Pymaceuticals Inc.

Analysis

- This study experimented with 10 variables across 248 mice. The mice were divided almost equally between male and female mice.
- After isolating mouse ID l509 and plotting the tumor size of the trial period, it is clear the Capomuliun treatment reduced the tumor over a 30 day period.
- It is clear as the weight of the mouse increased so did the size of the tumor.

In [ ]:

In [97]:

```
# Dependencies and Setup
import matplotlib.pyplot as plt
import pandas as pd
import scipy.stats as st

# Study data files
mouse_metadata_path = "data/Mouse_metadata.csv"
study_results_path = "data/Study_results.csv"

# Read the mouse data and the study results
mouse_metadata = pd.read_csv(mouse_metadata_path)
study_results = pd.read_csv(study_results_path)

# Combine the data into a single DataFrame
mouse_study = pd.merge(mouse_metadata, study_results, how="left", on="Mouse ID")

# Display the data table for preview
mouse_study.head()
```

Out[97]:

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	Tumor Volume (mm3)	Metastatic Sites
0	k403	Ramicane	Male	21	16	0	45.000000	0
1	k403	Ramicane	Male	21	16	5	38.825898	0
2	k403	Ramicane	Male	21	16	10	35.014271	1
3	k403	Ramicane	Male	21	16	15	34.223992	1
4	k403	Ramicane	Male	21	16	20	32.997729	1

In [37]:

```
# Checking the number of mice.
mice_count = mouse_study["Mouse ID"].nunique()
mice_count
```

Out[37]:

```
249
```

In [107…
```
# Our data should be uniquely identified by Mouse ID and Timepoint
mouse_duplicates = mouse_study.loc[mouse_study.duplicated(subset=["Mouse ID", "Timepoi

# Get the duplicate mice by ID number that shows up for Mouse ID and Timepoint.
mouse_duplicates_2
```

Out[107]:
```
array(['g989'], dtype=object)
```

In [108…
```
# Optional: Get all the data for the duplicate mouse ID.
mouse_duplicates_3 = mouse_study.loc[mouse_study["Mouse ID"] == mouse_duplicates_2[0]]
mouse_duplicates_3
```

Out[108]:

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	Tumor Volume (mm3)	Metastatic Sites
908	g989	Propriva	Female	21	26	0	45.000000	0
909	g989	Propriva	Female	21	26	0	45.000000	0
910	g989	Propriva	Female	21	26	5	48.786801	0
911	g989	Propriva	Female	21	26	5	47.570392	0
912	g989	Propriva	Female	21	26	10	51.745156	0
913	g989	Propriva	Female	21	26	10	49.880528	0
914	g989	Propriva	Female	21	26	15	51.325852	1
915	g989	Propriva	Female	21	26	15	53.442020	0
916	g989	Propriva	Female	21	26	20	55.326122	1
917	g989	Propriva	Female	21	26	20	54.657650	1
918	g989	Propriva	Female	21	26	25	56.045564	1
919	g989	Propriva	Female	21	26	30	59.082294	1
920	g989	Propriva	Female	21	26	35	62.570880	2

In [111…
```
# Create a clean DataFrame by dropping the duplicate mouse by its ID.
clean_DF = mouse_study[mouse_study["Mouse ID"].isin(mouse_duplicates_2)==False]
clean_DF.head()
```

Out[111]:

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	Tumor Volume (mm3)	Metastatic Sites
0	k403	Ramicane	Male	21	16	0	45.000000	0
1	k403	Ramicane	Male	21	16	5	38.825898	0
2	k403	Ramicane	Male	21	16	10	35.014271	1
3	k403	Ramicane	Male	21	16	15	34.223992	1
4	k403	Ramicane	Male	21	16	20	32.997729	1

In [115…
```
# Checking the number of mice in the clean DataFrame.
duplicate_mice_count = (clean_DF["Mouse ID"].nunique())
```

```
duplicate_mice_count
```

Out[115]:

```
248
```

Summary Statistics

In [126…

```
# Generate a summary statistics table of mean, median, variance, standard deviation, a

# Use groupby and summary statistical methods to calculate the following properties of
# mean, median, variance, standard deviation, and SEM of the tumor volume.
# Assemble the resulting series into a single summary DataFrame.
Tumor_Volume_Per = mouse_study.groupby("Drug Regimen")
mean = Tumor_Volume_Per["Tumor Volume (mm3)"].mean()
median = Tumor_Volume_Per["Tumor Volume (mm3)"].median()
variance = Tumor_Volume_Per["Tumor Volume (mm3)"].var()
standard_deviation = Tumor_Volume_Per["Tumor Volume (mm3)"].std()
sem = Tumor_Volume_Per["Tumor Volume (mm3)"].sem()

Tumor_Summary = pd.DataFrame({"Mean": mean,
                              "Median": median,
                              "Variance": variance,
                              "Standard Deviation": standard_deviation,
                              "SEM":sem})
Tumor_Summary
```

