

# Package ‘BiocCheck’

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**Version** 1.40.0

**Title** Bioconductor-specific package checks

**Description** BiocCheck guides maintainers through Bioconductor best practices. It runs Bioconductor-specific package checks by searching through package code, examples, and vignettes. Maintainers are required to address all errors, warnings, and most notes produced.

**Depends** R (>= 4.3.0)

**License** Artistic-2.0

**VignetteBuilder** knitr

**Imports** BiocBaseUtils, BiocFileCache, BiocManager, biocViews (>= 1.33.7), callr, codetools, graph, httr2, knitr, methods, rvest, stringdist, tools, utils

**Suggests** RUnit, BiocGenerics, Biobase, jsonlite, rmarkdown, downloader, devtools (>= 1.4.1), usethis, BiocStyle, GenomicRanges, gert

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**biocViews** Infrastructure

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

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## Contents

BiocCheck . . . . .	2
BiocCheck-class . . . . .	5
BiocCheck-methods . . . . .	6
BiocCheckGitClone . . . . .	7
Context . . . . .	8
Message-class . . . . .	9
Message-methods . . . . .	9
<b>Index</b>	<b>10</b>

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BiocCheck	<i>Check a package's adherence with the Bioconductor Package Guidelines</i>
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## Description

Analyzes an R package for adherence with Bioconductor package guidelines and best practices. The check outputs are categorized into ERROR, WARNING, and NOTE. See the vignette for more details. BiocCheck is complementary to R CMD check, which should always be run first.

## Usage

```
BiocCheck(
  package = getwd(),
  checkDir = dirname(package),
  debug = FALSE,
  callr = FALSE,
  ...
)
```

## Arguments

package	The path to an R package directory or tarball (.tar.gz). The BiocCheck function is intended to be run from the package directory; therefore, the current working directory (given by getwd()) is the default.
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checkDir	The directory where the BiocCheck output directory will be stored. By default, it will be placed in the same directory as the package directory i.e., <code>dirname(pkg_dir)</code> .
debug	Whether to append the names of functions that correspond to each condition raised by BiocCheck in the written log (i.e., in the ' <code>&lt;package_name&gt;.BiocCheck</code> ' folder). This option is only relevant to developers and contributors to BiocCheck.
callr	<code>logical(1)</code> Whether to use the <code>callr</code> package to run BiocCheck in an isolated R session to prevent namespace collisions.
...	See the details section for available options. When running BiocCheck, options can be specified as:  <code>BiocCheck(package, `no-check-vignettes`=TRUE)</code>

### Details

`BiocCheck()` reviews R packages for adherence with Bioconductor package guidelines and best practices. See <https://contributions.bioconductor.org> for the latest guidance for writing Bioconductor software. Some rationale behind these best practices can be seen in the vignette and pages in the references section. The vignette also provides detailed explanations of all the checks performed by BiocCheck.

BiocCheck is called within R with

```
BiocCheck(<package>)
```

where `package` points to the source directory or the `.tar.gz` tarball that was created using R CMD `build`.

*Note* that BiocCheck is complementary to R CMD `check`. R CMD `check` should always be run first for best results.

### Value

`BiocCheck()` is chiefly called for the side effect of the check reporting. The function also creates a `<package_name>.BiocCheck` folder and returns a BiocCheck reference class with three main list elements:

error	Items to address before the package can be accepted
warning	Strongly suggested items that may require attention
note	Items to consider, though not required, before acceptance

### dot-options

**new-package** enable checks specific to new packages

**no-check-dependencies** disable check for bad dependencies

**no-check-deprecated** disable check for usage of deprecated packages

**no-check-remotes** disable check for usage of remote packages other than those hosted on CRAN or Bioconductor

**no-check-version-num** disable check for valid version number

**no-check-R-ver** disable check for valid R version

**no-check-pkg-size** disable check for package tarball size  
**no-check-file-size** disable check for individual file size  
**no-check-bioc-views** disable biocViews-specific checks (for non-BioC packages)  
**no-check-bbs** disable BBS-specific checks (for non-BioC packages). Valid DESCRIPTION  
**no-check-description** disable DESCRIPTION file checks  
**no-check-vignettes** disable vignette checks  
**no-check-library-calls** disable check usage of functions that install or update packages  
**no-check-install-self** disable check for require or library of itself  
**no-check-coding-practices** disable check for some common best coding practices  
**no-check-function-len** disable check for function length  
**no-check-man-doc** disable checks for man page documentation  
**no-check-news** disable checks for NEWS file  
**no-check-unit-tests** disable checks for unit tests  
**no-check-skip-bioc-tests** disable check for tests that skip when on bioc  
**no-check-formatting** disable checks for file formatting  
**no-check-CRAN** disable check for if package exists in CRAN  
**no-check-bioc-help** disable check for registration on Bioconductor mailing list and support site  
**build-output-file** file containing R CMD build output, for additional analysis  
**quit-with-status** enable exit code option when performing check

