

Package ‘BiocStyle’

October 15, 2018

Title Standard styles for vignettes and other Bioconductor documents

Description Provides standard formatting styles for Bioconductor PDF and HTML documents. Package vignettes illustrate use and functionality.

Version 2.8.2

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Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Imports bookdown, knitr (>= 1.12), rmarkdown (>= 1.2), stats, utils, yaml

Suggests BiocGenerics, RUnit, htmltools

biocViews Software

License Artistic-2.0

VignetteBuilder knitr

Encoding UTF-8

URL <https://github.com/Bioconductor/BiocStyle>

BugReports <https://github.com/Bioconductor/BiocStyle/issues>

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| | |
|-------------------|---|
| BiocStyle-defunct | <i>Defunct functions in package ‘BiocStyle’</i> |
|-------------------|---|

Description

These functions are defunct and no longer available.

Details

The following functions are no longer available; use the replacement indicated below:

- latex_old, latex2: [latex](#)
- pdf_document_old, pdf_document2: [pdf_document](#)
- html_document_old, html_document2: [html_document](#)

| | |
|---------|--|
| helpers | <i>Specify Rmarkdown document metadata</i> |
|---------|--|

Description

Helper functions for including metadata in the document header.

Usage

```
pkg_ver(pkg)
```

```
doc_date()
```

Arguments

pkg character(1), package name

Details

Use doc_date to include document compilation date in the document metadata field 'date', and pkg_ver for package version specification in the 'package' field.

Value

Markdown-formatted character string.

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2014-2015

Examples

```
## current date
doc_date()

## package name with version
pkg_ver("BiocStyle")
```

| | |
|---------------|--|
| html_document | <i>Use Bioconductor style to format R Markdown HTML output</i> |
|---------------|--|

Description

Format for converting from R Markdown to an Bioconductor HTML document.

Usage

```
html_document(toc = TRUE, number_sections = TRUE, fig_width = NA,
  fig_height = NA, self_contained = TRUE, css = NULL,
  pandoc_args = NULL, ..., titlecaps = TRUE)
```

Arguments

| | |
|-----------------|---|
| toc | logical(1), TRUE to include a table of contents in the output |
| number_sections | logical(1), TRUE to number section headings |
| fig_width | numeric(1), default width (in inches) for figures |
| fig_height | numeric(1), default width (in inches) for figures |
| self_contained | numeric(1), TRUE to produce a standalone HTML file with no external dependencies, using data: URIs to incorporate the contents of linked scripts, stylesheets, images, and videos. Note that even for self contained documents MathJax is still loaded externally (this is necessary because of it's size). |
| css | character, one or more css files to include |
| pandoc_args | character, additional command line options to pass to pandoc |
| ... | Additional arguments passed to html_document |
| titlecaps | logical(1), TRUE to use the emphasize the first sentence in figure and table captions as title |

Details

BiocStyle:::html_document format extends the [html_document](#) format. See the [online documentation](#) and the package vignette "Authoring R Markdown Vignettes" for additional details on using the format,

Value

R Markdown output format to pass to [render](#)

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2014-2017

See Also

[pdf_document](#), [md_document](#)

Examples

```
## Not run:

# simple invocation
render("input.Rmd", BiocStyle::html_document())

# specify options
render("input.Rmd", BiocStyle::html_document(toc = FALSE))

## End(Not run)
```

latex

Use Bioconductor style to format LaTeX vignettes

Description

This function inserts code into a document preamble to provide a consistent style to Bioconductor vignettes.

Usage

```
latex(..., width, titlecaps = TRUE, short.fignames = FALSE, fig.path,
      use.unsrurl = TRUE, relative.path = FALSE)
```

Arguments

| | |
|----------------|--|
| ... | Additional arguments, passed to options . |
| width | integer(1), maximum number of columns on a line used in printing. See options . |
| titlecaps | logical(1), emphasize the first sentence of float captions |
| short.fignames | logical(1), indicates whether <code>\incfig</code> figures should be inserted and referred to using short names equal to corresponding code chunk labels without any additional prefix. |
| fig.path | character(1), custom prefix to be used for figure file names when used with <code>knitr</code> ; has no effect when compiled with <code>Sweave</code> . For details see opts_chunk . |
| use.unsrurl | logical(1), indicating that the ‘unsrurl’ style will be used (<code>\bibliographystyle</code> command <i>not</i> required). |
| relative.path | logical(1), copy supporting LaTeX files and use relative paths rather than absolute paths to system files. |

Details

Use is described in the ‘Bioconductor LaTeX Style 2.0’ vignette.

By default the ‘unsrturl’ bibliography style is used, which automatically creates links to URL, DOIs, etc. Use a different bibliography style with `use.unsrturl=FALSE` and standard LaTeX commands for styling bibliographies.

Value

The return value is a character string directing LaTeX to use the Bioconductor style file.

A side effect is setting any options specified as arguments.

Author(s)

Andrzej Oleś, Martin Morgan, Wolfgang Huber

Examples

```
## location of the .sty file
BiocStyle:::bioconductor.sty
```

macros

Link to packages on Bioconductor, CRAN and GitHub

Description

Functions for adding links to Bioconductor, CRAN and GitHub packages into R Markdown documents.