Out[126]:

	Mean	Median	Variance	Standard Deviation	SEM
Drug Regimen					
Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
Ceftamin	52.591172	51.776157	39.290177	6.268188	0.469821
Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
Ketapril	55.235638	53.698743	68.553577	8.279709	0.603860
Naftisol	54.331565	52.509285	66.173479	8.134708	0.596466
Placebo	54.033581	52.288934	61.168083	7.821003	0.581331
Propriva	52.322552	50.854632	42.351070	6.507770	0.512884
Ramicane	40.216745	40.673236	23.486704	4.846308	0.320955
Stelasyn	54.233149	52.431737	59.450562	7.710419	0.573111
Zoniferol	53.236507	51.818479	48.533355	6.966589	0.516398

In [134…

```
# A more advanced method to generate a summary statistics table of mean, median, varia
# and SEM of the tumor volume for each regimen (only one method is required in the sol

# Using the aggregation method, produce the same summary statistics in a single line
Agg_df = {"Tumor Volume (mm3)": ["mean", "median", "var", "std", "sem"]}
clean_DF.groupby("Drug Regimen").agg(Agg_df)
```

Out[134]:

	Tumor Volume (mm3)				
	mean	median	var	std	sem
Drug Regimen					
Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
Ceftamin	52.591172	51.776157	39.290177	6.268188	0.469821
Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
Ketapril	55.235638	53.698743	68.553577	8.279709	0.603860
Naftisol	54.331565	52.509285	66.173479	8.134708	0.596466
Placebo	54.033581	52.288934	61.168083	7.821003	0.581331
Propriva	52.320930	50.446266	43.852013	6.622085	0.544332
Ramicane	40.216745	40.673236	23.486704	4.846308	0.320955
Stelasyn	54.233149	52.431737	59.450562	7.710419	0.573111
Zoniferol	53.236507	51.818479	48.533355	6.966589	0.516398

