

Package ‘BiocWorkflowTools’

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.24.0

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, git2r, httr, knitr, rmarkdown, rstudioapi, stringr, tools, utils, usethis

NeedsCompilation no

VignetteBuilder knitr

biocViews Software, ReportWriting

RoxygenNote 7.1.0

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

git_url <https://git.bioconductor.org/packages/BiocWorkflowTools>

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createBiocWorkflow *Create a New Bioconductor Workflow Package*

Description

Uses [create_package](#) 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. |
| open | if TRUE, opens the project in a new RStudio session. |

Value

File path to the R Markdown vignette (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 height (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. "unsrnat", "plainnat")
natbiboptions Options to natbib LaTeX package (e.g. "number", "super", "round")
biblatoptions Options to biblatox LaTeX package

Examples

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

| | |
|------------------|-------------------------------------------|
| uploadToOverleaf | <i>Upload a LaTeX project to Overleaf</i> |
|------------------|-------------------------------------------|

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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