Pymaceuticals Inc.

Analysis

- Add your analysis here.

In [1]:
```
# 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


# Display the data table for preview
```

Out[1]:

	Mouse ID	Timepoint	Tumor Volume (mm3)	Metastatic Sites	Drug Regimen	Sex	Age_months	Weight (g)
0	b128	0	45.0	0	Capomulin	Female	9	22
1	f932	0	45.0	0	Ketapril	Male	15	29
2	g107	0	45.0	0	Ketapril	Female	2	29
3	a457	0	45.0	0	Ketapril	Female	11	30
4	c819	0	45.0	0	Ketapril	Male	21	25

In [2]:
```
# Checking the number of mice.
```

Out[2]:
```
249
```

In [3]:
```
# Our data should be uniquely identified by Mouse ID and Timepoint
# Get the duplicate mice by ID number that shows up for Mouse ID and Timepoint.
```

Out[3]:
```
array(['g989'], dtype=object)
```

In [4]:
```
# Optional: Get all the data for the duplicate mouse ID.
```

Out[4]:

	Mouse ID	Timepoint	Tumor Volume (mm3)	Metastatic Sites	Drug Regimen	Sex	Age_months	Weight (g)
107	g989	0	45.000000	0	Propriva	Female	21	26
137	g989	0	45.000000	0	Propriva	Female	21	26
329	g989	5	48.786801	0	Propriva	Female	21	26
360	g989	5	47.570392	0	Propriva	Female	21	26
620	g989	10	51.745156	0	Propriva	Female	21	26
681	g989	10	49.880528	0	Propriva	Female	21	26
815	g989	15	51.325852	1	Propriva	Female	21	26
869	g989	15	53.442020	0	Propriva	Female	21	26
950	g989	20	55.326122	1	Propriva	Female	21	26
1111	g989	20	54.657650	1	Propriva	Female	21	26
1195	g989	25	56.045564	1	Propriva	Female	21	26
1380	g989	30	59.082294	1	Propriva	Female	21	26
1592	g989	35	62.570880	2	Propriva	Female	21	26

In [5]:
```
# Create a clean DataFrame by dropping the duplicate mouse by its ID.
```

Out[5]:

	Mouse ID	Timepoint	Tumor Volume (mm3)	Metastatic Sites	Drug Regimen	Sex	Age_months	Weight (g)
0	b128	0	45.0	0	Capomulin	Female	9	22
1	f932	0	45.0	0	Ketapril	Male	15	29
2	g107	0	45.0	0	Ketapril	Female	2	29
3	a457	0	45.0	0	Ketapril	Female	11	30
4	c819	0	45.0	0	Ketapril	Male	21	25

In [6]:
```
# Checking the number of mice in the clean DataFrame.
```

Out[6]:
```
248
```

Summary Statistics

In [7]:
```
# Generate a summary statistics table of mean, median, variance, standard deviation, and SEM of the tumor vol

# Use groupby and summary statistical methods to calculate the following properties of each drug regimen:
# mean, median, variance, standard deviation, and SEM of the tumor volume.
# Assemble the resulting series into a single summary DataFrame.
```

Out[7]:

Drug Regimen	Mean Tumor Volume	Median Tumor Volume	Tumor Volume Variance	Tumor Volume Std. Dev.	Tumor Volume Std. Err.
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

