

Package ‘RcwlPipelines’

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Title Bioinformatics pipelines based on Rcwl

Version 1.27.0

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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cwlHub-class	<i>cwlHub</i>
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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 ‘BiocFileCache‘ 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 ‘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$rname
cwlInstall("tl_bwa")
cwlInstall(tls$filepath[tls$rname == "tl_bwa"]) ## equivalent
bwa

## End(Not run)
```

cwlLoad

cwlLoad

Description

To source Rcwl scripts

Usage

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

Arguments

<code>rname</code>	The ‘rname’ or ‘filepath’ column from the ‘bfc’ object returned from ‘cwlSearch’). It can also be a CWL url or a github repo.
<code>bfc</code>	The ‘BiocFileCache’ object for the recipes. The default is NULL which automatically detect the "Rcwl" cache directory.
<code>env</code>	The R enviroment to export to. The default is ‘.GlobalEnv’.
<code>cwlfile</code>	For github repo input, The relative path of a CWL file inside of the github repo.
<code>dir</code>	For github repo input, the directory to clone the repo.
<code>...</code>	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$filepath[tls$rname == "tl_bwa"]) ## equivalent
bwa

## End(Not run)
```

cwlSearch

*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

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

## End(Not run)
```

`cwlUpdate`*cwlUpdate*

Description

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

Usage

```
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 switching branch.

Examples

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

`RcwlPipelines`*RcwlPipelines*

Description

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

<code>searchContainer</code>	<i>seawrch containers</i>
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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

<code>tool</code>	The tool to search.
<code>repo</code>	The repository to lookup.
<code>source</code>	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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