

Practical courses

Amin Madoui and Romuald Laso-Jadart

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Estimation of the genomic differentiation

Allele frequency spectrum

```
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") ##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.