Observations and Insights

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In [609]:
```
# Dependencies and Setup
import matplotlib.pyplot as plt
import pandas as pd
import scipy.stats as st
import numpy as np

# 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 dataset
df1 = mouse_metadata.merge(study_results, on="Mouse ID")

# Display the data table for preview
df1
```

Out[609]:

	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
...	...	...	...	...	...	...	...	...
1888	z969	Naftisol	Male	9	30	25	63.145652	2
1889	z969	Naftisol	Male	9	30	30	65.841013	3
1890	z969	Naftisol	Male	9	30	35	69.176246	4
1891	z969	Naftisol	Male	9	30	40	70.314904	4
1892	z969	Naftisol	Male	9	30	45	73.867845	4

1893 rows × 8 columns

In [384]:
```
# Checking the number of mice.
number_of_mice = df1.nunique()["Mouse ID"]
number_of_mice
```

Out[384]: 249

In [401]:
```
# Getting the duplicate mice by ID number that shows up for Mouse ID an
df1.loc[df1.duplicated(subset=['Mouse ID', 'Timepoint']), 'Mouse ID'].u
df1.loc[df1['Mouse ID'] == 'g989']
```

Out[401]:

	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
910	g989	Propriva	Female	21	26	5	48.786801	0
912	g989	Propriva	Female	21	26	10	51.745156	0
914	g989	Propriva	Female	21	26	15	51.325852	1
916	g989	Propriva	Female	21	26	20	55.326122	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 [402]:
```
# Create a clean DataFrame by dropping the duplicate mouse by its ID.
df1.drop_duplicates(subset = ['Mouse ID', 'Timepoint'], inplace = True)
df = df1
df
```

	ID	Regimen	Sex	Age_months	(g)	Timepoint	(mm3)	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
...	...	...	...	...	...	...	...	...
1888	z969	Naftisol	Male	9	30	25	63.145652	2
1889	z969	Naftisol	Male	9	30	30	65.841013	3
1890	z969	Naftisol	Male	9	30	35	69.176246	4
1891	z969	Naftisol	Male	9	30	40	70.314904	4
1892	z969	Naftisol	Male	9	30	45	73.867845	4

In [403]:
```
# Checking the number of mice in the clean DataFrame.
number_of_mice = df.nunique()["Mouse ID"]
number_of_mice
```

Out[403]: 249

In [404]:
```
#WATCH END OF 1/26 LECTURE FOR HW INSIGHTS
```

Summary Statistics

Summary Statistics

In [405]:
```
# Generate a summary statistics table of mean, median, variance, standard dev
# Use groupby and summary statistical methods to calculate the following prop
# mean, median, variance, standard deviation, and SEM of the tumor volume.
# Assemble the resulting series into a single summary dataframe.

summ = df.groupby('Drug Regimen')['Tumor Volume (mm3)'].mean()
drugs = df['Drug Regimen'].unique()
tumormean = list(summ)
tumormedian = list(df.groupby('Drug Regimen')['Tumor Volume (mm3)'].median())
tumorvar = list(df.groupby('Drug Regimen')['Tumor Volume (mm3)'].var(ddof=0))
tumorstd = list(df.groupby('Drug Regimen')['Tumor Volume (mm3)'].std(ddof=0))
tumorSEM = list(df.groupby('Drug Regimen')['Tumor Volume (mm3)'].sem(ddof=0))
data = list(zip(drugs,tumormean,tumormedian,tumorvar,tumorstd,tumorSEM))
summary1 = pd.DataFrame(data, columns = ['Drug Regimen','Mean of Tutor Volume
summary1
```

Out[405]:

