**Summary**

The data generated by the Pymaceuticals company using different drug regimens to treat squamous cell carcinoma (SCC) shows that Python libraries are effective in generating plots, graphs, and bar charts that can help understand data better. From this analysis, the summary statistics showed that the mean, median, and variance were all the same, which was 45.0. The SEM and standard deviation were both 0, indicating that the dataset may be evenly distributed from the lowest to the highest values for the mean and median. The 0 observed for SEM and standard deviation suggests that the values in the datasets were the same, with no deviation from the average, and that there was no random error in the statistics, making the data more accurate. The bar plots show that pandas and matplotlib can be used to generate graphs, charts, and plots to tell a story for data. The results also show that more male rats were used than female mice across the treatment groups. Additionally, looking at the mouse weight vs. the average observed tumor of the entire Capomulin regimen, regardless of the weight of the mouse, it did not affect the average tumor value of 45.

This data will help the Pymaceuticals company make informed decisions regarding the various treatments used to treat SCC.