

Practical courses

Amin Madoui and Romuald Laso-Jadart

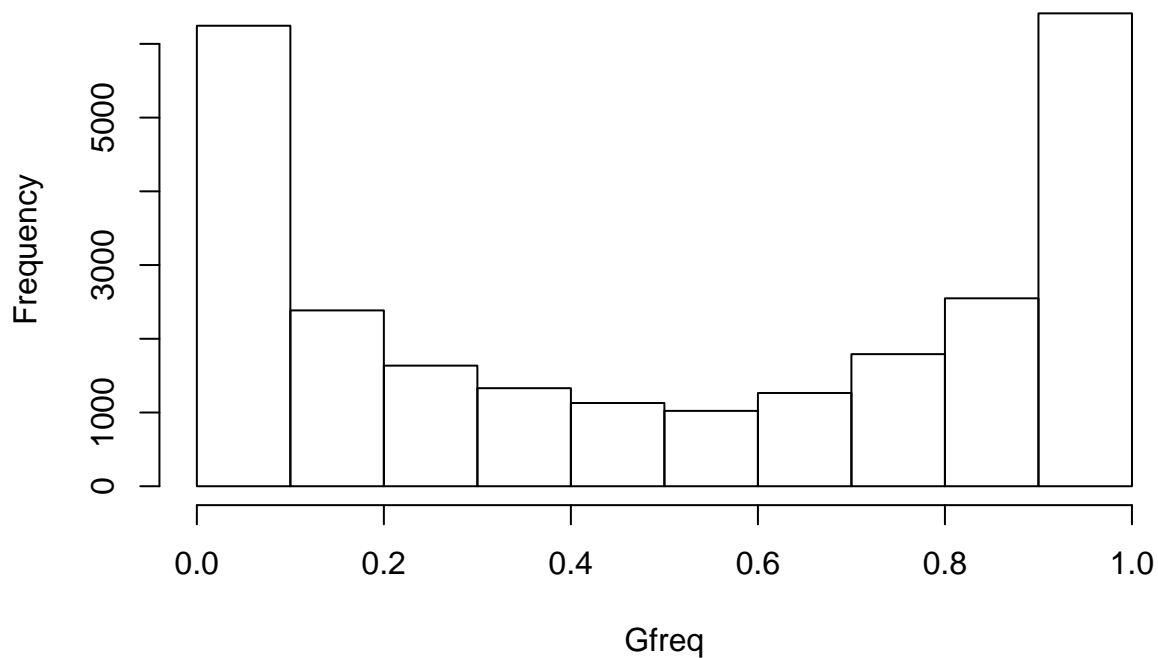
26 février 2021

Estimation of the genomic differentiation

Allele frequency spectrum

```
r data=read.table('RC/S155.txt') colnames(data) = c("GA","GB","TA","TB") Gfreq =  
data$GB/(data$GA+data$GB) hist(Gfreq, breaks = 10, main="B allele frequency distribution")
```

B allele frequency distribution



##Pairwise-FST

##Isolation by currents2

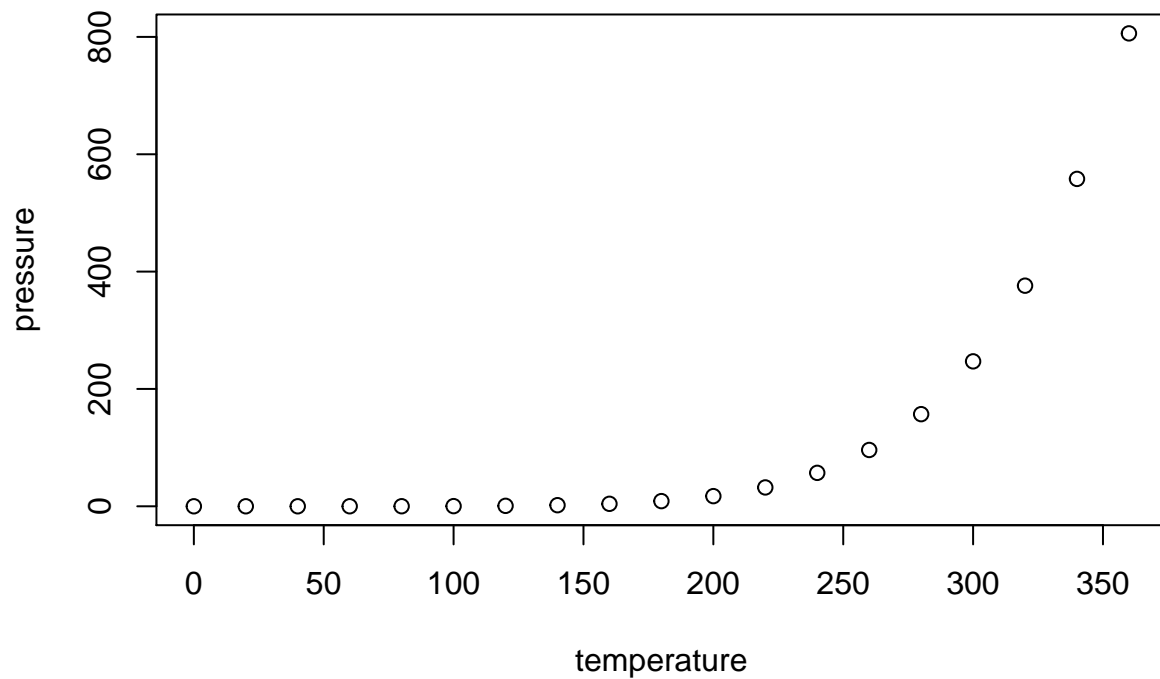
Detection of loci under natural selection ##FSToutliers method ##pcadapt method #Population-scale allele expression ##Comparison of allele expression to genomic abundance ##Detection of allele-specific expression ##Link between natural selection and allele specific ex-pression #Reference-free approach and metavariant species ##Genomic differentiation of MVS ##Role of the environmental factors ##Variance partitioning of environmental factors

```
summary(cars)
```

```
##      speed      dist
##  Min.   : 4.0    Min.    : 2.00
## 1st Qu.:12.0    1st Qu.: 26.00
##  Median :15.0    Median : 36.00
##   Mean  :15.4    Mean     : 42.98
## 3rd Qu.:19.0    3rd Qu.: 56.00
##   Max.  :25.0    Max.     :120.00
```

Including Plots

You can also embed plots, for example:



Note that the `echo = FALSE` parameter was added to the code chunk to prevent printing of the R code that generated the plot.