## lab11

## Zijing

## 2022-11-03

```
library(dplyr)

##
## Attaching package: 'dplyr'
## The following objects are masked from 'package:stats':
##
## filter, lag
## The following objects are masked from 'package:base':
##
## intersect, setdiff, setequal, union
library(ggplot2)

Q13

file <- "population_data.txt"
data <- read.table(file)</pre>
```

```
file <- "population_data.txt"

data <- read.table(file)
geno <- as.factor(data$geno)
table(geno)

## geno
## A/A A/G G/G
## 108 233 121

summary(data %>% filter(geno == "A/A"))
```

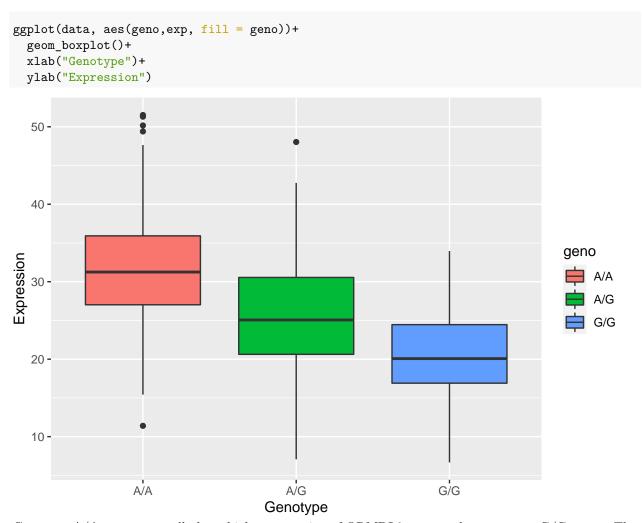
```
##
       sample
                           geno
                                                exp
  Length:108
                       Length: 108
                                          Min.
                                                 :11.40
##
                                           1st Qu.:27.02
##
   Class :character
                       Class :character
   Mode :character
##
                       Mode :character
                                           Median :31.25
##
                                                  :31.82
                                           Mean
##
                                           3rd Qu.:35.92
##
                                          Max.
                                                  :51.52
summary(data %>% filter(geno == "A/G"))
```

```
##
       sample
                           geno
                                                exp
##
    Length:233
                       Length: 233
                                           Min.
                                                  : 7.075
##
    Class :character
                       Class :character
                                           1st Qu.:20.626
##
    Mode :character
                       Mode :character
                                           Median :25.065
##
                                           Mean
                                                 :25.397
```

```
3rd Qu.:30.552
##
##
                                            Max.
                                                    :48.034
summary(data %>% filter(geno == "G/G"))
##
       sample
                            geno
                                                 exp
##
    Length: 121
                        Length: 121
                                            Min.
                                                   : 6.675
##
    Class :character
                        Class :character
                                            1st Qu.:16.903
##
    Mode :character
                        Mode :character
                                            Median :20.074
##
                                            Mean
                                                    :20.594
                                            3rd Qu.:24.457
##
##
                                            Max.
                                                    :33.956
```

Genotype A/A: sample size 108, median expression level 31.25 Genotype A/G: sample size 233, median expression level 25.065 Genotype G/G: sample size 121, median expression level 20.074

## Q14



Genotype A/A group generally have higher expression of ORMDL3 compared to genotype G/G group. The SNP does affect the expression of ORMDL3.