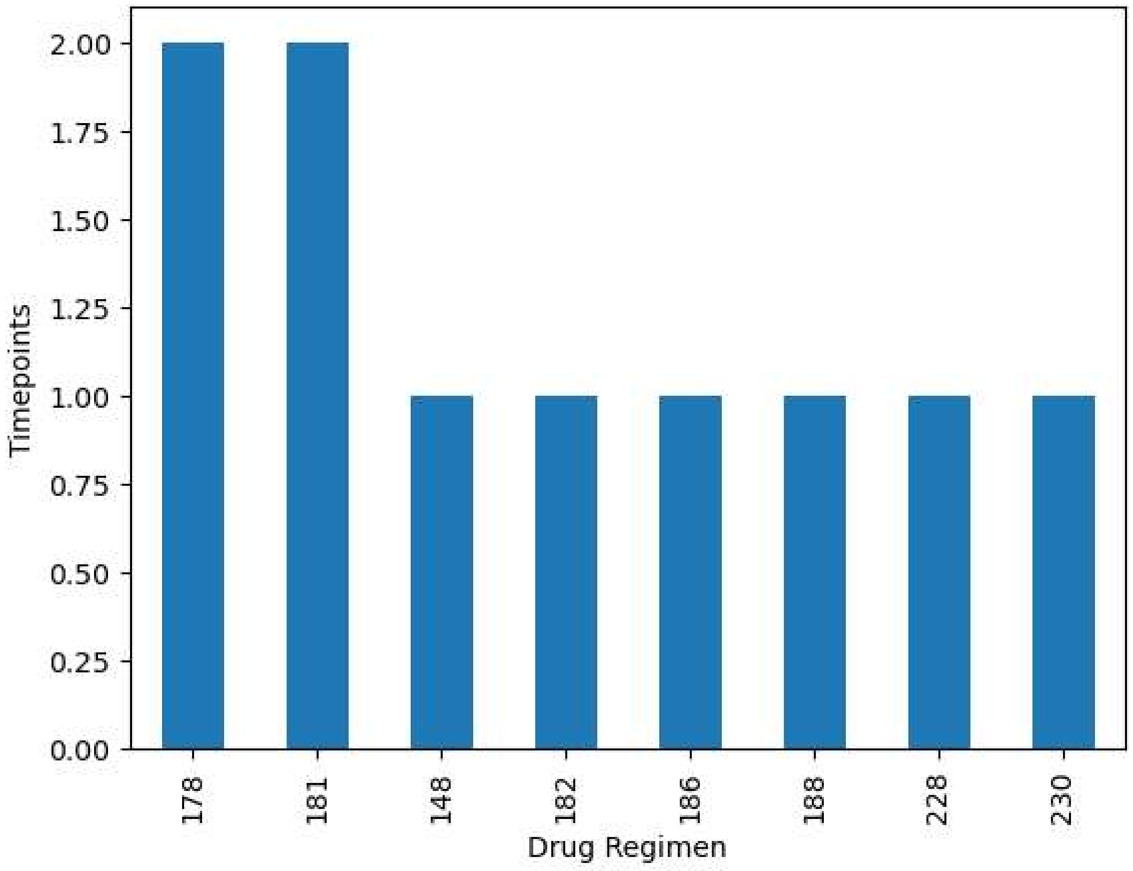
Bar and Pie Charts

In [139…

```
# Generate a bar plot showing the total number of rows (Mouse ID/Timepoints) for each
timepoints = clean_DF["Drug Regimen"].value_counts()
timepoints_df = pd.DataFrame(timepoints)
timepoints_df.columns = ["Total Timepoints"]
timepoints_plot = timepoints_df.value_counts("Total Timepoints", ascending=False).plot
timepoints_plot.set_xlabel('Drug Regimen')
timepoints_plot.set_ylabel("Timepoints")
plt.show
```

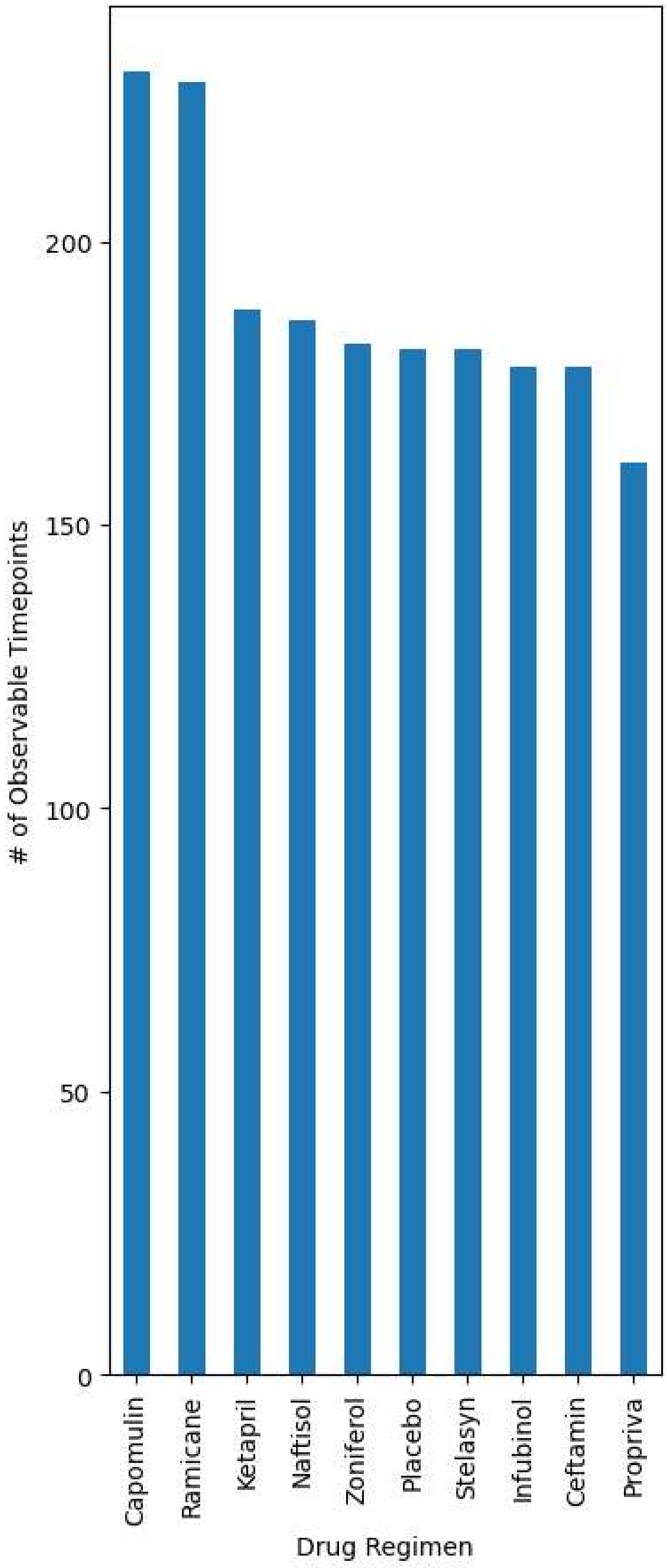
Out[139]:

```
<function matplotlib.pyplot.show(close=None, block=None)>
```



