Class 11 Introduction to Genome Informatics Lab

Justin Robinson (PID: A16307501)

2024-05-07

Population Scale Analysis Homework

Q13: Read this file into R and determine the sample size for each genotype and their corresponding median expression levels for each of these genotypes.

```
geno_table <- read.table(url("https://bioboot.github.io/bggn213_W19/class-material/rs8067378_ENSG000001
sum(geno_table$geno == "A/G")
## [1] 233
sum(geno_table$geno == "A/A")
## [1] 108
sum(geno_table$geno == "G/G")
## [1] 121
Stats for the A/A group:
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
AA_geno <- geno_table %>%
 filter(geno == "A/A")
summary(AA_geno)
```

```
##
       sample
                            geno
                                                  exp
##
    Length: 108
                        Length: 108
                                            Min.
                                                    :11.40
    Class : character
                                            1st Qu.:27.02
##
                        Class :character
##
    Mode :character
                                            Median :31.25
                        Mode :character
##
                                            Mean
                                                    :31.82
##
                                            3rd Qu.:35.92
##
                                                    :51.52
                                            Max.
```

The median expression of ORMDL3 for the A/A genotype is 31.25 Stats for the A/G group:

```
AG_geno <- geno_table %>%
filter(geno == "A/G")
summary(AG_geno)
```

```
##
       sample
                             geno
                                                   exp
##
    Length: 233
                         Length: 233
                                             Min.
                                                     : 7.075
##
    Class : character
                         Class : character
                                             1st Qu.:20.626
    Mode :character
                                             Median :25.065
                        Mode :character
##
                                                     :25.397
                                             Mean
##
                                             3rd Qu.:30.552
##
                                             Max.
                                                     :48.034
```

For the A/G genotype it is 25.065

Stats for the G/G group:

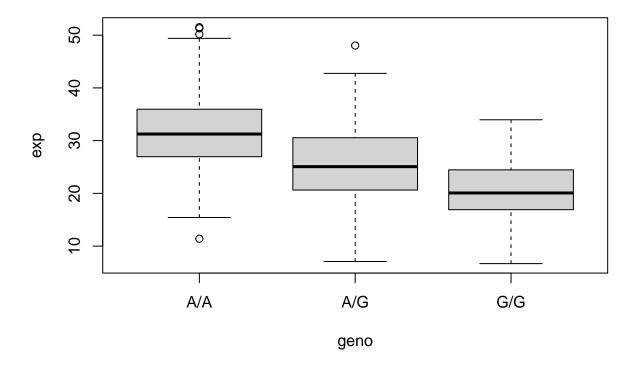
```
GG_geno <- geno_table %>%
filter(geno == "G/G")
summary(GG_geno)
```

```
##
       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
##
                                                    :20.594
                                            Mean
##
                                            3rd Qu.:24.457
##
                                            Max.
                                                    :33.956
```

For the G/G genotype it is 20.074

Q14: Generate a boxplot with a box per genotype, what could you infer from the relative expression value between A/A and G/G displayed in this plot? Does the SNP effect the expression of ORMDL3?

```
boxplot(exp ~ geno, data = geno_table)
```



Based on the above boxplot, it would seem that the A/A genotype has a higher expression of the ORMDL3 gene. A/G is second and G/G is last in terms of ORMDL3 expression.