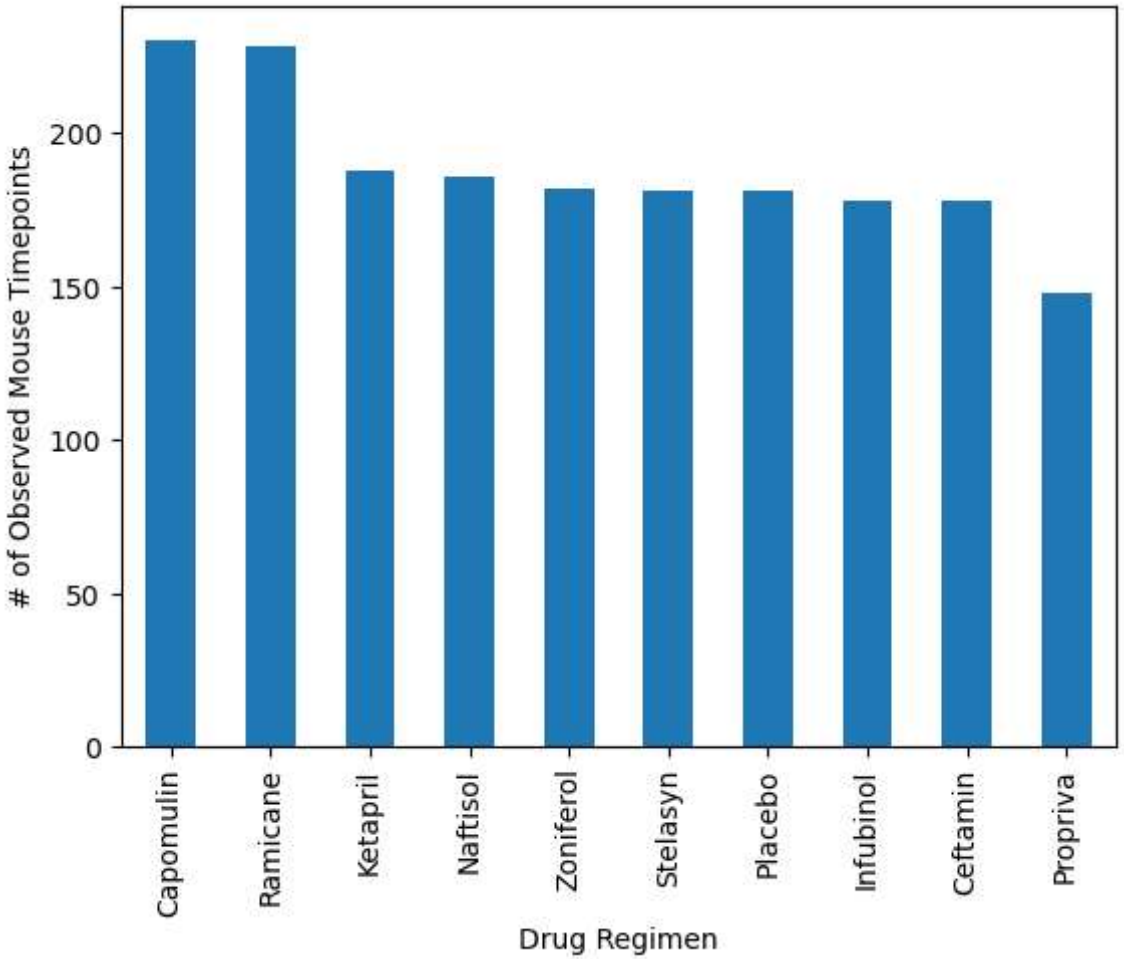
In [8]:
```
# A more advanced method to generate a summary statistics table of mean, median, variance, standard deviation
# and SEM of the tumor volume for each regimen (only one method is required in the solution)

# Using the aggregation method, produce the same summary statistics in a single line
```

Out[8]:

