

# Class12

Jae Kim

## Section 1. Proportion of G/G in a population

```
mxl <- read.csv("MXL.csv", row.names = 1)
mxl
```

	Genotype..forward.strand.	Population.s.	Father	Mother
NA19648 (F)	A A	ALL, AMR, MXL	-	-
NA19649 (M)	G G	ALL, AMR, MXL	-	-
NA19651 (F)	A A	ALL, AMR, MXL	-	-
NA19652 (M)	G G	ALL, AMR, MXL	-	-
NA19654 (F)	G G	ALL, AMR, MXL	-	-
NA19655 (M)	A G	ALL, AMR, MXL	-	-
NA19657 (F)	A G	ALL, AMR, MXL	-	-
NA19658 (M)	A A	ALL, AMR, MXL	-	-
NA19661 (M)	A G	ALL, AMR, MXL	-	-
NA19663 (F)	A A	ALL, AMR, MXL	-	-
NA19664 (M)	G A	ALL, AMR, MXL	-	-
NA19669 (F)	A A	ALL, AMR, MXL	-	-
NA19670 (M)	A A	ALL, AMR, MXL	-	-
NA19676 (M)	G G	ALL, AMR, MXL	-	-
NA19678 (F)	A A	ALL, AMR, MXL	-	-
NA19679 (M)	A G	ALL, AMR, MXL	-	-
NA19681 (F)	A G	ALL, AMR, MXL	-	-
NA19682 (M)	A G	ALL, AMR, MXL	-	-
NA19684 (F)	A G	ALL, AMR, MXL	-	-
NA19716 (F)	G A	ALL, AMR, MXL	-	-
NA19717 (M)	A G	ALL, AMR, MXL	-	-
NA19719 (F)	G G	ALL, AMR, MXL	-	-
NA19720 (M)	G G	ALL, AMR, MXL	-	-
NA19722 (F)	G A	ALL, AMR, MXL	-	-

NA19723 (M)	G G ALL, AMR, MXL	-	-
NA19725 (F)	A G ALL, AMR, MXL	-	-
NA19726 (M)	A A ALL, AMR, MXL	-	-
NA19728 (F)	A A ALL, AMR, MXL	-	-
NA19729 (M)	A G ALL, AMR, MXL	-	-
NA19731 (F)	A A ALL, AMR, MXL	-	-
NA19732 (M)	A G ALL, AMR, MXL	-	-
NA19734 (F)	G A ALL, AMR, MXL	-	-
NA19735 (M)	G G ALL, AMR, MXL	-	-
NA19740 (F)	A A ALL, AMR, MXL	-	-
NA19741 (M)	A A ALL, AMR, MXL	-	-
NA19746 (F)	A A ALL, AMR, MXL	-	-
NA19747 (M)	G A ALL, AMR, MXL	-	-
NA19749 (F)	A G ALL, AMR, MXL	-	-
NA19750 (M)	A G ALL, AMR, MXL	-	-
NA19752 (F)	A G ALL, AMR, MXL	-	-
NA19755 (F)	A A ALL, AMR, MXL	-	-
NA19756 (M)	G A ALL, AMR, MXL	-	-
NA19758 (F)	A G ALL, AMR, MXL	-	-
NA19759 (M)	G A ALL, AMR, MXL	-	-
NA19761 (F)	G A ALL, AMR, MXL	-	-
NA19762 (M)	A A ALL, AMR, MXL	-	-
NA19764 (F)	A A ALL, AMR, MXL	-	-
NA19770 (F)	A G ALL, AMR, MXL	-	-
NA19771 (M)	A A ALL, AMR, MXL	-	-
NA19773 (F)	A A ALL, AMR, MXL	-	-
NA19774 (M)	A G ALL, AMR, MXL	-	-
NA19776 (F)	A G ALL, AMR, MXL	-	-
NA19777 (M)	A A ALL, AMR, MXL	-	-
NA19779 (F)	G A ALL, AMR, MXL	-	-
NA19780 (M)	A A ALL, AMR, MXL	-	-
NA19782 (F)	G A ALL, AMR, MXL	-	-
NA19783 (M)	A G ALL, AMR, MXL	-	-
NA19785 (F)	A A ALL, AMR, MXL	-	-
NA19786 (M)	G A ALL, AMR, MXL	-	-
NA19788 (F)	A G ALL, AMR, MXL	-	-
NA19789 (M)	G G ALL, AMR, MXL	-	-
NA19792 (M)	A A ALL, AMR, MXL	-	-
NA19794 (F)	G A ALL, AMR, MXL	-	-
NA19795 (M)	A G ALL, AMR, MXL	-	-

```
table(mx1$Genotype..forward.strand.)
```

```
A|A A|G G|A G|G
22  21  12   9
```

```
table(mx1$Genotype..forward.strand.) / nrow(mx1)*100
```

```
      A|A      A|G      G|A      G|G
34.3750 32.8125 18.7500 14.0625
```

