Package 'RcwlPipelines'

March 30, 2021

Title Bioinformatics pipelines based on Rcwl

Version 1.6.2

Description A collection of Bioinformatics tools and pipelines based on R and the Common Workflow Language.

Depends R (>= 3.6), Rcwl, BiocFileCache

Imports rappdirs, methods, utils

License GPL-2

Encoding UTF-8

Suggests testthat, knitr, rmarkdown, BiocStyle, dplyr

VignetteBuilder knitr

RoxygenNote 7.1.1

biocViews Software, WorkflowStep, Alignment, Preprocessing, QualityControl, DNASeq, RNASeq, DataImport, ImmunoOncology

SystemRequirements nodejs

git_url https://git.bioconductor.org/packages/RcwlPipelines

git_branch RELEASE_3_12

git_last_commit 350f433

git_last_commit_date 2021-03-05

Date/Publication 2021-03-29

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R topics documented:

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cwlInstall   *cwlInstall*

Description

To source Rcwl scripts

Usage

```
cwlInstall(rname, bfc = NULL, env = .GlobalEnv)
```

Arguments

rname   The name or filepath of tool or pipeline to install ('rname' or 'fpath' column
                from the 'bfc' object returned from 'cwlSearch').

bfc   The 'BiocFileCache' object for the recipes returned from 'cwlUpdate'. The
                default is NULL which automatically detect the "Rcwl" cache directory.

env   The R enviroment to export to. The default is '.GlobalEnv'.

Details

Note to developers that the dependent Rcwl scripts should be included in the recipe with '@include'
tag.

Examples

```
## Not run:
tls <- cwlSearch("bwa")
tls$rname
cwlInstall("tl_bwa")
cwlInstall(tls$fpath[tls$rname == "tl_bwa"])  ## equivalent
bwa

## End(Not run)
```

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cwlLoad   *cwlLoad*

Description

To source Rcwl scripts

Usage

```
cwlLoad(rname, bfc = NULL, env = .GlobalEnv)
```

Arguments

rname	The name or filepath of tool or pipeline to install ('rname' or 'fpath' column from the 'bfc' object returned from 'cwlSearch').
bfc	The 'BiocFileCache' object for the recipes returned from 'cwlUpdate'. The default is NULL which automatically detect the "Rcwl" cache directory.
env	The R enviroment to export to. The default is '.GlobalEnv'.

Details

Note to developers that the dependent Rcwl scripts should be included in the recipe with '@include' tag.

Value

A 'cwlParam' object. For pipelines, the dependent tools will also loaded.

Examples

```
## Not run:
tls <- cwlSearch("bwa")
tls$rname
bwa <- cwlLoad("tl_bwa")
bwa <- cwlLoad(tls$fpath[tls$rname == "tl_bwa"])  ## equivalent
bwa

## End(Not run)
```

---

cwlSearch	*cwlSearch*

Description

Function to search Rcwl tools and pipelines.

Usage

```
cwlSearch(keyword, bfc = NULL, ...)
```

Arguments

keyword	A (vector of) character string as keywords to search for tools or pipelines. Will be used to match patterns against 'rname', 'rpath', 'fpath', 'Command' and 'Container' column in the 'bfc' object.
bfc	The 'BiocFileCache' object for the recipes returned from 'cwlUpdate'. The default is NULL which automatically detect the "Rcwl" cache directory.
...	More options from the internal 'bfcquery' function.

Value

A BiocFileCache tibble.

Examples

```
## Not run:
tls <- cwlSearch(c("bwa", "mem"))
data.frame(tls)

## End(Not run)
```

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cwlUpdate *cwlUpdate*

Description

Function to sync and get the most updated Rcwl recipes from the RcwlRecipes github

Usage

```
cwlUpdate(cachePath = "Rcwl", force = FALSE, branch = "rcwl1.6")
```

Arguments

cachePath	The cache path of the BiocFileCache object to store the Rcwl tools and pipelines recipes.
force	Whether to clean existing recipes cache.
branch	The branch of github recipes repository. It can be "master" and "dev". "force = TRUE" is recommended when swithing branch.

Examples

```
## Not run:
tools <- cwlUpdate()

## End(Not run)
```

RcwlPipelines *RcwlPipelines*

Description

A package for a collection of Rcwl pipelines. Currently four pipeplines have been collected in the package.

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