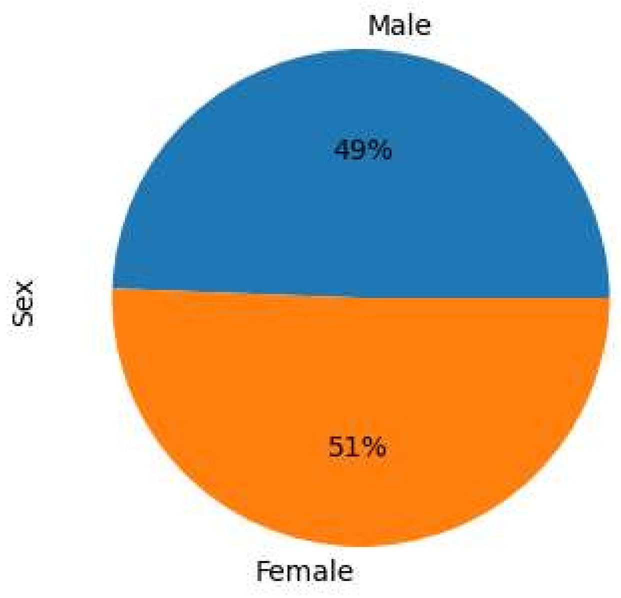
In [143…

```
# Generate a bar plot showing the total number of rows (Mouse ID/Timepoints) for each
timepoints = mouse_study["Drug Regimen"].value_counts()
timepoints.plot(kind="bar", figsize=(4, 10))
plt.xlabel("Drug Regimen")
plt.ylabel("# of Observable Timepoints")
plt.show()
```

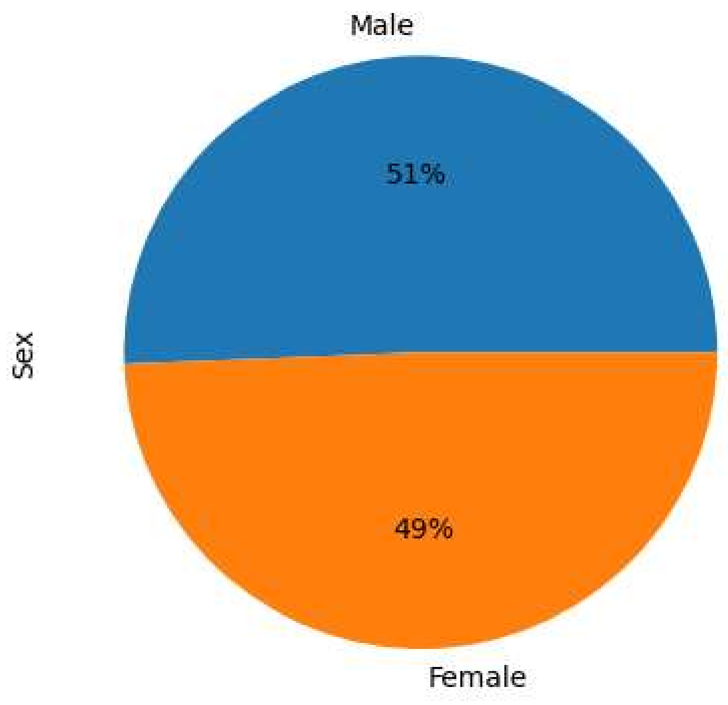


In [146…

```
# Generate a pie plot showing the distribution of female versus male mice using Pandas
gender_dist = mouse_study.groupby("Sex")
gender_dist_len = gender_dist["Sex"].count()
gender_dist_plot = gender_dist_len.plot(labels = ["Male", "Female"], kind = "pie", y =
```



In [155…
```
# Generate a pie plot showing the distribution of female versus male mice using pyplot
gender_dist_pyplot = [gender_dist_len["Male"], gender_dist_len["Female"]]
gender_dist_labels = ["Male", "Female"]
plt.pie(gender_dist_pyplot, labels = ["Male", "Female"], autopct = "%1.0f%%")
plt.ylabel("Sex")
plt.show()
```



Quartiles, Outliers and Boxplots

In [196…
```
# Calculate the final tumor volume of each mouse across four of the treatment regimens
# Capomulin, Ramicane, Infubinol, and Ceftamin
# Start by getting the last (greatest) timepoint for each mouse
last_tp = clean_DF.groupby("Mouse ID")
last_tp = last_tp["Timepoint"].max()
last_tp_df = pd.DataFrame(last_tp)

# Merge this group df with the original DataFrame to get the tumor volume at the last
last_tv = pd.merge(last_tp_df, clean_DF, on = ["Mouse ID", "Timepoint"])
last_tv.head(30)
```

Out[196]:

