

# Package ‘BiocBuildReporter’

April 26, 2026

**Type** Package

**Title** Functions to process a bioconductor build report database

**Version** 0.99.2

**Description** This package reads remote parquet files that have processed Bioconductor build report logs. Users may query the tables directly for specific information or use pre-defined helper functions for common queries. The logs processed are from <https://bioconductor.org/checkResults/>. In the future we will extend this package out to include processing of r-universe logs.

**Depends** R (>= 4.6.0)

**Imports** arrow, dplyr, BiocFileCache

**License** Apache License (>= 2)

**Encoding** UTF-8

**RoxygenNote** 7.3.3

**Suggests** BiocStyle, testthat (>= 3.0.0), knitr, rmarkdown, ggplot2, tidyr, stringr

**Config/testthat/edition** 3

**VignetteBuilder** knitr

**URL** <https://github.com/lshep/BiocBuildReporter.git>

**BugReports** <https://github.com/lshep/BiocBuildReporter/issues>

**biocViews** Software, Infrastructure

**git\_url** <https://git.bioconductor.org/packages/BiocBuildReporter>

**git\_branch** devel

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|           |  |
|-----------|--|
| bbs_cache | <i>Custom Environment to store downloaded parquet tibbles.</i> |
|-----------|--|

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### Description

A custom environment to store remotely read parquet files of Bioconductor build reports. Once one of the three valid parquet files are read in, the table is cached in this environment for quick easy reference either to use ad hocly by the user or to be used within pre-defined queries provided by this package.

### Usage

.bbs\_cache

### Format

An environment

---

|                   |   |
|-------------------|---|
| BiocBuildReporter | <i>BiocBuildReporter: Functions to process a bioconductor build report database</i> |
|-------------------|---|

---

### Description

The BiocBuildReporter package provides access to years of Bioconductor build system data, representing a comprehensive record of package builds across: - **Thousands of packages** in the Bioconductor ecosystem - **Multiple R versions** spanning several years of development - **Multiple platforms** including Linux, macOS, and Windows - **Different build stages** (install, build, check)

### Details

Please see vignette("BiocBuildReporter") for details on usage and pre-built query functions.

**Author(s)**

**Maintainer:** Lori Shepherd <lori.shepherd@roswellpark.org> ([ORCID](#))

Authors:

- Sean Davis <seandavi@gmail.com>

**See Also**

Useful links:

- <https://github.com/lshep/BiocBuildReporter.git>
- Report bugs at <https://github.com/lshep/BiocBuildReporter/issues>

---

get\_all\_bbs\_tables      *Retrieve all available Bioconductor build system parquet files*

---

**Description**

Retrieve all available parquet tables at once.

**Usage**

```
get_all_bbs_tables(  
  assign_to_global = FALSE,  
  useLocal = TRUE,  
  updateLocal = FALSE  
)
```

**Arguments**

|                  |  |
|------------------|--|
| assign_to_global | logical(1) indicating if downloaded tables should be assigned to the current global environment for access. Default is FALSE and only assigned to custom environment through call to get_bbs_table.  |
| useLocal         | A logical indicating if files should be read/downloaded from a local file or read remotely.  |
| updateLocal      | A logical indicating if using locally cached files, if the files should be re-downloaded/updated. Theoretically build reports are updated daily so the local data may be out of date if not updated. |

**Details**

This function is a quick wrapper around get\_bbs\_table to download all available parquet files as tibbles. By default no value is returned and the tibbles are stored to the custom environment and can be easily accessed through a call to get\_bbs\_table. If useLocal and updateLocal are TRUE, this also becomes an easy helper to update/redownload all files to the locally downloaded location.

**Value**

invisible. tables are cached to custom environment unless assign\_to\_global is TRUE.