### Author(s)

Dan Tenenbaum, Lori Shepherd, and Marcel Ramos

### References

<https://contributions.bioconductor.org>

### See Also

[BiocCheck-class](#), [Message-class](#)

### Examples

```
packageDir <- system.file("testpackages", "testpkg0", package="BiocCheck")
BiocCheck(packageDir, `quit-with-status`=FALSE)
```

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BiocCheck-class	<i>A class for composing BiocCheck reports.</i>
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## Description

The BiocCheck class provides a framework for reporting checks based on Bioconductor guidelines. The class has several methods for working with the provided checks that handle and display messages and the display of the metadata. These methods also record the output of the BiocCheck() report in both plain text and JSON formats.

**Note** that currently, multiple BiocCheck runs will interfere with each other given that they are implemented via a reference class semantic. When running multiple checks in the same session, you can separate these instances by running them in separate processes (e.g., via BiocParallel).

## Details

The metadata includes a number of standard fields to allow easier troubleshooting and display of potentially relevant information. Currently, the fields included are

**BiocCheckVersion** The version of the BiocCheck package

**BiocVersion** The version of Bioconductor

**Package** The name of the package in check

**PackageVersion** The version of the package in check

**sourceDir** The directory of the package source or tarball in check

**installDir** The directory where the package is installed for testing, a temporary location by default

**BiocCheckDir** The directory where the <package>.BiocCheck folder is saved. Usually the same folder as the package in check

**platform** The platform/OS where the check is taking place

**isTarBall** Whether the package in check is a source directory or a tarball

## Value

A BiocCheck instance

## Fields

`log list()` A running list of all conditions raised (i.e., notes, warnings, errors)

`check character(1)` The title of the last check used for logging purposes.

`error, warning, note list()` Finer extraction of each condition type

`metadata list()` A list of additional information relevant to the package and its state. See details.

`verbose logical(1)` Whether to show the full information pertaining to the checks. A FALSE value will only show the condition messages and not any relevant files or additional information. The defaults are FALSE and TRUE for BiocCheck and BiocCheckGitClone, respectively.

**See Also**[Message-class](#)**Examples**

```
bc <- BiocCheck:::.BiocCheck
```

```
bc$verbose
```

---

BiocCheck-methods      *A list of methods for the BiocCheck reference class*

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**Description**

A list of methods for the BiocCheck reference class

**Arguments**

...	character() A vector that makes up the BiocCheck exception message (e.g., 'Vignette must be built by R CMD build'). The character vector is handled with <code>paste0</code> and made into a list and appended with <code>help_text</code> and <code>messages</code> .
<code>help_text</code>	character(1) Additional text prompting a list of files (e.g., "Found in files:").
<code>condition</code>	character(1) One of the three conditions handled: error, warning, or note
<code>messages</code>	character() Often a vector of file names where the check was triggered.
<code>verbose</code>	logical(1) Whether or not to output both the <code>help_text</code> and <code>messages</code> as part of the report
<code>debug</code>	logical(1) Whether to append the name of the originating check name into for trace-ability
<code>checkName</code>	character(1) The title of the current group of checks. It can be set with <code>handleCheck</code> , e.g., <code>handleCheck("Checking for version number mismatch...")</code> . Internally, it is saved with <code>setCheck</code> and obtained with <code>getLastCheck</code> .
<code>isOnBBS</code>	logical(1) Indicates whether the checks are being run on the Bioconductor Build System (BBS). This is helpful for avoiding the creation of folders in the BBS.
<code>file</code>	character(1) A path to a JSON file for writing or reading as created by <code>toJSON</code> and <code>fromJson</code> BiocCheck methods.

