Package ‘BiocWorkflowTools’

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.8.0

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 (>= 3.4)

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

NeedsCompilation no

VignetteBuilder knitr

biocViews Software, ReportWriting

RoxygenNote 6.0.1

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

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`createBiocWorkflow` *Create a New Bioconductor Workflow Package*

Description

Uses `create` to set up a skeleton for a new Bioconductor workflow package.

Usage

```
createBiocWorkflow(path, description = getOption("devtools.desc"),
  rstudio = TRUE, ..., open = rstudio)
```

Arguments

`path`	location to create new package. The last component of the path will be used as the package name.
`description`	list of description values to override default values or add additional values.
`rstudio`	if `TRUE`, creates an RStudio project file.
`...`	other arguments passed to `create`.
`open`	if `TRUE`, opens the RStudio project.

Value

File path to the R Markdown vignete (invisibly).

Examples

```
createBiocWorkflow(file.path(tempdir(), "MyWorkflow"), open = FALSE)
```

`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)
```

`uploadToOverleaf` *Upload a LaTeX project to Overleaf*

Description

Upload a LaTeX project to Overleaf

Usage

```
uploadToOverleaf(path)
```

Arguments

`path`	File path to a directory or a single zip file to be uploaded.

Value

Does not return any value. The Overleaf project page will automatically open in the default browser.

Examples

```
## Not run:
## don't run this code chunk in the example as we don't want to spam Overleaf
uploadToOverleaf(files = 'MyWorkflow', openInBrowser = TRUE)

## End(Not run)
```

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