Running R on server

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Copy files from local machine to your coli home folder

scp -r ./analyses username@login.coli.uni-saarland.de:/home/CE/username/expt

Copying from the analyses folder in the local working directory to expt in the login home.

A password prompt will appear. Provide the password that you use to login to your coli email.

Create a secure connection

Connect to the coli login

ssh username@login.coli.uni-saarland.de

Again, provide your coli login credentials as a prompt appears.

Copy files from coli login to desired server

jones-3 is just an example here.

```
scp -r username@login.coli.uni-saarland.de:/home/CE/username/expt \
username@jones-3:/home/CE/username/expt/analysis
```

Copying from expt in the coli login to analysis in jones-3 server.

Connect to the server

```
# From the coli login:
ssh -X username@jones-3.coli.uni-saarland.de
#0r:
ssh jones-3
```

Navigate to your home directory and open R

Change my current working directory from /home/CE/username to ./expt/analysis. And open R in this directory.

```
pwd
cd expt/analysis
```

Find R libraries

```
.libPaths()
```

Likely output is:

- [1] "/usr/local/lib/R/site-library"
- [2] "/usr/lib/R/site-library"
- [3] "/usr/lib/R/library"

Add R libraries

```
.libPaths(new="/local/home/CE/pratikb/R/x86_64-pc-linux-gnu-library/4.0")
```

By this, you are adding additional path to R libraries which points to the path of pratikb's libraries so that you don't have to install packages required for LMM again.

Warning: I haven't tried this, so can't tell if it gives any error.

Resources:

- 1: Link stackoverflow-1
- 2: Link stackoverflow-2
- 3: Link stackoverflow-3
- 4: Check documentation help(.libPaths)

Load prerequsities for analyses

Load packages, data files, functions, etc. and run your analyses.

```
library(lme4)
library(dplyr)

load('analyses/datfiles/dat.RData')
source('analyses/functions/customfn.R')
```

N.B.: It is clear that the analyses folder that was imported from your computer to the server should have contained datafiles and functions.

Run the analyses of interest

You know what to do next – just run the good old Imer model.

```
m0 <- glmer(...)
```

Save the model output.\ Export it as an RDS file (e.g.results.RDS'), or export multiple model outputs as one .RData file.

Then copy them back to your computer.

Shortcut

It is not always necessary to hand-run the models in R.

You can write a single script with library, load, source, lmer, save, etc. and run it in the background.

One potential drawback: You might not be able to see what/where the error occurs. But you can run them in small chunks anyway. Or, maybe create a custom alert message? I don't have an experience with it; it should be possible, in principle.

Copy back

First copy the outputs to the coli login then to the local machine.

• Run this in the jones-3 terminal:

```
scp -r username@jones-3.coli.uni-saarland.de:/home/CE/username/
expt/analyses/results.RDS \
username@login.coli.uni-saarland.de:/home/CE/username/expt
```

This copies the files from the jones server to the coli login.

Copy back

Run this in your local terminal

scp -r username@login.coli.uni-saarland.de:/home/CE/username/expt ./analyses/

This copies the files from expt in coli login to the local machine.

Final thoughts

- Everything discussed today can be further simplified with some (?smart?) bash scripting.
- It might not always be useful to run our (?my?) analyses on the server.
 - Time-effort and long-term usefulness tradeoff :wink:
- Familiarizing oneself with basic bash commands is very helpful regardless of running R on server.
- It is fun to try new things anyway :smile:

Let me know if there is anything wrong and/or to correct or improvise here.

Resourceful people

Please consult:

- Iza and Margarita for general approach about connecting to server and R in particular respectively.
- Marian about GUI approach to connect to the server.