Package ‘RcwlPipelines’

May 15, 2024

Title  Bioinformatics pipelines based on Rcwl
Version  1.20.0
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, git2r, httr, S4Vectors
License  GPL-2
Encoding  UTF-8
Suggests  testthat, knitr, rmarkdown, BiocStyle
VignetteBuilder  knitr
RoxygenNote  7.2.3
biocViews  Software, WorkflowStep, Alignment, Preprocessing, QualityControl, DNASeq, RNASeq, DataImport, ImmunoOncology
SystemRequirements  nodejs
git_url  https://git.bioconductor.org/packages/RcwlPipelines
git_branch  RELEASE_3_19
git_last_commit  9cb016c
git_last_commit_date  2024-04-30
Repository  Bioconductor 3.19
Date/Publication  2024-05-14
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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 '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

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 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

```r
## Not run:
tls <- cwlSearch("bwa")
tls$rname

cwlInstall("tl_bwa")
cwlInstall(tls$fpath[tls$rname == "tl_bwa"] )  ## equivalent

bwa

## End(Not run)
```

### cwlLoad

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 enviroment 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
cwlSearch

Description

Function to search RcwI 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 “RcwI” cache directory.
- **type**: The ‘Type’ to filter the results, “pipeline” or “tool”.
- **...**: More options from the internal ‘bfquery’ 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

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

description

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

searchContainer(seawrch containers)

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

<table>
<thead>
<tr>
<th>Argument</th>
<th>Description</th>
</tr>
</thead>
<tbody>
<tr>
<td>tool</td>
<td>The tool to search.</td>
</tr>
<tr>
<td>repo</td>
<td>The repository to lookup.</td>
</tr>
<tr>
<td>source</td>
<td>The container server to search, quay.io or dockerhub.</td>
</tr>
</tbody>
</table>

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

Examples

searchContainer("samtools")
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