

Package ‘BiocCheck’

October 13, 2022

Version 1.32.1

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 7.1.2

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

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Author Bioconductor Package Maintainer [aut, cre],

Lori Shepherd [aut],

Daniel von Twisk [ctb],

Kevin Rue [ctb],

Marcel Ramos [ctb],

Leonardo Collado-Torres [ctb],

Federico Marini [ctb]

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

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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 = ".", 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 BiocCheck.
...	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.

... 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

Value

Mostly called for the side effect of the information displayed. When called interactively, returns a list with three components:

ERROR	Items that must be fixed before the package can be accepted into Bioconductor.
WARNING	We strongly suggest fixing these items.
NOTE	Fixing these items is not required, there is no expectation that considerations will escalate in severity.

Author(s)

Dan Tenenbaum, Lori Shepherd, and Marcel Ramos

References

<https://contributions.bioconductor.org>

Examples

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

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 <code>quit-with-status</code> is available. See <code>BiocCheck</code>

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

Mostly called for the side effect of the information displayed. When called interactively, returns a list with three components:

ERROR	Items that must be fixed before the package can be accepted into Bioconductor.
WARNING	We strongly suggest fixing these items.
NOTE	Fixing these items is not required, there is no expectation that considerations will escalate in severity.

Author(s)

Lori Shepherd

References

<https://contributions.bioconductor.org>

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(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

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