

Package ‘RcwlPipelines’

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Title Bioinformatics pipelines based on Rcwl

Version 1.23.0

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

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License GPL-2

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Author Qiang Hu [aut, cre],
Qian Liu [aut],
Shuang Gao [aut]

Maintainer Qiang Hu <qiang.hu@roswellpark.org>

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| | |
|--------------|---------------|
| cwlHub-class | <i>cwlHub</i> |
|--------------|---------------|

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

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

## End(Not run)
```

| | |
|---------|----------------|
| cwlLoad | <i>cwlLoad</i> |
|---------|----------------|

Description

To source Rcwl scripts

Usage

```
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.

Value

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

Examples

```
## 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

cwlSearch

Description

Function to search Rowl 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 "Rowl" cache directory. |
| type | The ‘Type’ to filter the results, "pipeline" or "tool". |
| ... | 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)
```

cwIUpdate

cwIUpdate

Description

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

Usage

```
cwIUpdate(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

```
## Not run:  
tools <- cwIUpdate()  
  
## End(Not run)
```

RcwlPipelines*RcwlPipelines*

Description

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

| | |
|-----------------|---------------------------|
| searchContainer | <i>seawrch containers</i> |
|-----------------|---------------------------|

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")
```

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