

Package ‘BiocCheck’

April 14, 2017

Version 1.10.1

Title Bioconductor-specific package checks

Description Executes Bioconductor-specific package checks.

Depends R (>= 3.3.0)

License Artistic-2.0

LazyData true

VignetteBuilder knitr

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

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

Enhances codetoolsBioC

biocViews Infrastructure

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

NeedsCompilation no

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R topics documented:

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BiocCheck	<i>Check a package for compliance with Bioconductor package guidelines</i>
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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)

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)
```

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

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