

Package: AnVILPublish (via r-universe)

May 29, 2026

Title Publish Packages and Other Resources to AnVIL Workspaces

Version 1.22.0

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, AnVILGCP, BiocBaseUtils, BiocManager, httr, jsonlite, rmarkdown, yaml, readr, whisker, tools, utils, stats

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

biocViews Infrastructure, Software

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

VignetteBuilder knitr

Config/testthat/edition 3

Date 2026-04-24

Config/pak/sysreqs
cmake make libicu-dev libsecret-1-dev libuv1-dev libssl-dev libx11-dev zlib1g-dev

Repository <https://bioc-release.r-universe.dev>

Date/Publication 2026-04-28 12:54:06 UTC

RemoteUrl <https://github.com/bioc/AnVILPublish>

RemoteRef RELEASE_3_23

RemoteSha 245d3082453fe05623b3fbbba39de7667f8bb24

Contents

add_access	2
as_notebook	2
as_workspace	3
create_workspace	4

Index	6
--------------	----------

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

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.

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

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 <code>jupyter notebook *ipynb</code> .
type	character(1) The type of notebook to be copied to the workspace. Must be one of <code>ipynb</code> , <code>rmd</code> , or <code>both</code> . <code>ipynb</code> copies only the Jupyter notebook. <code>rmd</code> copies Rmarkdown and Quarto vignettes. <code>both</code> copies both notebooks and vignettes.
quarto	character(1) If the program Quarto is installed, this parameter indicates whether the <code>.Rmd</code> 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.

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

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 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

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.

create_workspace	<i>Create an AnVIL Workspace</i>
------------------	----------------------------------

Description

Call the Terra() API to create a new AnVIL workspace. This is a helper function for as_workspace(), but can be used directly if you want to create a workspace without populating it with content from an R package. This is typically used by developers who want to create a workspace and then run other functions to populate it with content, e.g., importing data into the workspace.

Usage

```
create_workspace(namespace, name)
```

Arguments

namespace	character(1) AnVIL namespace (billing project) to be used.
name	character(1) AnVIL workspace name.

Value

`create_workspace()` returns TRUE invisibly if the workspace was created successfully; otherwise, an error is raised.

Examples

```
create_workspace("my-namespace", "my-workspace")
```

Index

[add_access](#), [2](#)

[as_notebook](#), [2](#)

[as_workspace](#), [3](#)

[create_workspace](#), [4](#)