

Package ‘BiocStyle’

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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 1.4.1

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Suggests knitr (>= 1.7), rmarkdown, BiocGenerics, RUnit

biocViews Software

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VignetteBuilder knitr

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

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

Usage

```
html_document(css, theme = NULL, ...)
```

Arguments

css	character, additional CSS files to include
theme	Visual theme ("default", "cerulean", "journal", "flatly", "readable", "spacelab", "united", or "cosmo"). Pass NULL for no theme (in this case you can use the css parameter to add your own styles).
...	Additional arguments, passed to html_document .

Value

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

Author(s)

Andrzej Oles, 2014

See Also

[pdf_document](#)

Examples

```
## Not run:  
  
# simple invocation  
render("input.Rmd", BiocStyle::html_document())  
  
# specify options  
render("input.Rmd", BiocStyle::html_document(toc = TRUE))  
  
## 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.unsrurl=TRUE)
```

Arguments

<code>...</code>	Additional arguments, passed to options .
<code>width</code>	integer(1), maximum number of columns on a line used in printing. See options .
<code>short.fignames</code>	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.
<code>fig.path</code>	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 .
<code>error</code>	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 .
<code>use.unsrurl</code>	logical(1), indicating that the 'unsrurl' style will be used (<code>\bibliographystyle</code> command <i>not</i> required).

Details

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

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

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Examples

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

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 Oles, 2014

Examples

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

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.unsrurl = 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.unsrurl` logical(1), indicating that the ‘unsrurl’ 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 Oles, 2014

See Also

[html_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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