Package 'BiocWorkflowTools'

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.4.2

Encoding UTF-8

Description Provides functions to ease the transition between Rmarkdown and LaTeX documents when authoring a Bioconductor Workflow.

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Depends R (>= 3.3)

Imports BiocStyle, bookdown, git2r, httr, knitr, rmarkdown, stringr, tools, utils

NeedsCompilation no

VignetteBuilder knitr

biocViews Software, ReportWriting

RoxygenNote 6.0.1

Collate 'f1000_article.R' 'uploadToOverleaf.R' 'markdownToLatex.R' 'utils.R'

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R topics documented:

f1000_article *F1000Research article format*

Description

Format for creating F1000Research software tool articles.

Usage

```
f1000_article(toc = FALSE, number_sections = FALSE, fig_width = 5.67,
  fig_height = fig_width, fig_align = "center", keep_tex = TRUE,
  citation_package = "natbib", md_extensions = "+link_attributes",
  pandoc_args = "--wrap=preserve", ...)
```

Arguments

toc	TRUE to include a table of contents in the output
number_sections	TRUE to number section headings
fig_width	Default width (in inches) for figures
fig_height	Default width (in inches) for figures
fig_align	Default alignment of figures. Possible values are "center" (default) "left" and "right".
keep_tex	Keep the intermediate tex file used in the conversion to PDF
citation_package	The LaTeX package to process citations, natbib or biblatex. Use none if neither package is to be used.
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
...	Arguments to pdf_document

Details

Creates LaTeX sources which can be submitted to F1000Research through Overleaf.

Value

R Markdown output format to pass to render

Citations

R Markdown supports automatic generation of citations. You can find more information on the markdown citation syntax in the Bibliographies and Citations article in the R Markdown online documentation.

A bibliography file can be specified using the bibliography metadata field in the document's YAML header. Metadata variables for customizing citation style include:

biblio-style Bibliography style (e.g. "unsrtnat", "plainnat")

natbiboptions Options to natbib LaTeX package (e.g. "number", "super", "round")

biblatexoptions Options to biblatex LaTeX package

Examples

```
## Not run:

rmarkdown::draft("MyArticle.Rmd", template="f1000_article", package="BiocWorkflowTools")

## End(Not run)
```

`markdownToLatex` *Convert R markdown to F1000 latex*

Description

Turn Rmarkdown version of workflow document into latex file that can be uploaded to F1000 Overleaf.

Usage

```
markdownToLatex(input, output = NULL, compress = TRUE)
```

Arguments

`input`	path to Rmd file to be converted
`output`	Specifies the folder where the output should be written. If left NULL this defaults to the same folder as the input file.
`compress`	If TRUE a zip file of the output directory is created, which can be uploaded to Overleaf

Details

This function has been deprecated. The recommended way to create the F1000 LaTeX and pdf version is to ensure your Rmarkdown document has the property 'output: BiocWorkflowTools::f1000_article' in the YAML header, and to use the function `render` in the `rmarkdown` pacakge on the document (or use the 'knit' button in RStudio).

Value

No value is returned, but a tex file is written to disk, and is given an identical name to the input Rmd except for the file extension. Accompanying figures are copied to the output directory long with style files and figures required to match the F1000 Research format.

Optionally the output directory can be compressed into a zip archive, which can then be uploaded to Overleaf either manually, or by passing it to the function `uploadToOverleaf`.

Examples

```
## Not run:
example_Rmd <- system.file('examples/f1000_software_example.Rmd',
                           package = "BiocWorkflowTools")
output_dir <- file.path(tempdir(), 'example')
markdownToLatex(input = example_Rmd, output = output_dir,
```

```
                compress = TRUE)

## End(Not run)
```

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uploadToOverleaf *Upload a LaTeX project to Overleaf*

Description

Upload a LaTeX project to Overleaf

Usage

```
uploadToOverleaf(path, forceNewProject = FALSE, openInBrowser = FALSE,
  git = FALSE)
```

Arguments

path	File path to a directory or a single zip file to be uploaded.
forceNewProject	Logical specifying if a new Overleaf project should be create, even if the function detects this document has already has an associated project. Default value is FALSE.
openInBrowser	Boolean determining whether to open a browser at the created Overleaf project or not. Default value is FALSE.
git	Boolean specifying whether to initialize a local clone of the Overleaf project's git repository

Value

The URL where the uploaded project can be accessed is printed to the screen and invisibly returned from the function. If the argument `openInBrowser` is set to `TRUE`, then the Overleaf project page will automatically open in the default browser.

Examples

```
## Not run:
example_Rmd <- system.file('examples/f1000_software_example.Rmd',
                           package = "BiocWorkflowTools")
output_dir <- file.path(tempdir(), 'example')
markdownToLatex(input = example_Rmd, output = output_dir,
                compress = TRUE)

## don't run this code chunk in the example as we don't want to spam Overleaf
zip_file <- paste0(output_dir, '.zip')
uploadToOverleaf(files = zip_file, openInBrowser = TRUE)

## End(Not run)
```

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