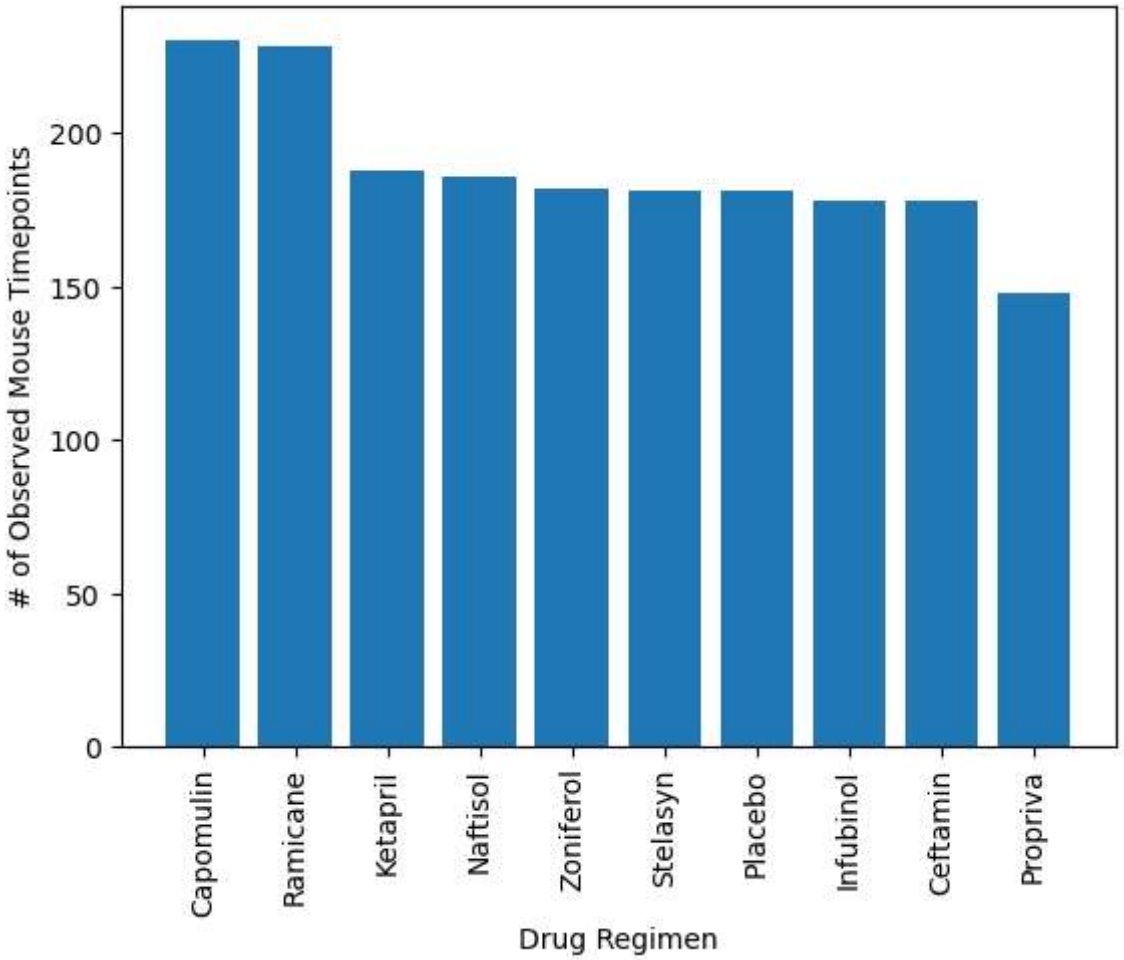
	Tumor Volume (mm3)				
	mean	median	var	std	sem
Drug Regimen					
Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
Ceftamin	52.591172	51.776157	39.290177	6.268188	0.469821
Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
Ketapril	55.235638	53.698743	68.553577	8.279709	0.603860
Naftisol	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

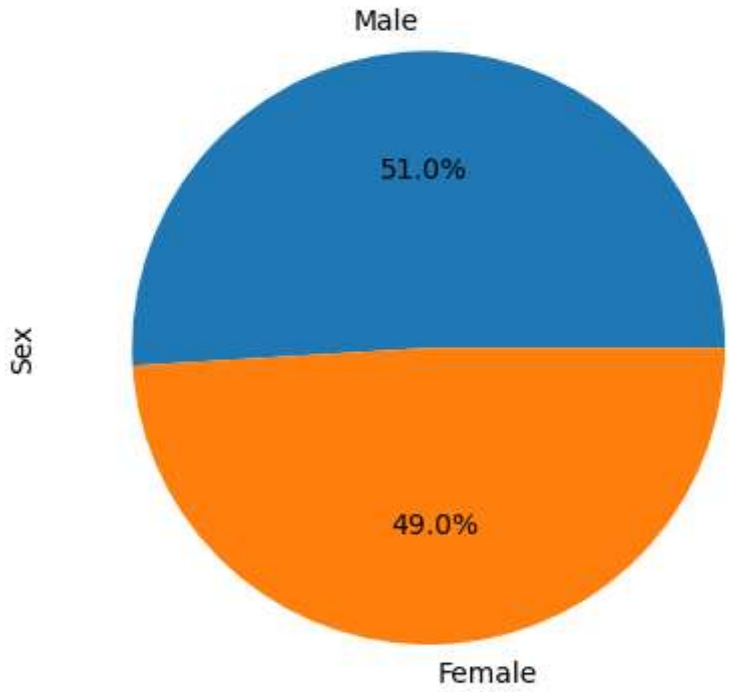
In [9]:
```
# Generate a bar plot showing the total number of rows (Mouse ID/Timepoints) for each drug regimen using Panc
```



