Practical courses

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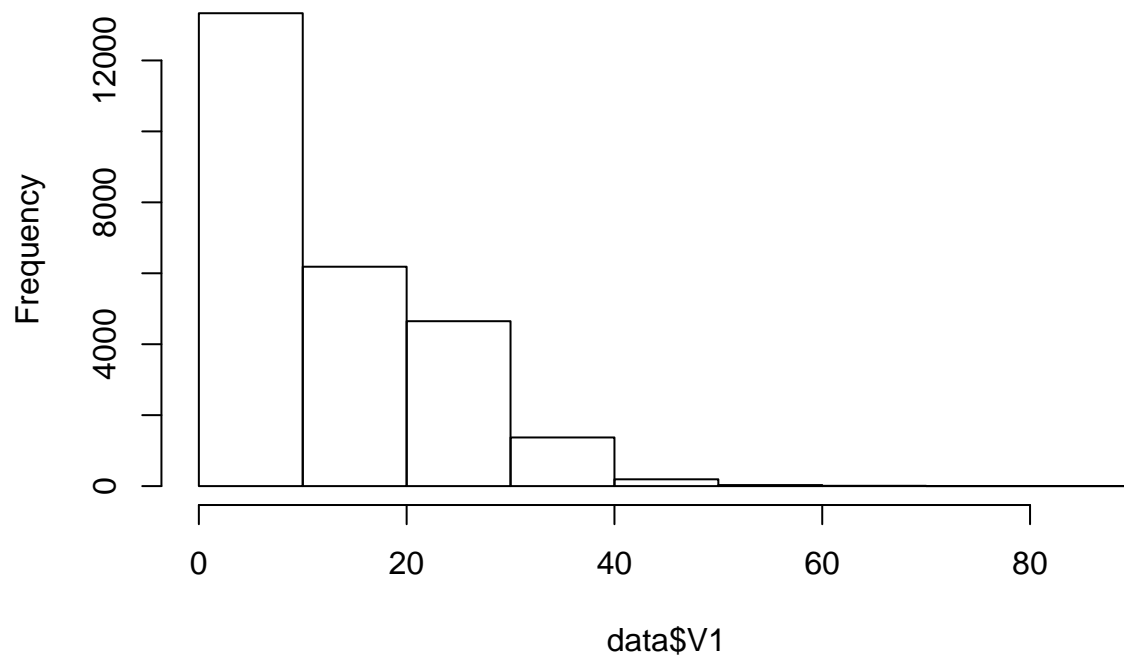
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Estimation of the genomic differentiation1

Allele frequency spectrum

`r  data=read.table( 'RC/S155.txt' )  hist(data$V1, breaks = 10)`

Histogram of data$V1

##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
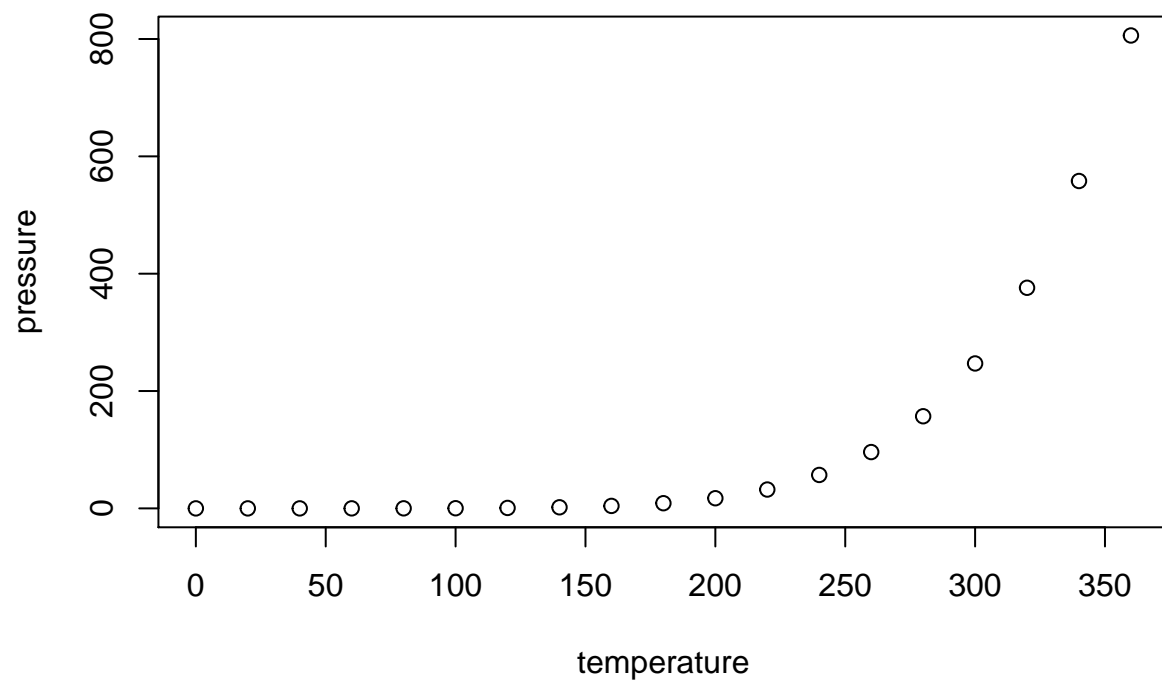
```r
summary(cars)
```

```
##      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.