

# Package ‘BiocManager’

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**Title** Access the Bioconductor Project Package Repository

**Description** A convenient tool to install and update Bioconductor packages.

**Version** 1.30.3

**Depends** R (>= 3.5.0)

**Imports** utils

**Suggests** BiocStyle, BiocVersion, remotes, testthat, knitr, withr

**BugReports** <https://github.com/Bioconductor/BiocManager/issues>

**VignetteBuilder** knitr

**License** Artistic-2.0

**RoxygenNote** 6.1.0

**NeedsCompilation** no

**Author** Martin Morgan [aut] (<<https://orcid.org/0000-0002-5874-8148>>),  
Marcel Ramos [ctb, cre] (<<https://orcid.org/0000-0002-3242-0582>>)

**Maintainer** Marcel Ramos <[marcel.ramos@roswellpark.org](mailto:marcel.ramos@roswellpark.org)>

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available                      *Discover packages available for installation.*

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### **Description**

Discover packages available for installation.

### **Usage**

```
available(pattern = "", include_installed = TRUE)
```

### **Arguments**

pattern                      character(1) pattern to filter (via `grep(pattern=...)`) available packages; the filter is not case sensitive.

include\_installed            logical(1) When TRUE, include installed packages in list of available packages; when FALSE, exclude installed packages.

### **Value**

character() vector of package names available for installation.

### **Examples**

```
avail <- BiocManager::available()
length(avail)

BiocManager::available("bs.*hsapiens")
```

---

BiocManager-pkg                      *Install or update Bioconductor, CRAN, or GitHub packages*

---

### **Description**

This package provides tools for managing *Bioconductor* and other packages in a manner consistent with *Bioconductor*'s package versioning and release system.

## Details

Main functions are as follows; additional help is available for each function, e.g., `?BiocManager::version`.

`BiocManager::install()` Install or update packages from *Bioconductor*, CRAN, and GitHub.

`BiocManager::version()` Report the version of *Bioconductor* in use.

`BiocManager::available()` Return a `character()` vector of package names available (at `BiocManager::repositories()` for installation).

`BiocManager::valid()` Determine whether installed packages are from the same version of *Bioconductor*.

`BiocManager::repositories()` *Bioconductor* and other repository URLs to discover packages for installation.

## Author(s)

**Maintainer:** Marcel Ramos <marcel.ramos@roswellpark.org> (0000-0002-3242-0582) [contributor]

Authors:

- Martin Morgan <martin.morgan@roswellpark.org> (0000-0002-5874-8148)

## See Also

Useful links:

- Report bugs at <https://github.com/Bioconductor/BiocManager/issues>

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install

*Install or update Bioconductor, CRAN, and GitHub packages*

---

## Description

The `BiocManager::install()` function installs or updates *Bioconductor* and CRAN packages in a *Bioconductor* release. Upgrading to a new *Bioconductor* release may require additional steps; see <https://bioconductor.org/install>.

## Usage

```
install(pkgs = character(), ..., site_repository = character(),
        update = TRUE, ask = TRUE, version = BiocManager::version())
```

## Arguments

<code>pkgs</code>	character() vector of package names to install or update. A missing value updates installed packages according to <code>update =</code> and <code>ask =</code> . Package names containing a <code>'/'</code> are treated as GitHub repositories and installed using <code>remotes::install_github()</code> .
<code>...</code>	Additional arguments used by <code>install.packages()</code> .
<code>site_repository</code>	(Optional) character(1) vector 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 <code>BiocManager::repositories()</code> ).
<code>update</code>	logical(1). When FALSE, <code>BiocManager::install()</code> does not attempt to update old packages. When TRUE, update old packages according to <code>ask</code> .
<code>ask</code>	logical(1) indicating whether to prompt user before installed packages are updated. If TRUE, user can choose whether to update all outdated packages without further prompting, to pick packages to update, or to cancel updating (in a non-interactive session, no packages will be updated unless <code>ask = FALSE</code> ).
<code>version</code>	character(1) <i>Bioconductor</i> version to install, e.g., <code>version = "3.8"</code> . The special symbol <code>version = "devel"</code> installs the current 'development' version.

## 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 `remotes::install_github()`.

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

`BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS` is an environment variable or global `options()` which, when set to FALSE, avoids the R and *Bioconductor* version checks that are done by querying an on-line configuration file. Setting `BIOCONDUCTOR_ONLINE_VERSION_DIAGNOSIS` 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

`BiocManager::install()` returns the `pkgs` argument, invisibly.

