

# Package ‘RcwlPipelines’

April 12, 2022

**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>

**git\_branch** RELEASE\_3\_14

**git\_last\_commit** 02f40ac

**git\_last\_commit\_date** 2021-10-26

**Date/Publication** 2022-04-12

**Author** Qiang Hu [aut, cre],  
Qian Liu [aut],  
Shuang Gao [aut]

**Maintainer** Qiang Hu <[qiang.hu@roswellpark.org](mailto:qiang.hu@roswellpark.org)>

## 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> |
|--------------|----------|

---

|        |               |
|--------|---------------|
| cwlHub | <i>cwlHub</i> |
|--------|---------------|

---

### Description

The ‘cwlHub’ constructor for ‘BiocFileCache’ object.

### Usage

```
cwlHub(BFC)
```

### Arguments

BFC                    A BiocFileCache created for ‘RcwlRecipes’.

---

|            |                   |
|------------|-------------------|
| cwlInstall | <i>cwlInstall</i> |
|------------|-------------------|

---

### 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)
```

---

cwlSearch

*cwlSearch*


---

**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 |
|---|-------------------|

---

|               |                      |
|---------------|----------------------|
| RcwlPipelines | <i>RcwlPipelines</i> |
|---------------|----------------------|

---

### Description

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

---

|                 |                           |
|-----------------|---------------------------|
| searchContainer | <i>seawrch containers</i> |
|-----------------|---------------------------|

---

### 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](#)