Package 'BiocInstaller'

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Title Install/Update Bioconductor and CRAN Packages

Description Install4/updates Bioconductor and CRAN packages

Version 1.4.7

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biocViews Software

Depends R (>= 2.15.0)

Suggests RUnit

License Artistic-2.0

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())
```

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Arguments

siteRepos   character() representing an additional repository in which to look for pack-
                 ages to install. This repository will be prepended to the default repositories
                 returned by the function.

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, ensuring that packages from the
appropriate version of Bioconductor are installed, and that all packages remain up to date.

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 value of character(0)
                 and suppressUpdates=FALSE updates packages without installing new ones.

suppressUpdates

                 logical(1) indicating whether to suppress automatic updating of all installed
                 packages, or character() of regular expressions specifying which packages to
                 NOT automatically 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. `lib.loc` is passed to `old.packages` (used to determine the library location of installed packages to be updated). `lib` is passed to `install.packages` (used to determine the library location where pkgs are to be installed).

Details

The `biocLite()` function is generally used after sourcing the file `biocLite.R`. This will install the `BiocInstaller` package if it is not already installed. See example section for more information.

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("http://bioconductor.org/biocLite.R")


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

```
## 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")

## don't install any packages, but update installed packages
biocLite(character(0), ask=FALSE)

## 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()
```

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 packages.

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 subsequent invocations of [biocLite](#) and [biocinstallRepos](#).

Details

With R going to a yearly release schedule and Bioconductor keeping its twice-yearly release schedule, the same version of R (2.15) can be used with two different versions of Bioconductor (2.10, release, and 2.11, devel). The version number of the BiocInstaller package is what is used to determine whether to download packages from the BioC 2.10 or 2.11 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-2.15, it will be set up to download BioC 2.10 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 2.11 (devel) repository. You should run useDevel only once.

It is possible to keep BioC 2.10 and 2.11 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/2.15-bioc-release

~/R/x86_64-unknown-linux-gnu-library/2.15-bioc-devel

Mac OS:

~/Library/R/2.15-bioc-release/library

~/Library/R/2.15-bioc-devel/library

Windows:

C:\Users\YOUR_USER_NAME\Documents\R\win-library\2.15-bioc-release

C:\Users\YOUR_USER_NAME\Documents\R\win-library\2.15-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/2.15-bioc-release R

R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/2.15-bioc-devel R

Mac OS X:

R_LIBS_USER=~~/Library/R/2.15-bioc-release/library R R_LIBS_USER=~~/Library/R/2.15-bioc-devel/library R

Windows:

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\2.15-bioc-release && R"

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\Documents\R\win-library\2.15-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/2.15-bioc-devel R'

alias Rrelease='R_LIBS_USER=~/R/x86_64-unknown-linux-gnu-library/2.15-bioc-release R'

Mac OS X

alias Rdevel='R_LIBS_USER=~/Library/R/2.15-bioc-devel/library R' alias Rrelease='R_LIBS_USER=~/Library/R/2.1 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\2.15-bioc-release && R"

...for release and

cmd /C "set R_LIBS_USER=C:\Users\YOUR_USER_NAME\DocumentsR\win-library\2.15-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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