Package 'BiocCheck'

April 15, 2019

Version 1.18.0

Title Bioconductor-specific package checks

Description Executes Bioconductor-specific package checks.

Depends R (>= 3.5.0)

License Artistic-2.0

LazyData true

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)

Enhances codetoolsBioC

biocViews Infrastructure

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

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

git_branch RELEASE_3_8

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R topics documented:

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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. This function is mostly meant to be called from the operating system's command line (via R CMD BiocCheck; see the vignette). 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 typically called from the operating system's command line, as
R CMD 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.

Installing BiocCheck will attempt to install the BiocCheck script, which could fail; details in the vignette.

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

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)

## or from the operating system's command line as:
## R CMD BiocCheck myPackage
```

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 mostly meant to be called from the operating system's command line (via R CMD BiocCheckGitClone). Not meant to replace R CMD check or R CMD BiocCheck, which should always be run first.

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 typically called from the operating system's command line, as
R CMD BiocCheckGitClone package

where package is a directory containing an R source package.

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

Installing BiocCheck will attempt to install the BiocCheckGitClone script, which could fail; details in the vignette.

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)

## or from the operating system's command line as:
## R CMD BiocCheckGitClone myPackage
```

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