Package ‘RcwlPipelines’

February 23, 2024

**Title**  Bioinformatics pipelines based on Rcwl

**Version**  1.18.0

**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

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**Suggests**  testthat, knitr, rmarkdown, BiocStyle

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**SystemRequirements**  nodejs

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Description

'cwlHub' class, constructor, and methods.

Usage

```r
## S4 method for signature 'cwlHub'
```

```r
cwlHub(BFC)

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

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

```r
## S4 method for signature 'cwlHub,ANY,ANY,ANY'
x[value]
```

```r
title(object)
```

```r
Command(object)
```

```r
Container(object)
```

```r
Type(object)
```

Arguments

- **BFC**  
  A BiocFileCache created for 'RcwIRecipes'.

- **x**  
  A 'cwlHub' object.

- **object**  
  A 'cwlHub' object

- **value**  
  The "BFC" ID to extract the subset.
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 `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.
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)
```

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 `bfcquery` function.

Value

A Bioconductor 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

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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