

class 17- Introduction to Genome Informatics Lab

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section 1. Proportion on G/G in a population

downloaded a CSV file from Eensembl < https://useast.ensembl.org/Homo_sapiens/Variation/Sample?db=core;r40395098;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
1	NA19648 (F)	A A	ALL, AMR, MXL	-
2	NA19649 (M)	G G	ALL, AMR, MXL	-
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	NA19655 (M)	A G	ALL, AMR, MXL	-
	Mother			
1	-			
2	-			
3	-			
4	-			
5	-			
6	-			

```
table(mxl$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

Now lets look at a different population, I picked the GBR.

```
gbr<- read.csv("373522-SampleGenotypes-Homo_sapiens_Variation_Sample_rs8067378.csv")
```

find the prportion of G/G

```
round (table(gbr$Genotype..forward.strand.) / nrow(gbr) * 100,2 )
```

A A	A G	G A	G G
25.27	18.68	26.37	29.67

this variant that is associated with childhood asthma is more frequent in the GBR population than MKL population.

Lets now dig into this further.

Section 4: Population Scale Analysis

One sample is obviously not enough to know what is happening in a population. You are interested in assessing genetic differences on a population scale. So, you processed about ~230 samples and did the normalization on a genome level. Now, you want to find whether there is any association of the 4 asthma-associated SNPs (rs8067378...) on ORMDL3 expression.

How many samples do we have?

```
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)
```

```
[1] 462
```

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

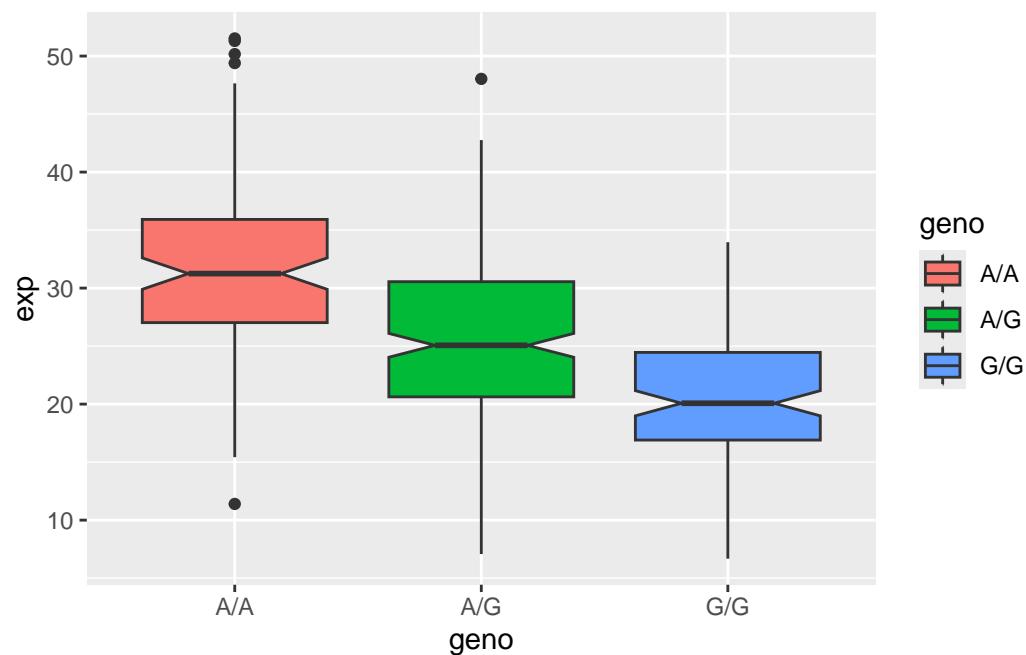
```
A/A A/G G/G  
108 233 121
```

```
library(ggplot2)
```

```
Warning: package 'ggplot2' was built under R version 4.4.3
```

lets make a boxplot

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



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?

A/A has the highest median expression, and G/G is the lowest. The SNP affects ORMDL3 expression because the expression difference between A and G is really different.