Package ‘RcwlPipelines’

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Title  Bioinformatics pipelines based on Rcwl
Version 1.18.1
Description A collection of Bioinformatics tools and pipelines based on R and the Common Workflow Language.
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\textbf{R topics documented:}

cwlHub-class ........................................... 2
cwlInstall ............................................. 3
Description

'cwlHub' class, constructor, and methods.

Usage

cwlHub(BFC)

## S4 method for signature 'cwlHub'
mcols(x)

## S4 method for signature 'cwlHub'
show(object)

## S4 method for signature 'cwlHub,ANY,ANY,ANY'
x[value, ..., drop = TRUE]

title(object)

Command(object)

Container(object)

Type(object)

Arguments

BFC A BiocFileCache created for 'RcwlRecipes'.

x A 'cwlHub' object.

object A 'cwlHub' object

value The "BFC" ID to extract the subset.

... Option from '[].

drop Option from '[].
Value

cwlHub: a ‘cwlHub’ object with slots of ‘rid’ and ‘cache’ path.
mcols: a ‘DataFrame’ with information from the ‘BicFileCache’ object.
[]: a subset of ‘cwlHub’ records.
title: the ‘Rcwl’ recipe names for tools or pipelines.
Command: The name of ‘Rcwl’ wrapped command line tools.
Container: the container name for the ‘Rcwl’ recipe if exist. Otherwise ‘NA’.
Type: The type of the ‘Rcwl’ recipe, "pipeline" or "tool".

Examples

## Not run:
tools <- cwlUpdate()
t1 <- tools["BFC178"]
title(t1)
Command(t1)
Container(t1)
Type(t1)

## End(Not run)

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 ‘BicFileCache’ object for the recipes returned from ‘cwlUpdate’. The default is NULL which automatically detect the "Rcwl" cache directory.
env  The R environment 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

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

## End(Not run)
```

Description

To source Rcwl scripts

Usage

```r
cwlLoad(
  rname,
  bfc = NULL,
  env = .GlobalEnv,
  cwlfile = NULL,
  dir = tempdir(),
  ...
)
```

Arguments

- **rname**: The name or filepath of tool or pipeline to install (`rname` or `fpath` column from the `bfc` object returned from `cwlSearch`). It can also be a CWL url or a github repo.
- **bfc**: The `BiocFileCache` object for the recipes. The default is NULL which automatically detect the "Rcwl" cache directory.
- **env**: The R environment to export to. The default is `.GlobalEnv`.
- **cwlfile**: For github repo input, The relative path of a CWL file inside of the github repo.
- **dir**: For github repo input, the directory to clone the repo.
- **...**: More options from `git2r::clone`.

Details

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

Value

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

Examples

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

## End(Not run)
```

cwlSearch

Description

Function to search Rcwl tools and pipelines.

Usage

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

Arguments

- **keyword**
  - A (vector of) character string as keywords to search for tools or pipelines. Will be used to match patterns (case-insensitive) 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.

- **type**
  - The ‘Type’ to filter the results, "pipeline" or "tool".

- **...**
  - More options from the internal ‘bfcquery’ function.

Value

A BiocFileCache tibble.

Examples

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

## End(Not run)
```
**cwlUpdate**  

**Description**  

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

**Usage**

```r
cwlUpdate(cachePath = "Rcwl", force = FALSE, branch = NULL)
```

**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**

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

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**RcwlPipelines**  

**Description**

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

searchContainer  seawrch containers

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Description

To search container images for a tool in certain repository from quay.io or dockerhub.

Usage

searchContainer(tool, repo = "biocontainers", source = c("quay", "dockerhub"))

Arguments

  tool       The tool to search.
  repo       The repository to lookup.
  source     The container server to search, quay.io or dockerhub.

Value

A DataFrame contains image tag names, updated dates and image sizes.

Examples

searchContainer("samtools")
Index

[,cwlHub,ANY,ANY,ANY-method
 (cwlHub-class), 2

Command (cwlHub-class), 2
Container (cwlHub-class), 2
cwlHub (cwlHub-class), 2
cwlHub-class, 2
cwlInstall, 3
cwlLoad, 4
cwlSearch, 5
cwlUpdate, 6

mcols,cwlHub-method (cwlHub-class), 2

RcwlPipelines, 6

searchContainer, 7
show,cwlHub-method (cwlHub-class), 2

title (cwlHub-class), 2
Type (cwlHub-class), 2