

## SNP Analysis using dartR



# Installing dartR



**Copies of the full workshop notes are available from:**

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## Install R and RStudio

Install R version 3.6.0 from the web page <https://cran.r-project.org/bin/windows/base/> and install in the usual manner for your computer, selecting the defaults.

RStudio is a graphical user interface for R that is commonly used. This can be installed as version 1.2.1335 from the web page <https://www.rstudio.com/products/rstudio/download/>.

## Install dartR

There is considerable advantage to having a clean installation before the workshop begins, because installation may require individual attention. This will delay us from getting into the materials proper.

If you experience problems, post the details to the dartR google group.

<https://groups.google.com/forum/#!forum/dartR>

To be able to install dartR properly we recommend installation of a recent version of R (at least version 3.5) and Rstudio (at least version 1.1.463).

Apple users need to ensure Xcode (available on the App Store) is installed before starting the dartR installation process.

## Installing from GitHub

The latest stable version can be installed directly from GitHub.

```
install.packages("devtools")
library(devtools)
install_github("green-striped-gecko/dartR")
library(dartR)
```

or if you have trouble with SNPRelate,

```
install.packages("devtools")
library(devtools)
install.packages("BiocManager")
BiocManager::install(c("SNPRelate", "qvalue"))
install_github("green-striped-gecko/dartR")
library(dartR)
```



Install dartR from GitHub and then load the library

## If something goes wrong



If you already have a version of R installed, you may need to install the new version by running RStudio as administrator.

If there is some masking going on, perhaps use `rm(list=ls())`

If some packages have not been loaded, an error message will be given and you will need to install those packages manually. You should read the warnings and errors, identify the packages that have not loaded, install them manually using `install.packages`, and try again.

For example:

```
loading required package: adegenet
Error: package or namespace load failed for 'adegenet'
in loadNamespace(i, c(lib.loc, .libPaths()),
versionCheck = vI[[i]]): namespace 'rlang' 0.3.0.1 is
already loaded, but >= 0.3.1 is required
Error: package 'adegenet' could not be loaded
```

If this happens, install the required package listed in the error (here `adegenet`), and then reinstall `dartR` from CRAN:

```
install.packages("adegenet")
install.packages("dartR")
library(dartR)
```

You may have to do this several times if different packages fail to install.

## Hint for Mac

Some (older) Mac Systems are not able to install the `rgl` package and you need to install the `quartz` software from `quartz.org` manually, before you can install the `rgl` package. Try this if package `rgl` fails to install.

## Testing your installation

You can test your installation by running a function on the test dataset, for example:

```
gl.plot(testset.gl)
```

## Help

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You can post questions via Google group dartR at any point leading up to the workshop if you are having trouble. You will need to join the group.

<https://groups.google.com/forum/#!forum/dartr>