

# 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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**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

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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 <code>usage()</code> to see the available options. When running <code>BiocCheck</code> interactively, options can be passed like so: <code>BiocCheck(package, `no-check-vignettes`=TRUE)</code>

**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 <code>check</code> , though note that a single error does not cause <code>BiocCheck</code> to stop, thus multiple requirements are possible.
recommendations	We strongly suggest fixing these items. Equivalent in severity to WARNINGS in R CMD <code>check</code> .
considerations	Fixing these items is not required. Equivalent in severity to NOTES in 'R CMD <code>check</code> ', 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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