## Observations and Insights

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In [ ]:
```
# Obersvations from the data study:
# 1)  Count of Male mouse participated in the study is nore than Female.
# 2)  Drug Infubinol have Tumor volume data in the outliner.
# 3)  Correlation between average tumor volume vs. mouse weight for the Capomulir
```

In [1]:
```
# Dependencies and Setup
import matplotlib.pyplot as plt
import pandas as pd
import scipy.stats as st
import numpy as np
from scipy.stats import linregress
from sklearn import datasets

# 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
Combined_1 = pd.merge(mouse_metadata, study_results, on="Mouse ID", how = 'outer'

# Display the data table for preview
Combined_1
```

Out[1]:

| | 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 [2]:
```
# Checking the number of mice.
Unique_no_mouse = Combined_1["Mouse ID"].nunique()
Unique_no_mouse
```

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

In [3]:
```
# Getting the duplicate mice by ID number that shows up for Mouse ID and Timepoir
Duplicate_mice_data =  Combined_1[Combined_1.duplicated(['Mouse ID', 'Timepoint']
```

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

```
    Mouse ID Drug Regimen     Sex  Age_months  Weight (g)  Timepoint  \
908     g989     Propriva  Female          21          26          0   
909     g989     Propriva  Female          21          26          0   
910     g989     Propriva  Female          21          26          5   
911     g989     Propriva  Female          21          26          5   
912     g989     Propriva  Female          21          26         10   
913     g989     Propriva  Female          21          26         10   
914     g989     Propriva  Female          21          26         15   
915     g989     Propriva  Female          21          26         15   
916     g989     Propriva  Female          21          26         20   
917     g989     Propriva  Female          21          26         20   

     Tumor Volume (mm3)  Metastatic Sites  
908           45.000000                 0  
909           45.000000                 0  
910           48.786801                 0  
911           47.570392                 0  
912           51.745156                 0  
913           49.880528                 0  
914           51.325852                 1  
915           53.442020                 0  
916           55.326122                 1  
917           54.657650                 1  
```

In [5]:
```
# Create a clean DataFrame by dropping the duplicate mouse by its ID.
Combined_1 = Combined_1.set_index('Mouse ID')
Combined_2 = Combined_1.drop('g989')
Combined_2
```

Out[5]:

| | Drug Regimen | Sex | Age_months | Weight (g) | Timepoint | Tumor Volume (mm3) | Metastatic Sites |
|---|---|---|---|---|---|---|---|
| **Mouse ID** | | | | | | | |
| **k403** | Ramicane | Male | 21 | 16 | 0 | 45.000000 | 0 |
| **k403** | Ramicane | Male | 21 | 16 | 5 | 38.825898 | 0 |
| **k403** | Ramicane | Male | 21 | 16 | 10 | 35.014271 | 1 |
| **k403** | Ramicane | Male | 21 | 16 | 15 | 34.223992 | 1 |
| **k403** | Ramicane | Male | 21 | 16 | 20 | 32.997729 | 1 |
| **...** | ... | ... | ... | ... | ... | ... | ... |
| **z969** | Naftisol | Male | 9 | 30 | 25 | 63.145652 | 2 |
| **z969** | Naftisol | Male | 9 | 30 | 30 | 65.841013 | 3 |
| **z969** | Naftisol | Male | 9 | 30 | 35 | 69.176246 | 4 |
| **z969** | Naftisol | Male | 9 | 30 | 40 | 70.314904 | 4 |
| **z969** | Naftisol | Male | 9 | 30 | 45 | 73.867845 | 4 |

1880 rows × 7 columns

In [6]:
```
# Checking the number of mice in the clean DataFrame.
Combined_2 = Combined_2.reset_index()

Unique_no_mouse_1 = Combined_2["Mouse ID"].nunique()
Unique_no_mouse_1
```

