BEFORE STARTING: please install the required *R* packages

You will need *R* **version 3.5.1.**

If you are using an older R version, please update R to this version. Once you have updated R, please follow the below steps below (<mark>If you have any technical issues with the installation please e-mail Margot Paris at margot.paris@unifr.ch</mark>)

The analyses we will perform require two packages from the bioconductor version 3.4, namely:

- SNPrelate (https://www.bioconductor.org/packages/release/bioc/html/SNPRelate.html)

- LEA (https://www.bioconductor.org/packages/release/bioc/html/LEA.html)

plus

- RColorBrewer (http://colorbrewer2.org/)

Please use the following commands in R to install them:

```
# LEA
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install("LEA", version = "3.8")

# SNPrelate
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install("SNPRelate", version = "3.8")

# To check if the packages were installed correctly
library("LEA")
library("SNPRelate")

# Install RColorBrewer
install.packages("RColorBrewer")

# load the package RColorBrewer
library("RColorBrewer")
```