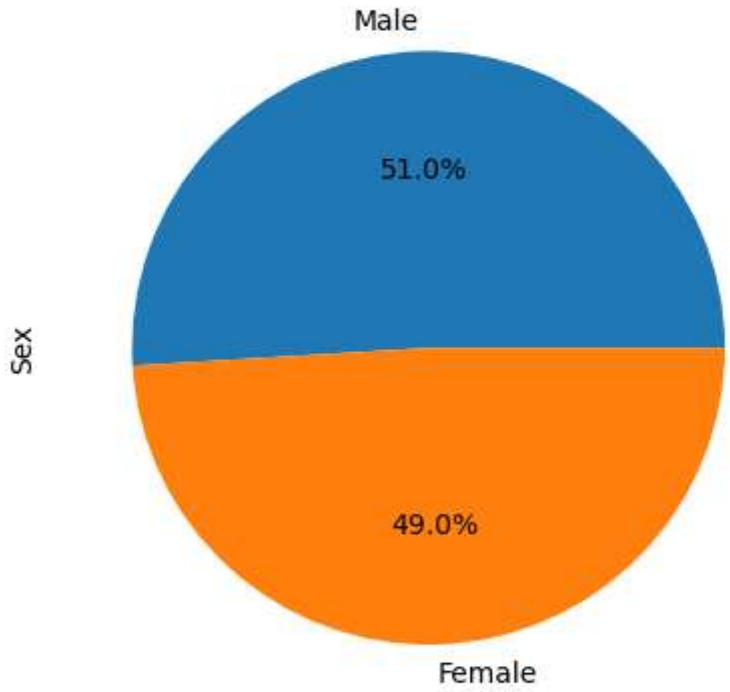
In [10]:
```
# Generate a bar plot showing the total number of rows (Mouse ID/Timepoints) for each drug regimen using pypl
```



In [11]:
```
# Generate a pie plot showing the distribution of female versus male mice using Pandas

```



In [12]:
```
# Generate a pie plot showing the distribution of female versus male mice using pyplot