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

## Summary Statistics

In [18]:
```
# Generate a summary statistics table of mean, median, variance, standard deviati

# Use groupby and summary statistical methods to calculate the following properti
# mean, median, variance, standard deviation, and SEM of the tumor volume.
# Assemble the resulting series into a single summary dataframe.
Drug_regimen_grp = Combined_2.groupby(['Drug Regimen'])

Mean_tumor_volume = Drug_regimen_grp["Tumor Volume (mm3)"].mean()
Median_tumor_volume = Drug_regimen_grp["Tumor Volume (mm3)"].median()
Var_tumor_volume = Drug_regimen_grp["Tumor Volume (mm3)"].var()
SD_tumor_volume = Drug_regimen_grp["Tumor Volume (mm3)"].std()
SEM_tumor_volume = Drug_regimen_grp["Tumor Volume (mm3)"].sem()

Drug_regimen_summary = pd.DataFrame({"Mean": Mean_tumor_volume,
                                    "Median": Median_tumor_volume,
                                    "Variance": Var_tumor_volume,
                                    "SD": SD_tumor_volume,
                                    "SEM": SEM_tumor_volume})
Drug_regimen_summary["Mean"] = Drug_regimen_summary["Mean"].map("{:,.2f}".format
Drug_regimen_summary["Median"] = Drug_regimen_summary["Median"].map("{:,.2f}".for
Drug_regimen_summary["Variance"] = Drug_regimen_summary["Variance"].map("{:,.2f}"
Drug_regimen_summary["SD"] = Drug_regimen_summary["SD"].map("{:,.2f}".format)
Drug_regimen_summary["SEM"] = Drug_regimen_summary["SEM"].map("{:,.2f}".format)
Drug_regimen_summary
```

Out[18]:

| | Mean | Median | Variance | SD | SEM |
|---|---|---|---|---|---|
| **Drug Regimen** | | | | | |
| **Capomulin** | 40.68 | 41.56 | 24.95 | 4.99 | 0.33 |
| **Ceftamin** | 52.59 | 51.78 | 39.29 | 6.27 | 0.47 |
| **Infubinol** | 52.88 | 51.82 | 43.13 | 6.57 | 0.49 |
| **Ketapril** | 55.24 | 53.70 | 68.55 | 8.28 | 0.60 |
| **Naftisol** | 54.33 | 52.51 | 66.17 | 8.13 | 0.60 |
| **Placebo** | 54.03 | 52.29 | 61.17 | 7.82 | 0.58 |
| **Propriva** | 52.32 | 50.45 | 43.85 | 6.62 | 0.54 |
| **Ramicane** | 40.22 | 40.67 | 23.49 | 4.85 | 0.32 |
| **Stelasyn** | 54.23 | 52.43 | 59.45 | 7.71 | 0.57 |
| **Zoniferol** | 53.24 | 51.82 | 48.53 | 6.97 | 0.52 |

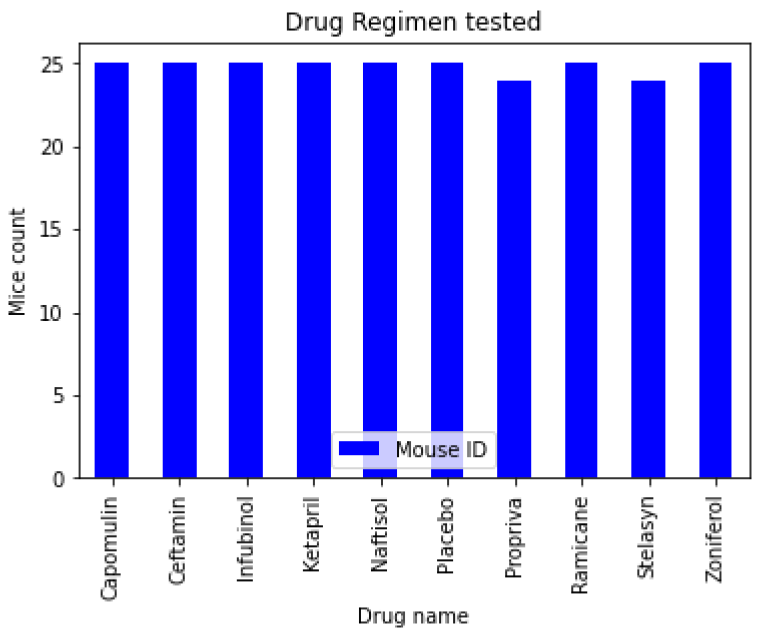
In [8]:
```
# Generate a summary statistics table of mean, median, variance, standard deviati

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

Drug_regimen_reg_summary = Drug_regimen_grp.aggregate({"Tumor Volume (mm3)":['mea

Drug_regimen_reg_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 |
| **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 |

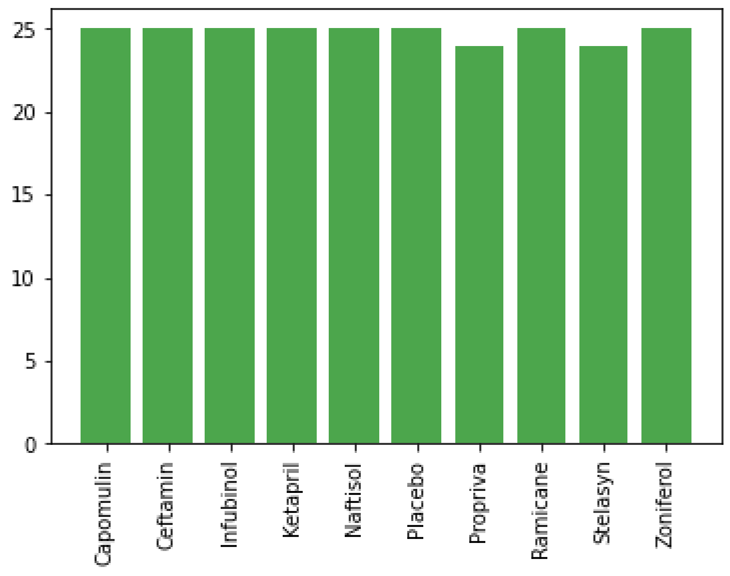
## Bar and Pie Charts

In [9]:
```
# Generate a bar plot showing the total number of unique mice tested on each drug

