

# Package ‘RcwlPipelines’

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**Title** Bioinformatics pipelines based on Rcwl

**Version** 1.25.0

**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** 7.2.3

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

**SystemRequirements** nodejs

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

**git\_branch** devel

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| cwlHub-class | <i>cwlHub</i> |
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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**

```
## Not run:
tools <- cwlUpdate()
t1 <- tools["BFC178"]
title(t1)
Command(t1)
Container(t1)
Type(t1)

## End(Not run)
```

cwlInstall

*cwlInstall***Description**

To source Rcw1 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 "Rcw1" cache directory. |
| env   | The R enviroment to export to. The default is '.GlobalEnv'.                                                                                      |

**Details**

Note to developers that the dependent Rcw1 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)
```

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*cwlSearch**cwlSearch*

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**Description**

Function to search Rcw1 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 "Rcw1" 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*

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**Description**

Function to sync and get the most updated Rcw1 recipes from the Rcw1Recipes github

**Usage**

```
cwlUpdate(cachePath = "Rcw1", force = FALSE, branch = NULL)
```

**Arguments**

|           |                                                                                                                            |
|-----------|----------------------------------------------------------------------------------------------------------------------------|
| cachePath | The cache path of the BiocFileCache object to store the Rcw1 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)
```

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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")
```

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