Package 'BiocCheck'

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Version 1.33.7

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)

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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

Enhances codetoolsBioC

biocViews Infrastructure

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

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

RoxygenNote 7.2.0

Encoding UTF-8

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BiocCheck	*Check a package's adherence with the Bioconductor Package Guidelines*

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 = ".", checkDir = dirname(package), debug = FALSE, ...)
```

Arguments

package	A directory or tarball (`.tar.gz` file) of an R package.
checkDir	A directory where the BiocCheck output directory will go. By default, it will be placed in the same directory as the package directory.
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 Bioc-Check.
...	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

Mainly, the side effect of the information displayed. When run interactively, BiocCheck() 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 `paste0` and made into a list and appended with `help_text` 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 `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 `00BiocCheck.log` report into the `BiocCheck` folder

writeNSsuggests Write the namespace suggestions (`00NAMESPACE.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

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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

Mainly, the side effect of the information displayed. When run interactively, `BiocCheckGitClone()` 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	*Report context of events to user with a data.frame of events and locations*

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	*A lower level Message helper class for BiocCheck*

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.

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