# Systems Genetics: Installation instructions

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## 1 Requirements

To follow the exercises and not waste unnecessary time, please try to get all the software running in advance.

### 1.1 Software

#### 1.1.1 R and RStudio

Please prepare your laptop with R and RStudio. You can find the installation instructions here:

1. https://www.r-project.org
2. - Windows users only: https://mirror.its.sfu.ca/mirror/CRAN/bin/windows/Rtools/
   - Linux/Mac users only: https://www.xquartz.org/index.html
3. once you have installed R, install RStudio: https://www.rstudio.com/products/rstudio/download/

#### 1.1.2 other software

- You can use **markdown** & **knitr** to create reports. To create pdf's, you would need a TeX installation

#### 1.1.3 Installation and resources for R packages

In general, to install Bioconductor packages you can use the following commands:

```r
if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install("package")
```

for R version 3.4 or older:

```r
source("https://bioconductor.org/biocLite.R")
BiocInstaller::biocLite("package")
```

To install packages from a git repository, the package **devtools** is required:

```r
install.packages("devtools")
library(devtools)
devtools::install_github(package)
```

### 1.1.4  R packages

- VariantAnnotation (install with: **BiocManager::install("VariantAnnotation")**)

- genetics (install with: **install.packages("genetics")**)

- biomaRt (install with: **BiocManager::install("biomaRt")**)

- Gviz (install with: **BiocManager::install("Gviz")**)

- markdown, rmarkdown & knitr (needs a valid TeX installation to create pdf-reports)

- devtools (install with: **install.packages("devtools")**)

- data.table (install with: **install.packages("data.table")**)

- dplyr (install with: **install.packages("dplyr")**)

- MatrixEQTL (install with: **devtools::install_github("andreyshabalin/MatrixEQTL", force=T)**)
  In the current **MatrixEQTL** version on CRAN, which is used when installing the package with **install.packages()**, the parameter *noFDRsaveMemory* is not implemented correctly. However, we want to use this functionality, therefore, please reinstall the package over the github repository, where the error is already corrected.

- eQTLpipeline (install with: **devtools::install_github("matthiasheinig/eQTLpipeline", force=T)**)

- qqman (install with: **install.packages("qqman")**)

If you started from scratch and followed the instructions above, you should be able to use this code chunk to install all packages:

```r
install.packages("devtools", dependencies = T, clean = T)
install.packages(c("markdown", "rmarkdown", "knitr"),
                 dependencies = T, clean = T)
install.packages(c("data.table", "dplyr", "ggplot2", "genetics", "qqman"),
                 dependencies = T, clean = T)

if (!requireNamespace("BiocManager", quietly = TRUE))
    install.packages("BiocManager")
BiocManager::install(c("biomaRt", "VariantAnnotation", "Gviz"),
                     version = "3.8", dependencies = T, clean = T)

library(devtools)
devtools::install_github("andreyshabalin/MatrixEQTL", force=T)
devtools::install_github("matthiasheinig/eQTLpipeline", force=T)
```

## 1.2  Data:

- filtered 1000 genomes genotypes
  vcf file (*e-geuv-1_filtered.vcf.bgz* and *e-geuv-1_filtered.vcf.bgz.tbi*, 1.4 MB / 114 KB)

- sample annotations (*e-geuv-1_filtered_pheno.tsv*, 72 KB)