```



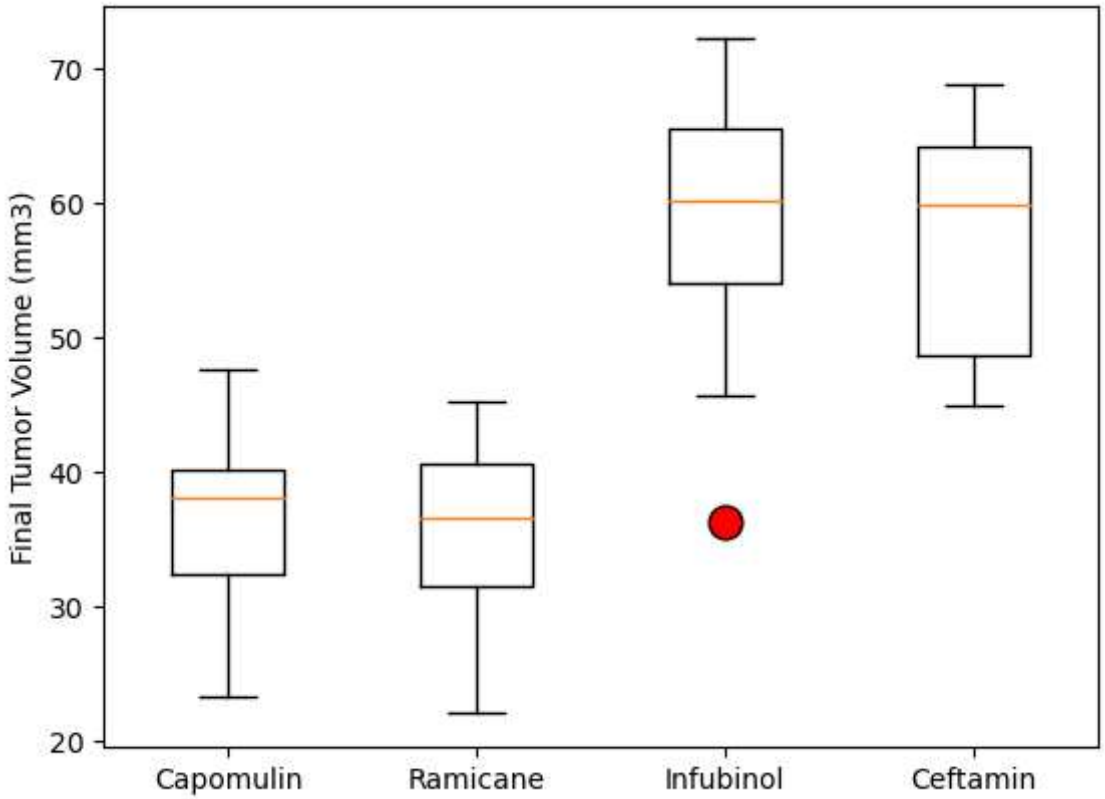
Quartiles, Outliers and Boxplots

In [13]:
```
# 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


# Merge this group df with the original DataFrame to get the tumor volume at the last timepoint

```

In [14]:
```
# Put treatments into a list for for loop (and later for plot labels)

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

# Calculate the IQR and quantitatively determine if there are any potential outliers.

    # Locate the rows which contain mice on each drug and get the tumor volumes

    # add subset

    # Determine outliers using upper and lower bounds
```

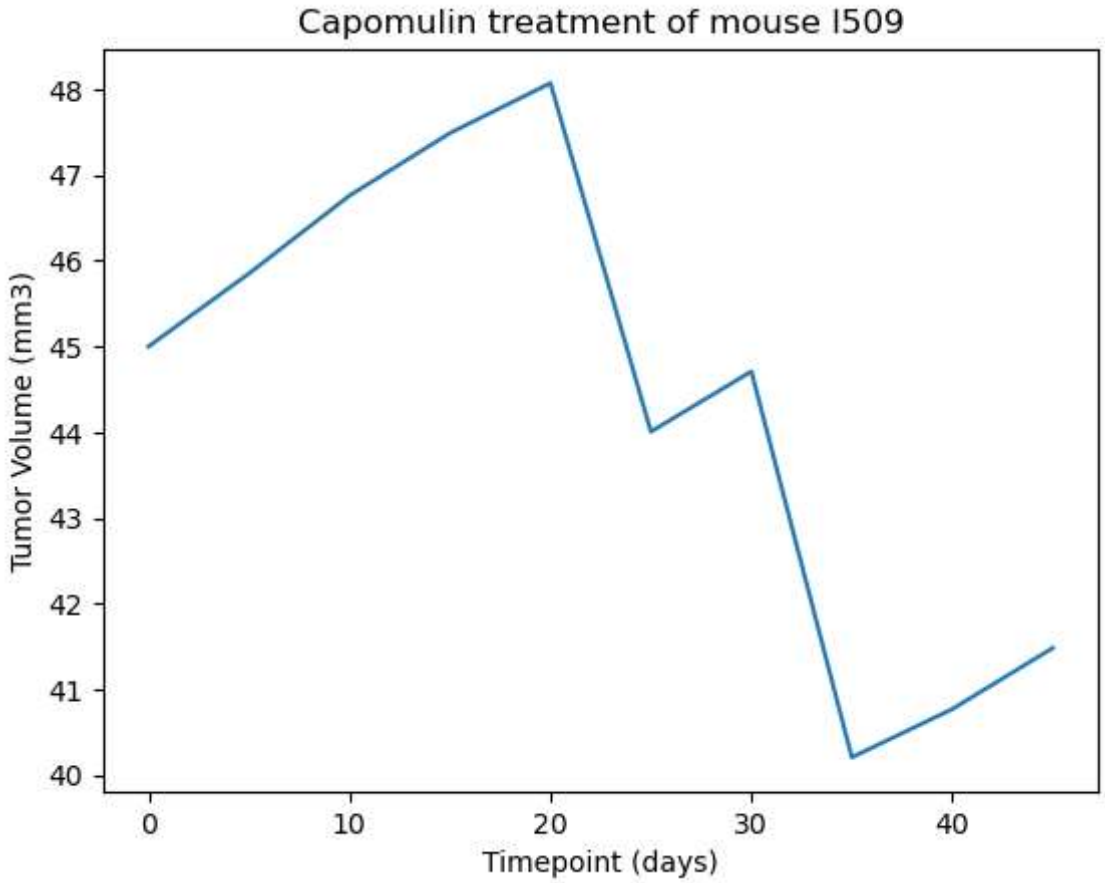
```
Capomulin's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
Ramicane's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
Infubinol's potential outliers: 31    36.321346
Name: Tumor Volume (mm3), dtype: float64
Ceftamin's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
```