	Drug Regimen	Mean of Tutor Volume Per Drug	Median of Tutor Volume Per Drug	Variance of Tutor Volume Per Drug	Standard Deviation of Tutor Volume Per Drug	SEM of Tutor Volume Per Drug
0	Ramicane	40.675741	41.557809	24.839296	4.983904	0.328629
1	Capomulin	52.591172	51.776157	39.069446	6.250556	0.468499
2	Infubinol	52.884795	51.820584	42.886388	6.548770	0.490851
3	Placebo	55.235638	53.698743	68.188930	8.257659	0.602252
4	Ceftamin	54.331565	52.509285	65.817708	8.112811	0.594860
5	Stelasyn	54.033581	52.288934	60.830138	7.799368	0.579722
6	Zoniferol	52.393463	50.909965	42.862273	6.546928	0.524174
7	Ketapril	40.216745	40.673236	23.383692	4.835669	0.320250
8	Propriva	54.233149	52.431737	59.122106	7.689090	0.571526
9	Naftisol	53.236507	51.818479	48.266689	6.947423	0.514977

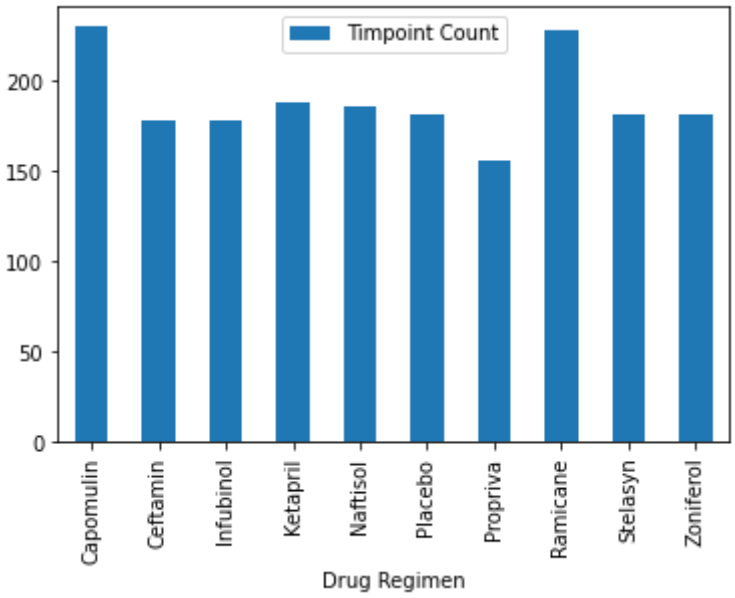
In [406]:
```
# Using the aggregation method, produce the same summary statistics in
# .grouby then .agg
summ2 = df.groupby('Drug Regimen')['Tumor Volume (mm3)'].agg(['mean','m
summ2
```

Out[406]:

Drug Regimen	mean	median	var	std	sem
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	52.393463	50.909965	43.138803	6.568014	0.525862
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

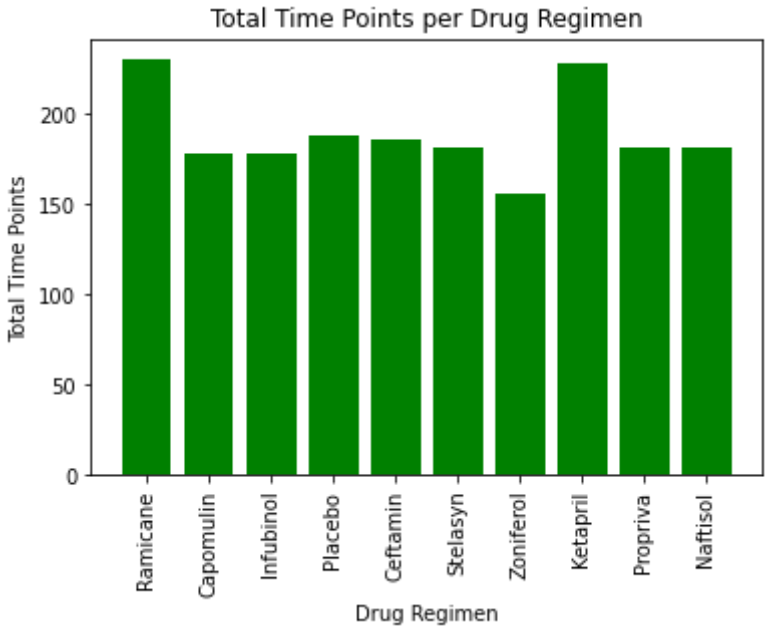
Bar and Pie Charts

In [407]:
```
# Generate a bar plot showing the total number of timepoints for all mic
x = drugs
yax = df.groupby('Drug Regimen').count()['Timepoint']
df1 = pd.DataFrame({'Drugs': x, 'Timpoint Count': yax})
ax = df1.plot.bar(rot=90)
```



