


Develop Bioconductor packages with docker container

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Readings

links to read:

- <https://www.bioconductor.org/developers/package-guidelines/#rcode>
(<https://www.bioconductor.org/developers/package-guidelines/#rcode>)
- <https://github.com/Bioconductor/Contributions> (<https://github.com/Bioconductor/Contributions>)
- use container https://github.com/Bioconductor/bioconductor_full
(https://github.com/Bioconductor/bioconductor_full)

I am following the last link.

pull the container

```
docker pull bioconductor/bioconductor_full:devel
docker images
```

REPOSITORY	TAG	IMAGE ID	CREATED
bioconductor/bioconductor_full	devel	ae3ec2be7376	3 hours ago
seuratv3	latest	9b358ab1fd63	2 days ago

It is 5.7G in size.

start the Rstudio from the image. I have another Rstudio instance using port 8787, let me use a different one (e.g. 8080). docker Rstudio default port is 8787 , change the host port to 8080 .

```
mkdir -p ~/R/host-site-library

docker run \
  -e PASSWORD="xyz" \
  -p 8080:8787 \
  -v ~/R/host-site-library:/usr/local/lib/R/host-site-library \
  -v ~/github_repos:/home/rstudio \
  bioconductor/bioconductor_full:devel
```

NOTE: The path `~/R/host-site-library` is mapped to `.libPaths()` in R. So, when R is started, all the libraries in the host directory `host-site-library` are available to R. It is stored on your machine mounted from the volume you fill in place of `host-site-library`.

The mounted path must be an **absolute path**.

I also mounted the `github_repo` folder in my host machine to the docker home directory. Because every time you exit a container and start it again, the modification you did to the container will be gone (unless you make an modified image and use that for the next time). I will save the R package in my `~/github_repo` folder in the host machine.

type `localhost:8080`, you should see the Rstudio login page. username is `rstudio`, password is `xyz` in this dummy example.

In Rstudio:

```
> .libPaths()
[1] "/usr/local/lib/R/host-site-library" "/usr/local/lib/R/site-library"
[3] "/usr/local/lib/R/library"
```

you will see `/usr/local/lib/R/host-site-library` is in the `libpath`, that corresponds to the `~/R/host-site-library` in the host machine, if you do package installation, it will be installed in the `~/R/host-site-library`.

start an R package use usethis

follow these two blog posts and R packages book (<http://r-pkgs.had.co.nz/>) by Hadley Wickham:

- <https://blog.methodsconsultants.com/posts/developing-r-packages-using-gitlab-ci-part-i/> (<https://blog.methodsconsultants.com/posts/developing-r-packages-using-gitlab-ci-part-i/>)
- <https://www.hvitfeldt.me/blog/usethis-workflow-for-package-development/> (<https://www.hvitfeldt.me/blog/usethis-workflow-for-package-development/>)

```
install.packages(c("devtools", "roxygen2", "usethis", "available", "rmarkdown"))

## check if the package name is available (not used by others)
library(available)
available("myawesomepackage")

library(usethis)
usethis::create_package("~/myawesomepackage")

use_git()
use_github()
use_mit_license("Ming Tang")
usethis::use_pipe()
```

Add a function

```
usethis::use_r("myawesomefunc")
```

On mac:

command + option + shift + R for inserting roxygen comment.

command + shift + D for documentation.

command + shift + B for building package.

add more functions, repeat.

Next

Next is to add test and setup some continuous integration. Read this Automate testing of your R package using Travis CI, Codecov, and testthat (<https://jef.works/blog/2019/02/17/automate-testing-of-your-R-package/>) by Jean Fan.

[Bioconductor](https://divingintogeneticsandgenomics.rbind.io/tags/bioconductor/) (<https://divingintogeneticsandgenomics.rbind.io/tags/bioconductor/>)

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