Total_mouse_count = pd.DataFrame(Drug_regimen_grp["Mouse ID"].nunique())

# Total_mouse_count
Total_mouse_count.plot(kind="bar", facecolor="blue")

plt.title("Drug Regimen tested")
plt.ylabel("Mice count")
plt.xlabel("Drug name")
plt.legend(loc="best")

plt.show()
```



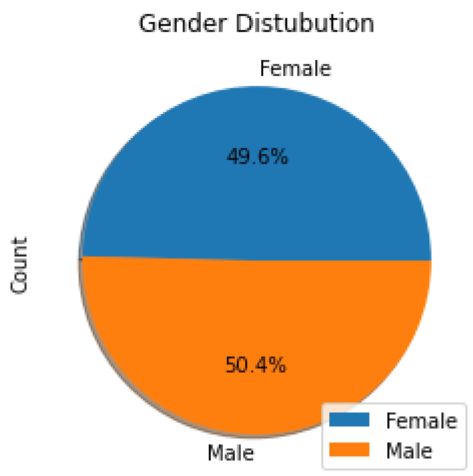
In [10]:
```
# Generate a bar plot showing the total number of unique mice tested on each drug
Total_mouse_count = Total_mouse_count.reset_index()

x_axis = np.arange(len(Total_mouse_count))
tick_locations = [value for value in x_axis]
# plt.figure(figsize=(20,3))
plt.bar(x_axis,Total_mouse_count["Mouse ID"] , color='g', alpha=0.7, align="cente
plt.xticks(tick_locations, Total_mouse_count["Drug Regimen"], rotation="vertical'
```

Out[10]:
```
([<matplotlib.axis.XTick at 0x2031640ca58>,
  <matplotlib.axis.XTick at 0x2031640ca20>,
  <matplotlib.axis.XTick at 0x2031640c668>,
  <matplotlib.axis.XTick at 0x20316450160>,
  <matplotlib.axis.XTick at 0x203164505c0>,
  <matplotlib.axis.XTick at 0x20316450a58>,
  <matplotlib.axis.XTick at 0x20316450438>,
  <matplotlib.axis.XTick at 0x20316457160>,
  <matplotlib.axis.XTick at 0x203164575c0>,
  <matplotlib.axis.XTick at 0x20316457a58>],
 [Text(0, 0, 'Capomulin'),
  Text(0, 0, 'Ceftamin'),
  Text(0, 0, 'Infubinol'),
  Text(0, 0, 'Ketapril'),
  Text(0, 0, 'Naftisol'),
  Text(0, 0, 'Placebo'),
  Text(0, 0, 'Propriva'),
  Text(0, 0, 'Ramicane'),
  Text(0, 0, 'Stelasyn'),
  Text(0, 0, 'Zoniferol')])
```

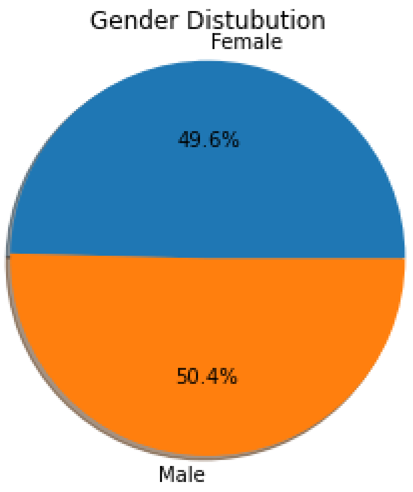


In [11]:
```
# Generate a pie plot showing the distribution of female versus male mice using p
Gender_count = Combined_2.groupby(['Sex'])
Gender_count_1 = Gender_count['Mouse ID'].nunique()