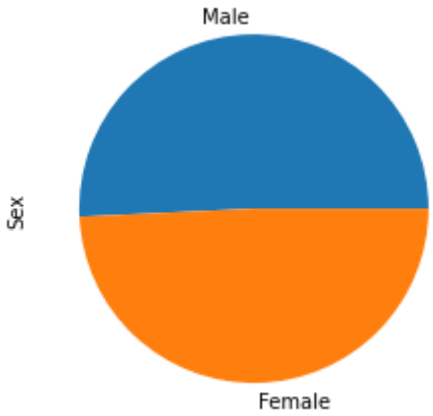
In [408]:
```
# Generate a bar plot showing the total number of timepoints for all mic
plt.bar(drugs, yax, color = 'g')
plt.xticks(rotation = 90)
plt.xlabel("Drug Regimen")
plt.ylabel("Total Time Points")
plt.title("Total Time Points per Drug Regimen")
```

Out[408]: Text(0.5, 1.0, 'Total Time Points per Drug Regimen')



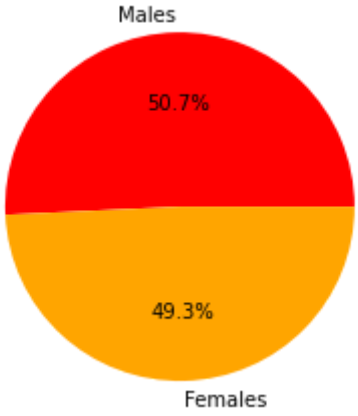
In [409]:
```
# Generate a pie plot showing the distribution of female versus male mi
genderdist = df['Sex'].value_counts()
print(genderdist)
malecount = genderdist[0]
femalecount = genderdist[1]
dist_df = pd.DataFrame({'count': [malecount, femalecount]}, index = ['M
plot = genderdist.plot.pie(y = 'count')
```

```
Male      958
Female    930
Name: Sex, dtype: int64
```



In [410]:
```
# Generate a pie plot showing the distribution of female versus male mi
labels = ['Males','Females']
sizes = [int(malecount), int(femalecount)]
plt.pie(sizes, labels=labels, colors = ['red','orange'], autopct="%1.1f

```

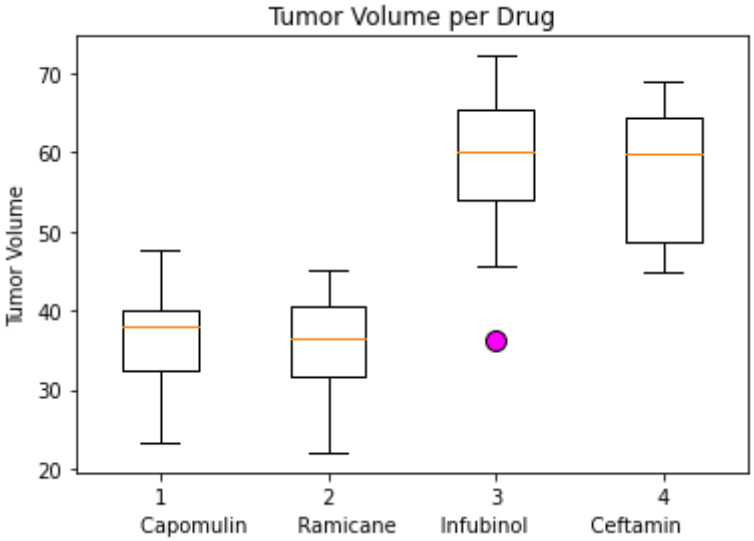
Out[410]:
```
([<matplotlib.patches.Wedge at 0x7fbe2c728e50>,
  <matplotlib.patches.Wedge at 0x7fbe2c735340>],
 [Text(-0.025622895044835736, 1.0997015355311284, 'Males'),
  Text(0.025622792083347525, -1.099701537930112, 'Females')],
 [Text(-0.013976124569910401, 0.5998372011987972, '50.7%'),
  Text(0.01397606840909865, -0.5998372025073339, '49.3%')])
```