**Author(s)**

Lori Shepherd

**See Also**

get\_bbs\_table

**Examples**

```
get_all_bbs_tables()

# Now that all are downloaded. Retrieve cached build_summary tibble
build_summary <- get_bbs_table("build_summary")

library(stringr)
library(dplyr)
# find the times the package BiocFileCache failed on linux nebbiolo builders

build_summary |>
  filter(
    package == "BiocFileCache",
    status %in% c("TIMEOUT", "ERROR"),
    str_starts(node, "nebbiolo")
  )
```

---

`get_bbs_table`*Retrieve a remotely read parquet file of Bioconductor build data*

---

**Description**

Bioconductor Build results are at times cumbersome to work with and interrogate. Parquet files of condensed reports are provided remotely. These functions read the remote parquet files using the arrow package and return a tibble. Once retrieved the table is stored in a custom environment for easy quick reference either to use ad hocly or within pre-defined queries provided by this package. If `useLocal` is chosen, the remote parquet files are downloaded locally and cached using `BiocFileCache`. If already downloaded, the local file is utilized unless `updateLocal` is also `TRUE` in which case the file will be redownloaded to the local location before reading into the session. If `useLocal` is `FALSE`, the files will be read remotely.

**Usage**

```
get_bbs_table(
  tblname = c("build_summary", "info", "propagation_status"),
  useLocal = TRUE,
  updateLocal = FALSE
)
```

**Arguments**

|             |  |
|-------------|--|
| tblname     | A valid parquet file name. Currently available: build_summary, info, or propagation_status.  |
| useLocal    | A logical indicating if files should be read/downloaded locally or read remotely.  |
| updateLocal | A logical indicating if using locally cached files, if the files should be re-downloaded/updated. Theoretically build reports are updated daily so the local data may be out of date if not updated. |

**Details**

The `get_bbs_table` returns a tibble but is also saved in a custom environment for quick easy subsequent reference. There are three tables available and can be specified in `get_bbs_table`: `build_summary`, `info`, or `propagation_status`. `build_summary` returns a tibble with the results of each stage of the Bioconductor build process. `info` returns a tibble with information regarding the package maintainer and git commit status. `propagation_status` returns a tibble with data on if a package propagated to the community.

**Value**

returns a tibble.

**Author(s)**

Lori Shepherd

**See Also**

`get_all_bbs_tables`

**Examples**

```
info <- get_bbs_table("info")
info

library(dplyr)
# all the package Lori Shepherd maintains
info |> filter(Maintainer == "Lori Shepherd") |> distinct(Package)
```

---

`get_build_report`*Get a report for any given day from the Bioconductor Build System*

---

**Description**

Get a report for any given day from the Bioconductor Build System, optionally specifying a git branch or build machine name.

**Usage**

```
get_build_report(build_date = Sys.Date(), branch = NULL, builder = NULL)
```

**Arguments**

|            |   |
|------------|---|
| build_date | Date of report to retrieve (eg. '2025-12-19')               |
| branch     | a bioconductor branch (eg. 'devel', 'RELEASE_3_22')         |
| builder    | name of a valid Bioconductor build machine (ie 'nebbiolol') |

**Details**

Utilizes data from the build\_summary and info parquet files to retrieve a reconstructed Bioconductor Build Report for any given day. Optionally a given build machine name or Bioconductor branch may be specified for further filtering. By default it will use today's date and retrieve both devel and current release for all Bioconductor build machines. NOTE: Traditionally Bioconductor splits builds into software, data-experiment, annotation, workflow, books; this distinction is not available in these functions and packages regardless of 'type' will be included. The returned tibble includes: package name, build node, build stage, package version number, status of stage, when the run started and ended, the command the builder ran, branch of bioconductor and relevant git commit information.

**Value**

tibble representing a Bioconductor build report for a given day

**Author(s)**

Lori Shepherd

**See Also**

get\_bbs\_table

**Examples**

```
get_build_report("2025-12-29", branch="RELEASE_3_22", builder="nebbiolol2")
```

---

get\_failing\_packages *Get list of failing packages for the most recent build*

---

**Description**

Get a list of failing (ERROR/TIMEOUT) packages for any given branch and builder

**Usage**

```
get_failing_packages(branch = NULL, builder = NULL)
```

**Arguments**

|         |   |
|---------|---|
| branch  | a bioconductor branch (eg. 'devel', 'RELEASE_3_22')         |
| builder | name of a valid Bioconductor build machine (ie 'nebbiolol') |

**Details**

Utilizes data from the build\_summary and info parquet files to list all packages failing (ERROR/TIMEOUT) in any stage of the process. Optionally a Bioconductor git branch can be specified and by default will do both the current devel and release. The report can be further filtered by optionally specifying a build machine name. The returned tibble includes: git branch, package name, package version number, build machine node, collapsed column of stages and statuses.