Gender_count_df = pd.DataFrame({"Count": Gender_count_1})
Gender_count_df.plot(kind="pie",subplots=True, autopct="%1.1f%%", shadow=True)
plt.title("Gender Distubution")
plt.legend(loc="lower right")
```

Out[11]:
```
<matplotlib.legend.Legend at 0x203164a4198>
```



In [12]:
```
# Generate a pie plot showing the distribution of female versus male mice using p
Gender_count_1 = Gender_count_1.reset_index()
Gender_count_1
plt.title("Gender Distubution")
plt.pie(Gender_count_1['Mouse ID'], labels=Gender_count_1['Sex'] ,autopct="%1.1f%
plt.axis("equal")
plt.show()
```



## Quartiles, Outliers and Boxplots

In [13]:
```
# Calculate the final tumor volume of each mouse across four of the treatment reg
# Capomulin, Ramicane, Infubinol, and Ceftamin
Treatment_regimen = Combined_2.loc[(Combined_2['Drug Regimen'] == "Capomulin") |
                                   (Combined_2['Drug Regimen'] == "Ramicane")  |
                                   (Combined_2['Drug Regimen'] == "Infubinol") |
                                   (Combined_2['Drug Regimen'] == "Ceftamin")]

# Start by getting the last (greatest) timepoint for each mouse
Timepoint_count = Treatment_regimen.groupby(['Mouse ID', 'Drug Regimen'])
Timepoint_max = Timepoint_count["Timepoint"].max()

Timepoint_max= Timepoint_max.reset_index()
# Timepoint_max
# Merge this group df with the original dataframe to get the tumor volume at the
Timepoint_Merge = pd.merge(Timepoint_max, Combined_2, on=["Mouse ID" ,"Drug Regin
Timepoint_Merge
```

Out[13]:

| | Mouse ID | Drug Regimen | Timepoint | Sex | Age_months | Weight (g) | Tumor Volume (mm3) | Metastatic Sites |
|---|---|---|---|---|---|---|---|---|
| **0** | a203 | Infubinol | 45 | Female | 20 | 23 | 67.973419 | 2 |
| **1** | a251 | Infubinol | 45 | Female | 21 | 25 | 65.525743 | 1 |
| **2** | a275 | Ceftamin | 45 | Female | 20 | 28 | 62.999356 | 3 |
| **3** | a411 | Ramicane | 45 | Male | 3 | 22 | 38.407618 | 1 |
| **4** | a444 | Ramicane | 45 | Female | 10 | 25 | 43.047543 | 0 |
| **...** | ... | ... | ... | ... | ... | ... | ... | ... |
| **95** | y769 | Ceftamin | 45 | Female | 6 | 27 | 68.594745 | 4 |
| **96** | y793 | Capomulin | 45 | Male | 17 | 17 | 31.896238 | 2 |
| **97** | y865 | Ceftamin | 45 | Male | 23 | 26 | 64.729837 | 3 |
| **98** | z578 | Ramicane | 45 | Male | 11 | 16 | 30.638696 | 0 |
| **99** | z581 | Infubinol | 45 | Female | 24 | 25 | 62.754451 | 3 |

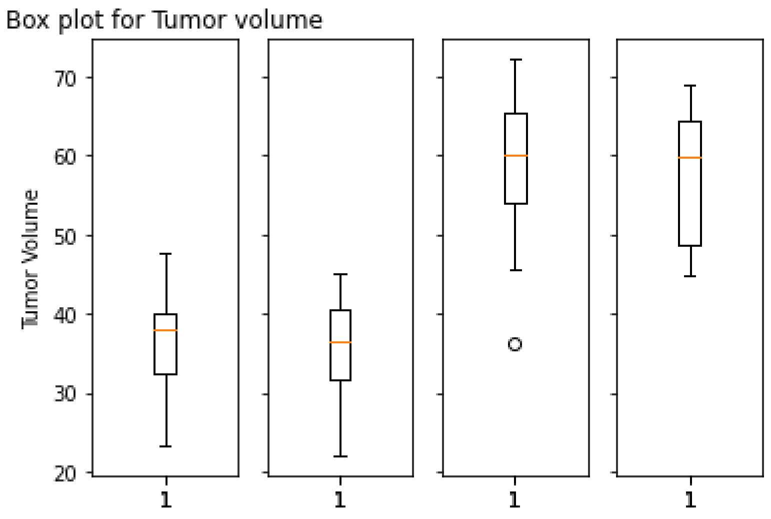
100 rows × 8 columns

In [14]:
```
# Put treatments into a list for for loop (and later for plot labels)
Treatment_list = ['Capomulin', 'Ramicane', 'Infubinol', 'Ceftamin']
Treatment_list

