Week 12: RNAseq Galaxy

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Part 4: Population Scale Analysis

~230 gene samples were processed from a population and placed in the file "PopAnalysis.txt".

> Q13: Determine the sample size for each genotype and their corresponding median expression levels for each of these genotypes.

Let's first look at what we've got.

```
x <- read.table("PopAnalysis.txt")
```

There are 462 samples in this table based on the `nrow()` function:

```
nrow(x)
```

```
[1] 462
```

We can use the `sum()` function and logicals to find the sample size of each genotype:

```
# Sample size A/A
sum(x[,2] == "A/A")
```

```
[1] 108
```

```
# Sample size A/G
sum(x[,2] == "A/G")
```

```
[1] 233
```

```
# Sample size G/G
sum(x[,2] == "G/G")
```

```
[1] 121
```

Now how do we get the median of each? Using the dplyr package, we can `group_by()` genotype then use `summarize()` to find median expression levels:

```
library(dplyr)
```

```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

    filter, lag

The following objects are masked from 'package:base':

    intersect, setdiff, setequal, union
```

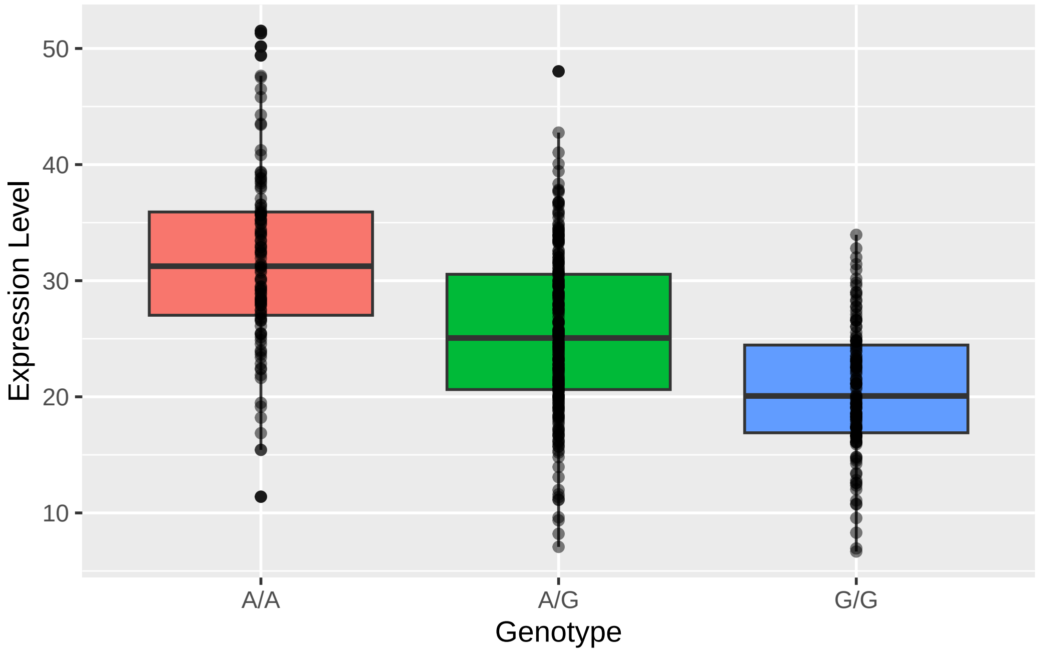
```
x %>%
  group_by(geno) %>%
  summarize(medianGeno = median(exp))
```

```
# A tibble: 3 x 2
  geno  medianGeno
  <chr>      <dbl>
1 A/A         31.2
2 A/G         25.1
3 G/G         20.1
```

> 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 affect the expression of ORMDL3?

```
# Boxplot using ggplot
library(ggplot2)
```

```
ggplot(x, aes(geno, exp, fill = geno)) +
  geom_boxplot() +
  geom_point(alpha = 0.5) +
  labs(x = "Genotype", y = "Expression Level") +
  theme(legend.position = "none")
```



Based on this plot, you can infer that A/A tend to have higher expression levels than G/G. The SNP seems to affect ORMDL3 expression.