

# Package ‘BiocWorkflowTools’

December 17, 2025

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

**Version** 1.37.0

**Encoding** UTF-8

**Description** Provides functions to ease the transition between  
Rmarkdown and LaTeX documents when authoring a Bioconductor  
Workflow.

**License** MIT + file LICENSE

**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** 23b271e

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.23

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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. "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)
```

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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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