

Package ‘BiocWorkflowTools’

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.0.0

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 rmarkdown, tools, stringr, httr, knitr, utils

NeedsCompilation no

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VignetteBuilder knitr

Suggests BiocStyle

biocViews Software, ReportWriting

RoxygenNote 5.0.1

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markdownToLatex	<i>Convert R markdown to F1000 latex</i>
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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

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)
```

uploadToOverleaf	<i>Upload a LaTeX project to Overleaf</i>
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Description

Upload a LaTeX project to Overleaf

Usage

```
uploadToOverleaf(files = NULL, 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.
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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