Package ‘RcwlPipelines’

May 30, 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 Work-flow 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
Repository  Bioconductor 3.19
Date/Publication  2024-05-29
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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

```r
## 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 'BiocFileCache' 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)
```

cwlInstall(cwlInstall, cwlInstall)

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.
...

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"])
## 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)
RcwlPipelines

**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)
```

RcwlPipelines

**Description**

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

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

Usage

```r
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

```r
searchContainer("samtools")
```
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