	Mouse ID	Timepoint	Drug Regimen	Sex	Age_months	Weight (g)	Tumor Volume (mm3)	Metastatic Sites
0	a203	45	Infubinol	Female	20	23	67.973419	2
1	a251	45	Infubinol	Female	21	25	65.525743	1
2	a262	45	Placebo	Female	17	29	70.717621	4
3	a275	45	Ceftamin	Female	20	28	62.999356	3
4	a366	30	Stelasyn	Female	16	29	63.440686	1
5	a401	45	Zoniferol	Female	8	25	66.794156	4
6	a411	45	Ramicane	Male	3	22	38.407618	1
7	a444	45	Ramicane	Female	10	25	43.047543	0
8	a457	10	Ketapril	Female	11	30	49.783419	0
9	a492	45	Stelasyn	Male	20	25	60.122011	1
10	a520	45	Ramicane	Male	13	21	38.810366	1
11	a577	30	Infubinol	Female	6	25	57.031862	2
12	a644	45	Ramicane	Female	7	17	32.978522	1
13	a685	45	Infubinol	Male	8	30	66.083066	3
14	a699	45	Propriva	Female	5	28	62.191414	1
15	a788	30	Zoniferol	Male	5	30	60.413709	1
16	a818	45	Naftisol	Female	12	28	74.997764	2
17	a897	45	Placebo	Male	7	28	72.255963	4
18	a963	45	Stelasyn	Female	23	27	62.765093	1
19	b128	45	Capomulin	Female	9	22	38.982878	2
20	b313	25	Zoniferol	Male	12	27	55.745146	1
21	b447	0	Ceftamin	Male	2	30	45.000000	0
22	b487	25	Ceftamin	Female	6	28	56.057749	1
23	b559	45	Naftisol	Male	20	26	73.051363	1
24	b742	45	Capomulin	Male	7	21	38.939633	0
25	b759	30	Ceftamin	Female	12	25	55.742829	1
26	b879	45	Stelasyn	Female	4	26	72.555239	2
27	c139	45	Infubinol	Male	11	28	72.226731	2
28	c264	45	Zoniferol	Female	11	27	67.942121	2
29	c282	45	Placebo	Male	12	27	65.815165	2

In [241…

```python
treatments = ["Capomulin", "Ramicane", "Infubinol", "Ceftamin"]

# Create empty list to fill with tumor vol data (for plotting)
```

```
tumor_vol = []
UQ = []
LQ = []

# Calculate the IQR and quantitatively determine if there are any potential outliers.
for drug in treatments:
    quartiles = last_tv[last_tv["Drug Regimen"] == drug]["Tumor Volume (mm3)"].quantil
    LQ_2 = quartiles[.25]
    UQ_2 = quartiles[.75]
    IQR = UQ_2 - LQ_2

    UQ.append(UQ_2)
    LQ.append(LQ_2)
    print(f"The IQR for {drug} is {IQR}")

    # Determine outliers using upper and lower bounds
    lower_bound = LQ_2 - (1.5*IQR)
    upper_bound = UQ_2 + (1.5*IQR)
    print(f"Values below {lower_bound} could be outliers.")
    print(f"Values above {upper_bound} could be outliers.")
```

