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 1.22.3

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biocViews Infrastructure

Depends R (>= 3.3.0)

Suggests devtools, RUnit, BiocGenerics

License Artistic-2.0

NeedsCompilation no

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.

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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.

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 devtools 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 **devtools** package functions [install_github](#) and [install](#). 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 devtools 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.

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()
```

---

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 Bio-conductor 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 pack-
ages.

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

Usage

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

Arguments

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

Details

With R going to a yearly release schedule and Bioconductor keeping its twice-yearly release sched-
ule, the same version of R (3.2) can be used with two different versions of Bioconductor (3.1, re-
lease, and 3.2, devel). The version number of the BiocInstaller package is what is used to determine
whether to download packages from the BioC 3.1 or 3.2 repositories. 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 on R-3.2, it will be set up to download BioC 3.1
packages.

If you want to change this, you can run the useDevel function. With argument TRUE (the default),
it will download the devel version of BiocInstaller and subsequently all packages downloaded with
biocLite will be from the BioC 3.2 (devel) repository. You should run useDevel only once.

It is possible to keep BioC 3.1 and 3.2 libraries separate, within the same installation of R.

The trick is to 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)

You can then 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

Invisible NULL.

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

```
## Not run:
useDevel()

## End(Not run)
```

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