# Final Project Foundations of Data Science in LaTeX

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#### 1 Summary Table Demonstration

This is a table of summary statistics generated in Base R. It shows the vast variation in the expression of particular genes. Although the assignment stated that one used two genes, I used five to show off.

Table 1: Summary Statistics for Various RNA SEQ Counts

|         | TSPAN6 | DPM1 | SCYL3 | C1orf112 | FGR  |
|---------|--------|------|-------|----------|------|
| Min.    | 1262   | 2922 | 1287  | 5617     | 2830 |
| 1st Qu. | 1262   | 2922 | 1287  | 5617     | 2830 |
| Median  | 1262   | 2922 | 1287  | 5617     | 2830 |
| Mean    | 1262   | 2922 | 1287  | 5617     | 2830 |
| 3rd Qu. | 1262   | 2922 | 1287  | 5617     | 2830 |
| Max.    | 1262   | 2922 | 1287  | 5617     | 2830 |

## 2 Histogram of TSPAN6

I improved this histogram by adding color, adjusting the bins, and taking the log10 of the TSPAN6 values. As with other plots, this diminished the skew of extreme outliers. I wanted to overlay several transparent histograms of various genes, but after hours of frustration, I decided to keep it simple so I can turn this in on time.

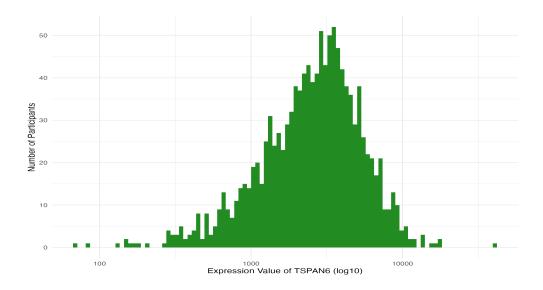


Figure 1: Histogram of log10-transformed TSPAN6 expression counts.

## 3 Scatter Plot of TSPAN6 and DPM1

This plot really shows the benefit of p-values and trend lines. The blob of points hints at a correlation, but the math proves it. Not the axes are logarithmic. This is, again, to compensate for extreme outliers.

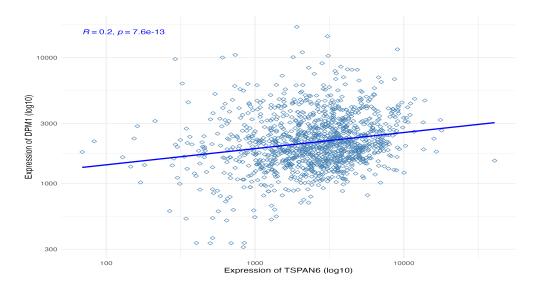


Figure 2: Scatter plot of the expression count for TSPAN6 versus DPM1 (log10).

#### 4 Violin Duodectet Plot

This plot shows the density - that is, the most common values expressed - TSPAN6 in 12 disease stages. I have removed the grid lines to allow the shapes to tell the story, and again logged the y axis to account for outliers. The differing shapes show that TSPAN6 has distinct variation in the disease progression.

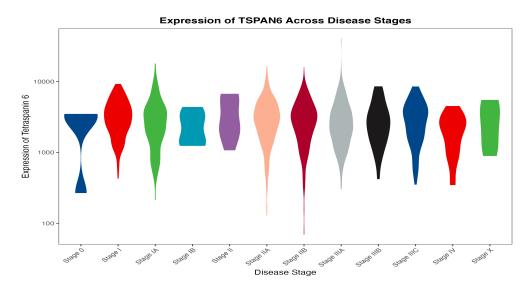


Figure 3: Violin plot mapping the expression of TSPAN6 to disease stages.

## 5 A Heat-Map of 10 Genes

This heat map shows the values of RNA SEQ counts. Each column represents a gene, and the rows represent the degree to which a participant expresses that gene. Most genes in my list exhibit low values. The plot is stretched to show the higher values within the heat map.

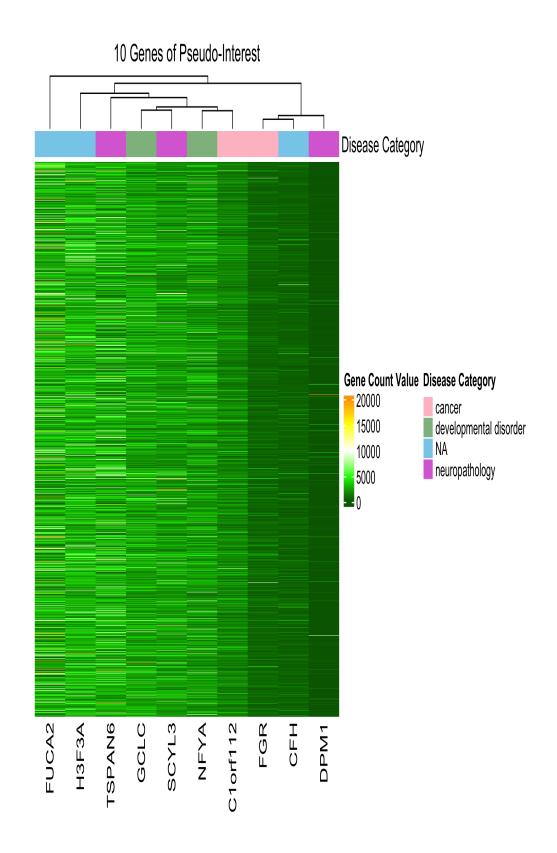


Figure 4: A heat map showing the similarity among participants of several genes.

# 6 My Chosen Plot

I chose a line plot, the classic "over time" plot. I looked to see if there was a variation in TSPAN6 expression and age of diagnosis. There is quite a bit of variation, but no trend showing a relationship.

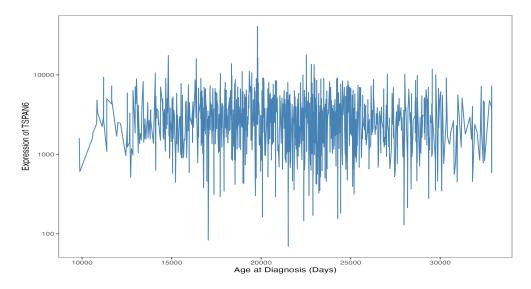


Figure 5: A line plot seeking a correlation with the expression of TSPAN6 and the age in which the patient was diagnosed.