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

```
url <- "https://bioboot.github.io/bimm143_S23/class-material/rs8067378_ENSG00000172057.6.t
expr <- read.table(url)

nrow(expr)
```

```
[1] 462
```

```
table(expr$geno)
```

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

```
result <- aggregate(expr$exp ~ expr$geno, data = expr, FUN = median)
result
```

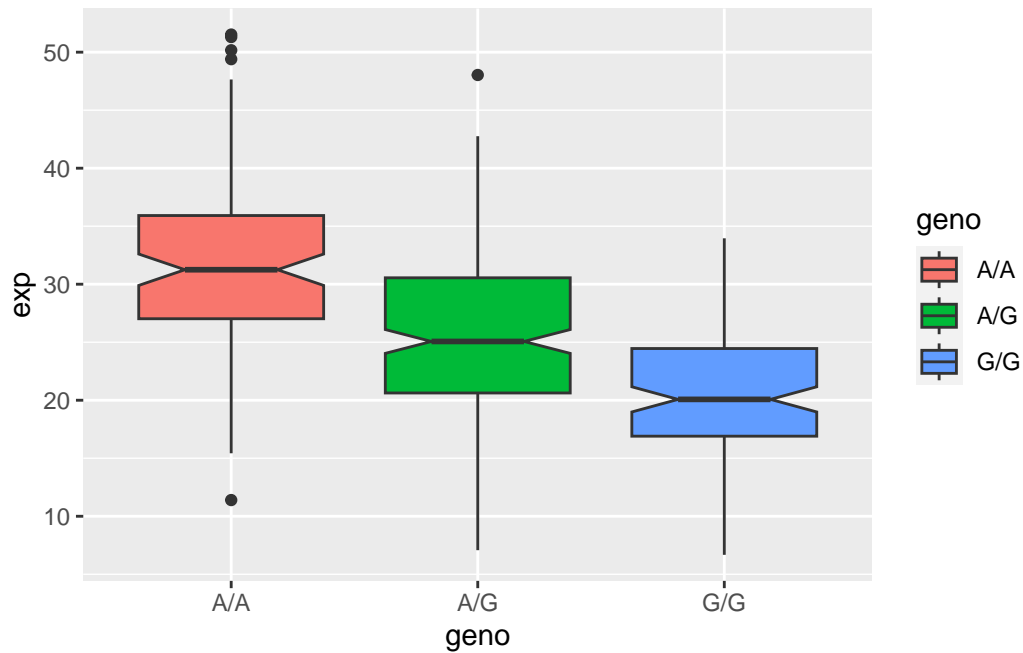
```
expr$geno expr$exp
1      A/A 31.24847
2      A/G 25.06486
3      G/G 20.07363
```

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)
```

Making a boxplot

```
x <- ggplot(expr) +  
  aes(geno, exp, fill=geno) +  
  geom_boxplot(notch=TRUE)  
x
```



```
boxplot_data <- ggplot_build(x)$data[[1]]  
boxplot_data$middle
```

```
[1] 31.24847 25.06486 20.07363
```

From the boxplot, we can see that the expression of ORMDL3 is higher if the genotype is A/A than if it is G/G. It seems like SNP does affect the expression of ORMDL3.