

Bioconductor

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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,
          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 Bioconductor package updates itself.
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. Passed to update.packages .
...	Additional arguments passed to install.packages .

Details

The biocLite () function is generally used after sourcing the file biocLite.R. This will install the Bioconductor 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.

Examples

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

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

## The most recent version of the Bioconductor 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")

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

<code>biocinstallRepos</code>	<i>Display current Bioconductor and CRAN repositories.</i>
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Description

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

Usage

```
biocinstallRepos()
```

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)
```

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