

In [166]:

```
#Dependencies and Setup
%matplotlib inline
import matplotlib.pyplot as plt
import pandas as pd
import numpy as np

#Hide warning messages in notebook
import warnings
warnings.filterwarnings('ignore')

#File to Load (Remember to Change These)
mouse_drug_data_load = "data/mouse_drug_data.csv"
clinical_trial_data_load = "data/clinicaltrial_data.csv"

#Read the Mouse and Drug Data and the Clinical Trial Data
mouse_drug=pd.read_csv(mouse_drug_data_load)
clinical_trial_data=pd.read_csv(clinical_trial_data_load)

#Combine the data into a single dataset
complete_clinical_data=pd.merge(mouse_drug, clinical_trial_data, how="left", on=["Mouse ID"])

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

Out[166]:

	Mouse ID	Drug	Timepoint	Tumor Volume (mm3)	Metastatic Sites
0	f234	Stelasyn	0	45.000000	0
1	f234	Stelasyn	5	47.313491	0
2	f234	Stelasyn	10	47.904324	0
3	f234	Stelasyn	15	48.735197	1
4	f234	Stelasyn	20	51.112713	2

Tumor Response to Treatment

In [167]:

```
#Make a copy of the original complete data set for manipulation
complete_clinical_copy=complete_clinical_data.copy()

#Use 'Drug','Timepoint', and 'Tumor Volume (mm3)' columns for analysis
tumor_data_df= complete_clinical_copy[['Drug', 'Timepoint','Tumor Volume (mm3)']]

#Preview DataFrame
#tumor_data_df

#Use Groupby Function (Drug and Timepoint) to find mean of Tumor Volume(mm3) + convert to DataFrame
tumor_vol_mean=pd.DataFrame(tumor_data_df.groupby(['Drug', 'Timepoint'])['Tumor Volume (mm3)'].mean())

#Preview DataFrame
#tumor_vol_mean

#Clean data by using the Pivot Table function [Index = timepoint, column = Drug, values = Tumor Volume (mm3)]
tumor_vol_mean_clean=tumor_vol_mean.pivot_table(index='Timepoint',columns='Drug',values='Tumor Volume (mm3)')

#Preview DataFrame
tumor_vol_mean_clean
```

Out[167]:

	Drug	Capomulin	Ceftamin	Infubinol	Ketapril	Naftisol	Placebo	Propriva	Ramicane	Stelasyn	Zoniferol
Timepoint											
0		45.000000	45.000000	45.000000	45.000000	45.000000	45.000000	45.000000	45.000000	45.000000	45.000000
5		44.266086	46.503051	47.062001	47.389175	46.796098	47.125589	47.248967	43.944859	47.527452	46.851818
10		43.084291	48.285125	49.403909	49.582269	48.694210	49.423329	49.101541	42.531957	49.463844	48.689881
15		42.064317	50.094055	51.296397	52.399974	50.933018	51.359742	51.067318	41.495061	51.529409	50.779059
20		40.716325	52.157049	53.197691	54.920935	53.644087	54.364417	53.346737	40.238325	54.067395	53.170334
25		39.939528	54.287674	55.715252	57.678982	56.731968	57.482574	55.504138	38.974300	56.166123	55.432935
30		38.769339	56.769517	58.299397	60.994507	59.559509	59.809063	58.196374	38.703137	59.826738	57.713531
35		37.816839	58.827548	60.742461	63.371686	62.685087	62.420615	60.350199	37.451996	62.440699	60.089372
40		36.958001	61.467895	63.162824	66.068580	65.600754	65.052675	63.045537	36.574081	65.356386	62.916692
45		36.236114	64.132421	65.755562	70.662958	69.265506	68.084082	66.258529	34.955595	68.438310	65.960888

In [168]:

```
#Store the Standard Error of Tumor Volumes Grouped by Drug and Timepoint
tumor_data_df["Standard Error of Tumor Volume"] = tumor_data_df['Tumor Volume (mm3)'].sem()
tumor_data_df.reset_index(inplace = True)

#Preview DataFrame
tumor_data_df.head()
```

Out[168]:

	index	Drug	Timepoint	Tumor Volume (mm3)	Standard Error of Tumor Volume
0	0	Stelasyn	0	45.000000	0.203161
1	1	Stelasyn	5	47.313491	0.203161
2	2	Stelasyn	10	47.904324	0.203161
3	3	Stelasyn	15	48.735197	0.203161
4	4	Stelasyn	20	51.112713	0.203161

In [169]:

```
#Create a pivot table with the Standard Error of Total Volume with Timepoint and Drug Name then print for preview
tumor_error_pivot = tumor_data_df.pivot_table(index='Timepoint',columns='Drug',values='Standard Error of Tumor Volume')
tumor_error_pivot.head()
```

Out[169]:

	Drug	Capomulin	Ceftamin	Infubinol	Ketapril	Naftisol	Placebo	Propriva	Ramicane	Stelasyn	Zoniferol
Timepoint											
0		0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161
5		0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161
10		0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161
15		0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161
20		0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161	0.203161

In [234]:

```
#Generate the Plot (with Error Bars)
plt.errorbar(tumor_vol_mean_clean.index, tumor_vol_mean_clean["Capomulin"], yerr=tumor_error_pivot["Capomulin"],
             color='red', marker='o', markersize=5, linestyle='-', linewidth=0.5,label="Copumulin")

plt.errorbar(tumor_vol_mean_clean.index, tumor_vol_mean_clean["Infubinol"], yerr=tumor_error_pivot["Infubinol"],
```

```

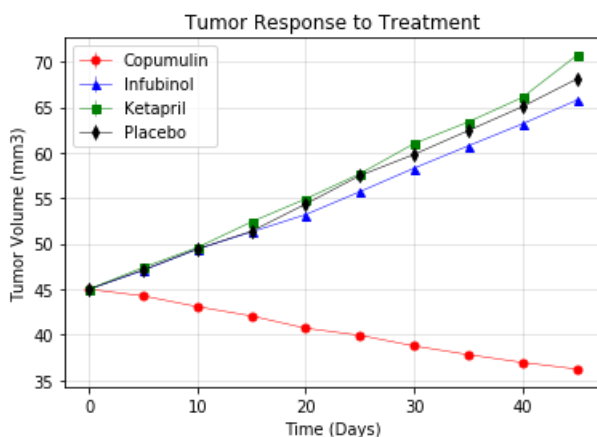
        color='blue', marker='^', markersize=5, linestyle='--', linewidth=0.5,
label="Infubinol")

plt.errorbar(tumor_vol_mean_clean.index, tumor_vol_mean_clean["Ketapril"], yerr=tumor_error_pivot[
"Ketapril"],
        color='green', marker='s', markersize=5, linestyle='--', linewidth=0.5,
label="Ketapril")

plt.errorbar(tumor_vol_mean_clean.index, tumor_vol_mean_clean["Placebo"], yerr=tumor_error_pivot["
Placebo"],
        color='black', marker='d', markersize=5, linestyle='--', linewidth=0.5, label=
"Placebo")

x_lim = len(tumor_vol_mean_clean.index)
#Add the Chart Title - "Tumor Response to Treatment"
plt.title("Tumor Response to Treatment")
#Add the x-label - "Time (Days)"
plt.xlabel("Time (Days)")
# Add the y-label - "Tumor Volume (mm3)"
plt.ylabel("Tumor Volume (mm3)")
#Add the legend to best location (upper left)
plt.legend(loc="best")
#Add grid lines to plot
plt.grid(b=True, which='major', color='#666666', linestyle='--', alpha=0.2)
#Save Graph
plt.savefig("../Images/TumorResponse.png")
#Show the Figure
plt.show()

```



Metastatic Response to Treatment

In [172]:

```

#Make a copy of the original complete data set for manipulation
complete_clinical_copy2=complete_clinical_data.copy()

#Use 'Drug', 'Timepoint', and 'Metastatic Sites' columns for analysis
meta_data_df= complete_clinical_copy[['Drug', 'Timepoint', 'Metastatic Sites']]

#Preview DataFrame
#meta_data_df

#Use Groupby Function (Drug and Timepoint) to find mean Metastatic Sites + convert to DataFrame
meta_site_mean=pd.DataFrame(meta_data_df.groupby(['Drug', 'Timepoint'])['Metastatic Sites'].mean()
)

#Preview DataFrame
#meta_site_mean

#Clean data by using the Pivot Table function [Index = timepoint, column = Drug, values = Metastat
ic Sites]
meta_site_mean_clean=meta_site_mean.pivot_table(index='Timepoint',columns='Drug',values='Metastatic
Sites')

