Package ‘BiocWorkflowTools’

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Title Tools to aid the development of Bioconductor Workflow packages

Version 1.33.0

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'

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Contents

`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. "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)
```

`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)
```

Index