# Create empty list to fill with tumor vol data (for plotting)
Tumor_vol_list_Cap = []
Tumor_vol_list_Ram = []
Tumor_vol_list_Inf = []
Tumor_vol_list_Cef = []

for i in range(len(Timepoint_Merge)):
    Drug = Timepoint_Merge.iloc[i,:]["Drug Regimen"]
    Volume = Timepoint_Merge.iloc[i,:]["Tumor Volume (mm3)"]
    if Drug == 'Capomulin':
       Tumor_vol_list_Cap.append(Volume)
    if Drug == 'Ramicane':
       Tumor_vol_list_Ram.append(Volume)
    if Drug == 'Infubinol':
       Tumor_vol_list_Inf.append(Volume)
    if Drug == 'Ceftamin':
       Tumor_vol_list_Cef.append(Volume)
```

In [15]:
```
# Locate the rows which contain mice on each drug and get the tumor volumes
# add subset
for drug in Treatment_list:
    # From drug df , if drug name matches the one from list, add tumor volume to
    drug_df = Timepoint_Merge.loc[Timepoint_Merge["Drug Regimen"]== drug,"Tumor V

# Calculate the IQR and quantitatively determine if there are any potential outli
    quartiles = drug_df.quantile([.25,.5,.75])
    lowerq = quartiles[0.25]
    upperq = quartiles[0.75]
    iqr = upperq-lowerq
    lower_bound = lowerq - (1.5*iqr)
    upper_bound = upperq + (1.5*iqr)
    print(f"The lower quartile of {drug} occupancy is: {lowerq}")
    print(f"The upper quartile of {drug} occupancy is: {upperq}")
    print(f"The interquartile range of {drug} occupancy is: {iqr}")
    print(f"The the median of {drug} occupancy is: {quartiles[0.5]} ")
    print("-----------------------------------------------------------")

    # Determine outliers using upper and lower bounds

    print(f"Values below {drug} {lower_bound} could be outliers.")
    print(f"Values above {drug} {upper_bound} could be outliers.")
    print("-----------------------------------------------------------")
```

