

Package: AnVILPublish (via r-universe)

October 9, 2026

Title Publish Packages and Other Resources to AnVIL Workspaces

Version 1.23.5

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.

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

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

biocViews Infrastructure, Software

SystemRequirements Quarto command line tool
(<<https://github.com/quarto-dev/quarto-cli>>)

URL <https://github.com/Bioconductor/AnVILPublish/>

BugReports <https://github.com/Bioconductor/AnVILPublish/issues>

Encoding UTF-8

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

Config/testthat/edition 3

Date 2026-05-29

Config/roxygen2/version 8.0.0

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

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

Date/Publication 2026-05-30 03:35:42 UTC

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

RemoteRef HEAD

RemoteSha 06e578a38e1073777c4773bcbf3c1632afa80cf7

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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, dry.run = FALSE)

Arguments

- namespace character(1) namespace (billing account) under which the workspace belongs.
- name character(1) name of the workspace to add access credentials.
- dry.run logical(1) When TRUE, no changes are made to the workspace ACL. A message is printed describing what would have been done.

Value

add_access() returns TRUE, invisibly.

Examples

add_access("landmarknavil2", "Bioconductor-Package-AnVILHCAR", TRUE)

`as_notebook`*Render vignettes as .ipynb notebooks*

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"),  
  dry.run = FALSE  
)
```

Arguments

<code>rmd_paths</code>	<code>character()</code> paths to Rmd or Qmd files.
<code>namespace</code>	<code>character(1)</code> AnVIL namespace (billing project) to be used.
<code>name</code>	<code>character(1)</code> AnVIL workspace name.
<code>update</code>	<code>logical(1)</code> Update (over-write any similarly named notebooks) an existing workspace? The default (FALSE) creates notebooks locally, e.g., for previewing via jupyter notebook *ipynb.
<code>type</code>	<code>character(1)</code> 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.
<code>quarto</code>	<code>character(1)</code> Method to convert vignettes to .ipynb. Either "render" (runs <code>quarto render --to ipynb</code>) or "convert" (runs <code>quarto convert</code>). Note that the quarto CLI must be installed.
<code>dry.run</code>	<code>logical(1)</code> When TRUE, notebooks are created locally but no files are copied to the workspace. Use this to preview the conversion without modifying the workspace.

Details

See the vignette "Publishing R / Bioconductor Packages To AnVIL Workspaces" for details on the conversion process; best results are obtained when the quarto command line interface (CLI) is available.

Value

as_notebook() returns the paths to the local (if update = FALSE or dry.run = TRUE) or the workspace notebooks.

Examples

```
exampleRmd <-
  system.file("extdata", "example.Rmd", package = "AnVILPublish")
as_notebook(
  exampleRmd,
  "landmarkanvil2",
  "Bioconductor-Package-AnVILHCAR",
  dry.run = TRUE
)
```

as_workspace

*Render R packages as AnVIL workspaces***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"),
  dry.run = 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.
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) Method to convert vignettes to .ipynb. Either "render" (runs quarto render --to ipynb) or "convert" (runs quarto convert). Note that the quarto CLI must be installed.
dry.run	logical(1) When TRUE, all local processing (dashboard rendering, notebook conversion) is performed but no changes are pushed to the workspace. Overrides create and update. Use this to preview results without modifying AnVIL.

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.

Examples

```
as_workspace(
  path = "../AnVILPublish",
  namespace = "landmarkanvil2",
  name = "Bioconductor-Package-AnVILHCAR",
  dry.run = TRUE
)
```

create_workspace	<i>Create an AnVIL Workspace</i>
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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")
```

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