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 1.6.0

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

biocViews Software

License Artistic-2.0

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

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

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)
```

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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 Oles, Wolfgang Huber

Examples

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

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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 beincluded into the html file or should they be saved as separte 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
```

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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 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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