

BGGN213-Class11

AUTHOR

Lisanne Stouthart (PID A69036187)

Quarto

Quarto enables you to weave together content and executable code into a finished document. To learn more about Quarto see <https://quarto.org>.

Question 13

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

	sample	geno	exp
1	HG00367	A/G	28.96038
2	NA20768	A/G	20.24449
3	HG00361	A/A	31.32628
4	HG00135	A/A	34.11169
5	NA18870	G/G	18.25141
6	NA11993	A/A	32.89721

```
nrow(expr) #462
```

```
[1] 462
```

```
table(expr$geno) #A/A = 108, A/G = 233, G/G = 121
```

A/A	A/G	G/G
108	233	121

```
str(expr)
```

```
'data.frame':  462 obs. of  3 variables:
 $ sample: chr  "HG00367" "NA20768" "HG00361" "HG00135" ...
 $ geno  : chr  "A/G" "A/G" "A/A" "A/A" ...
 $ exp   : num  29 20.2 31.3 34.1 18.3 ...
```

```
# Check the column names to ensure the data is correct
names(expr) #sample, geno, exp
```

```
[1] "sample" "geno"   "exp"
```

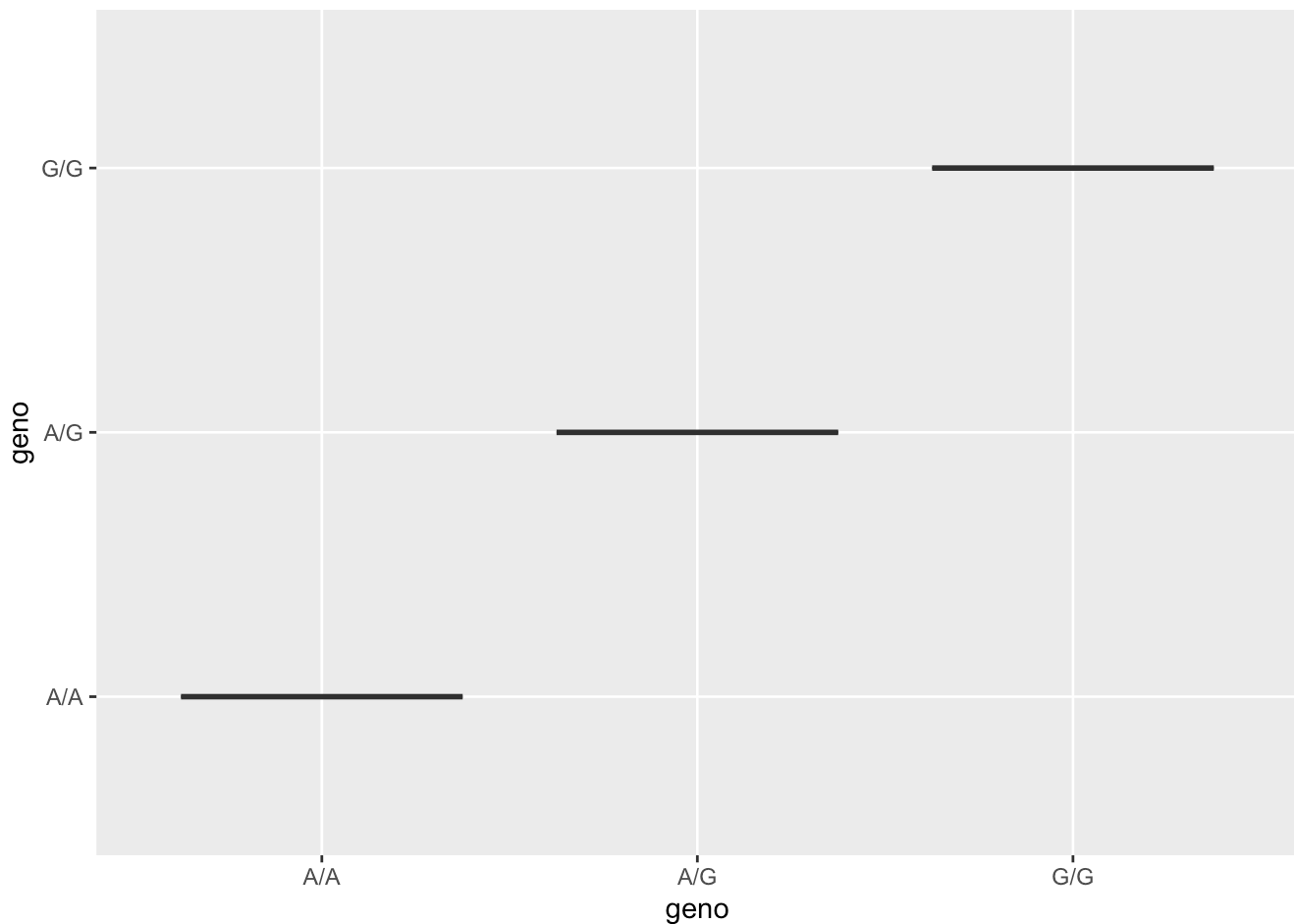
```
median_expression <- tapply(expr$exp, expr$geno, median)
print(median_expression)
```

```
      A/A      A/G      G/G
31.24847 25.06486 20.07363
```