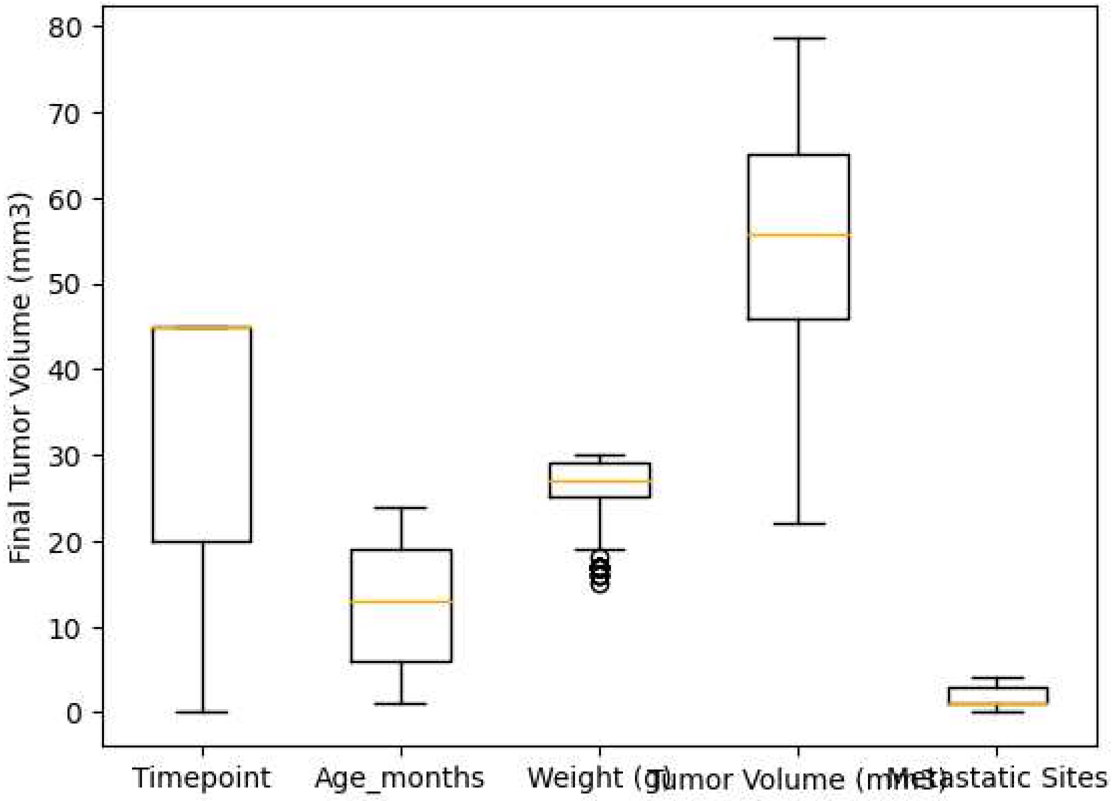
```
The IQR for Capomulin is 7.781863460000004
Values below 20.70456164999999 could be outliers.
Values above 51.83201549 could be outliers.
The IQR for Ramicane is 9.098536719999998
Values below 17.912664470000003 could be outliers.
Values above 54.30681135 could be outliers.
The IQR for Infubinol is 11.477135160000003
Values below 36.83290494999999 could be outliers.
Values above 82.74144559000001 could be outliers.
The IQR for Ceftamin is 15.577752179999997
Values below 25.355449580000002 could be outliers.
Values above 87.66645829999999 could be outliers.
```

In [269…

```
# Generate a box plot that shows the distrubution of the tumor volume for each treatme
# set the x and y axis labels
# show the plot


boxplot = last_tv.boxplot(grid = False, color = dict(boxes = "black", whiskers = "blac
boxplot.set_ylabel("Final Tumor Volume (mm3)")
boxplot.set_xlabel("")
```

Out[269]:

