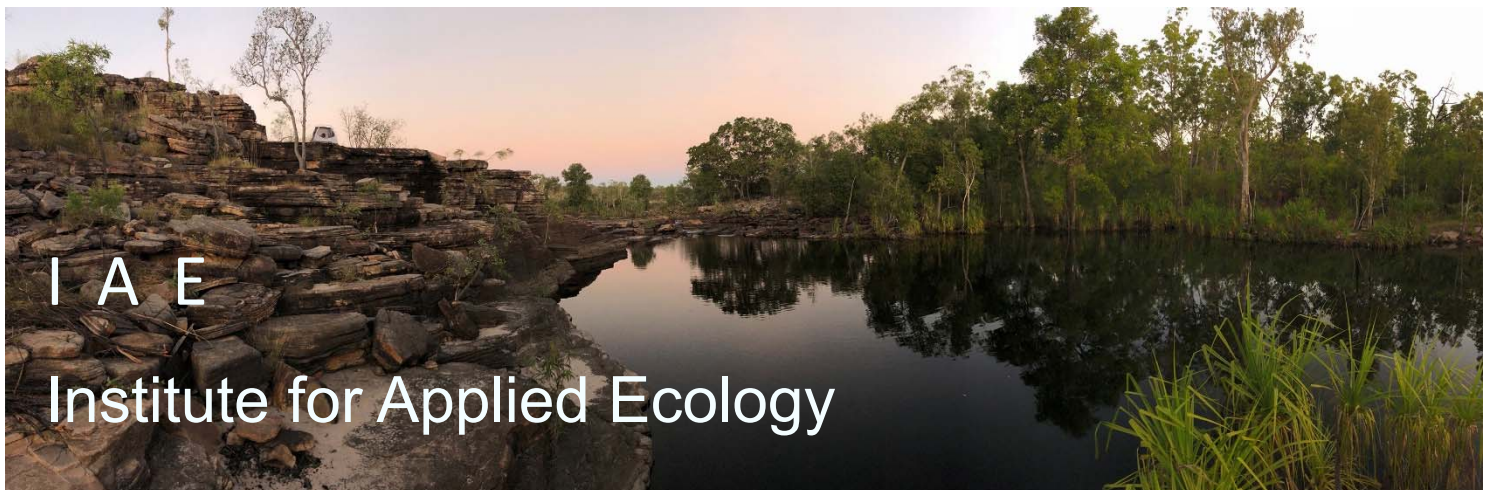


## SNP Analysis using dartR



# Installing dartR

Version 1.8.3



**Copies of the latest version of this tutorial are available from:**

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## Install dartR

### Installing from CRAN

---

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

To be able to install dartR properly we recommend installation of a recent version of R (at least version 4.0) 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

---

#### Latest Stable Version

```
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)
```

#### Latest Beta Version

```
install.packages("devtools")
library(devtools)
install.packages("leaflet.providers")
install.packages("lifecycle")
install.packages("farver")
install_github("green-striped-gecko/dartR", ref="dev")
# no need to upgrade prior installs, answer no.
```

```
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

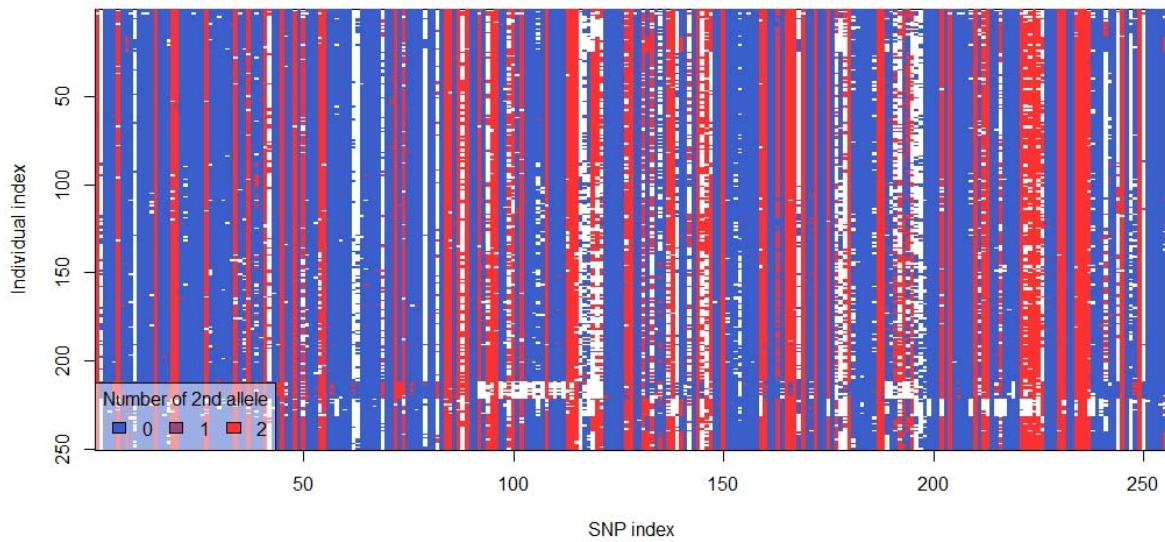
Some (older) Mac Systems are not able to install the `rgl` package and you need to install the `quartz` software from [quartz.org](http://quartz.org) manually, before you can install the `rgl` package. Try this if package `rgl` fails to install.

## Testing your installation

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

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

to yield a plot as follows:



## Help

You can post questions via Google group dartR if you are having trouble. You will need to join the group.

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

If you are a developer and wish to contribute to the development of dartR, you should link through RStudio to

<http://github.com/green-striped-gecko/dartR>

develop locally and push to the /dev version. Raise any issues you believe require attention.