```
The lower quartile of Capomulin occupancy is: 32.37735684
The upper quartile of Capomulin occupancy is: 40.1592203
The interquartile range of Capomulin occupancy is: 7.781863460000004
The the median of Capomulin occupancy is: 38.125164399999996
-----------------------------------------------------------
Values below Capomulin 20.70456164999999 could be outliers.
Values above Capomulin 51.83201549 could be outliers.
-----------------------------------------------------------
The lower quartile of Ramicane occupancy is: 31.56046955
The upper quartile of Ramicane occupancy is: 40.65900627
The interquartile range of Ramicane occupancy is: 9.098536719999998
The the median of Ramicane occupancy is: 36.56165229
-----------------------------------------------------------
Values below Ramicane 17.912664470000003 could be outliers.
Values above Ramicane 54.30681135 could be outliers.
-----------------------------------------------------------
The lower quartile of Infubinol occupancy is: 54.04860769
The upper quartile of Infubinol occupancy is: 65.52574285
The interquartile range of Infubinol occupancy is: 11.477135160000003
The the median of Infubinol occupancy is: 60.16518046
-----------------------------------------------------------
Values below Infubinol 36.83290494999999 could be outliers.
Values above Infubinol 82.74144559000001 could be outliers.
-----------------------------------------------------------
The lower quartile of Ceftamin occupancy is: 48.72207785
The upper quartile of Ceftamin occupancy is: 64.29983003
The interquartile range of Ceftamin occupancy is: 15.577752179999997
The the median of Ceftamin occupancy is: 59.85195552
-----------------------------------------------------------
Values below Ceftamin 25.355449580000002 could be outliers.
Values above Ceftamin 87.66645829999999 could be outliers.
-----------------------------------------------------------
```

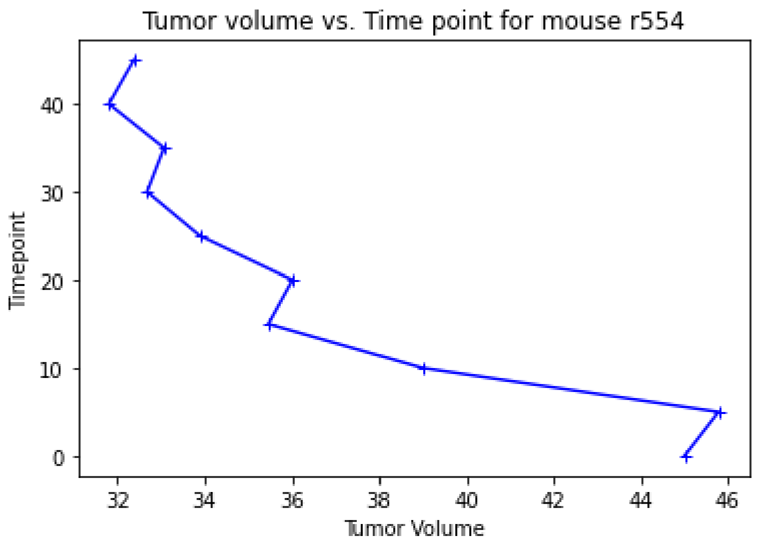
In [19]:
```
# Generate a box plot of the final tumor volume of each mouse across four regimen
fig1,(ax1, ax2, ax3, ax4) = plt.subplots(ncols = 4, sharex='all', sharey='all')
ax1.set_title('Box plot for Tumor volume')
ax1.set_ylabel('Tumor Volume')
ax1.boxplot(Tumor_vol_list_Cap)
ax2.boxplot(Tumor_vol_list_Ram)
ax3.boxplot(Tumor_vol_list_Inf)
ax4.boxplot(Tumor_vol_list_Cef)
plt.show()
```



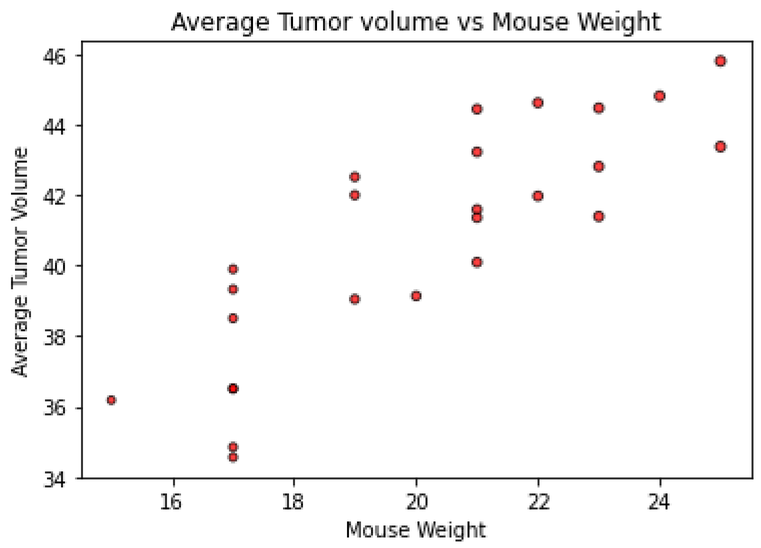
## Line and Scatter Plots

In [16]:
```
# Generate a line plot of tumor volume vs. time point for a mouse treated with Ca
Capomulin_data = Combined_2.loc[(Combined_2['Drug Regimen'] == "Capomulin") &
                                (Combined_2['Mouse ID'] == "r554")]
# Capomulin_data
x_axis = Capomulin_data['Tumor Volume (mm3)']
y_axis = Capomulin_data['Timepoint']
plt.plot(x_axis,y_axis, marker="+",color="blue", linewidth=1.5)
plt.title("Tumor volume vs. Time point for mouse r554")
plt.xlabel("Tumor Volume")
plt.ylabel("Timepoint")
plt.show
```

Out[16]:
```
<function matplotlib.pyplot.show(*args, **kw)>
```



In [17]:
```
# Generate a scatter plot of average tumor volume vs. mouse weight for the Capomu
Capomulin_data_avg = Combined_2.loc[(Combined_2['Drug Regimen'] == "Capomulin")]

