invoke `.libPaths`, you'll see that the first item is your special release or devel directory. Packages will be installed to that directory and that is the first place that `library` will look for them. `biocLite`, `install.packages`, `update.packages` and friends all respect this setting.

On Linux and Mac OS X, you can create a bash alias to save typing. Add the following to your ~/bash_profile:

Linux

alias Rdevel='R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-devel R'

alias Rrelease='R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/3.2-bioc-release R'

Mac OS X

alias Rdevel='R_LIBS_USER=~/Library/R/3.2-bioc-devel/library R' alias Rrelease='R_LIBS_USER=~/Library/R/3.2-bioc-release/library R'

You can then invoke these from the command line as

Rdevel

...and...

Rrelease

On Windows, you can create two shortcuts, one for devel and one for release. Go to My Computer and navigate to a directory that is in your PATH. Then right-click and choose New->Shortcut.

in the "type the location of the item" box, put:

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.2-bioc-release && R"

...for release and

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\3.0-bioc-devel && R"

...for devel.

(again, it's assumed R.exe is in your PATH)

Click "Next".

In the "Type a name for this shortcut" box, type

Rdevel

or

Rrelease

You can invoke these from the command line as

Rdevel.lnk

...and...

Rrelease.lnk

(You must type in the .lnk extension.)

Because `R_LIBS_USER` is an environment variable, its value should be inherited by any subprocesses started by R, so they should do the right thing as well.

Value

useDevel(): Invisible NULL.

isDevel(): logical(1) TRUE or FALSE.

See Also

biocinstallRepos returns the Bioconductor and CRAN repositories used by biocLite.

biocLite Installs/updates Bioconductor/CRAN packages.

install.packages installs the packages themselves.

chooseBioCmirror lets you choose from a list of all public Bioconductor mirror URLs.

chooseCRANmirror lets you choose from a list of all public CRAN mirror URLs.

Examples

```
isDevel()

## Not run: useDevel()
```

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