

# Class 17: Genome Informatics

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```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.1      v stringr    1.6.0
v ggplot2     4.0.0      v tibble     3.3.0
v lubridate  1.9.4      v tidyr      1.3.1
v purrr       1.2.0
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(ggplot2)
library(readr)
```

```
galaxy_data <- read.table("rs8067378_ENSG00000172057.6.txt")
```

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.

```
galaxy_data |>
  group_by(geno) |>
  summarize(
    Sample_Size = n(),
    Median_Expression = median(exp)
  )
```

```
# A tibble: 3 x 3
  geno Sample_Size Median_Expression
```

	<chr>	<int>	<dbl>
1	A/A	108	31.2
2	A/G	233	25.1
3	G/G	121	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 effect the expression of ORMDL3?

ORMDL3 expression is highest in individuals with the A/A genotype and lowest in those with the G/G genotype. This suggests that the SNP affects ORMDL3 expression, with the G allele associated with reduced expression in a dose-dependent manner.

```
ggplot(galaxy_data) +
  geom_boxplot(aes(x = geno, y = exp, fill = geno, notch=TRUE)) +
  labs(
    x = "Genotype",
    y = "Expression Level"
  ) + theme_minimal()
```

Warning in geom\_boxplot(aes(x = geno, y = exp, fill = geno, notch = TRUE)):  
Ignoring unknown aesthetics: notch