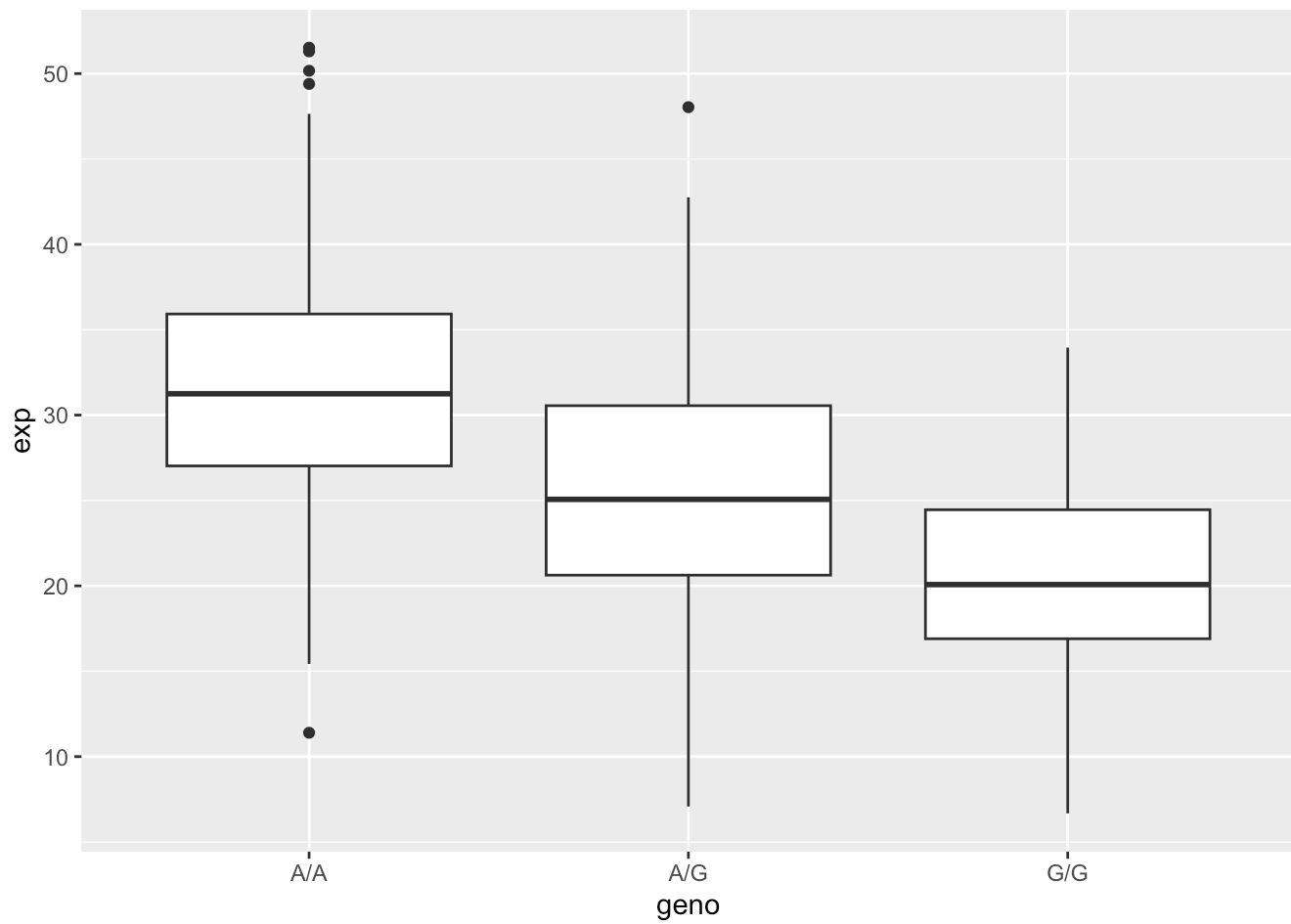
Question 14

```
library(ggplot2)

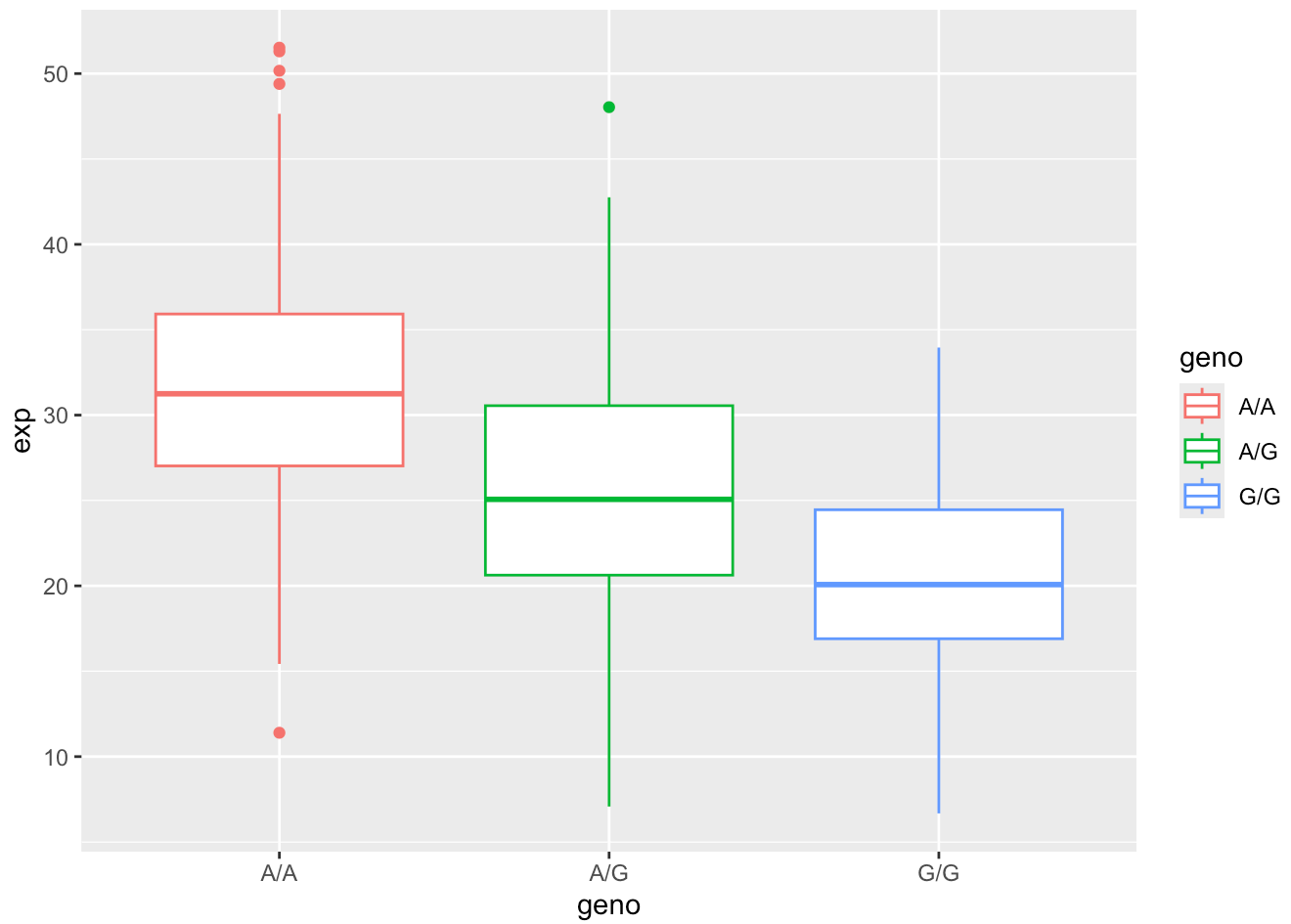
# lets make a boxplot
ggplot(expr) + aes(x=geno, y=geno) +
  geom_boxplot()
```



