

# BiocInstaller

March 24, 2012

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biocLite

*Install or update Bioconductor and CRAN packages*

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## 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 BiocInstaller 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. If TRUE, user can choose whether to update all outdated packages without further prompting, to pick and choose packages to update, or to cancel updating (in a non-interactive session, no packages will be updated).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 <a href="#">update.packages</a> .
...	Additional arguments passed to <a href="#">install.packages</a> .

## 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()
```

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biocinstallRepos    *Display current Bioconductor and CRAN repositories.*

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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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Package Groups	<i>Convenience functions to return package names associated with Bioconductor publications.</i>
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### 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()
```

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