Pymaceuticals Inc.

Data Analyst

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Analysis

Clinical study highlights:

- Capomulin and Ramicane have better performance compared with the rest of the treatments
- Capomulin treatment was associated to the highest mice population while Zoniferol was to the smallest
- As the chart shows, the correlation between mouse weight and average tumor volume is 0.84. This means that when the mouse weight increases so does the average tumor volume.
- The total population of mice was almost identical in terms of gender. With 125 males (51%) and 124 females (49%)

In [1]:

```
# Dependencies and Setup
%matplotlib notebook

import matplotlib.pyplot as plt
import pandas as pd
from scipy import 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 dataset
study_data_complete = pd.merge(study_results, mouse_metadata, how="left", on="Mouse ID

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

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.
mice_count = len(study_data_complete['Mouse ID'].value_counts())
mice_count
```

Out[2]:

```
249
```

In [3]:

```
# Getting the duplicate mice by ID number that shows up for Mouse ID and Timepoint.
duplicate_mice = study_data_complete[study_data_complete.duplicated(subset=['Mouse ID'
duplicate_mice['Mouse ID'].unique()
```

Out[3]:

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

In [4]:

```
# Optional: Get all the data for the duplicate mouse ID.
duplicate_mice_data = study_data_complete[study_data_complete['Mouse ID']==duplicate_m
duplicate_mice_data
```

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.
study_data_clean = study_data_complete[study_data_complete['Mouse ID'] != duplicate_mi
study_data_clean.head()
```

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.
mice = len(study_data_clean['Mouse ID'].value_counts())
mice
```

Out[6]:

```
248
```

Summary Statistics

In [7]:

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

# Use groupby and summary statistical methods to calculate the following properties of
drug_regimen_data=study_data_clean.groupby(['Drug Regimen'])

# mean, median, variance, standard deviation, and SEM of the tumor volume.
mean = drug_regimen_data['Tumor Volume (mm3)'].mean()
median = drug_regimen_data['Tumor Volume (mm3)'].median()
var = drug_regimen_data['Tumor Volume (mm3)'].var()
std = drug_regimen_data['Tumor Volume (mm3)'].std()
sem = drug_regimen_data['Tumor Volume (mm3)'].sem()

# Assemble the resulting series into a single summary DataFrame.
tumor_summary = pd.DataFrame({'Mean Tumor Volume': mean, 'Median Tumor Volume': mediar
tumor_summary
```

Out[7]:

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

In [8]:

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

# Using the aggregation method, produce the same summary statistics in a single line.
agg_tumor_summary = drug_regimen_data.agg({'Tumor Volume (mm3)':['mean','median','var'
agg_tumor_summary
```

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
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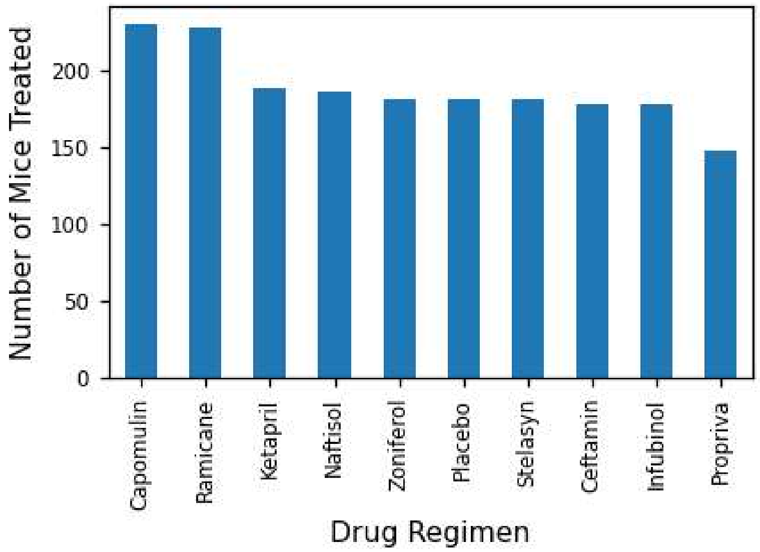
Zoniferol	53.236507	51.818479	48.533355	6.966589	0.516398

