Package: RcwlPipelines (via r-universe)

November 1, 2026

Title Bioinformatics pipelines based on Rcwl

Version 1.29.0

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

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VignetteBuilder knitr

RoxygenNote 7.2.3

biocViews Software, WorkflowStep, Alignment, Preprocessing, QualityControl, DNASeq, RNASeq, DataImport, ImmunoOncology

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Config/Bioconductor/UnsupportedPlatforms windows

Config/pak/sysreqs cmake libglpk-dev make libgit2-dev libicu-dev libpng-dev libssh2-1-dev libuv1-dev libxml2-dev libssl-dev python3 libx11-dev zlib1g-dev

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`cwlHub-class` *cwlHub*

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 ‘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$rname
cwlInstall("tl_bwa")
cwlInstall(tls$fpath[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

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.

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 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 swithing branch.

Examples

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

## End(Not run)
```

RcwlPipelines *RcwlPipelines*

Description

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

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

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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