Quartiles, Outliers and Boxplots

In [711]:
```
# Calculate the final tumor volume of each mouse across four of the tre

grouped = df1.drop_duplicates('Mouse ID', keep='last')
cap = grouped.loc[grouped['Drug Regimen'] == 'Capomulin', 'Tumor Volume
ram = grouped.loc[grouped['Drug Regimen'] == 'Ramicane', 'Tumor Volume
inf = grouped.loc[grouped['Drug Regimen'] == 'Infubinol', 'Tumor Volume
ceft = grouped.loc[grouped['Drug Regimen'] == 'Ceftamin', 'Tumor Volume
d = {'Capomulin': cap, 'Ramicane': ram, 'Infubinol': inf, 'Ceftamin': c
ser = pd.Series(data = d, index = ['Capomulin', 'Ramicane', 'Infubinol'

```

In [726]:
```
# Generate a box plot of the final tumor volume of each mouse across fo
fig1, ax1 = plt.subplots()
ax1.set_title('Tumor Volume per Drug')
ax1.set_ylabel('Tumor Volume')
ax1.set_xlabel('Capomulin       Ramicane       Infubinol          Ceft
ax1.boxplot(ser, flierprops={'marker': 'o', 'markersize': 10, 'markerfa
plt.show()
outliers = inf[(inf <= lower_bound) | (inf >= upper_bound)]
print('The following are the outliers in the boxplot:{}'.format(outlier
```




```
The following are the outliers in the boxplot:669    36.321346
Name: Tumor Volume (mm3), dtype: float64
```

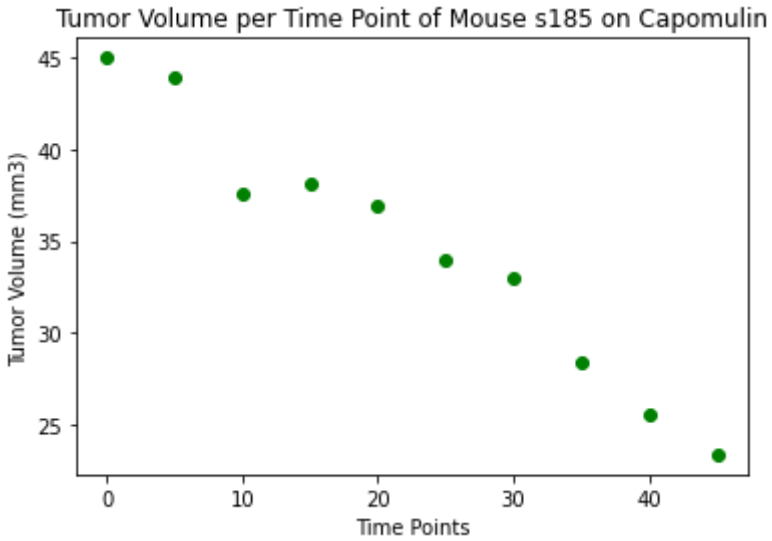
In [727]:
```
# Only showing statistics for Infubinol as the box plot showed it's the

quartiles = inf.quantile([.25,.5,.75])
lowerq = quartiles[0.25]
upperq = quartiles[0.75]
iqr = upperq-lowerq

print(f"The lower quartile of Infubinol is: {lowerq}")
print(f"The upper quartile of Infubinol is: {upperq}")
print(f"The interquartile range of Infubinol is: {iqr}")

lower_bound = lowerq - (1.5*iqr)
upper_bound = upperq + (1.5*iqr)
print(f"Values below {lower_bound} could be outliers.")
print(f"Values above {upper_bound} could be outliers.")
```

```
The lower quartile of Infubinol is: 54.04860769
The upper quartile of Infubinol is: 65.52574285
The interquartile range of Infubinol is: 11.477135160000003
Values below 36.83290494999999 could be outliers.
Values above 82.74144559000001 could be outliers.
```