In [15]:
```
# Generate a box plot that shows the distrubution of the tumor volume for each treatment group.
```

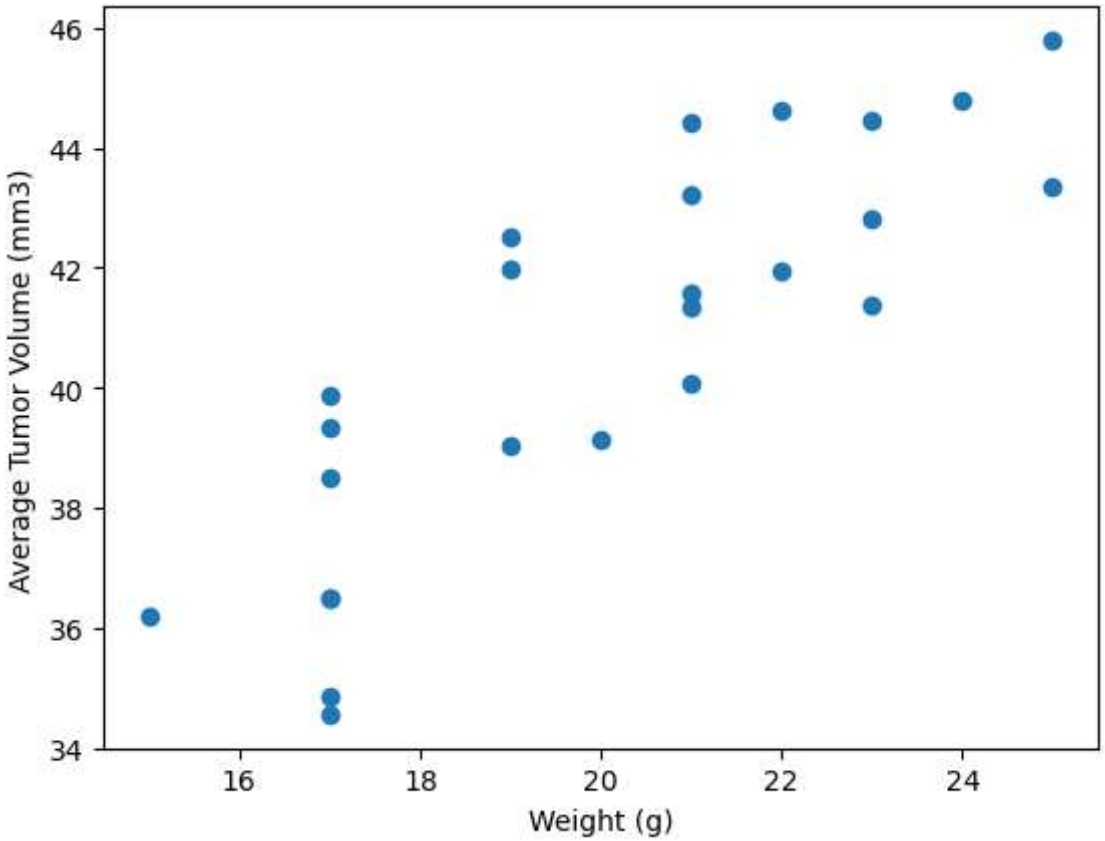


Line and Scatter Plots

In [16]:
```
# Generate a line plot of tumor volume vs. time point for a single mouse treated with Capomulin