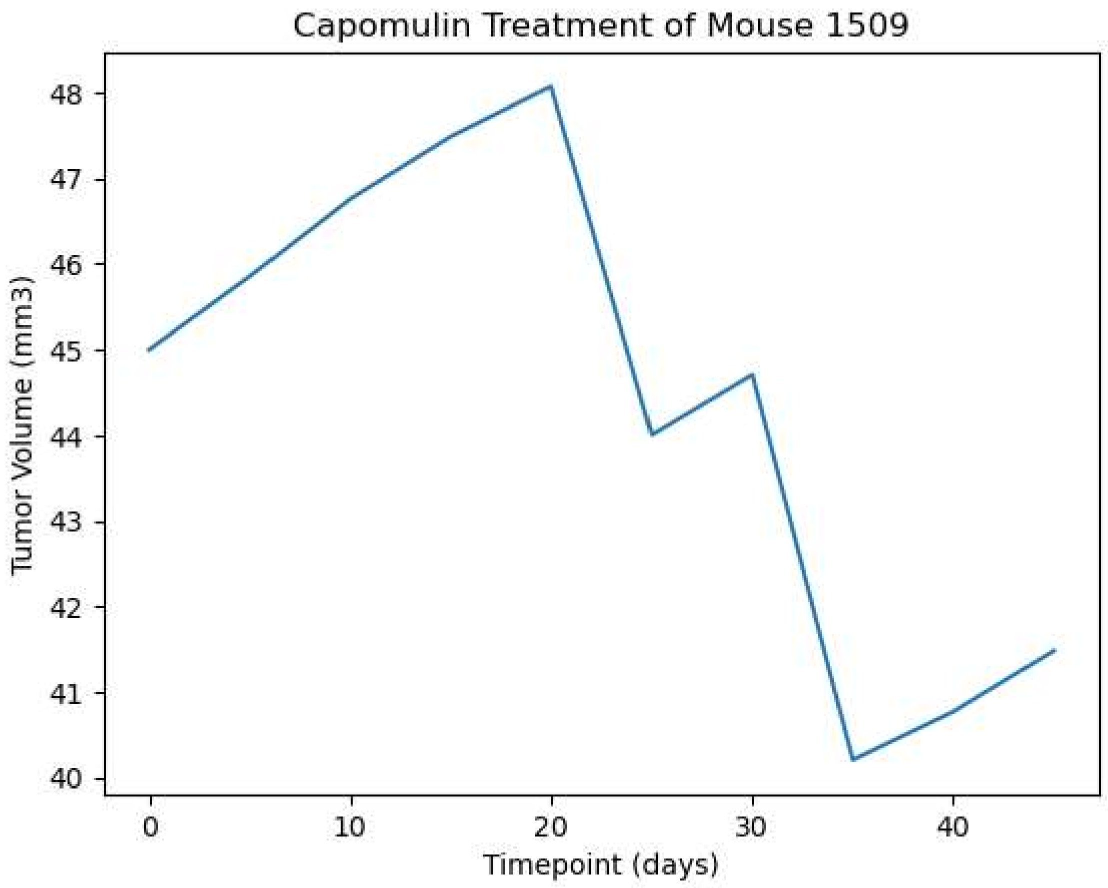
```
Text(0.5, 0, '')
```



Line and Scatter Plots

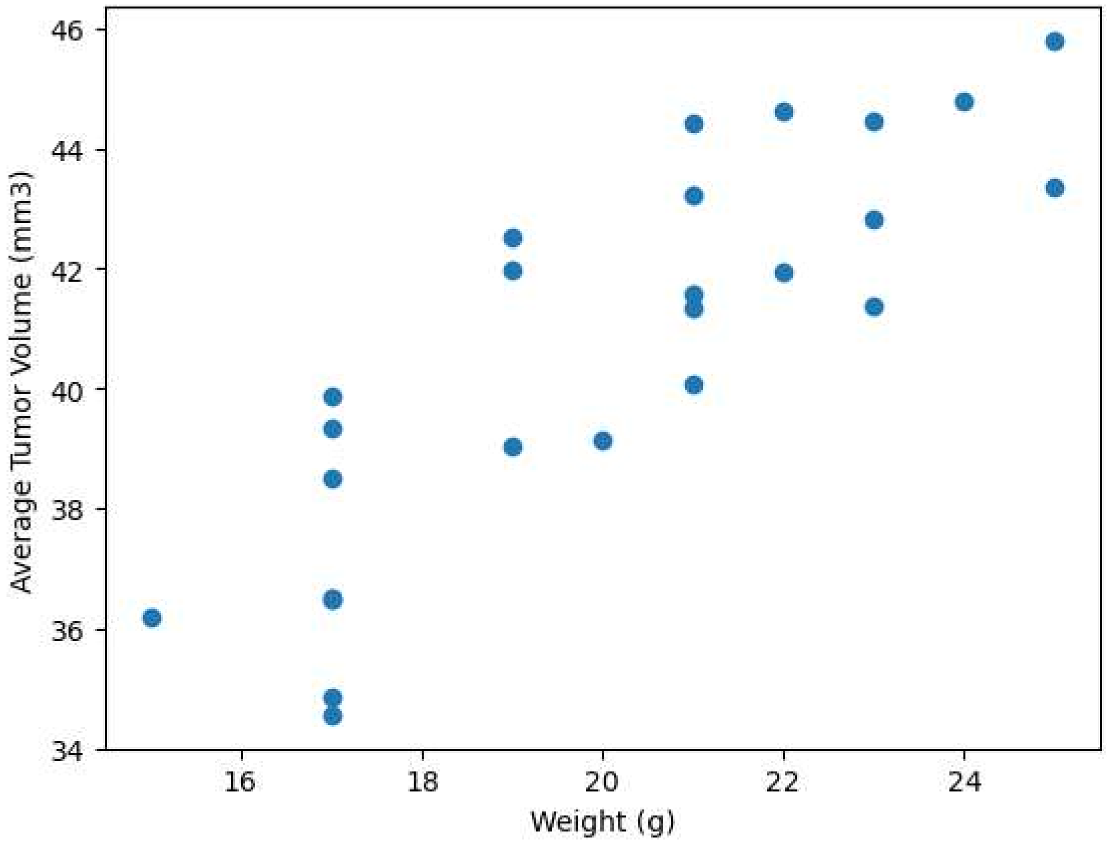
In [291…

```
# Generate a line plot of tumor volume vs. time point for a single mouse treated with
capomulin_plot = clean_DF.loc[clean_DF["Mouse ID"] == "l509"]
plt.plot(capomulin_plot["Timepoint"], capomulin_plot["Tumor Volume (mm3)"])

plt.title("Capomulin Treatment of Mouse 1509")
plt.xlabel("Timepoint (days)")
plt.ylabel("Tumor Volume (mm3)")

plt.show()
```



