

Package ‘BiocCheck’

February 2, 2023

Version 1.34.2

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 (>= 4.2.0)

License Artistic-2.0

VignetteBuilder knitr

Imports biocViews (>= 1.33.7), BiocManager, stringdist, graph, httr, tools, codetools, methods, utils, knitr

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

Enhances codetoolsBioC

biocViews Infrastructure

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

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

RoxygenNote 7.2.1

Encoding UTF-8

git_url <https://git.bioconductor.org/packages/BiocCheck>

git_branch RELEASE_3_16

git_last_commit e352395

git_last_commit_date 2022-11-16

Date/Publication 2023-02-02

Author Bioconductor Package Maintainer [aut],
Lori Shepherd [aut],
Daniel von Twisk [ctb],
Kevin Rue [ctb],
Marcel Ramos [aut, cre] (<<https://orcid.org/0000-0002-3242-0582>>),
Leonardo Collado-Torres [ctb],
Federico Marini [ctb]

Maintainer Marcel Ramos <marcel.ramos@roswellpark.org>

R topics documented:

BiocCheck	2
BiocCheck-methods	4
BiocCheckGitClone	5
Context	7
Message-class	7
Message-methods	8

Index	9
--------------	----------

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

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: <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-namespace disable namespace 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

...	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: <code>error</code> , <code>warning</code> , or <code>note</code>
<code>messages</code>	character() Often a vector of file names where the check was triggered.

verbose	logical(1) Whether or not to output both the help_text and messages as part of the report
debug	logical(1) Whether to append the name of the originating check name into for traceability
checkName	character(1) The title of the current group of checks. It can be set with handleCheck, e.g., handleCheck("Checking for version number mismatch..."). Internally, it is saved with setCheck and obtained with getLastCheck.
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 toJSON and fromJSON BiocCheck methods.

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 @BiocCheck.log report into the BiocCheck folder
- writeNSsuggests** Write the namespace suggestions (@NAMESPACE.log) to 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(pkg = "", file = "", lines = character(), idx = logical())
```

Arguments

pkg	character(1) name of the package
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

Value

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

Message-class	<i>A lower level Message helper class for BiocCheck</i>
---------------	---

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.

Index

add, BiocCheck-method
(BiocCheck-methods), 4

BiocCheck, 2
BiocCheck-class, 4, 6, 7
BiocCheck-methods, 4
BiocCheckGitClone, 5

Context, 7

getCondition, Message-method
(Message-methods), 8

Message-class, 4, 7
Message-methods, 8

setCondition, Message-method
(Message-methods), 8

setMessage, Message-method
(Message-methods), 8