Package 'BiocCheck'

April 12, 2022

Version 1.30.0

Title Bioconductor-specific package checks

Description Executes Bioconductor-specific package checks.

Depends R (>= 3.5.0)

License Artistic-2.0

VignetteBuilder knitr

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

Suggests RUnit, BiocGenerics, Biobase, RJSONIO, rmarkdown, devtools
(>= 1.4.1), usethis, BiocStyle

Enhances codetoolsBioC

biocViews Infrastructure

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

RoxygenNote 7.1.1

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

git_branch RELEASE_3_14

git_last_commit 31109f8

git_last_commit_date 2021-10-26

Date/Publication 2022-04-12

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>

R topics documented:

BiocCheck	*Check a package for compliance with Bioconductor package guidelines*

Description

Analyzes R packages for compliance with Bioconductor package guidelines and best practices. Divides output into three categories: ERROR, WARNING, and NOTE. See the vignette for more details. Not meant to replace R CMD check, which should always be run first.

Usage

```
BiocCheck(package = ".", ...)
usage()
```

Arguments

package	A directory or tarball (.tar.gz file) containing an R source package.
...	Run usage() to see the available options. When running BiocCheck interactively, options can be passed like so: BiocCheck(package, `no-check-vignettes`=TRUE)

Details

BiocCheck() analyzes R packages for compliance with Bioconductor package guidelines and best practices. For the rationale behind these guidelines and best practices, see the vignette and pages in the references section. usage() displays the options that can be passed to BiocCheck().

BiocCheck is called within R with
BiocCheck(<package>)

where package is a directory or .tar.gz file containing an R source package.

BiocCheck is not meant as a replacement for R CMD check, which should always be run first for best results.

See the vignette for detailed explanations of all the checks performed by BiocCheck.

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 and Lori Shepherd

References

http://www.bioconductor.org/developers/how-to/coding-style/ http://www.bioconductor.org/developers/package-guidelines/ http://www.bioconductor.org/developers/how-to/version-numbering/ http://www.bioconductor.org/developers/how-to/unitTesting-guidelines/

Examples

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

BiocCheckGitClone	*Additional checks for a package for compliance with Bioconductor package guidelines*

Description

Analyzes R packages for compliance with Bioconductor package guidelines and best practices. Divides output into three categories: ERROR, WARNING, and NOTE. This function is not meant to replace R CMD check or BiocCheck.

Usage

```
BiocCheckGitClone(package=".", ...)
usage2()
```

Arguments

package	A directory containing an R source package. Not a package tar ball.
...	Only available option currently is quit-with-status. See BiocCheck

Details

`BiocCheckGitClone()` analyzes R packages for compliance with Bioconductor package guidelines and best practices. This function should only be run on a open source directory not a tarball.

`BiocCheckGitClone` is called within R with, as
BiocCheckGitClone(<package>)

where `package` is a directory containing an R source package.

`BiocCheckGitClone` is not meant as a replacement for R `CMD` check or `BiocCheck`.

See the vignette for detailed explanations of all the checks performed by `BiocCheckGitClone`.

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

<http://www.bioconductor.org/developers/how-to/coding-style/> <http://www.bioconductor.org/developers/package-guidelines/> <http://www.bioconductor.org/developers/how-to/version-numbering/> <http://www.bioconductor.org/developers/how-to/unitTesting-guidelines/>

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())

handleContext(ctxt, nlines = 6, width = getOption("width"))
```

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
ctxt	Object derived from Context()
nlines	numeric(1) The number of lines to provide context for.
width	numeric(1) The width of the console; defaults to the value given by getOption("width")

Value

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

handleContext: side effect is output on the message stream

Index