Package 'BiocCheck'

October 11, 2016

Version 1.8.2

Title Bioconductor-specific package checks

Description Executes Bioconductor-specific package checks.

Depends R (>= 3.2.0)

License Artistic-2.0

LazyData true

VignetteBuilder knitr

Imports biocViews (>= 1.33.7), BiocInstaller, graph, devtools (>= 1.4.1), httr, knitr, tools, optparse, codetools, methods

Suggests RUnit, BiocGenerics, Biobase, RJSONIO, rmarkdown

Enhances codetoolsBioC

biocViews Infrastructure

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

NeedsCompilation no

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R topics documented:

BiocCheck   *Check a package for compliance with Bioconductor package guide-*
                                   lines

Description

Analyzes R packages for compliance with Bioconductor package guidelines and best practices. Divides output into three categories: requirements, recommendations, and considerations. 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:

requirements	Items that must be fixed before the package can be accepted into Bioconductor. Equivalent in severity to ERRORs in R CMD check, though note that a single error does not cause BiocCheck to stop, thus multiple requirements are possible.

recommendations

    We strongly suggest fixing these items. Equivalent in severity to `WARNINGs` in `R CMD check`.

considerations Fixing these items is not required. Equivalent in severity to `NOTEs` in 'R CMD check', though unlike `NOTEs`

, there is no expectation that considerations will escalate in severity.

Author(s)

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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)

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

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