

Livestock Breeding and Genomics - Exercise 3

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Problem 1: Breeding Value

We are considering a quantitative trait that depends on a given bi-allelic locus G . The frequency of the favorable allele corresponds to 0.08. Suppose that genotype frequencies follow the Hardy-Weinberg equilibrium. The difference between the homozygous genotypes corresponds to 15. The heterozygous genotype has a value of -1.5 .

- Compute the breeding values and the dominance deviations for the three genotypes.
- Because of selecting the positive allele the frequency has increased to 0.096. How does this increased allele frequency change the breeding values?

Hint: Have a look at the summary table of all values in the course notes.

Problem 2: Allele Substitution

What is the meaning of the term **allele substitution** and how big is it in 1a) and 1b)?

Problem 3: Reading Data into R

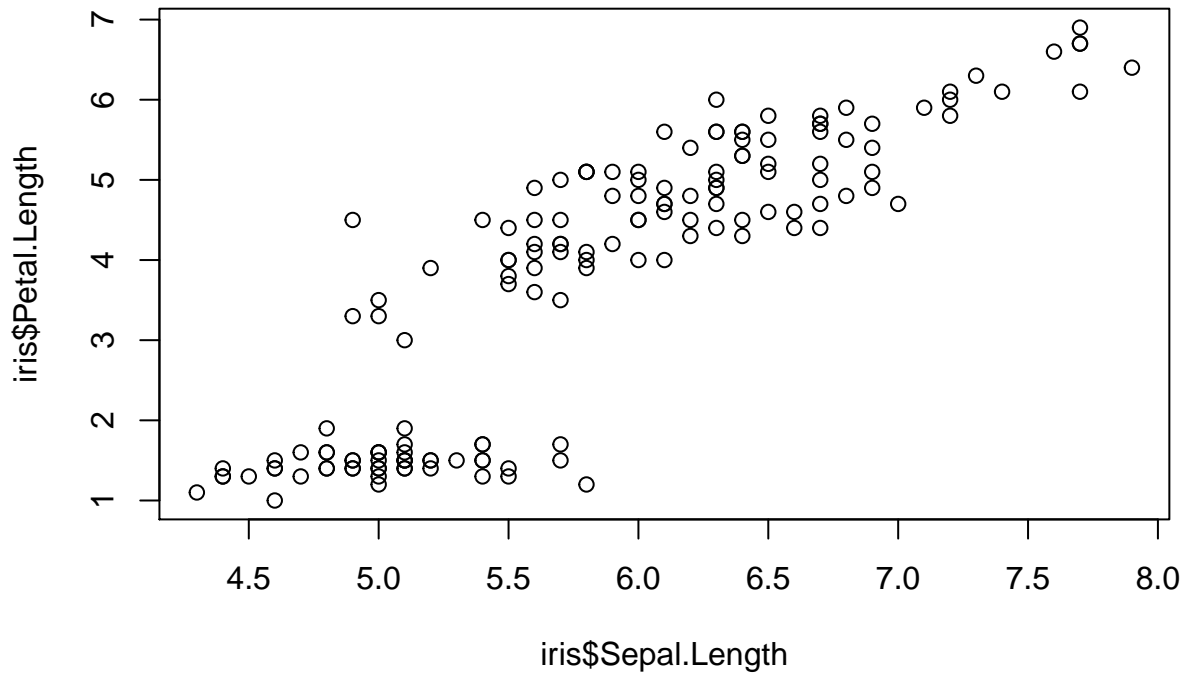
You can download a file in csv-format from the course website. The URL is https://charlotte-ngs.github.io/lbgfs2020/misc/iris_ex03.csv. Read the data from that csv-file into R using the function `read.csv2()`. Test the consequences of specifying the option `stringsAsFactors=TRUE`. The function `read_csv2()` from the `readr` package is an alternative way to import data from a .csv-file. The result is a little different. While the function `read.csv2()` returns an ordinary 'data.frame' as a result, the function `read_csv2()` returns a 'tibble' which is a more modern version of a 'data.frame'.

Hints:

- You can first download the csv-file to your local computer and then read the data, or you can directly indicate the URL when reading the data. You get more information with the command `?read.csv2` at the R-console.
- Assign the result of `read.csv2()` to a variable
- Use the function `str()` on the result of `read.csv2()` to see the difference between the two results of reading the data.
- Use the description at <https://bookdown.org/rdpeng/rprogdatascience/getting-data-in-and-out-of-r.html> as a reference to read data into R. There is also a video on the same subject under https://youtu.be/Z_dc_FADyi4.
- Use the function `read_csv2()` to import the data and inspect the difference between a 'data.frame' and a 'tibble'.

Additional Problem: Create a plot in R

Plot the values in the columns `Sepal.Length` and `Petal.Length` of the Iris data set. The plot should look like the following figure.



The above plot was produced using the standard plotting function of the base-R system. The R-package `ggplot2` provides an interesting alternative to the basic plotting function. A plot with `ggplot2` looks as follows.

