# Package ‘BiocDockerManager’

October 18, 2022

**Type** Package

**Title** Access Bioconductor docker images

**Version** 1.8.1

**Description** Package works analogous to BiocManager but for docker images. Use the BiocDockerManager package to install and manage docker images provided by the Bioconductor project. A convenient package to install images, update images and find which Bioconductor based docker images are available.

**biocViews** Software, Infrastructure, ThirdPartyClient

**Depends** R (>= 4.1)

**Imports** httr, whisker, readr, dplyr, utils, methods, memoise

**Suggests** BiocStyle, knitr, rmarkdown, testthat (>= 2.1.0)

**SystemRequirements** docker

**VignetteBuilder** knitr

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** false

**BugReports** `https://github.com/Bioconductor/BiocDockerManager/issues`

**RoxygenNote** 7.1.1

**git_url** https://git.bioconductor.org/packages/BiocDockerManager

**git_branch** RELEASE_3_15

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**Maintainer** Bioconductor Package Maintainer `<maintainer@bioconductor.org>`

# R topics documented:

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## `available` *List available images with tags for Bioconductor*

### Description

List available images with tags for Bioconductor

### Usage

```
available(pattern, organization = "bioconductor", deprecated = FALSE)
```

### Arguments

| | |
|---|---|
| `pattern` | ‘character(1)‘, a pattern to filter the names of images. |
| `organization` | ‘character(1)‘, organization whose list of images hosted on dockerhub will be displayed. Default is ’bioconductor’. |
| `deprecated` | ‘logical(1)‘, TRUE will show deprecated images. |

### Details

Return a tibble of all the available docker images in an organization. The tibble will show the Image name, description, tags, repository-name, pull-count. By default this function is designed to show the available images under the Bioconductor organization in dockerhub.

### Value

‘tibble‘ of available images

## Examples

```
res <- available()

res <- available("bioconductor_docker")

res <- available(pattern = "rstudio", organization = "rocker")

res <- available(deprecated = TRUE)
```

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`BiocDockerManager` *BiocDockerManager: Manage Bioconductor docker images.*

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## Description

A convenient package to install images, update images and find which Bioconductor based docker images are available.

## BiocDockerManager functions

available()

installed()

install()

maintainer()

version()

valid()

use_dockerfile()

## Author(s)

maintainer@bioconductor.org

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`help` *Help function to direct brower to Bioconductor dockerhub*

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## Description

Help function to direct brower to Bioconductor dockerhub

## Usage

```
help(repository = "bioconductor/bioconductor_docker")
```

### Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository name of image. Default image is the main ’bioconductor/bioconductor_docker’ image. |

### Value

Open a browser tab with docker repository

### Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if(do_it) {
    BiocDockerManager::help()
}
```

---

## `install` *Install a docker image on your local machine*

### Description

Install a docker image on your local machine

### Usage

```
install(repository, tag, quiet = FALSE, all_tags = FALSE)
```

### Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository name of the docker image. |
| `tag` | ‘character(1)‘, tag of the docker image. |
| `quiet` | ‘logical(1)‘, if TRUE suppress verbose output generated from the download. |
| `all_tags` | ‘logical(1)‘, pull all the tags of the image |

### Details

The function works similar to the ’docker pull’ command. It downloads a docker image from Dockerhub on to the local machine, in a place which the docker engine knows about, building your local registry of docker images.

### Value

invisible

### Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if (do_it) {
    BiocDockerManager::install(
        repository = "bioconductor/bioconductor_docker",
        tag = "latest"
    )
}
```

---

## `installed` *Get installed docker images*

### Description

Get installed docker images

### Usage

```
installed(repository)
```

### Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository name of image; if not given all images will be shown. |

### Value

stdout of docker images on your local machine.

### Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if (do_it) {
    BiocDockerManager::installed()

    BiocDockerManager::installed(
        repository = "bioconductor/bioconductor_docker"
    )
}
```

---

`maintainer` *Get maintainer of bioconductor docker image*

---

### Description

Get maintainer of bioconductor docker image

### Usage

```
maintainer(repository = "bioconductor/bioconductor_docker", tag)
```

### Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository of the docker image. |
| `tag` | ‘character(1)‘, tag of the docker image. |

### Details

The maintainer name and email provides information for who you can contact in case the image isn’t working as expected.

### Value

‘character‘ vector representing the maintainer.

### Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if (do_it) {
    BiocDockerManager::maintainer(
        "bioconductor/bioconductor_docker",
        tag = "latest"
    )
}
```

---

`use_dockerfile` *Use dockerfile template*

---

### Description

Use dockerfile template

### Usage

```
use_dockerfile(
  name,
  person,
  description,
  license = "Artistic-2.0",
  path = tempdir()
)
```

### Arguments

| | |
|---|---|
| `name` | ‘character(1)‘, name of the image. |
| `person` | ‘person(1)‘, class person which holds information. Only the maintainer is listed on the LABEL information of the Docker image. |
| `description` | ‘character(1)‘, description of image. |
| `license` | ‘character(1)‘, license of image. |
| `path` | ‘character(1)‘, parent path where folder repository should be created. |

### Details

The ’use_dockerfile’ function is used to create new dockerfiles based on the bioconductor/bioconductor_docker set of images. The function provides a template for creating your image.

### Value

invisible

### Examples

```
## detailed example

use_dockerfile(
    name = "custom_image",
    person = person("Foo", "Bar",
        email="foo@bar.com", role = c("aut", "cre")
    ),
    description = "My image",
    license = "GPL",
    path = tempdir()
)

## minimal exmaple
use_dockerfile("custom_image",
    person(
        "abc", "def",
        email = "abc@def.com",
        role = c("cre", "aut")
    )
)
```

---

## `valid` *Check if all images available are valid*

---

### Description

Check if all images available are valid

### Usage

```
valid(repository = "bioconductor/bioconductor_docker", tag)
```

### Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository name of the docker image. |
| `tag` | ‘character(1)‘, tag of the docker image. |

### Details

Check if the image is valid, i.e to see if the image is up to date with the image hosted by bioconductor on the Dockerhub organization page.

### Value

tibble with the repository and tag of image which needs to be updated.

### Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if (do_it) {

    BiocDockerManager::valid()

    BiocDockerManager::valid(
        "bioconductor/bioconductor_docker",
        tag = "devel"
    )
}
```

---

`version` *Get version of bioconductor docker image*

---

## Description

Get version of bioconductor docker image

## Usage

```
version(repository = "bioconductor/bioconductor_docker", tag)
```

## Arguments

| | |
|---|---|
| `repository` | ‘character(1)‘, repository of the docker image. |
| `tag` | ‘character(1)‘, tag of the docker image. |

## Details

The version of the images provided by Bioconductor are unique. They are represented by ’x.y.z’ where, the ’x.y’ represent the version of Bioconductor and the ’.z’ represents the version of the Dockerfile used to build the Docker image. This is especially useful in terms of reproducibility and tracking changes when using the Docker images provided by Bioconductor.

## Value

‘character‘ vector representing the version number.

## Examples

```
do_it <- BiocDockerManager:::.is_docker_installed()

if (do_it) {
    BiocDockerManager::version(
        "bioconductor/bioconductor_docker",
        tag = "latest"
    )

    BiocDockerManager::version(
        "bioconductor/bioconductor_docker",
        tag = "devel"
    )
}
```

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