Capomulin_data_comb = pd.DataFrame(Capomulin_data_avg.groupby(["Mouse ID", "Weigh
Capomulin_data_comb = Capomulin_data_comb.reset_index()
# Capomulin_data_comb
plt.scatter(Capomulin_data_comb['Weight (g)'], Capomulin_data_comb['Tumor Volume
            edgecolors="black", s=Capomulin_data_comb['Weight (g)'], alpha=0.75)

plt.title("Average Tumor volume vs Mouse Weight")
plt.xlabel("Mouse Weight")
plt.ylabel("Average Tumor Volume")
plt.show()
```



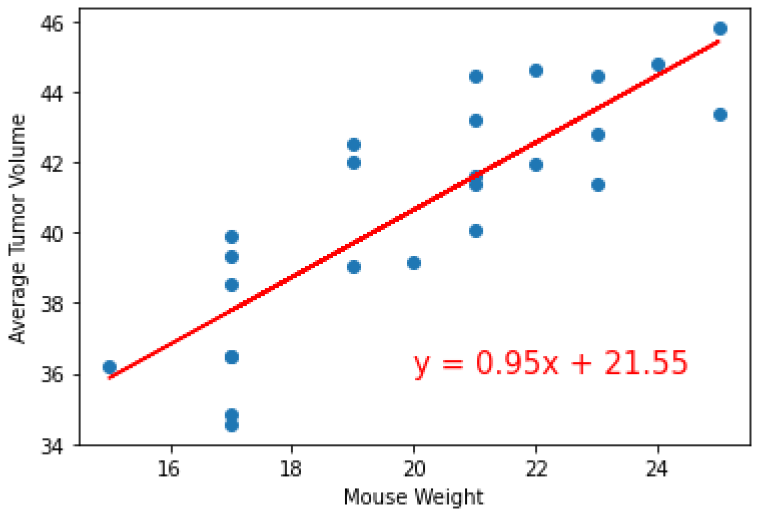
## Correlation and Regression

In [18]:
```
# Calculate the correlation coefficient and linear regression model
# for mouse weight and average tumor volume for the Capomulin regimen
correlation_coeff = st.pearsonr(Capomulin_data_comb['Tumor Volume (mm3)'], Capomu
print(f"The correlation between both factors is {round(correlation_coeff[0],2)}"
```

```
The correlation between both factors is 0.84
```

In [19]:
```
x_values = Capomulin_data_comb['Weight (g)']
y_values = Capomulin_data_comb['Tumor Volume (mm3)']

(slope, intercept, rvalue, pvalue, stderr) = linregress(x_values, y_values)
regress_values = x_values * slope + intercept
line_eq = "y = " + str(round(slope,2)) + "x + " + str(round(intercept,2))

plt.scatter(x_values,y_values)
plt.plot(x_values,regress_values,"r-")
plt.annotate(line_eq,(20,36),fontsize=15,color="red")
plt.xlabel('Mouse Weight')
plt.ylabel('Average Tumor Volume')
print(f"The r-squared is: {rvalue**2}")
plt.show()
```

```
The r-squared is: 0.7088568047708717
```


y = 0.95x + 21.55
Average Tumor Volume
Mouse Weight