

# Package ‘RcwlPipelines’

December 2, 2021

**Title** Bioinformatics pipelines based on Rcwl

**Version** 1.10.0

**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** 7.1.1

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

**SystemRequirements** nodejs

**git\_url** <https://git.bioconductor.org/packages/RcwlPipelines>

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## R topics documented:

cwlHub	2
cwlInstall	2
cwlLoad	3
cwlSearch	4

cwlUpdate . . . . .	5
mcols,cwlHub-method . . . . .	5
RcwlPipelines . . . . .	6
searchContainer . . . . .	6
[,cwlHub,ANY,ANY,ANY-method . . . . .	7

<b>Index</b>	<b>8</b>
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cwlHub	<i>cwlHub</i>
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### Description

The 'cwlHub' constructor for 'BiocFileCache' object.

### Usage

```
cwlHub(BFC)
```

### Arguments

BFC	A BiocFileCache created for 'RcwlRecipes'.
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cwlInstall	<i>cwlInstall</i>
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### 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**

```
## 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 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'.
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")
tls$rname
bwa <- cwlLoad("tl_bwa")
bwa <- cwlLoad(tls$fpath[tls$rname == "tl_bwa"]) ## equivalent
bwa

## End(Not run)
```

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cwlSearch

*cwlSearch*


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**Description**

Function to search Rowl 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 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 "Rowl" 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)
```

---

 mcols, cwlHub-method

*mcols*


---

**Description**

DataFrame information from the 'BiocFileCache' object.

**Usage**

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

**Arguments**

x	A 'cwlHub' object
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RcwlPipelines	<i>RcwlPipelines</i>
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### Description

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

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searchContainer	<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

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")
```

---

[,cwlHub,ANY,ANY,ANY-method  
*extract*

---

### **Description**

extract  
title  
Command  
Container  
Type

### **Usage**

```
## S4 method for signature 'cwlHub,ANY,ANY,ANY'  
x[value]  
  
title(object)  
  
Command(object)  
  
Container(object)  
  
Type(object)
```

### **Arguments**

x	A 'cwlHub' object.
value	The "BFC" ID to extract the subset.
object	A 'cwlHub' object.

### **Examples**

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

# Index

[, cwlHub, ANY, ANY, ANY-method, [7](#)

Command ([, cwlHub, ANY, ANY, ANY-method), [7](#)

Container  
    ([, cwlHub, ANY, ANY, ANY-method),  
    [7](#)

cwlHub, [2](#)

cwlInstall, [2](#)

cwlLoad, [3](#)

cwlSearch, [4](#)

cwlUpdate, [5](#)

mcols, cwlHub-method, [5](#)

RcwlPipelines, [6](#)

searchContainer, [6](#)

title ([, cwlHub, ANY, ANY, ANY-method), [7](#)

Type ([, cwlHub, ANY, ANY, ANY-method), [7](#)