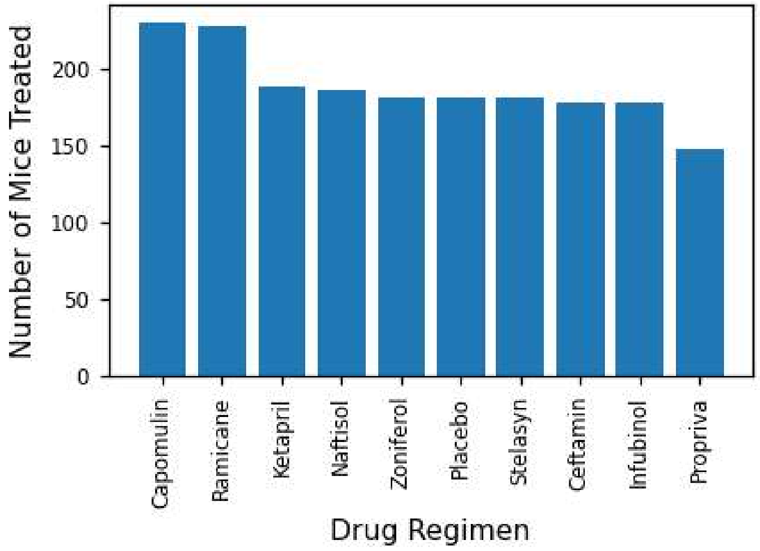
Bar and Pie Charts

In [10]:

```
# Generate a bar plot showing the total number of timepoints for all mice tested for e
timepoints_by_regimen = pd.DataFrame(drug_regimen_data.count()["Timepoint"].sort_value
ax = timepoints_by_regimen.plot(kind='bar',fontsize = 7.5, figsize=(4,3),
                                xlabel='Drug Regimen', ylabel='Number of Mice Treated'
plt.tight_layout()
```

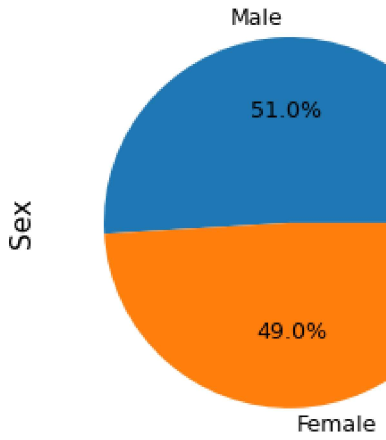


In [11]:
```
# Generate a bar plot showing the total number of timepoints for all mice tested for e
timepoint_dict = timepoints_by_regimen.to_dict()

x = list(timepoint_dict.get('Timepoint', {}).keys())
height = list(timepoint_dict.get('Timepoint', {}).values())

plt.figure(figsize=(4,3))
plt.bar(x, height, width=0.8, align='center')
plt.xlabel("Drug Regimen", fontsize=10)
plt.ylabel("Number of Mice Treated", fontsize=10)
plt.xticks(fontsize=7.5,rotation=90)
plt.yticks(fontsize=7.5)
plt.tight_layout()
```



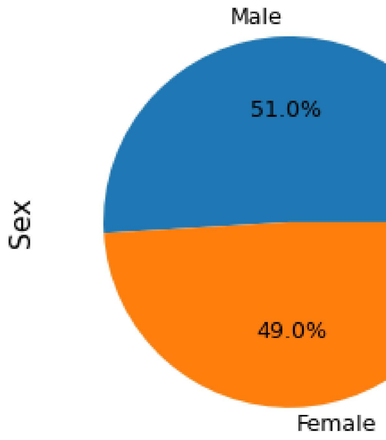
In [12]:

```python
# Generate a pie plot showing the distribution of female versus male mice using Pandas
sex_distro = pd.DataFrame(study_data_clean["Sex"].value_counts())
ax = sex_distro.plot(kind='pie', subplots=True, fontsize = 8, figsize=(3,3), legend=Fa
```



In [13]:

```python
# Generate a pie plot showing the distribution of female versus male mice using pyplot
sex_dict = sex_distro.to_dict()

labels = list(sex_dict.get('Sex', {}).keys())
sizes = list(sex_dict.get('Sex', {}).values())

plt.figure(figsize=(3,3))
plt.pie(sizes, labels=labels, autopct='%1.1f%%',textprops = {'fontsize':8})
plt.ylabel('Sex', fontsize=10)
plt.show()
```



