

# Managing the lab server/desktop

Cedric Arisdakessian

2022-09-14

## About our lab computer

- Not a typical server (“normal” macOS)
- Enhanced desktop

```
> system_profiler SPHardwareDataType  
  Hardware Overview:
```

```
    Model Name: iMac  
    Model Identifier: iMac20,1  
    Processor Name: 8-Core Intel Core i7  
    Processor Speed: 3.8 GHz  
    Number of Processors: 1  
    Total Number of Cores: 8  
    L2 Cache (per Core): 256 KB  
    L3 Cache: 16 MB  
    Hyper-Threading Technology: Enabled  
    Memory: 128 GB
```

## Part 1: Managing rstudio-server

# Generalities

- Many things here are for your understanding, you don't need to memorize much. I feel like it is important to understand what you are working with to demystify it.
- The rstudio-server is a “service” (special type of background program) that:
  - Starts automatically when the computer starts and stops when it is turned off
  - Serves Rstudio on port 8787  
Note: port=“door” to use when we arrive at address graphics2.kewalo.hawaii.edu)  
Default door on web browser: 80
- Never delete the rstudio user. It is needed to run rstudio-server
- Testing it locally: on the lab iMAC, go to localhost:8787. If you can log in, the server works.
- To restart the server without turning it off:

```
sudo rstudio-server restart  
# or  
sudo rstudio-server stop  
sudo rstudio-server start
```

# Before we start

## Challenges

- We want users to be able to use and install libraries
- We don't avoid installing the same library multiple times
- We don't avoid users affecting each other too much

## Setup

For each of these components, should be defined at the user level? system level? somewhere in between?

- Rstudio
- R program
- R libraries

## Notes:

- “system” level vs “lab admin” level
- why conda

# R setup

- R not installed system-wide, just available in a conda environment:  
/Users/labhuiofrank/.miniconda3/envs/rserver
- Environment specifications in yaml file at:  
/Users/labhuiofrank/Public/conda-environments/rserver.yml
- This is our main folder for storing libraries that are useful for most people in the lab (e.g. ggplot2). We want to keep it lean.

## R Libraries setup

The main library folder belongs to the labhuiofrank user: other users cannot modify it (if they try, they can have a “Permission Denied” error)

```
$ whoami
labhuiofrank # OK!
$ conda activate rserver
$ conda install ...
```

*# otherwise*

```
EnvironmentNotWritableError: The current user does not have
write permissions to the target environment.
  environment location: /Users/labhuiofrank/.miniconda3/envs/rserver
  uid: 512
  gid: 20
```

OR (if possible, avoid and use conda)

```
> install.packages()
> devtools::install_github()
> biocManager::install()
```

## When to use the labhuiofrank account

- If you want to add more base packages and make it available to everyone.
- Usually to avoid, as modifying those packages can affect other users.
- Log in with the labhuiofrank account for that. Don't use your own and force your way through with sudo, it might get things messy (where different libraries belong to different users).

## The issue

R is configured to look in the labhuiofrank account, and it's a problem because:

- We can't install libraries there
- But we still need R to check that because we want to use the default libraries

What to do then? Just tell R to look and install packages in multiple places



## Where does R find installed libraries?

- Next to where R is installed. In our case:

```
> R.home()  
/Users/labhuiofrank/.miniconda3/envs/rserver/lib/R  
# Libraries are in R_HOME/library
```

- Order matters: if a library is installed in multiple location, R will get the first one that it finds.

Note:

- Wherever we are telling R to look. All folders need to be compatible: you cannot have libraries compiled with R-4.1 in one and others with R-4.2 in others.

## Installing new R libraries

- We want a modular system: each user will add to the base environment but not affect other users.
- I set up R in the labhuiofrank account to add automatically the following location:  
~/Library/R/x86\_64/4.1/library (no need to remember it)

```
> .libPaths()  
[1] "/Users/cedric/Library/R/x86_64/4.1/library"  
[2] "/Users/labhuiofrank/.miniconda3/envs/rserver/lib/R/library"  
  
less /Users/labhuiofrank/.miniconda3/envs/rserver/lib/R/etc/Renviron
```

Great! For each user, this is automatically working (no need to do anything):

- If he tries to install a package, R will try first in his home directory, which he is allowed to access
- If he loads a library, R will first look at his personal library (good if you want to override base packages), then labhuiofrank's, the R base
- All libraries are isolated, no risk of breaking other users setup (as long as sudo is not used).

