# 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** 2.37.0

**Imports** bookdown, knitr (>= 1.30), rmarkdown (>= 1.2), stats, utils, yaml, BiocManager

**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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**Author** Andrzej Oleś [aut] (ORCID: <https://orcid.org/0000-0003-0285-2787>),
Mike Smith [ctb] (ORCID: <https://orcid.org/0000-0002-7800-3848>),
Martin Morgan [ctb],
Wolfgang Huber [ctb],
Bioconductor Package Maintainer [cre]

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

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`BiocStyle-defunct` *Defunct functions in package 'BiocStyle'*

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## 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` *Specify Rmarkdown document metadata*

---

## 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` *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, 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.unsrturl = 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 \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). |
| 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 `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:::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, vignette = NULL, label = NULL)

Biocbook(pkg, label = NULL)

Biocannopkg(pkg)

Biocexptpkg(pkg)

CRANpkg(pkg)

Rpackage(pkg)

Githubpkg(repo, pkg)
```

## Arguments

| | |
|---|---|
| pkg | character(1), package name |
| vignette | character(1), basename of vignette link, including html or pdf extension, e.g., "work-0-intro.html". |
| label | character(1) label used to identify the package or vignette. If NULL, defaults to pkg. |
| repo | Repository address in the format username/repo[/subdir] |

## Details

Use Biocpkg for Bioconductor software, annotation, experiment data, and workflow packages. When vignette=NULL, the function automatically includes a link to the package landing page, the version of which depends on the current Bioconductor version (i.e. if run in a devel environment, it will point towards the devel landing page; otherwise it will point to the release landing page).

Use Biocbook for Bioconductor webbooks. This will create a link to the index page of the book rather than to the landing page of the package used for the book's deployment.

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. If vignette != NULL, the address of the specified vignette is returned.

## Author(s)

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

## Examples

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

## link to a Bioconductor annotation package
Biocpkg("org.Mm.eg.db")

## link to a Bioconductor experiment data package
Biocpkg("affydata")

## link to a Bioconductor workflow
Biocpkg("simpleSingleCell")
Biocpkg(
    "simpleSingleCell",
    vignette = "work-0-intro.html",
    label = "Episode 1: analyzing scRNA-seq data with R/Bioconductor"
)
```

```
## 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 specifing 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_unsrturl = 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_unsrturl | logical(1), indicating that the 'unsrturl' style will be used (\bibliographystyle command *not* 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)
```

use_vignette_html *Create 'Rmd' vignette templates for HTML or PDF output*

## Description

Create 'Rmd' vignette templates for HTML or PDF output

## Usage

```
use_vignette_html(destination = tempfile(fileext = ".Rmd"))

use_vignette_pdf(destination = tempfile(fileext = ".Rmd"))
```

## Arguments

| | |
|---|---|
| destination | character(1) file path to destination. The directory of the destination must already exist, and the file must not. The default creates a file in the temporary directory, and so is removed when the R session ends. |

## Examples

```
use_vignette_html()
```

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