

# class 11 hw

## Quarto

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

## Running Code

When you click the **Render** button a document will be generated that includes both content and the output of embedded code. You can embed code like this:

```
1 + 1
```

```
[1] 2
```

You can add options to executable code like this

```
[1] 4
```

The `echo: false` option disables the printing of code (only output is displayed).

```
hw <- read.table("rs8067378_ENSG00000172057.6.txt", row.names = 1)
head(hw)
```

	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

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.

```
table(hw$geno)
```

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

```
aggregate(exp~geno, data = hw, FUN=median)
```

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

