

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)

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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

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

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

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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><package_name>.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)
```

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

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 messages.
help_text	character(1) Additional text prompting a list of files (e.g., "Found in files:").
condition	character(1) One of the three conditions handled: error, warning, or note
messages	character() Often a vector of file names where the check was triggered.
verbose	logical(1) Whether or not to output both the <code>help_text</code> and messages as part of the report
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

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>
---------	---

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
- 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.

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