Package 'AnVILPublish'

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Title Publish Packages and Other Resources to AnVIL Workspaces

Version 1.2.0

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.

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Imports AnVIL, httr, jsonlite, 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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R topics documented:

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add_access   *Add Bioconductor_User group to workspace access*

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   *Render vignettes as .ipynb notebooks*

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   *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
)
```

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 niether create nore 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'.

Details

Information from the DESCRIPTION file and Rmd YAML files are used to populate the 'DASH-BOARD' 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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