Package 'BiocStyle'

April 14, 2017

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 2.2.1

Author Andrzej Oleś, Martin Morgan, Wolfgang Huber

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Imports stats, utils

Suggests base64enc, knitr (>= 1.12), rmarkdown (>= 1.2), BiocGenerics,
RUnit, yaml, 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

NeedsCompilation no

R topics documented:

| helpers | *Specify Rmarkdown document metadata* |

Description

Helper functions for including metadata in the document header.

Usage

```
doc_date()
pkg_ver(pkg)
```

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 | *Use Bioconductor style to format R Markdown HTML output* |

Description

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

Usage

```
html_document(toc = TRUE, toc_depth = 3, number_sections = TRUE,
  fig_width = 7, fig_height = 5, fig_retina = NULL,
  fig_caption = FALSE, dev = "png", smart = TRUE, self_contained = TRUE,
  highlight = "default", mathjax = "default", extra_dependencies = NULL,
  css = NULL, includes = NULL, keep_md = FALSE,
  lib_dir = NULL, md_extensions = NULL, pandoc_args = NULL, ...)
```

Arguments

toc	TRUE to include a table of contents in the output
toc_depth	Depth of headers to include in table of contents
number_sections	
	TRUE to number section headings
fig_width	Default width (in inches) for figures
fig_height	Default width (in inches) for figures
fig_retina	Scaling to perform for retina displays
fig_caption	TRUE to render figures with captions
dev	Graphics device to use for figure output (defaults to png)
smart	Produce typographically correct output, converting straight quotes to curly quotes, — to em-dashes, – to en-dashes, and ... to ellipses.
self_contained	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).
highlight	Syntax highlighting style. Supported styles include "default", "tango", "pygments", "kate", "monochrome", "espresso", "zenburn", "haddock", and "textmate". Pass NULL to prevent syntax highlighting.
mathjax	Include mathjax. The "default" option uses an https URL from the official MathJax CDN. The "local" option uses a local version of MathJax (which is copied into the output directory). You can pass an alternate URL or pass NULL to exclude MathJax entirely.
css	One or more css files to include
includes	Named list of additional content to include within the document (typically created using the [includes](#) function).
keep_md	Keep the markdown file generated by knitting.
lib_dir	Directory to copy dependent HTML libraries (e.g. jquery, bootstrap, etc.) into. By default this will be the name of the document with _files appended to it.
md_extensions	Markdown extensions to be added or removed from the default definition or R Markdown. See the [rmarkdown_format](#) for additional details.
pandoc_args	Additional command line options to pass to pandoc
extra_dependencies, ...	
	Additional function arguments to pass to the base R Markdown HTML output formatter [html_document_base](#)

Details

The BiocStyle::html_document format is based on the [html_document](#) format. See the [online documentation](#) for additional details on using the html_document format.

R Markdown documents can have optional metadata that is used to generate a document header that includes the title, author, date, package info and abstract. For more details see the documentation on R Markdown [metadata](#).

R Markdown documents also support citations. You can find more information on the markdown syntax for citations in the [Bibliographies and Citations](#) article in the online documentation.

Value

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

Author(s)

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

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 styles to format LaTeX vignettes*

Description

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

Usage

```
latex(..., width=90, short.fignames=FALSE, fig.path, error=FALSE,
      use.unsrturl=TRUE)
```

Arguments

`...`	Additional arguments, passed to `options`.
`width`	integer(1), maximum number of columns on a line used in printing. See `options`.
`short.fignames`	logical(1), indicates whether `\incfig` 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 `knitr`; has no effect when compiled with Sweave. For details see `opts_chunk`.
`error`	logical(1), behavior of `knitr` when errors occur in vignette code chunks, has no effect when compiled with Sweave. The default (FALSE) means that errors stop vignette processing, which is appropriate when packages are being built and checked. For details see `opts_chunk`.
`use.unsrturl`	logical(1), indicating that the 'unsrturl' style will be used (`\bibliographystyle` command *not* required).

Details

Use is described in the 'Bioconductor LaTeX Style' vignette.

By default the 'unsrturl' bibliography style is used, which automatically creates links to URL, DOIs, etc. Use a different `bibliographystyle` 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)

Martin Morgan mtmorgan@fhcrc.org, Andrzej Oleś, Wolfgang Huber

Examples

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

---

latex2 *Use Bioconductor styles to format LaTeX vignettes*

Description

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

Usage

```
latex2(..., width, titlecaps = TRUE, short.fignames=FALSE, fig.path,
       use.unsrturl=TRUE)
```

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 `\incfig` 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 `knitr`; has no effect when compiled with Sweave. For details see `opts_chunk`.
`use.unsrturl`	logical(1), indicating that the 'unsrturl' style will be used (`\bibliographystyle` command *not* required).

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 `bibliographystyle` 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:::bioconductor2.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)
CRANpkg(pkg)
Githubpkg(repo, pkg)
Rpackage(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 FHCRC CRAN mirror 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   *Enable BiocStyle macros and a hyperlinked TOC in markdown output*

Description

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

Usage

```
md_document(toc = TRUE, toc_depth = 3, ...)
```

Arguments

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

Details

The BiocStyle::md_document format extends the md_document format by a hyperlinked TOC. 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

See Also

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

Examples

```
## Not run:

# simple invocation
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, use.unsrturl = TRUE, includes, ...)
```

Arguments

toc
: logical(1), TRUE to include a table of contents in the output.

number_sections
: logical(1), TRUE to number section headings.

use.unsrturl
: logical(1), indicating that the 'unsrturl' style will be used (\bibliographystyle command *not* required).

includes
: Named list of additional content to include within the document

...
: Additional arguments, passed to [pdf_document](#).

Value

R Markdown output format to pass to rmarkdown::render.

Author(s)

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

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)
```

Index