Class 11

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Section 1. Proportion of G/G in a population

 $Downloaded \ the \ csv \ file \ from \ Ensemble < https://useast.ensembl.org/Homo_sapiens/Variation/Sample?db=cor39962692;v=rs8067378;vdb=variation;vf=959672880\#373531_tablePanel>$

Here we read this CSV file

```
mxl <- read.csv("373531-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv")
head(mxl)

Sample..Male.Female.Unknown. Genotype..forward.strand. Population.s. Father

NA19648 (F)

ALA ALL. AMB MXL. -
```

```
1
                    NA19648 (F)
                                                        A|A ALL, AMR, MXL
2
                                                        G|G ALL, AMR, MXL
                    NA19649 (M)
3
                    NA19651 (F)
                                                        A|A ALL, AMR, MXL
4
                    NA19652 (M)
                                                        G|G ALL, AMR, MXL
5
                    NA19654 (F)
                                                        G|G ALL, AMR, MXL
6
                                                        A|G ALL, AMR, MXL
                   NA19655 (M)
 Mother
```

1 - 2 - 3 - 4 - 5 - 6 - -

We want to find proportion that are homozygous (G|G) for asthma. Use the table() function.

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

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

Section 4 Population Scale Analysis

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.

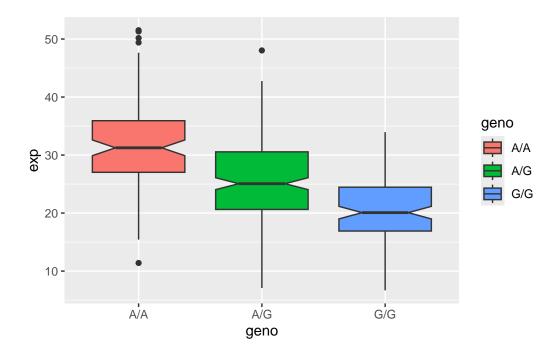
```
#need to read in the file first
  expr <- read.table("rs8067378_ENSG00000172057.6.txt", row.names=1)</pre>
  head(expr)
   sample geno
1 HG00367 A/G 28.96038
2 NA20768 A/G 20.24449
3 HG00361 A/A 31.32628
4 HG00135 A/A 34.11169
5 NA18870 G/G 18.25141
6 NA11993 A/A 32.89721
Sample size for each genotype
  table(expr$geno)
A/A A/G G/G
108 233 121
Median Expression levels for each genotype
  medis <- tapply(expr$exp, expr$geno, median)</pre>
  medis
     A/A
              A/G
                        G/G
31.24847 25.06486 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?

Make a boxplot

```
library (ggplot2)

genobox <- ggplot(expr) + aes(geno, exp, fill=geno) +
    geom_boxplot(notch=TRUE)
genobox</pre>
```



G/G has a lower expression level relative to A/A genotype The SNP does effect the expression of ORMDL3.