

Package ‘BiocWorkflowTools’

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.34.0

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	<i>Create a New Bioconductor Workflow Package</i>
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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	<i>F1000Research article format</i>
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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

<code>toc</code>	TRUE to include a table of contents in the output
<code>number_sections</code>	TRUE to number section headings
<code>fig_width</code>	Default width (in inches) for figures
<code>fig_height</code>	Default height (in inches) for figures
<code>fig_align</code>	Default alignment of figures. Possible values are "center" (default) "left" and "right".
<code>keep_tex</code>	Keep the intermediate tex file used in the conversion to PDF
<code>citation_package</code>	The LaTeX package to process citations, natbib or biblatex. Use none if neither package is to be used.
<code>md_extensions</code>	Markdown extensions to be added or removed from the default definition or R Markdown. See the rmarkdown_format for additional details.
<code>pandoc_args</code>	Additional command line options to pass to pandoc
<code>...</code>	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")
 biblatexoptions Options to biblatex 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>
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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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