

# Package ‘AnVILPublish’

February 27, 2021

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

**Version** 1.0.0

**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, httr, rmarkdown, whisker, tools, utils, stats,

**Suggests** knitr, BiocStyle, BiocManager

**biocViews** Infrastructure, Software

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

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

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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 .Rmd vignettes as .ipynb notebooks, and updates the notebooks in an AnVIL workspace.

**Usage**

```
as_notebook(rmd_paths, namespace, name, update = FALSE)
```

**Arguments**

rmd_paths	character() paths to to Rmd 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.

**Details**

.Rmd Vignettes are processed to .md using rmarkdown::render(..., md\_document()), and then translated to .ipynb using python software called notedown; notedown is available at <https://github.com/aaren/notedown>.

The translation is not perfect, for instance code chunks marked as `eval = FALSE` are not marked as such in the python notebook.

**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)
```

**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 or NULL. If NULL, the workspace name is set to "Bioconductor-Package-<pkgname>", where <pkgname> is the name of the package (from the DESCRIPTION file) at path.
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.

**Details**

Information from the DESCRIPTION file and Rmd YAML files are used to populate the 'DASHBOARD' tab.

See `?as_notebook()` for details on how vignettes are processed to notebooks, and the limitations of the current approach.

**Value**

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

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