

# Package ‘AnVILPublish’

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**Title** Publish Packages and Other Resources to AnVIL Workspaces

**Version** 1.13.3

**Description** Use this package to create or update AnVIL workspaces from resources such as R / Bioconductor packages. The metadata about the package (e.g., select information from the package DESCRIPTION file and from vignette YAML headings) are used to populate the 'DASHBOARD'. Vignettes are translated to python notebooks ready for evaluation in AnVIL.

**License** Artistic-2.0

**Imports** AnVIL, BiocBaseUtils, BiocManager, httr, jsonlite, rmarkdown, yaml, readr, whisker, tools, utils, stats

**Suggests** knitr, BiocStyle, testthat (>= 3.0.0)

**biocViews** Infrastructure, Software

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**VignetteBuilder** knitr

**Config/testthat/edition** 3

**git\_url** <https://git.bioconductor.org/packages/AnVILPublish>

**git\_branch** devel

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**Repository** Bioconductor 3.19

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|------------|--|
| add_access | <i>Add Bioconductor_User group to workspace access</i> |
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### Description

add\_access() adds the Bioconductor\_User group to a workspace with READER permissions. Users gain access to the workspace (and others) by being added to the Bioconductor\_User group.

### Usage

```
add_access(namespace, name)
```

### Arguments

|           |   |
|-----------|---|
| namespace | character(1) namespace (billing account) under which the workspace belongs. |
| name      | character(1) name of the workspace to add access credentials.               |

### Value

add\_access() returns TRUE, invisibly.

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|             |   |
|-------------|---|
| as_notebook | <i>Render vignettes as .ipynb notebooks</i> |
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### Description

as\_notebook() renders Rmarkdown (.Rmd) or Quarto (.Qmd) vignettes as Jupyter (.ipynb) notebooks. The vignettes and notebooks are updated in an AnVIL workspace.

### Usage

```
as_notebook(
  rmd_paths,
  namespace,
  name,
  update = FALSE,
  type = c("ipynb", "rmd", "both"),
  quarto = c("render", "convert")
)
```

**Arguments**

|           |  |
|-----------|--|
| rmd_paths | character() paths to Rmd or Qmd files.   |
| namespace | character(1) AnVIL namespace (billing project) to be used.   |
| name      | character(1) AnVIL workspace name.   |
| update    | logical(1) Update (over-write any similarly named notebooks) an existing workspace? The default (FALSE) creates notebooks locally, e.g., for previewing via jupyter notebook *ipynb.   |
| type      | character(1) The type of notebook to be copied to the workspace. Must be on of ipynb, rmd, or both. ipynb copies only the Jupyter notebook. rmd copies Rmarkdown and Quarto vignettes. both copies both notebooks and vignettes. |
| quarto    | character(1) If the program Quarto is installed, this parameter indicates whether the .Rmd files will be rendered or converted. See vignette for more details.   |

**Details**

See the vignette "Publishing R / Bioconductor Packages To AnVIL Workspaces" for details on the conversion process; best results are obtained when Quarto software is available.

**Value**

as\_notebook() returns the paths to the local (if update = FALSE) or the workspace notebooks.

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|              |  |
|--------------|--|
| as_workspace | <i>Render R packages as AnVIL workspaces</i> |
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**Description**

as\_workspace() renders a package source tree (e.g., from a git checkout) as an AnVIL workspace.

**Usage**

```
as_workspace(
  path,
  namespace,
  name = NULL,
  create = FALSE,
  update = FALSE,
  use_readme = FALSE,
  type = c("ipynb", "rmd", "both"),
  quarto = c("render", "convert")
)
```

**Arguments**

|            |  |
|------------|--|
| path       | character(1) path to the location of the package source code.  |
| namespace  | character(1) AnVIL namespace (billing project) to be used.   |
| name       | character(1) AnVIL workspace name.   |
| create     | logical(1) Create a new project?   |
| update     | logical(1) Update (over-write the existing DASHBOARD and any similarly named notebooks) an existing workspace? If neither create nor update is TRUE, the code to create a workspace is run but no output generated; this can be useful during debugging. |
| use_readme | logical(1) Defaults to FALSE; if TRUE the content of README.md in package top-level folder is used with the package DESCRIPTION version and provenance metadata for rendering in the workspace 'DASHBOARD'.  |
| type       | character(1) The type of notebook to be copied to the workspace. Must be one of ipynb, rmd, or both. ipynb copies only the Jupyter notebook. rmd copies Rmarkdown and Quarto vignettes. both copies both notebooks and vignettes.                        |
| quarto     | character(1) If the program Quarto is installed, this parameter indicates whether the .Rmd files will be rendered or converted. See vignette for more details.   |

**Details**

Information from the DESCRIPTION file and Rmd YAML are used to populate the 'DASHBOARD' tab. See ?as\_notebook() for details on how vignettes are processed to notebooks.

**Value**

as\_workspace() returns the URL of the updated workspace, invisibly.

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