

PhyloFactor Installation on R conda environment with IRkernel for Jupyter Notebooks

Erick Armingol, April 23, 2019

1. Using the terminal, connect to the server via ssh

```
conda create -n R anaconda
```

2. Activate environment

```
conda activate R
```

3. Install R

```
conda install -c conda-forge r=3.5.1 --yes
```

4. Install devtools

```
conda install -c r r-devtools --yes
```

5. Install BiocInstaller

```
conda install -c bioconda bioconductor-biocinstaller --yes
```

6. Open R from the terminal by executing

```
R
```

7. If an error occurs, related to libiconv, install it with:

```
conda install -c conda-forge libiconv --yes
```

8. In R, execute the following commands. **If asked, do NOT install packages compiled from source. Also, do NOT update packages (if asked, just select 'none').**

```
source("https://bioconductor.org/biocLite.R")
biocLite("Biostrings")
biocLite("ggtree")
devtools::install_github('reptalex/phylofactor')
```

9. If you got an error like "Installation failed: error in running command", run:

```
library(devtools)
options(unzip = "internal")
devtools::install_github('reptalex/phylofactor')
```

10. Go out from R (quit command) and Install IRkernel (for jupyter notebook - hub)

```
conda install -c r r-irkernel
```

11. Open R again, and activate IRkernel executing the command

```
IRkernel::installspec()
```