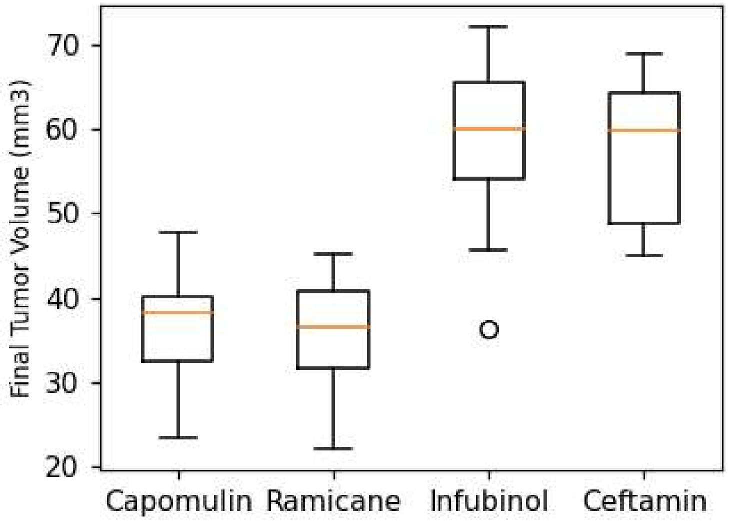
Quartiles, Outliers and Boxplots

In [17]:

```
# Calculate the final tumor volume of each mouse across four of the treatment regimens
# Capomulin, Ramicane, Infubinol, and Ceftamin
capomulin = study_data_clean.loc[study_data_clean["Drug Regimen"] == "Capomulin",:]
ramicane = study_data_clean.loc[study_data_clean["Drug Regimen"] == "Ramicane", :]
infubinol = study_data_clean.loc[study_data_clean["Drug Regimen"] == "Infubinol", :]
ceftamin = study_data_clean.loc[study_data_clean["Drug Regimen"] == "Ceftamin", :]

# Start by getting the last (greatest) timepoint for each mouse
capomulin_tumor_volume = pd.DataFrame(capomulin.groupby('Mouse ID').max()['Timepoint']
ramicane_tumor_volume = pd.DataFrame(ramicane.groupby('Mouse ID').max()['Timepoint'])
infubinol_tumor_volume = pd.DataFrame(infubinol.groupby('Mouse ID').max()['Timepoint']
ceftamin_tumor_volume = pd.DataFrame(ceftamin.groupby('Mouse ID').max()['Timepoint'])

# Merge this group df with the original DataFrame to get the tumor volume at the last
cap_group = pd.merge(capomulin_tumor_volume, study_data_clean, on=("Mouse ID","Timepoi
ram_group = pd.merge(ramicane_tumor_volume, study_data_clean, on=("Mouse ID","Timepoir
inf_group = pd.merge(infubinol_tumor_volume, study_data_clean, on=("Mouse ID","Timepoi
cef_group = pd.merge(ceftamin_tumor_volume, study_data_clean, on=("Mouse ID","Timepoir
```

In [18]:

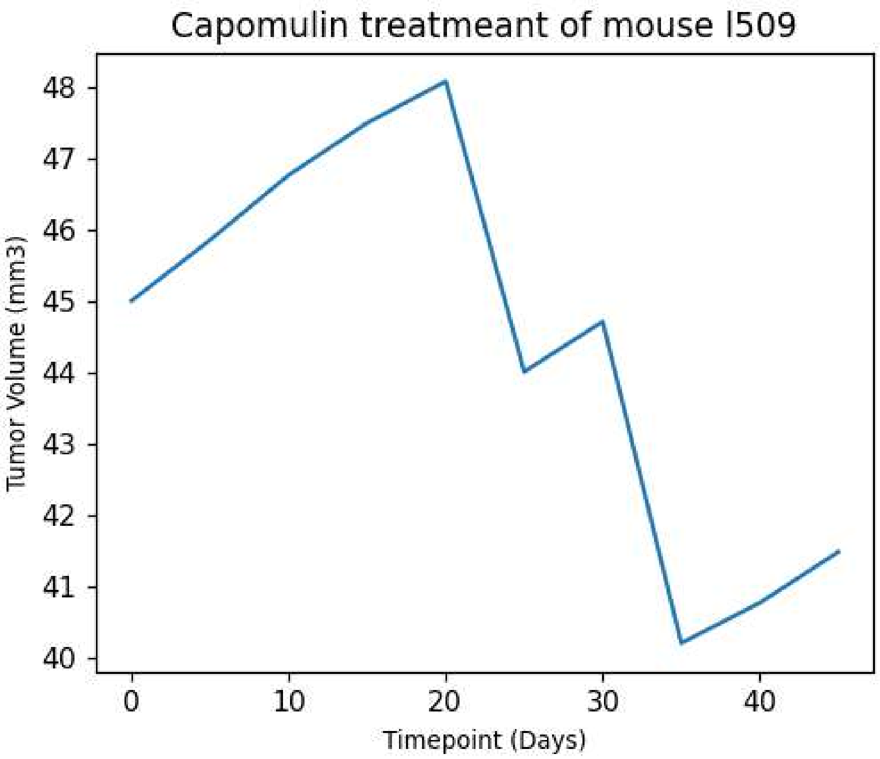
```
# Put treatments into a list for loop (and later for plot labels)
treatment_list = ["Capomulin", "Ramicane", "Infubinol", "Ceftamin"]
treatments = study_data_clean[study_data_clean["Drug Regimen"].isin(treatment_list)]

# Create empty list to fill with tumor vol data (for plotting)
tumor_vol_data=[]

# Locate the rows which contain mice on each drug and get the tumor volumes
max_timepoint = treatments.groupby(["Drug Regimen", "Mouse ID"]).agg(tumor_size=("Tumo

# add subset
max_timepoint = max_timepoint.stack(level=0).unstack(level=0)

treatment_idx = 0


for treatment in treatment_list:
    # Calculate the IQR and quantitatively determine if there are any potential outlie
    quartiles = max_timepoint[treatment].quantile([.25,.5,.75]).round(2)
    lower_quar = quartiles[0.25].round(2)
    upper_quar = quartiles[0.75].round(2)
    iquar = round(upper_quar-lower_quar,2)
    # Determine outliers using upper and lower bounds
    lower_bound = round(lower_quar - (1.5*iquar),2)
    upper_bound = round(upper_quar + (1.5*iquar),2)

# Generate a box plot that shows the distribution of the tumor volume for each treatme
for treatment in treatment_list:
    tumor_vol_data.append(list(max_timepoint[treatment].dropna()))

plt.figure(figsize=(4,3))
plt.ylabel("Final Tumor Volume (mm3)", fontsize=8.5)
plt.boxplot(tumor_vol_data,labels=treatment_list)
plt.show()
```



Line and Scatter Plots

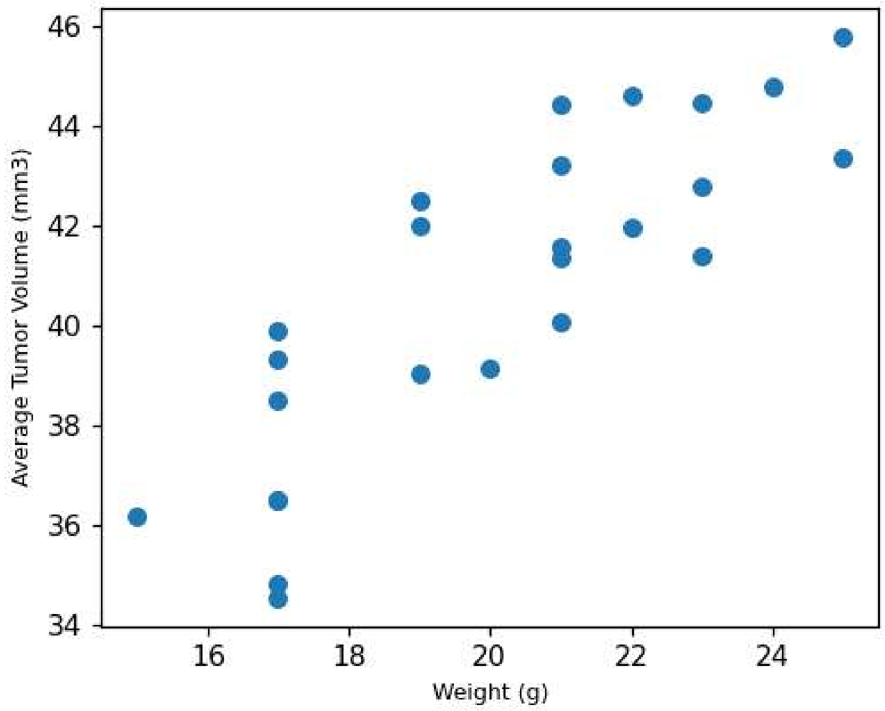
In [19]:

```
# Generate a line plot of tumor volume vs. time point for a mouse treated with Capomul
x = capomulin.loc[capomulin["Mouse ID"] == "l509",:]["Timepoint"]
y = capomulin.loc[capomulin["Mouse ID"] == "l509",:]["Tumor Volume (mm3)"]

plt.figure(figsize=(5,4))
plt.title('Capomulin treatmeant of mouse l509')
plt.plot(x, y)
plt.xlabel('Timepoint (Days)', fontsize=8.5)
plt.ylabel('Tumor Volume (mm3)', fontsize=8.5)
plt.show()
```



