

Package: BiocCheck (via r-universe)

September 8, 2024

Title Bioconductor-specific package checks

Version 1.41.17

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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.

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URL <https://github.com/Bioconductor/BiocCheck>

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

Depends R (>= 4.3.0)

Imports BiocBaseUtils, BiocFileCache, BiocManager, biocViews, callr, cli, codetools, graph, httr2, knitr, methods, rvest, stringdist, tools, utils

Suggests BiocStyle, devtools, gert, jsonlite, rmarkdown, tinytest, usethis

VignetteBuilder knitr

biocViews Infrastructure

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

Repository <https://bioc.r-universe.dev>

RemoteUrl <https://github.com/bioc/BiocCheck>

RemoteRef HEAD

RemoteSha aa7b6672a263d4b8be895c3cb6d9ee714cd66875

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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.
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., dirname(pkg_dir).
debug	Whether to append the names of functions that correspond to each condition raised by BiocCheck in the written log (i.e., in the '<package_name>.BiocCheck' folder). This option is only relevant to developers and contributors to BiocCheck.
callr	logical(1) Whether to use the callr 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: BiocCheck(package, `no-check-vignettes`=TRUE)

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)
```

BiocCheck-methods

A list of methods for the BiocCheck reference class

Description

A list of methods for the BiocCheck reference class

Arguments

<code>...</code>	<code>character()</code> 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>	<code>character(1)</code> Additional text prompting a list of files (e.g., "Found in files:")
<code>condition</code>	<code>character(1)</code> One of the three conditions handled: error, warning, or note
<code>messages</code>	<code>character()</code> Often a vector of file names where the check was triggered.

debug	logical(1) Whether to append the name of the originating check name into for trace-ability
checkName	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> .
isOnBBS	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.
file	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
- `addMetadata`: Add metadata to the BiocCheck object from a BiocPackage object
- `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

BiocCheckGitClone

Checks specific to a Git clone of a package repository

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:

- 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

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)
```

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

- file character(1) full path (including package name) of file being summarized.
- lines character() vector of text lines in file
- idx logical() same length as lines indicating lines in which event occurs
- offset 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

Message-class	<i>A lower level Message helper class for BiocCheck</i>
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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	<i>A list of methods for the Message reference class</i>
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Description

A list of methods for the Message reference class

Arguments

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

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