```



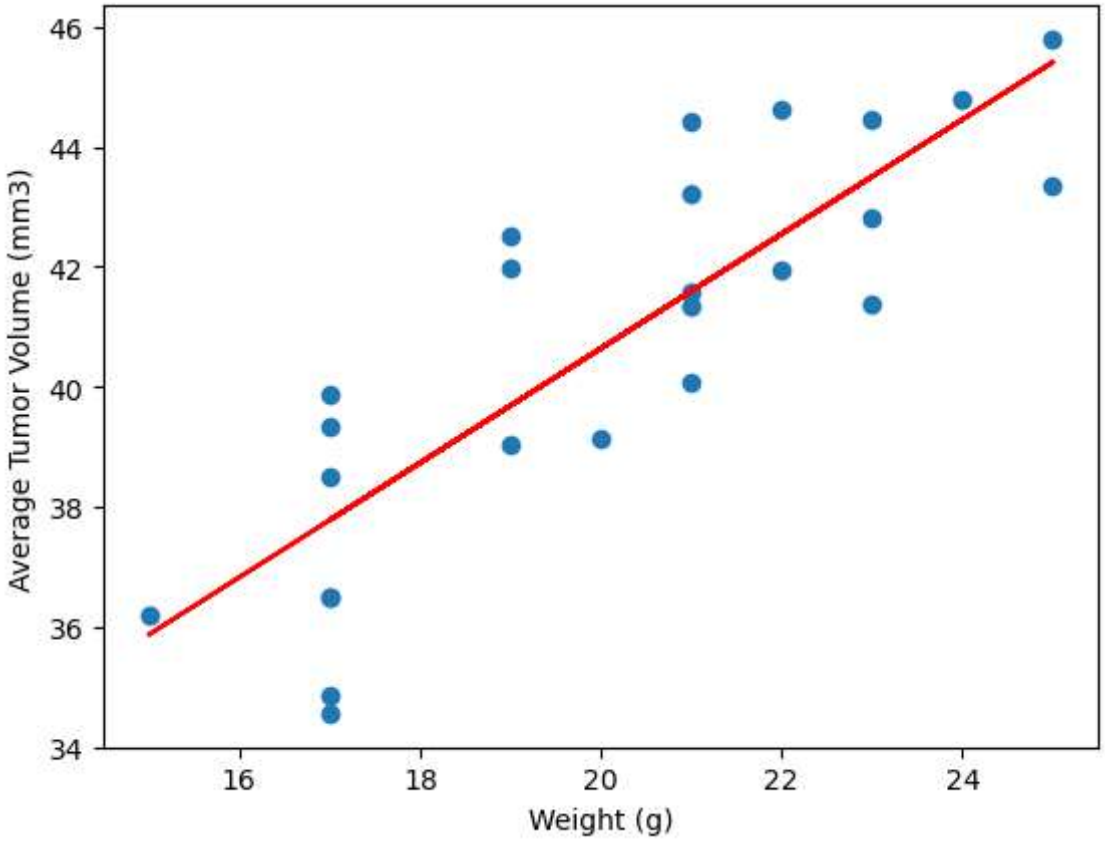
In [17]:
```
# Generate a scatter plot of mouse weight vs. the average observed tumor volume for the entire Capomulin regi
```



Correlation and Regression

In [18]:
```
# Calculate the correlation coefficient and a linear regression model
# for mouse weight and average observed tumor volume for the entire Capomulin regimen
```

```
The correlation between mouse weight and the average tumor volume is 0.84
```



In [ ]:
```
```