Line and Scatter Plots

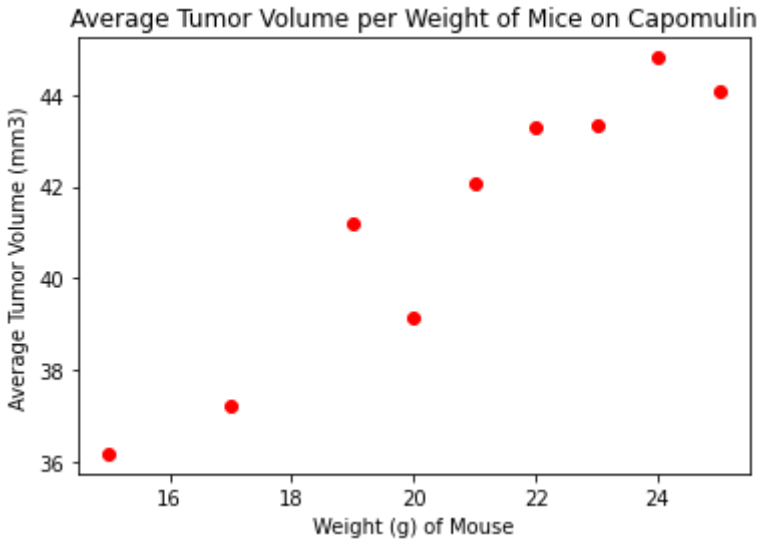
In [515]:
```
# Generate a line plot of tumor volume vs. time point for a mouse treat
df.loc[df['Drug Regimen'] == 'Capomulin']
df2 = df.loc[df['Mouse ID'] == 's185']
tumorvol = list(df2['Tumor Volume (mm3)'])
timepoint = list(df2['Timepoint'])
plt.title('Tumor Volume per Time Point of Mouse s185 on Capomulin')
plt.xlabel('Time Points')
plt.ylabel('Tumor Volume (mm3)')
plt.scatter(timepoint, tumorvol, color='green')
```

Out[515]: <matplotlib.collections.PathCollection at 0x7fbe2c957d30>



In [528]:
```
# Generate a scatter plot of average tumor volume vs. mouse weight for
df3 = df.groupby(['Drug Regimen','Weight (g)'])['Tumor Volume (mm3)'].m
new = pd.DataFrame(df3)
df4 = pd.DataFrame(new.groupby(['Drug Regimen']).get_group('Capomulin')
x = df4['Weight (g)'].tolist()
y = df4['Tumor Volume (mm3)'].tolist()
plt.title('Average Tumor Volume per Weight of Mice on Capomulin')
plt.xlabel('Weight (g) of Mouse')
plt.ylabel('Average Tumor Volume (mm3)')
plt.scatter(x, y, color='red')
```

Out[528]: <matplotlib.collections.PathCollection at 0x7fbe2caa4550>



Correlation and Regression

In [553]:
```
# Calculate the correlation coefficient and linear regression model for mouse
correlation = st.pearsonr(x, y)
int(f'The correlation coeffienct for mouse weight and average tumor volume f
```

```
The correlation coeffienct for mouse weight and average tumor volume for
the Capomulin regimen is: 0.95
```

In [569]:

```
(slope, intercept, rvalue, pvalue, stderr) = st.linregress(x, y)
regress_values = np.array(x) * slope + intercept
line_eq = "y = " + str(round(slope,2)) + "x + " + str(round(intercept,2
plt.scatter(x,y)
plt.plot(x,regress_values, "r-")
plt.annotate(line_eq, (6,10), fontsize=15,color="red",)
plt.title('Linear Regression Model for Weight vs. Tumor Vol.')
plt.xlabel('Weight (g)')
plt.ylabel('Average Tumor Volume per Weight of Mice on Capomulin')
plt.show()
print(line_eq)
```


```
y = 0.89x + 22.76
```

In [ ]:

```
1
```