Package 'BiocWorkflowTools'

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.2.0

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, rmarkdown, tools, stringr, httr, knitr,
utils

NeedsCompilation no

VignetteBuilder knitr

biocViews Software, ReportWriting

RoxygenNote 6.0.1

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

Author Mike Smith [aut, cre],
Andrzej Oleś [aut]

Maintainer Mike Smith <grimbough@gmail.com>

R topics documented:

f1000_article *F1000 article format*

Description

Format for creating F1000 software articles.

Usage

```
f1000_article(toc = FALSE, number_sections = FALSE, keep_tex = TRUE,
  md_extensions = "+link_attributes", extra_dependencies = NULL, ...)
```

Arguments

toc TRUE to include a table of contents in the output

number_sections

TRUE to number section headings

keep_tex Keep the intermediate tex file used in the conversion to PDF

md_extensions Markdown extensions to be added or removed from the default definition or R Markdown. See the [rmarkdown_format](#) for additional details.

extra_dependencies

A LaTeX dependency latex_dependency(), a list of LaTeX dependencies, a character vector of LaTeX package names (e.g. c("framed", "hyperref")), or a named list of LaTeX package options with the names being package names (e.g. list(hypreref = c("unicode=true", "breaklinks=true"), lmodern = NULL)). It can be used to add custom LaTeX packages to the .tex header.

... Arguments to rmarkdown::pdf_document

Details

Creates a latex file that can be uploaded to F1000 Overleaf

Value

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

Examples

```
## Not run:
rmarkdown::draft("MyArticle.Rmd", template="f1000_article", package="BiocWorkflowTools")

## End(Not run)
```

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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 de-
              faults 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

```
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)
```

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uploadToOverleaf   *Upload a LaTeX project to Overleaf*

Description

Upload a LaTeX project to Overleaf

Usage

```
uploadToOverleaf(files = NULL, forceNewProject = FALSE,
  openInBrowser = FALSE)
```

Arguments

files	Character vector of file names to upload. If the first entry is a zip file this is uploaded directly. Otherwise the files will be added to a zip archive and then 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.

Value

No value is returned. The URL where the uploaded project can be accessed is printed to the screen. If the argument openInBrowser is set to TRUE, then the default browser will automatically open at the Overleaf project page.

Examples

```
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)
## Not run:
## 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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