#Preview DataFrame
meta_site_mean_clean

```

Out[172]:

	Drug	Capomulin	Ceftamin	Infubinol	Ketapril	Naftisol	Placebo	Propriva	Ramicane	Stelasyn	Zoniferol
Timepoint											
0		0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000	0.000000
5		0.160000	0.380952	0.280000	0.304348	0.260870	0.375000	0.320000	0.120000	0.240000	0.166667
10		0.320000	0.600000	0.666667	0.590909	0.523810	0.833333	0.565217	0.250000	0.478261	0.500000
15		0.375000	0.789474	0.904762	0.842105	0.857143	1.250000	0.764706	0.333333	0.782609	0.809524
20		0.652174	1.111111	1.050000	1.210526	1.150000	1.526316	1.000000	0.347826	0.952381	1.294118
25		0.818182	1.500000	1.277778	1.631579	1.500000	1.941176	1.357143	0.652174	1.157895	1.687500
30		1.090909	1.937500	1.588235	2.055556	2.066667	2.266667	1.615385	0.782609	1.388889	1.933333
35		1.181818	2.071429	1.666667	2.294118	2.266667	2.642857	2.300000	0.952381	1.562500	2.285714
40		1.380952	2.357143	2.100000	2.733333	2.466667	3.166667	2.777778	1.100000	1.583333	2.785714
45		1.476190	2.692308	2.111111	3.363636	2.538462	3.272727	2.571429	1.250000	1.727273	3.071429

In [173]:

```
#Store the Standard Error of Tumor Volumes Grouped by Drug and Timepoint
meta_data_df["Standard Error of Metastatic Sites"] = meta_data_df['Metastatic Sites'].sem()
meta_data_df.reset_index(inplace = True)

#Preview DataFrame
meta_data_df.head()
```

Out[173]:

	index	Drug	Timepoint	Metastatic Sites	Standard Error of Metastatic Sites
0	0	Stelasyn	0	0	0.02602
1	1	Stelasyn	5	0	0.02602
2	2	Stelasyn	10	0	0.02602
3	3	Stelasyn	15	1	0.02602
4	4	Stelasyn	20	2	0.02602

In [174]:

```
#Create a pivot table with the Standard Error of Metastatic Sites with Timepoint and Drug Name the n print for preview
meta_error_pivot = meta_data_df.pivot_table(index='Timepoint',columns='Drug',values='Standard Error of Metastatic Sites')
meta_error_pivot.head()
```

Out[174]:

	Drug	Capomulin	Ceftamin	Infubinol	Ketapril	Naftisol	Placebo	Propriva	Ramicane	Stelasyn	Zoniferol
Timepoint											
0		0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602
5		0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602
10		0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602
15		0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602
20		0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602	0.02602

In [233]:

```
#Generate the Plot (with Error Bars)
plt.errorbar(meta_site_mean_clean.index, meta_site_mean_clean["Capomulin"], yerr=meta_error_pivot["Capomulin"],
             color='red', marker='o', markersize=5, linestyle='-', linewidth=0.5, label="Capomulin")
```

```

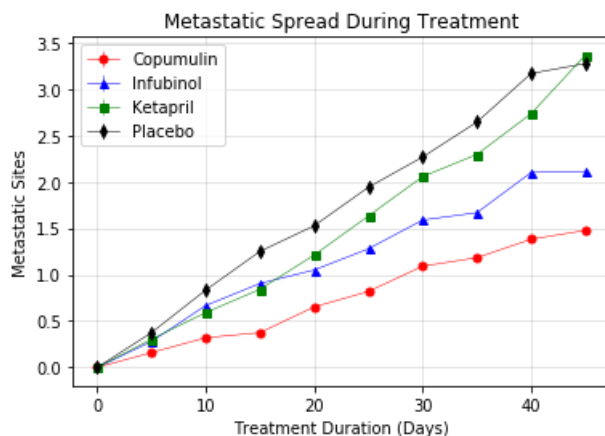
color='red', marker='o', markersize=5, linestyle='-', linewidth=0.5, label='Copumulin',
plt.errorbar(meta_site_mean_clean.index, meta_site_mean_clean["Infubinol"], yerr=meta_error_pivot[
"Infubinol"],
            color='blue', marker='^', markersize=5, linestyle='-', linewidth=0.5,
            label="Infubinol")

plt.errorbar(meta_site_mean_clean.index, meta_site_mean_clean["Ketapril"], yerr=meta_error_pivot["P
Ketapril"],
            color='green', marker='s', markersize=5, linestyle='-', linewidth=0.5,
            label="Ketapril")

plt.errorbar(meta_site_mean_clean.index, meta_site_mean_clean["Placebo"], yerr=meta_error_pivot["P
lacebo"],
            color='black', marker='d', markersize=5, linestyle='-', linewidth=0.5, label=
"Placebo")