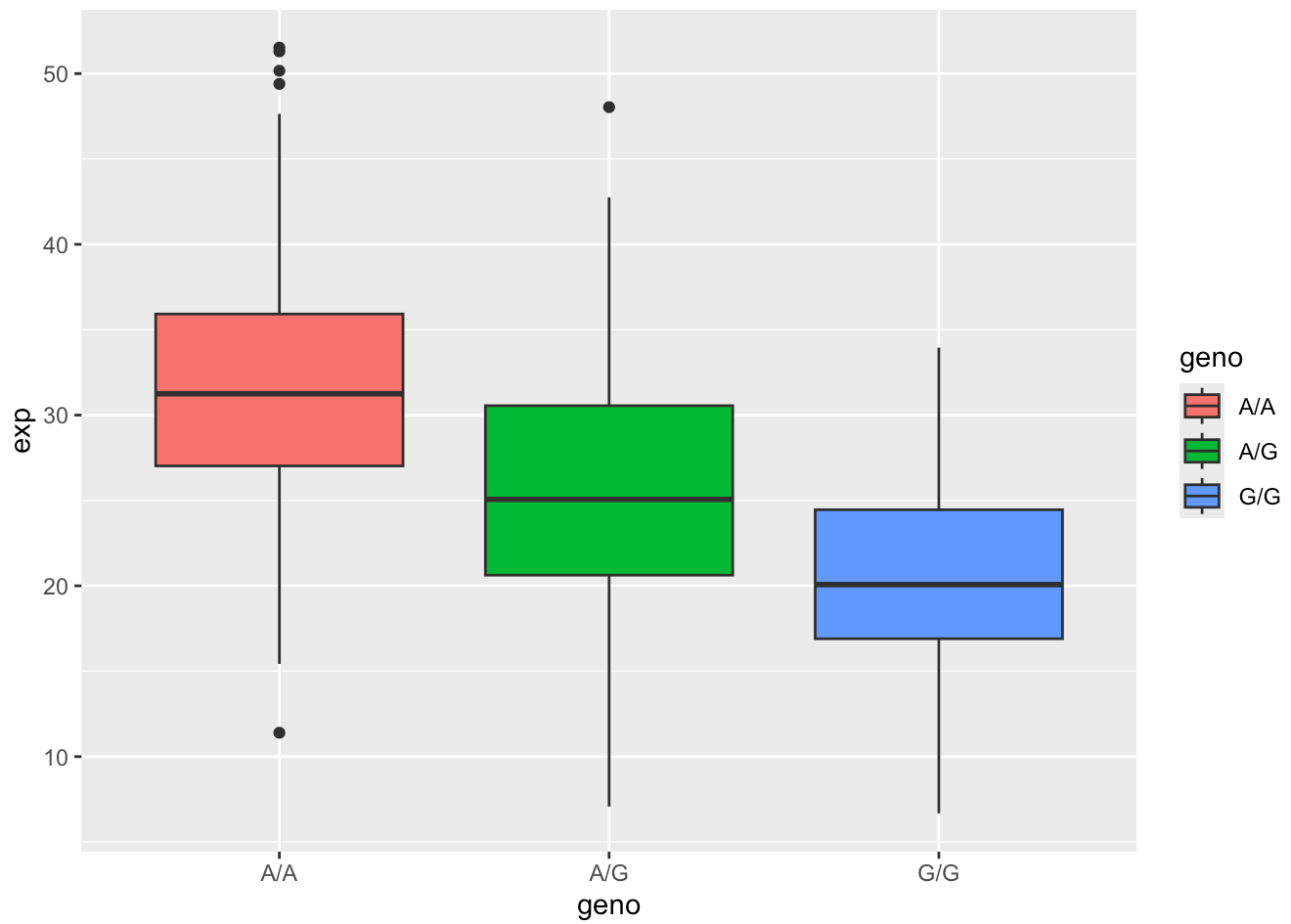
```
# lets try something different
ggplot(expr) + aes(x=geno, y=exp) +
  geom_boxplot()
```



