

PhyloFactor Installation on R conda environment with IRkernel for Jupyter Notebooks

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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
```

If needed, also install gcc and libgcc with "conda install gcc" "conda install libgcc"

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. If installation fails because of dependencies errors, see:

<https://stackoverflow.com/questions/6907937/how-to-install-dependencies-when-using-r-cmd-install-to-install-r-packages>

Other option is to install other version of devtools from R:

```
install.packages("devtools")
```

Then, run #8

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

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

If this fails, try opening R and executing:

```
library(devtools)
devtools::install_github("IRkernel/IRkernel")
```

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

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