Usage

`Biocpkg(pkg)`

`Biocannopkg(pkg)`

`Biocexptpkg(pkg)`

`CRANpkg(pkg)`

`Rpackage(pkg)`

`Githubpkg(repo, pkg)`

Arguments

`pkg` character(1), package name

`repo` Repository address in the format `username/repo[/subdir]`

Details

Use `Biocpkg` for Bioconductor software, annotation and experiment data packages. The function automatically includes a link to the release landing page or if the package is only in devel, to the devel landing page.

Use `CRANpkg` for R packages available on CRAN. The function automatically includes a link to the master CRAN landing page.

Use `Githubpkg` for R packages available on GitHub. The `repo` should include the repository address in the format `username/repo[/subdir]`. If `package` is missing, the package name is assumed to be equal the repository name and is extracted from `repo`.

For R packages which are not available on Bioconductor, CRAN or GitHub use `Rpackage`.

Value

Markdown-formatted character vector containing a hyperlinked package name.

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2014-2015

Examples

```
## link to a Bioconductor package
Biocpkg("IRanges")
```

```
## link to a CRAN package
CRANpkg("data.table")
```

```
## link to an R package on GitHub
Githubpkg("rstudio/rmarkdown")
```

markdown

Use Bioconductor CSS style to format HTML vignettes

Description

This function sets the Bioconductor style sheet to provide a consistent style across Bioconductor HTML vignettes.

Usage

```
markdown(css.files, self.contained = TRUE, links.target = TRUE)
```

Arguments

`css.files` character vector containing the location of additional `.css` files.

`self.contained` logical(1), should the content of the CSS stylesheet files be included into the html file or should they be saved as separate files.

`links.target` logical(1), should external links open in new browser tab/window.

Details

Use is described in the ‘Bioconductor CSS Style’ vignette.

Value

No value is returned. The function is called for its side effect of setting the markdown and/or knitr specific options controlling the inclusion of the Bioconductor CSS style file in the HTML output.

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2014-2015

Examples

```
## location of the .css file
BiocStyle:::bioconductor.css
```

md_document

Convert to a BiocStyle markdown document

Description

Enable BiocStyle macros and author affiliations in markdown documents.

Usage

```
md_document(toc = TRUE, ...)
```

Arguments

| | |
|-----|---|
| toc | TRUE to include a table of contents in the output |
| ... | Additional function arguments to pass to the base R Markdown md_document output formatter |

Details

The `BiocStyle::md_document` format extends the base [md_document](#) format by means of specifying complex author affiliations. It also loads the BiocStyle package namespace to enable the use of helper functions, such as [Biocpkg](#).

Value

R Markdown output format to pass to [render](#)

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2015-2016

See Also

[html_document](#), [pdf_document](#)

Examples

```
## Not run:  
  
rmarkdown::render("input.Rmd", BiocStyle::md_document())  
  
## End(Not run)
```

output

Output format of an R Markdown document

Description

Helper function to determine the document's current pandoc output format.

Usage

```
output()
```

Details

The function is useful for defining different behavior depending on the output format, e.g. figure settings.

Value

A character string specifying the pandoc output format.

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2016

Examples

```
## Not run:  
## Switch between SVG and PDF figures depending on document output format  
knitr::opts_chunk$set(  
  dev = switch(output(), html = "svg", latex = "pdf")  
)  
  
## End(Not run)
```

pdf_document *Use Bioconductor style to format R Markdown PDF output*

Description

This function sets the Bioconductor style in PDF documents rendered using R Markdown v2.

Usage

```
pdf_document(toc = TRUE, number_sections = TRUE, fig_width = NA,  
             fig_height = NA, includes = NULL, ..., titlecaps = TRUE,  
             toc_newpage = FALSE, use_unsrurl = TRUE, relative_path = FALSE)
```

Arguments

| | |
|-----------------|--|
| toc | logical(1), TRUE to include a table of contents in the output |
| number_sections | logical(1), TRUE to number section headings |
| fig_width | numeric(1), default width (in inches) for figures |
| fig_height | numeric(1), default width (in inches) for figures |
| includes | Named list of additional content to include within the document (typically created using the includes function). |
| ... | Additional arguments passed to pdf_document . |
| titlecaps | logical(1), TRUE to use the emphasize the first sentence in figure and table captions as title |
| toc_newpage | logical(1), TRUE to start the table of contents on a new page. |
| use_unsrurl | logical(1), indicating that the ‘unsrurl’ style will be used (<code>\bibliographystyle</code> command <i>not</i> required). |
| relative_path | logical(1), copy supporting LaTeX files and use relative paths rather than absolute paths to system files. |

Value

R Markdown output format to pass to [render](#).

Author(s)

Andrzej Oleś <andrzej.oles@embl.de>, 2014-2017

See Also

[html_document](#), [md_document](#)

Examples

```
## Not run:  
  
# simple invocation  
render("input.Rmd", BiocStyle::pdf_document())  
  
# specify an option for latex engine  
render("input.Rmd", BiocStyle::pdf_document(toc = FALSE))  
  
## End(Not run)
```

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