UNIVERSITY OF
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SNP Analysis using dartR

Installing dartR

Version 2

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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)
gl.install.vanilla.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.

If you have trouble because SNPRelate was not installed, try to run this:

```
install.packages("BiocManager")
BiocManager::install(c("SNPRelate", "qvalue"))
```

and then rerun

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

Installing from GitHub

Latest Stable Version

```
install.packages("devtools")
library(devtools)
install_github("green-striped-gecko/dartR")
library(dartR)
gl.install.vanilla.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)
gl.install.vanilla.dartR(flavour='master')
```

Latest Beta Version

```
install.packages(dartR)
library(dartR)
gl.install.vanilla.dartR(flavour='dev')
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)
```

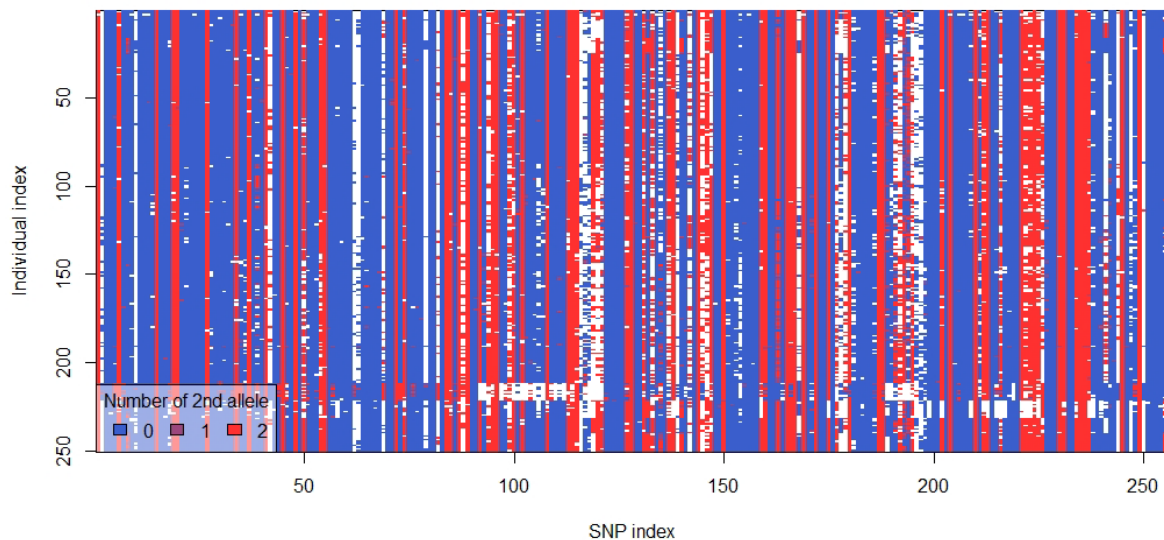You may have to do this several times if different packages fail to install.

Hint for Mac

Some (older) Mac Systems are not able to install the rgl package and you need to install the quarz 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)
```

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.