x_lim = len(meta_site_mean_clean.index)
#Add the Chart Title - "Metastatic Spread During Treatment"
plt.title("Metastatic Spread During Treatment")
#Add the x-label - "Treatment Duration (Days)"
plt.xlabel("Treatment Duration (Days)")
# Add the y-label - "Metastatic Sites"
plt.ylabel("Metastatic Sites")
#Add the legend to best location (upper left)
plt.legend(loc="best")
#Add grid lines to plot
plt.grid(b=True, which='major', color='#666666', linestyle='-', alpha=0.2)
#Save Graph
plt.savefig("../Images/MetastaticSpread.png")
#Show the Figure
plt.show()

```



Survival Rates

In [177]:

```

#Make a copy of the original complete data set for manipulation
complete_clinical_copy3=complete_clinical_data.copy()

#Use 'Drug', 'Timepoint', and 'Mouse ID' columns for analysis
mouse_survival_df= complete_clinical_copy3[['Drug', 'Timepoint', 'Mouse ID']]

#Preview DataFrame
mouse_survival_df.head()

```

Out[177]:

	Drug	Timepoint	Mouse ID
0	Stelasyt	0	f234
1	Stelasyt	5	f234
2	Stelasyt	10	f234
3	Stelasyt	15	f234

In [178]:

```
#Use Groupby Function (Drug and Timepoint) to find count of Mouse IDs + convert to DataFrame
mouse_survival_count=pd.DataFrame(mouse_survival_df.groupby(['Drug', 'Timepoint'])['Mouse ID'].count())

#Preview DataFrame
mouse_survival_count

#Clean data by using the Pivot Table function [Index = timepoint, column = Drug, values = Metastatic Sites]
mouse_survival_count_clean=mouse_survival_count.pivot_table(index='Timepoint',columns='Drug',values='Mouse ID')

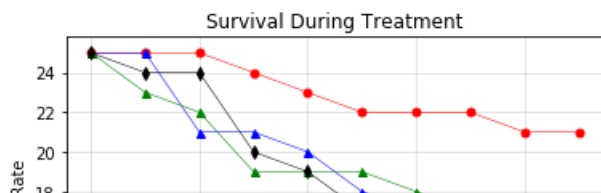
#Preview DataFrame
mouse_survival_count_clean
```

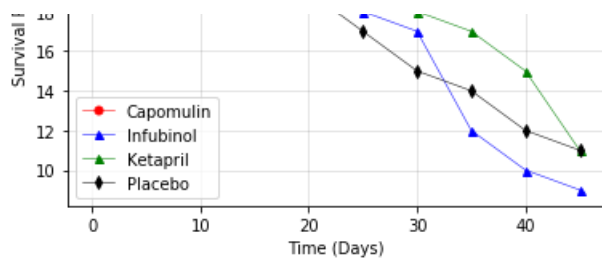
Out[178]:

Drug	Capomulin	Ceftamin	Infubinol	Ketapril	Naftisol	Placebo	Propriva	Ramicane	Stelasyf	Zoniferol
Timepoint										
0	25	25	25	25	25	25	26	25	26	25
5	25	21	25	23	23	24	25	25	25	24
10	25	20	21	22	21	24	23	24	23	22
15	24	19	21	19	21	20	17	24	23	21
20	23	18	20	19	20	19	17	23	21	17
25	22	18	18	19	18	17	14	23	19	16
30	22	16	17	18	15	15	13	23	18	15
35	22	14	12	17	15	14	10	21	16	14
40	21	14	10	15	15	12	9	20	12	14
45	21	13	9	11	13	11	7	20	11	14

In [232]:

```
#Generate the Plot
plt.errorbar(mouse_survival_count_clean.index, mouse_survival_count_clean["Capomulin"],
             color='red',marker='o',markersize=5,linestyle='-',linewidth=0.5,label="Capomulin")
plt.errorbar(mouse_survival_count_clean.index, mouse_survival_count_clean["Infubinol"],
             color='blue',marker='^',markersize=5,linestyle='-',linewidth=0.5,label="Infubinol")
plt.errorbar(mouse_survival_count_clean.index, mouse_survival_count_clean["Ketapril"],
             color='green',marker='^',markersize=5,linestyle='-',linewidth=0.5,label="Ketapril")
plt.errorbar(mouse_survival_count_clean.index, mouse_survival_count_clean["Placebo"],
             color='black',marker='d',markersize=5,linestyle='-',linewidth=0.5, label="Placebo")
#Add the Chart Title - "Survival During Treatment"
plt.title("Survival During Treatment")
#Add the x-label - "Time (Days)"
plt.xlabel("Time (Days)")
#Add the y-label - "Survival Rate"
plt.ylabel("Survival Rate")
#Add the legend to the best location (bottom left)
plt.legend(loc="best")
#Add grid lines to plot
plt.grid(b=True, which='major', color='#666666', linestyle='-', alpha=0.2)
#Save Graph
plt.savefig("../Images/SurvialRates.png")
#Show the Figure
plt.show()
```





Summary Bar Graph

In [195]:

```
#To calculate the total change in Tumor Volume, subtract the final tumor volume from the initial t
umor volume then divide by the initial tumor volume
#We want a percentage so we multiply that value by 100
#Print to confirm
tumor_change_percentage=((tumor_vol_mean_clean.iloc[-1]-tumor_vol_mean_clean.iloc[0])/tumor_vol_me
n_clean.iloc[0]) * 100
tumor_change_percentage
```

Out[195]:

```
Drug
Capomulin    -19.475303
Ceftamin      42.516492
Infubinol     46.123472
Ketapril      57.028795
Naftisol      53.923347
Placebo       51.297960
Propriva      47.241175
Ramicane     -22.320900
Stelasyn     52.085134
Zoniferol     46.579751
dtype: float64
```

In [200]:

```
drug=['Capomulin','Ceftamin','Infubinol','Ketapril','Naftisol','Placebo','Propriva','Ramicane','Ste
lasyn','Zoniferol']
change=[-19.475303,42.516492,46.123472,57.028795,53.923347,51.297960,47.241175,-22.320900,52.085134
,46.579751]
#Function to determine number of items in the array
x_axis=np.arange(len(change))
x_axis
```

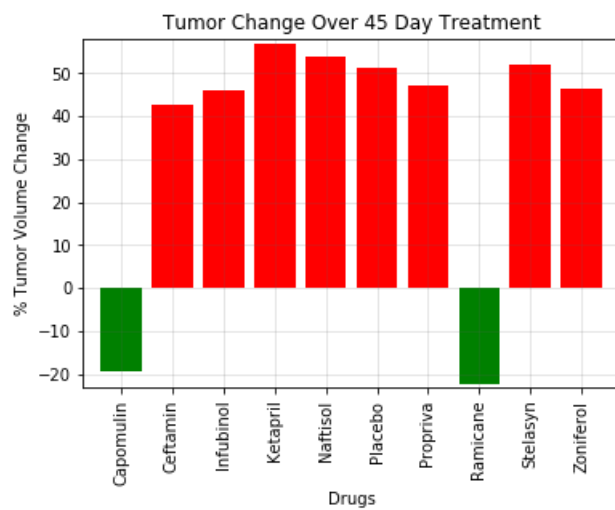
Out[200]:

```
array([0, 1, 2, 3, 4, 5, 6, 7, 8, 9])
```

In [230]:

```
#Plot bar graph with green values showing decrease in % Tumor Volume Change
#Red values indicate increase in % Tumor Volume Change
#Align in center
plt.bar(drug,change,color=['green','red','red','red','red','red','red','red','green','red','red'],align="
center")
#x-labels vertical for cleaner formatting
plt.xticks(drug, rotation='vertical')
#Add Title: "Tumor Change Over 45 Day Treatment"
plt.title("Tumor Change Over 45 Day Treatment")
#Add label to x-axis: "Drugs"
plt.xlabel("Drugs")
#Add label to y-axis: "% Tumor Volume Change"
plt.ylabel("% Tumor Volume Change")
#Add grid lines to plot
plt.grid(b=True, which='major', color='#666666', linestyle='--', alpha=0.2)
#Set the limits of the x-axis
plt.xlim(-0.75, len(x_axis)-0.25)
#Set the limits of the y-axis
plt.ylim(min(change)-1, max(change)+1)
```

```
plt.tight_layout()
#Save Bar Graph
plt.savefig("../Images/TumorChangeBar.png")
#Show Bar Graph
plt.show()
```



In []:

```
#Observations:
#1. Capomulin and Ramicane significantly lowered the growth and spread of tumors in the mouse subjects
#2. Stelasyn, Naftisol, Infubinol, and Ketapril were not good treatments for tumors in mice, as they performed equal or worse than the placebo group
#3. Infubinol showed the worst survival rate among tumorous mice, with a steep drop off after 30 days
```