**Value**

a tibble of failing packages

**Author(s)**

Lori Shepherd

**See Also**

get\_bbs\_table

**Examples**

```
get_failing_packages("RELEASE_3_22")
get_failing_packages("RELEASE_3_22", "nebbiolo2")
```

---

get\_latest\_branches    *Get currently active Bioconductor git branches*

---

**Description**

Get currently active Bioconductor git branches

**Usage**

```
get_latest_branches(infoTbl = NULL)
```

**Arguments**

infoTbl            downloaded paraquet info table retrieved from get\_bbs\_table('info') that includes git\_branch information.

**Details**

Get currently active Bioconductor git branches

**Value**

character(2) 'devel' and RELEASE\_X\_Y value equivalent to current release.

**See Also**

get\_bbs\_table

**Examples**

```
get_latest_branches()
```

---

```
get_package_build_results
```

*Get the most recent build result data for a given package on a given branch*

---

**Description**

Get the build status information for a given package on a specified branch.

**Usage**

```
get_package_build_results(packagename, branch = "devel")
```

**Arguments**

|             |   |
|-------------|---|
| packagename | a single valid Bioconductor package name            |
| branch      | a bioconductor branch (eg. 'devel', 'RELEASE_3_22') |

**Details**

Utilizes data from the info and build\_summary parquet files to retrieve the latest build results for a specified package on a given branch. If no branch is given it defaults to use 'devel'. The data returned includes the node (builder machine name), stage (install, build, check), package version number, status of stage, date stage completed, and git information for the build (git branch, git commit hash, git commit date).

**Value**

tibble of build status information or NULL if package or branch is not found

**Author(s)**

Lori Shepherd

**See Also**

```
get_bbs_table
```

**Examples**

```
get_package_build_results("BiocFileCache")  
get_package_build_results("BiocFileCache", branch="RELEASE_3_22")
```

---

`get_package_release_info`

*Get git information for a given package across all Bioconductor releases*

---

## **Description**

Get the package version and git commit data for all releases in Bioconductor.

## **Usage**

```
get_package_release_info(packagename)
```

## **Arguments**

`packagename` a single valid Bioconductor package name

## **Details**

Utilizes data from the info parquet file to retrieve the equivalent git information for every available Bioconductor release of a package. This include the git commit hash and last commit date along with the package version.

## **Value**

tibble of release information or NULL if package is not found

## **Author(s)**

Lori Shepherd

## **See Also**

`get_bbs_table`

## **Examples**

```
get_package_release_info("BiocFileCache")
```

---

list\_all\_branches      *Get list of all Bioconductor git branches*

---

**Description**

Get list of all Bioconductor git branches

**Usage**

```
list_all_branches(infoTbl = NULL)
```

**Arguments**

infoTbl      downloaded paraquet info table retrieved from `get_bbs_table('info')` that includes `git_branch` information.

**Details**

Get list of all Bioconductor git branches

**Value**

character() vector listing all options for "branch"

**See Also**

`get_bbs_table`

**Examples**

```
list_all_branches()
```

---

list\_all\_builders      *Get list of all Bioconductor builders*

---

**Description**

Get list of all Bioconductor builders

**Usage**

```
list_all_builders(summaryTbl = NULL)
```

**Arguments**

summaryTbl      downloaded paraquet `build_summary` table retrieved from `get_bbs_table('build_summary')` that includes builder (node) information.