**Value**

An internal BiocCheck R5 Reference Class used to document conditions such as errors, warnings, and notes

**methods**

- add** Include a condition to the BiocCheck report
- getLastCheck** Obtain the name of the last check run
- setCheck** Create a new element in the internal list for a check
- get** Extract the list of conditions raised by BiocCheck
- getNum** Tally the number of condition provided by the input
- zero** Reset the internal log of the condition provided
- getBiocCheckDir** Report and create the <package>.BiocCheck directory as obtained from the metadata
- composeReport** Simplify the list structure from the log and provide a character vector of conditions raised
- report** Write the 00BiocCheck.log report into the BiocCheck folder
- toJSON** Write a JSON file to the location indicated with the conditions raised
- fromJSON** Read a JSON file from the location indicated with the output of previous conditions raised in the check
- show** Display the information in the class. Currently empty.
- show\_meta** Display the metadata information stored in the metadata field

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 BiocCheckGitClone

*Checks specific to a Git clone of a package repository*


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**Description**

Analyzes an R package for adherence with Bioconductor package guidelines and best practices. The check outputs are categorized into ERROR, WARNING, and NOTE. This function is typically used in the Bioconductor Build System (BBS) and not intended for general use.

**Usage**

```
BiocCheckGitClone(package = ".", ...)
```

**Arguments**

package	A directory containing an R source package. Not a package tar ball.
...	Currently, only quit-with-status is available. See BiocCheck

**Details**

BiocCheckGitClone() reviews R packages for adherence with Bioconductor package guidelines and best practices. See <https://contributions.bioconductor.org> for the latest guidance for writing Bioconductor software. This function should only be run on a source directory and not on a tarball.

BiocCheckGitClone is called within R with, as

```
BiocCheckGitClone(<package>)
```

where package is the source directory containing the R package.

**Value**

`BiocCheckGitClone()` is chiefly called for the side effect of the check reporting. The function returns a `BiocCheck` reference class with three main list elements:

<code>error</code>	Items to address before the package can be accepted
<code>warning</code>	Strongly suggested items that may require attention
<code>note</code>	Items to consider, though not required, before acceptance

**Author(s)**

Lori Shepherd

**References**

<https://contributions.bioconductor.org>

**See Also**

[BiocCheck-class](#)

**Examples**

```
packageDir <- system.file("testpackages", "testpkg0", package="BiocCheck")
BiocCheckGitClone(packageDir, `quit-with-status`=FALSE)
```

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Context	<i>Report context of events to user with a data.frame of events and locations</i>
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**Description**

Report context of events to user with a data.frame of events and locations

**Usage**

```
Context(file = "", lines = character(), idx = logical(), offset = 0L)
```

**Arguments**

<code>file</code>	character(1) full path (including package name) of file being summarized.
<code>lines</code>	character() vector of text lines in file
<code>idx</code>	logical() same length as <code>lines</code> indicating lines in which event occurs
<code>offset</code>	'integer(1)' The number of lines to add to the 'Line' column calculation. It is mainly used to account for the number of lines that the YAML header occupies.

**Value**

Context: a data.frame() with columns File, Line, and Context



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Message-class      *A lower level Message helper class for BiocCheck*

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**Description**

A lower level Message helper class for BiocCheck

**Value**

A Message class instance

**Fields**

`msg list()` A list of character messages usually grown with `append` with conditions raised by a check

`condition character(1)` One of the three conditions handled: error, warning, or note

**See Also**

[BiocCheck-class](#)

---

Message-methods      *A list of methods for the Message reference class*

---

**Description**

A list of methods for the Message reference class

**Arguments**

`condition`      `character(1)` One of the three conditions handled: error, warning, or note

`verbose`      `logical(1)` Whether to output the full text in the check or only the check name itself in the report

`...`      `list()` A nested list with the check name as the top level layer. Second level lists include any `help_text` and messages that are part of the check.

**Value**

An internal R5 Reference Class to handle messages and their conditions, e.g., for errors, warnings, or notes.

# Index

## \* **internal**

    BiocCheck-class, [5](#)

add,BiocCheck-method  
    (BiocCheck-methods), [6](#)

BiocCheck, [2](#)

BiocCheck-class, [4](#), [5](#), [8](#), [9](#)

BiocCheck-methods, [6](#)

BiocCheckGitClone, [7](#)

Context, [8](#)

getCondition,Message-method  
    (Message-methods), [9](#)

Message-class, [4](#), [6](#), [9](#)

Message-methods, [9](#)

setCondition,Message-method  
    (Message-methods), [9](#)

setMessage,Message-method  
    (Message-methods), [9](#)