

Class 12 Homework

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2024-11-09

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.

```
file <- read.table("rs8067378_ENSG00000172057.6.txt")
```

```
summary(file)
```

```
##      sample      geno      exp
## Length:462      Length:462      Min.   : 6.675
## Class :character Class :character 1st Qu.:20.004
## Mode  :character Mode  :character Median :25.116
##                                     Mean  :25.640
##                                     3rd Qu.:30.779
##                                     Max.   :51.518
```

```
# Sample size for each genotype
table(file$geno)
```

```
##
## A/A A/G G/G
## 108 233 121
```

```
aa <- subset(file, geno == "A/A")
# Median Expression Levels of genotype A/A samples
median(aa$exp)
```

```
## [1] 31.24847
```

```
ag <- subset(file, geno == "A/G")
# Median Expression Levels of genotype A/G samples
median(ag$exp)
```

```
## [1] 25.06486
```

```
gg <- subset(file, geno == "G/G")
# Median Expression Levels of genotype G/G samples
median(gg$exp)
```

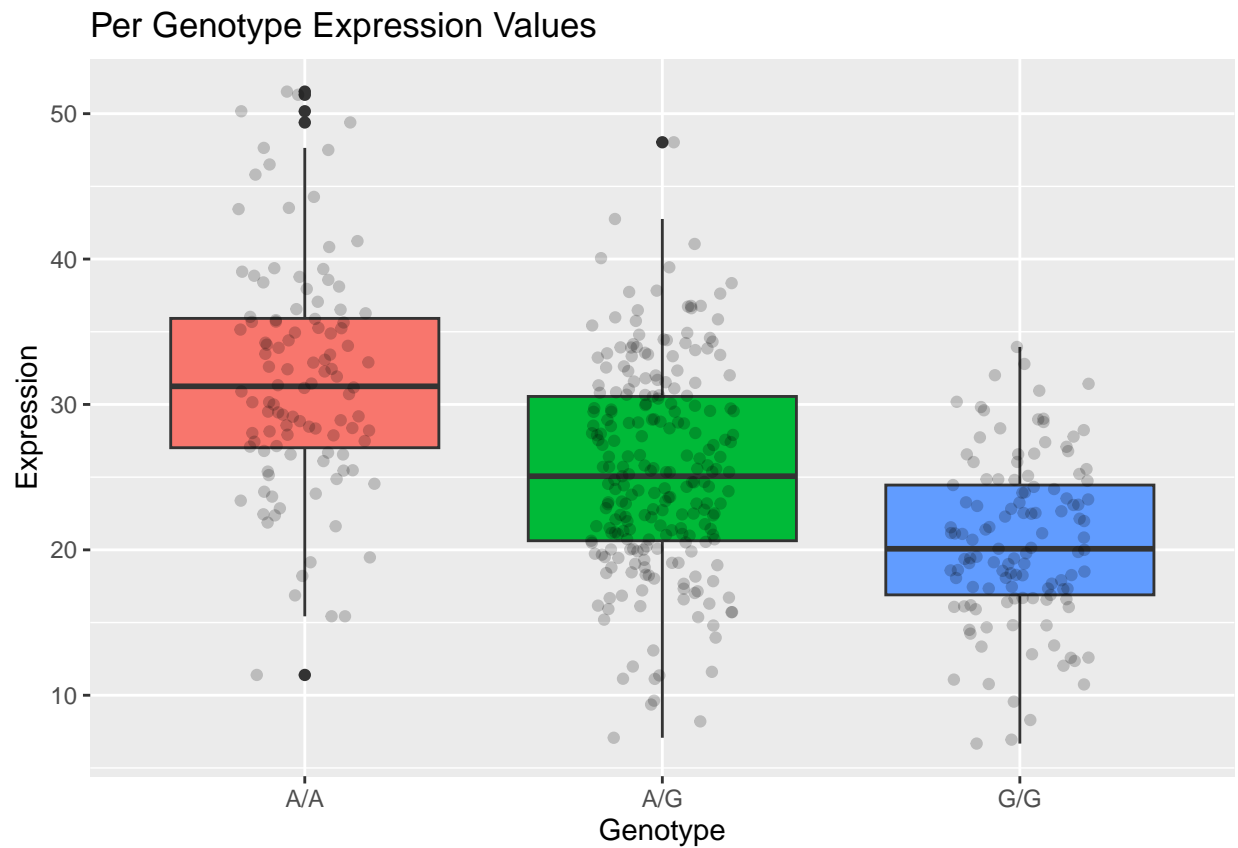
```
## [1] 20.07363
```

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?

```
library(ggplot2)
```

```
ggplot(file, aes(geno, exp, fill = geno)) +
  geom_boxplot() +
```

```
guides(fill="none") +
  geom_jitter(width = 0.2, alpha = 0.2) +
  labs(title="Per Genotype Expression Values", x = "Genotype", y = "Expression")
```



A/A is expressed more than G/G

Given the large difference in expression between the genotypes, I believe SNP affects the expression of ORM DL3.