**Details**

Get list of all Bioconductor builders

**Value**

character() vector listing all options for "builder"

**See Also**

get\_bbs\_table

**Examples**

```
list_all_builders()
```

---

|                     |   |
|---------------------|---|
| package_error_count | <i>Get a count of how many time a package failed on the Bioconductor Build System</i> |
|---------------------|---|

---

**Description**

Get a count of how many time a package failed (ERROR/TIMEOUT) on the Bioconductor Build System; optionally can specify a specific builder or branch to filter results.

**Usage**

```
package_error_count(packagename, builder = NULL, branch = NULL)
```

**Arguments**

|             |  |
|-------------|--|
| packagename | a single valid Bioconductor package name                   |
| builder     | name of a valid Bioconductor build machine (ie 'nebbiol1') |
| branch      | a bioconductor branch (eg. 'devel', 'RELEASE_3_22')        |

**Details**

Utilizes data from the build\_summary and info parquet files to retrieve a count of errors (TIMEOUT/ERROR) for a specified package. Optionally a given builder machine name or Bioconductor branch may be specified to filter request. If no builder is given it will return all. If no branch is give it will also return all. The data returned includes the node (builder machine name), package version number, stage (install, build, check), total number of times that stage/builder tried to run, total number of times the package failed during that stage, and the given Bioconductor git branch. NOTE: since 'devel' is on-going. There will be multiple 'devel' results across multiple years not just the current devel. See example to filtering to see most recent. NOTE: If builder or branch is not found, function will continue and return unfiltered results.

**Value**

tibble of data including counts of runs and errors or NULL if package is not found

**Author(s)**

Lori Shepherd

**See Also**

get\_bbs\_table

**Examples**

```

package_error_count("BiocFileCache")
package_error_count("BiocFileCache", branch="RELEASE_3_22")
package_error_count("BiocFileCache", builder = "nebbiolo2", branch="RELEASE_3_22")

library(dplyr)
## devel will have more than just current devel
devErrors <- package_error_count("BiocFileCache", branch="devel")
## can use package version number to filter to current devel
devErrors |> filter(version == max(version))

```

---

package\_failures\_over\_time

*Get rough timeline overview of package failing events*


---

**Description**

Get rough timeline overview of a package failing events on a specific builder

**Usage**

```
package_failures_over_time(packagename, builder, failure_cluster_hours = 72)
```

**Arguments**

packagename      a single valid Bioconductor package name  
builder            name of a valid Bioconductor build machine (ie 'nebbiolo1')  
failure\_cluster\_hours  
                  numeric indicating the number of hours to treat failures as a single event

**Details**

This function attempts to give an overview of how long a package has been failing on a given builder. The time to treat failures as a single event is distinguished by consecutive days and by the failure\_cluster\_hours argument. Currently there is a different cadence of builds for release compared to devel so this allows the flexibility to define the timeline. Let's use the following example for interpretation of the result table: ““ version episode first\_failure last\_failure n\_failures  
2 3.1.0 3 2025-12-15 02:57:57 2025-12-16 21:29:20 3 3 3.1.0 2 2025-12-13 02:32:33 2025-12-13 02:32:33 1 4 3.1.0 1 2025-12-08 21:30:14 2025-12-11 21:27:29 4 stages statuses 2 buildsrc, checksrc ERROR 3 checksrc ERROR 4 buildsrc ERROR ““ The package version being built on the build system for this package is 3.1.0. The episode refers to the number of failing episodic events. If we look at the episode 1, the package started failing on December 8 and continued to fail until

December 11. During that time period there were 4 number of failures and they occurred during the build stage. The time between the last failure of the first episode and the second episode is from December 11 to December 13; we can infer then that the package built cleanly on December 12. During episode 2 the package failed solely on December 13 but during the check stage. Episode 3 began on Dec 15 and lasted until December 16 and had 3 failures but they occurred in either the build or check stage.

This hopefully can help determine if package failures are intermittent and how long a package is failing on a given builder.

**Value**

tibble of failure event information or NULL if package or builder is not found

**Author(s)**

Lori Shepherd

**See Also**

`get_bbs_table`

**Examples**

```
package_failures_over_time("BiocFileCache", "nebbiolo1", 24)
```

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