In [20]:

```
# Generate a scatter plot of average tumor volume vs. mouse weight for the Capomulin r
avg_tumor_volume_cap =capomulin.groupby(['Mouse ID']).mean()

plt.figure(figsize=(5,4))
plt.scatter(avg_tumor_volume_cap['Weight (g)'],avg_tumor_volume_cap['Tumor Volume (mm3
plt.xlabel('Weight (g)',fontsize =8)
plt.ylabel('Average Tumor Volume (mm3)',fontsize =8)
plt.show()
```

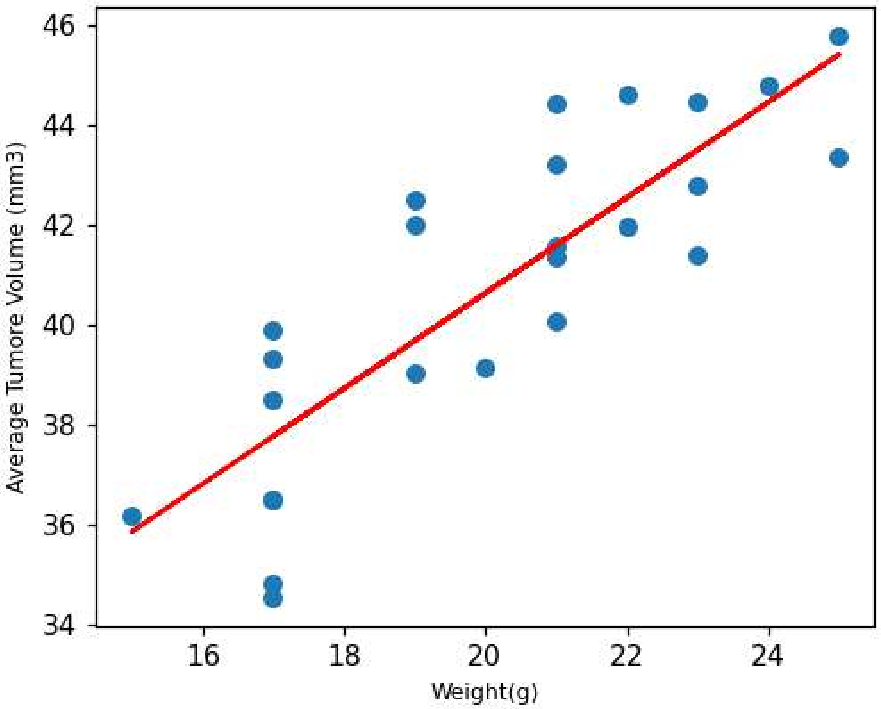


Correlation and Regression

In [21]:

```
# Calculate the correlation coefficient and linear regression model for mouse weight a
correlation=round(st.pearsonr(avg_tumor_volume_cap['Weight (g)'],avg_tumor_volume_cap[
print(f"The correlation between mouse weight and average tumor volume is {correlation}

x = avg_tumor_volume_cap['Weight (g)']
y = avg_tumor_volume_cap['Tumor Volume (mm3)']

(slope, intercept, rvalue, pvalue, stderr) = st.linregress(x, y)
regression_values  = x * slope + intercept

plt.figure(figsize=(5,4))
plt.scatter(x,y)
plt.plot(x,regression_values,"r-")
plt.xlabel('Weight(g)',fontsize =8)
plt.ylabel('Average Tumore Volume (mm3)',fontsize =8)
plt.show()
```

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


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