## See Also

`BiocManager::repositories()` returns the *Bioconductor* and CRAN repositories used by `install()`.

`install.packages()` installs the packages themselves (used by `BiocManager::install` internally).

`update.packages()` updates all installed packages (used by `BiocManager::install` internally).

`chooseBioCmirror()` allows choice of a mirror from all public *Bioconductor* mirrors.

`chooseCRANmirror()` allows choice of a mirror from all public CRAN mirrors.

## Examples

```
## Not run:
## update previously installed packages
BiocManager::install()

## install Bioconductor packages, and prompt to update all
## installed packages
BiocManager::install(c("GenomicRanges", "edgeR"))

## install a CRAN and Bioconductor packages:
BiocManager::install(c("survival", "SummarizedExperiment"))

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

## End(Not run)
```

---

repositories

*Display current Bioconductor and CRAN repositories.*

---

## Description

`repositories()` reports the URLs from which to install *Bioconductor* and CRAN packages. It is used by `BiocManager::install()` and other functions.

## Usage

```
repositories(site_repository = character(),
            version = BiocManager::version())
```

## Arguments

`site_repository`

(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., "3.8") for which repositories are required.

## Value

Named `character()` of repositories.

**See Also**

`BiocManager::install()` Installs or updates Bioconductor, CRAN, and GitHub packages.  
[chooseBioCmirror\(\)](#) choose an alternative Bioconductor mirror; not usually necessary.  
[chooseCRANmirror\(\)](#) choose an alternative CRAN mirror; not usually necessary.  
[setRepositories\(\)](#) Select additional repositories for searching.

**Examples**

```
BiocManager::repositories()
## Not run:
BiocManager::repositories(version="3.8")

## End(Not run)
```

---

valid

*Validate installed package versions against correct versions.*


---

**Description**

Check that installed packages are consistent (neither out-of-date nor too new) with the version of R and *Bioconductor* in use.

**Usage**

```
valid(pkgs = installed.packages(lib.loc, priority = priority),
      lib.loc = NULL, priority = "NA", type = getOption("pkgType"),
      filters = NULL, ..., site_repository = character())

## S3 method for class 'biocValid'
print(x, ...)
```

**Arguments**

<code>pkgs</code>	A <code>character()</code> vector of package names for checking, or a matrix as returned by <a href="#">installed.packages</a> .
<code>lib.loc</code>	A <code>character()</code> vector of library location(s) of packages to be validated; see <a href="#">installed.packages()</a> .
<code>priority</code>	<code>character(1)</code> Check validity of all, "base", or "recommended" packages; see <a href="#">installed.packages()</a> .
<code>type</code>	<code>character(1)</code> The type of available package (e.g., binary, source) to check validity against; see <a href="#">available.packages()</a> .
<code>filters</code>	<code>character(1)</code> Filter available packages to check validity against; see <a href="#">available.packages()</a> .
<code>...</code>	Additional arguments, passed to <code>BiocManager::install()</code> when <code>fix=TRUE</code> .
<code>site_repository</code>	<code>character(1)</code> . See <code>?install</code> .
<code>x</code>	A 'biocValid' object returned by <code>'BiocManager::valid()'</code> .

## Details

This function compares the version of installed packages to the version of packages associated with the version of *R* and *Bioconductor* currently in use.

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

## Value

biocValid list object with elements `too_new` and `out_of_date` containing data.frames with packages and their installed locations that are too new or out-of-date for the current version of *Bioconductor*.

``print()`` is invoked for its side effect.

## Author(s)

Martin Morgan <martin.morgan@roswellpark.org>

## See Also

`BiocManager::install()` to update installed packages.

## Examples

```
BiocManager::valid()
```

---

version

*Version of Bioconductor currently in use.*

---

## Description

`version()` reports the version of *Bioconductor* appropriate for this version of *R*, or the version of *Bioconductor* requested by the user.

**Usage**

```
version()
```

```
## S3 method for class 'unknown_version'  
print(x, ...)
```

**Arguments**

x	An <code>unknown_version</code> instance used to represent the situation when the version of Bioconductor in use cannot be determined.
...	Additional arguments, ignored.

**Details**

`version()` (and all functions requiring version information) fails when version cannot be validated e.g., because internet access is not available.

**Value**

A two-digit version, e.g., 3.8, of class `package_version` describing the version of *Bioconductor* in use.

**Examples**

```
BiocManager::version()
```



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