

Package ‘AnVILPublish’

December 5, 2024

Title Publish Packages and Other Resources to AnVIL Workspaces

Version 1.16.0

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, testthat (>= 3.0.0)

biocViews Infrastructure, Software

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.2

VignetteBuilder knitr

Config/testthat/edition 3

Date 2024-10-24

git_url <https://git.bioconductor.org/packages/AnVILPublish>

git_branch RELEASE_3_20

git_last_commit a7a8d50

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-12-05

Author Marcel Ramos [aut, cre] (<<https://orcid.org/0000-0002-3242-0582>>),
Martin Morgan [aut] (<<https://orcid.org/0000-0002-5874-8148>>),
Kayla Interdonato [aut],
Vincent Carey [ctb] (<<https://orcid.org/0000-0003-4046-0063>>)

Maintainer Marcel Ramos <marcel.ramos@sph.cuny.edu>

Contents

add_access	2
as_notebook	2
as_workspace	3

Index	5
--------------	----------

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.

Index

add_access, [2](#)
as_notebook, [2](#)
as_workspace, [3](#)