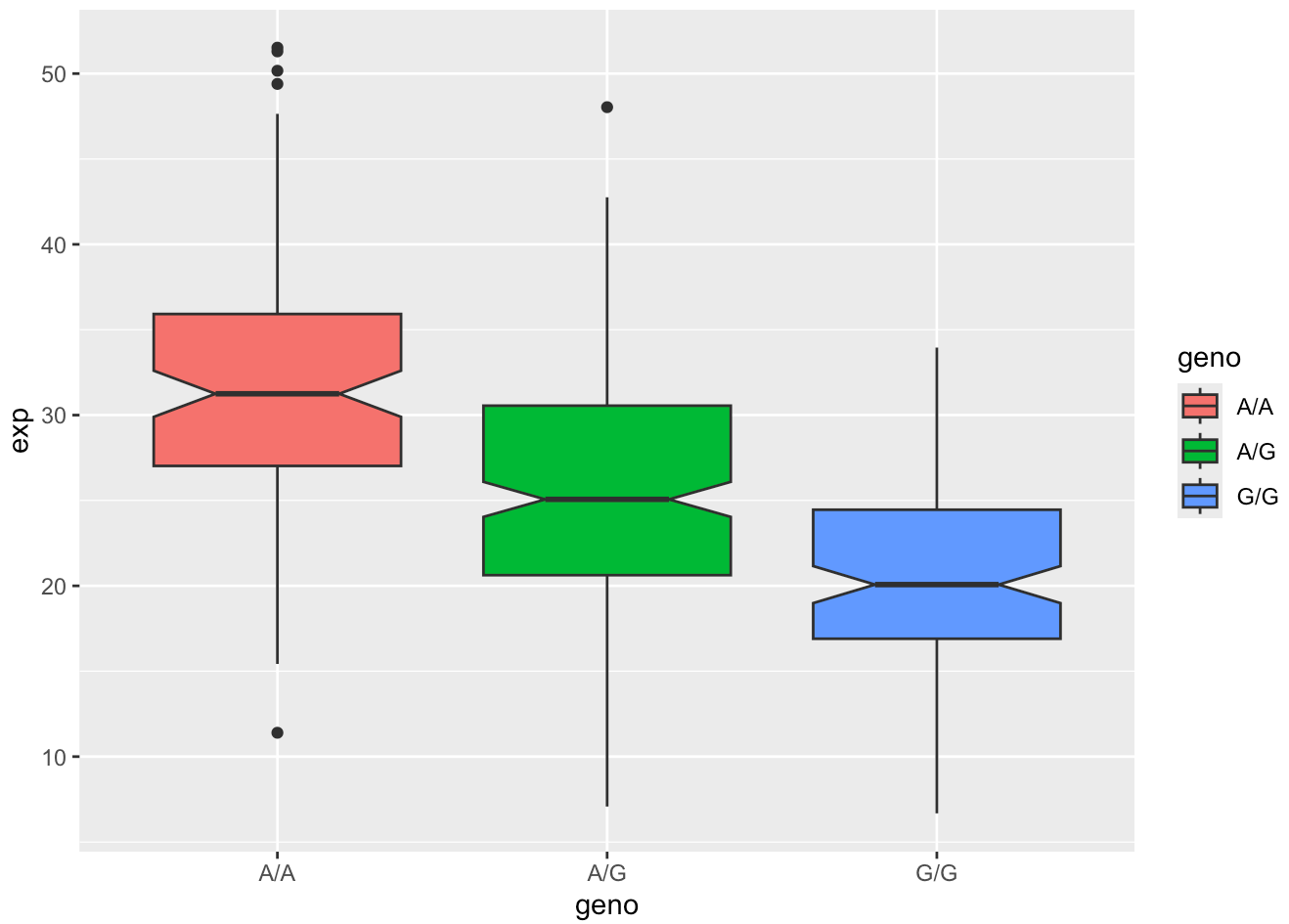
```
# lets try something different  
ggplot(expr) + aes(x=geno, y=exp, col=geno) +  
  geom_boxplot()
```



```
# lets try something different  
ggplot(expr) + aes(x=geno, y=exp, fill=geno) +  
  geom_boxplot()
```



```
# lets try something different
ggplot(expr) + aes(x=geno, y=exp, fill=geno) +
  geom_boxplot(notch=TRUE)
```



```
# conclusion; having a G/G really results in a low expression of this gene.  
# expression level of ORMDL3 decreases as you go from A/A to G/G.  
# The SNP appears to have an effect on the expression of ORMDL3.
```