But...

- R needs external tools to install libraries. Besides, R is installed in the labhuiofrank's conda environment, not ours.
- 2 options:
  - In Rstudio, the R from labhuiofrank is already loaded, we could use this one
  - In the terminal, we could activate labhuiofrank's environment and use it
- For now, it doesn't work from RStudio: RStudio is not well integrated with conda and cannot find all the programs necessary to install libraries.
- But that's okay, we have the other option.

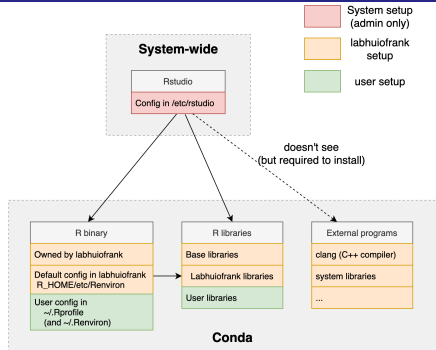
## Install a new library (most important part)

- 1 Log on your account on the iMAC with your account
- 2 Open a terminal and activate the labhuiofrank R environment:

```
$ conda activate /Users/labhuiofrank/.miniconda3/envs/rserver`
```

- 3 Open R and do your thing

```
$ R  
# opens R interactive interface  
> install.packages() # or something else
```



What does R sees					
User	Rstudio	R	base R libraries	labhufiofrank libraries	user-specific libraries
labhufiofrank					
other					

What can you edit					
User	Rstudio	R	base R libraries	labhufiofrank libraries	user-specific libraries
labhufiofrank					
other					

## Bonus: Rstudio-server configuration

Although you'll probably never edit them, let's look at the configuration files:

```
cat /etc/rstudio/rserver.conf  
cat /etc/rstudio/rsession.conf  
cat /etc/rstudio/database.conf
```

## Part 2: Managing users and files

## Create a new user

- Through the GUI (recommended): <https://support.apple.com/guide/mac-help/set-up-other-users-on-your-mac-mtusr001/mac>
- Through the command-line (replace USERNAME and PASSWORD with their respective values).

```
# Create user (admin)
```

```
sudo sysadminctl -addUser USERNAME -home /Users/USERNAME -admin -shell /bin/bas
```

```
# Set password
```

```
sudo dscl . -passwd /Users/USERNAME PASSWORD
```

```
# Create home directory
```

```
sudo createhomedir -c
```

Test: `su - USERNAME` (su=switch user)



## Delete an existing user

- Through the GUI (recommended): <https://support.apple.com/guide/mac-help/delete-a-user-or-group-mchlp1557/12.0/mac/12.0>
- Through the command-line (replace USERNAME with its value). You will need to run each command with `sudo` to get admin privileges:

```
# delete account
sudo sysadminctl -deleteUser USERNAME
# delete home directory (careful, it is not reversible)
sudo rm -rf /Users/USERNAME

# reboot computer
reboot
```

# Managing files

- On the command-line (via `scp` or `rsync`, see linux tutorial)
- SFTP access:
  - Install with `brew install --cask cyberduck`
  - Open Cyberduck
  - File > Open connection

### Cyberduck connection

Protocol: SFTP (SSH File Transfer Protocol)

Server: graphics2.kewalo.hawaii.edu

Username:

Either:

- Password:
- SSH Private Key: (default: ~/.ssh/id\_rsa)

## Shared folder

- File permissions (owner/group/other, read/write/execute)
- Mac computers have by default a folder called “Public” that any user can access
- You can find and retrieve many project data in the labhuiofrank’s Public folder at /Users/labhuiofrank/Public. Let’s create now a symbolic link to it (for Rstudio).
- We could also store databases in this folder as well (i.e. pathogens, primers, ...)