

Getting ready to jump into Genome Wide Association Studies in Plants !

Dear attendees,

During the course, we will be mostly working with R software.

1. It is required to install **the latest version of R-4.2.1 of R software** <https://cran.r-project.org/bin/windows/base/R-4.2.1-win.exe> on your own computer before the beginning of the course. Versions for Windows, Mac and Linux can be freely downloaded from <https://cran.r-project.org/>

2. **To understand the statistical models to be developed during the course, it will be useful to review basic matrix algebra. A quick reminder of such matrix operations may be found on the following link:** <http://ee263.stanford.edu/notes/matrix-primer-lect2.pdf>

Please pay attention, at least, to *matrix addition* and *matrix multiplication*.

3. Also, a R code editor such as **RStudio**, making R easier to use, may be helpful. The **latest version RStudio Desktop version**

can be freely downloaded from <https://www.rstudio.com/products/rstudio/download/>

4. For course attendees who are not familiar with R, great tutorial sources are available on <https://www.datacamp.com/> or <http://software-carpentry.org/>. There are many videos on youtube to learn R by your own.

5. Please find below the **list of the R packages required for the analysis** of the case studies to be discussed during the course this week. It will be very convenient and efficient, if you install them on your computer before the beginning of the course as the installation of some R packages may be time-consuming.

To do so, you will need an internet connection. We advice to install the packages directly from the R software console as some problems may occur in the R package installation if you do it on RStudio. The following R packages can be installed by typing (or copy/paste) these command lines (you are required to choose a 'Secure CRAN mirror' to download, any site in the proposed list is convenient):

```
if (!requireNamespace("BiocManager", quietly = TRUE))  
  install.packages("BiocManager")  
  
BiocManager::install("multtest")  
  
install.packages("gplots")  
install.packages("LDheatmap")  
install.packages("genetics")  
install.packages("agricolae", dependencies=TRUE)  
install.packages("dplyr", dependencies=TRUE)  
install.packages("emmeans", dependencies=TRUE)  
install.packages("ggplot2", dependencies=TRUE)  
install.packages("gridExtra", dependencies=TRUE)  
install.packages("Hmisc", dependencies=TRUE)  
install.packages("lmerTest", dependencies=TRUE)  
install.packages("lme4", dependencies=TRUE)  
install.packages("multcomp", dependencies=TRUE)  
install.packages("nlme", dependencies=TRUE)  
install.packages("pwr", dependencies=TRUE)  
install.packages("tidyverse", dependencies=TRUE)  
install.packages("lsmeans", dependencies=TRUE)  
install.packages("car", dependencies=TRUE)  
install.packages("reshape", dependencies=TRUE)
```

Looking forward jumping with you into GWAS for Plants !

Best regards,
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