

# Package ‘BiocWorkflowTools’

July 15, 2025

**Title** Tools to aid the development of Bioconductor Workflow packages

**Version** 1.35.0

**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>

**git\_branch** devel

**git\_last\_commit** 1a72194

**git\_last\_commit\_date** 2025-04-15

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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

|                  |                                                                                                                                                        |
|------------------|--------------------------------------------------------------------------------------------------------------------------------------------------------|
| 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 <a href="#">rmarkdown_format</a> for additional details. |
| pandoc_args      | Additional command line options to pass to pandoc                                                                                                      |
| ...              | Arguments to <a href="#">pdf_document</a>                                                                                                              |

## 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)
```

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|                  |                                           |
|------------------|-------------------------------------------|
| 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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