In [281…

```
# Generate a scatter plot of mouse weight vs. the average observed tumor volume for th
mouse = clean_DF.loc[clean_DF["Drug Regimen"] == "Capomulin"].groupby("Mouse ID")

average = mouse["Tumor Volume (mm3)"].mean()
weight = mouse["Weight (g)"].unique()
plt.scatter(weight, average)

plt.xlabel("Weight (g)")
plt.ylabel("Average Tumor Volume (mm3)")

plt.show()
```

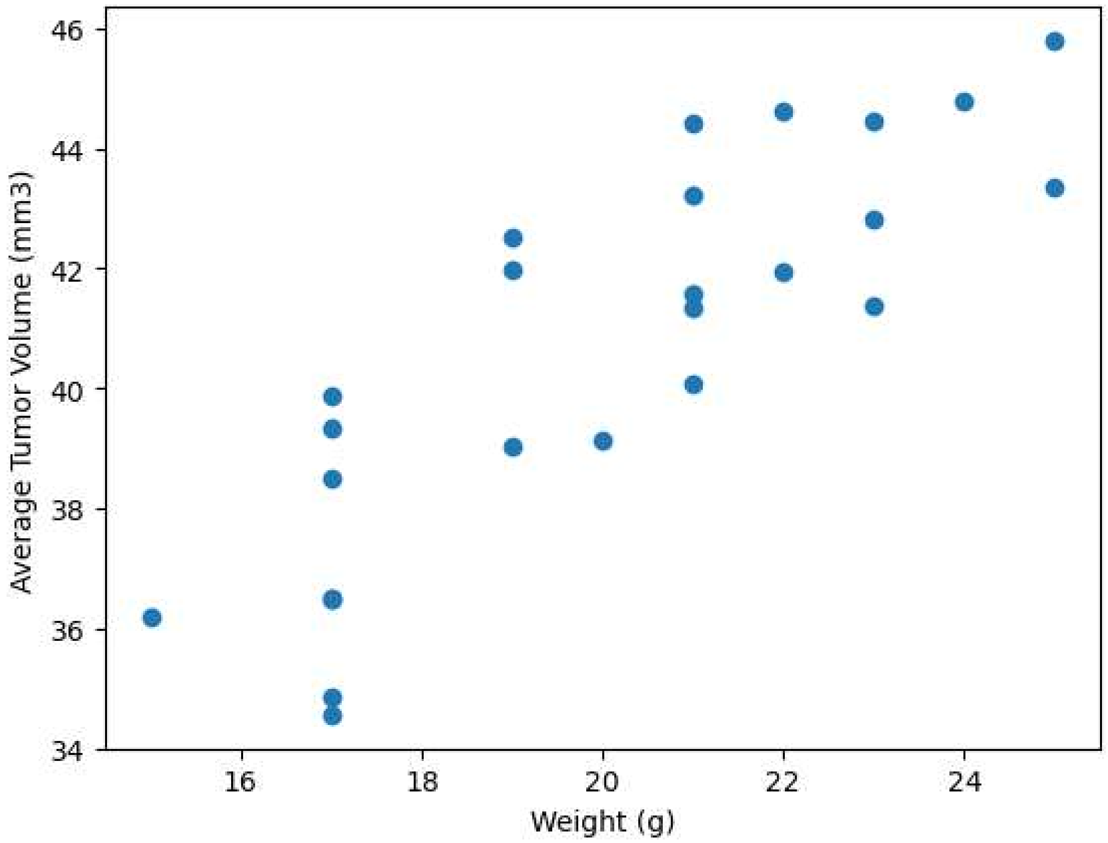


Correlation and Regression

In [290…

```
# Calculate the correlation coefficient and a linear regression model
corr = st.pearsonr(weight, average)
print("The correlatioin between mouse weight and the average tumor volume is 0.84")
# for mouse weight and average observed tumor volume for the entire Capomulin regimen

plt.scatter(weight, average)
plt.xlabel("Weight (g)")
plt.ylabel("Average Tumor Volume (mm3)")

regress_values = weight * slope + intercept
plt.plot(weight, regress_values, "r-")
line = "y =" + str(round(slope,2)) + "x +" + str(round(intercept,2))
plt.annotate(line,(19,38))

plt.show()
```

```
The correlatioin between mouse weight and the average tumor volume is 0.84
---------------------------------------------------------------------------
NameError                                 Traceback (most recent call last)
Cell In[290], line 10
      7 plt.xlabel("Weight (g)")
      8 plt.ylabel("Average Tumor Volume (mm3)")
---> 10 regress_values = weight * slope + intercept
     11 plt.plot(weight, regress_values, "r-")
     12 line = "y =" + str(round(slope,2)) + "x +" + str(round(intercept,2))

NameError: name 'slope' is not defined
```


46
44
42
40
38
36
34
16
18
20
22
24
Weight (g)
Average Tumor Volume (mm3)

```
In [ ]:
```