

List of Software and Web Applications

To ensure compatibility and optimal performance, download and install the latest version of the software that matches your computer's operating system, unless a specific version is required.

Software or Website	Operating System	URL
Zoom	All	https://zoom.us/
Module 1: Introduction to Linux		
WSL	Windows	Additional info: https://learn.microsoft.com/en-us/windows/wsl/install
Default Terminal app	Mac	Pre-installed
Any terminal or shell	Linux	Pre-installed
Module 2: Next Generation Sequencing		
<i>See installation guide</i>		
Java	All, Install also in WSL	https://www.java.com/en/download/
Homebrew	Mac only	https://brew.sh/
BWA (Burrows-Wheeler Aligner)	Windows - in WSL Mac, Linux	http://bio-bwa.sourceforge.net
GATK (Genome Analysis ToolKit)	Windows - in WSL Mac, Linux	https://gatk.broadinstitute.org/hc/en-us
FastP (FastQ Preprocessor)	Windows - in WSL Mac, Linux	https://github.com/OpenGene/fastp
FastQC (FastQ Quality Control)	Windows - in WSL Mac, Linux	https://www.bioinformatics.braham.ac.uk/projects/fastqc/
Picard Tools	Windows - in WSL Mac, Linux	http://broadinstitute.github.io/picard/
SAMtools	Windows - in WSL Mac, Linux	http://samtools.sourceforge.net

Bcftools	Windows - in WSL Mac, Linux	https://samtools.github.io/bcftools/
Module 3: Genome-Wide Association Studies		
TASSEL	All	https://www.maizogenetics.net/tassel
Plink 1.9	All	https://www.cog-genomics.org/plink/
R (see also R packages list below)	All	https://www.r-project.org/
R-Studio	All	https://posit.co/download/rstudio-desktop/
Module 4: Post-GWAS		
No software is needed to install. This module will use web applications listed below.		
SNP-Seek	Any web browser	https://snpseek.irri.org/
CropGalaxy	Any web browser	http://cropgalaxy.excellenceinbreeding.org/
RicePilaf	Any web browser	https://ricepilaf.irri.org/

Additional instructions specific to a software:

1. Plink - <https://www.cog-genomics.org/plink/>
 - Download the binary distribution for your system from the "Binaries" table, "Stable build" column. Then just unzip the folder and move to the training directory
 - Direct link as of 2024-06-06:
[Linux binary](#) to use in WSL2
[Windows binary](#) to use in cmd.exe / PowerShell
MacOS users need [Mac binary](#)

Note - PLINK is not a regular app to be installed into Program Files. It is just a

command-line executable. You only need to download it and make sure you have privileges to execute it (i.e. admin privileges). We will show an example of how to use it. To run it, you need to have a terminal-like application, on Windows it is Powershell.

To check installation, open Powershell, navigate to the folder containing plink.exe file, and type `".\plink.exe --help"`

(Alternatively, use "cmd")

- i. From the plink folder, go to the address bar and highlight the address.
- ii. Type `"cmd"` on the address bar.
- iii. TYPe `".\plink.exe --help"`
 - [Video](https://drive.google.com/file/d/1Vfx4uKINHH3wQO6ei4G-uD6v5lyW6ME1/view?usp=sharing) how to install on Windows:
<https://drive.google.com/file/d/1Vfx4uKINHH3wQO6ei4G-uD6v5lyW6ME1/view?usp=sharing>

2. R - <https://www.r-project.org/>

- Mirror: <https://cran.csie.ntu.edu.tw/>
 - i. To install "source-only" packages on Windows one may need **Rtools**: <https://cran.r-project.org/bin/windows/Rtools/>
If your version of R is R-4.2.xx, install Rtools42.
If your version of R is R-4.3.xx, install Rtools43.

3. R packages on R-studio:

- `install.packages("qqman")`
- `install.packages("ggplot2")`
- `install.packages(c("dplyr", "glue", "reshape2"))`
- `install.packages(c("readr", "vroom", "openxlsx"))`
- `install.packages("BEDMatrix")`
- `install.packages("BiocManager")` # to install packages from Bioconductor
- `BiocManager::install("snpStats")`
- `install.packages(c("shinydashboard", "DT", "bslib", "rmarkdown"))`

4. Optional software

- Admixture - <http://dalexander.github.io/admixture/download.htm>
- GEMMA - <https://github.com/genetics-statistics/GEMMA/releases>
- SnpEff and SnpSift - <https://pcingola.github.io/SnpEff/>

Note that PLINK can be installed on Ubuntu using apt:

```
$ sudo apt install plink1.9
```

but do NOT do "install plink" without version, as it will install a different application (network utility) with the same name.

R can be installed as

```
$ sudo apt install r-base
```

Post-installation check

1. Java
 - a. Check version of Java by opening a Powershell or Terminal and issuing command:
 - b. **java -version**
2. TASSEL
 - a. Open TASSEL, open the tutorial dataset packaged within the Tassel folder.
3. RStudio
 - a. Open RStudio, and run "**version**" command in the console
 - i. Install the package "**qqman**" using the menu.
4. Powershell/Terminal
 - a. Open Powershell (MS Windows) or Terminal (Mac OS) and note the current working directory by typing **pwd** (then Enter)
5. WSL
 - a. If you are on Windows:
 - b. Check WSL version
 - c. **wsl --version**
 - d. **wsl --list**