

Observations and Insights

```
In [ ]: #1.Percentages of male and female mice used for the study are almost same.
#2.Tumor volume decreases significantly with time for mice treated with capomulin
#3.there is a positive correlation between mouse weight and average tumor volume
#4.Final Tumor Volume for Capomulin and Ramincane regimens are lower than Infubinol and Ceffamin regimens.
```

```
In [1]: # Dependencies and Setup
import matplotlib.pyplot as plt
import pandas as pd
import scipy.stats as sts
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 dataframe
combined_df=pd.merge(mouse_metadata,study_results,ons="Mouse ID",how="outer")
# Display the data table for preview
combined_df.head()
```

```
Out[1]:
```

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	Tumor Volume (mm3)	Metastatic Sites
0	k403	Ramincane	Male	21	16	0	45.000000	0
1	k403	Ramincane	Male	21	16	5	38.825898	0
2	k403	Ramincane	Male	21	16	10	35.014271	1
3	k403	Ramincane	Male	21	16	15	34.223992	1
4	k403	Ramincane	Male	21	16	20	32.997729	1

```
In [2]: # Checking the number of mice.
combined_df[["Mouse ID"]].nunique()
```

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

```
In [3]: # Getting the duplicate mice by ID number that shows up for Mouse ID and Timepoint.
duplicate_df=combined_df[combined_df.duplicated(subset=["Mouse ID","Timepoint"],keep=False)]
duplicated_mouse_ID=duplicate_df["Mouse ID"].unique()
duplicated_mouse_ID
```

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

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

```
Out[4]:
```

	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
909	g989	Propriva	Female	21	26	0	45.000000	0
910	g989	Propriva	Female	21	26	5	48.766801	0
911	g989	Propriva	Female	21	26	5	47.570392	0
912	g989	Propriva	Female	21	26	10	51.745156	0

```
In [5]: # Create a clean DataFrame by dropping the duplicate mouse by its ID.
combined_df=combined_df.drop_duplicates(subset=["Mouse ID","Timepoint"],keep="last").reset_index(drop=True)
combined_df.head()
```

```
Out[5]:
```

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	Tumor Volume (mm3)	Metastatic Sites
0	k403	Ramincane	Male	21	16	0	45.000000	0
1	k403	Ramincane	Male	21	16	5	38.825898	0
2	k403	Ramincane	Male	21	16	10	35.014271	1
3	k403	Ramincane	Male	21	16	15	34.223992	1
4	k403	Ramincane	Male	21	16	20	32.997729	1

```
In [6]: # Checking the number of mice in the clean DataFrame.
combined_df[["Mouse ID"]].nunique()
```

```
Out[6]: 249
```

Summary Statistics

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

```
# Use groupby and summary statistical methods to calculate the following properties of each drug regimen:
regimen_group=combined_df.groupby("Drug Regimen")

# mean, median, variance, standard deviation, and SEM of the tumor volume.
mean_tumor_volume=regimen_group["Tumor Volume (mm3)"].mean()
mean_tumor_volume.rename("Mean",inplace=True)
median_tumor_volume=regimen_group["Tumor Volume (mm3)"].median()
median_tumor_volume.rename("Median",inplace=True)
variance_tumor_volume=regimen_group["Tumor Volume (mm3)"].var()
variance_tumor_volume.rename("Variance",inplace=True)
sdv_tumor_volume=regimen_group["Tumor Volume (mm3)"].std()
sdv_tumor_volume.rename("Standard Deviation",inplace=True)

sem_tumor_volume=regimen_group["Tumor Volume (mm3)"].sem()
sem_tumor_volume.rename("SEM",inplace=True)

# Assemble the resulting series into a single summary dataframe.
tumor_df=pd.concat([mean_tumor_volume,median_tumor_volume,variance_tumor_volume,svd_tumor_volume,sem_tumor_volume],axis=1)
tumor_df.head()
```

```
Out[7]:
```

	Mean	Median	Variance	Standard Deviation	SEM
Drug Regimen					
Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
Ceffamin	52.591172	51.776157	39.290177	6.268188	0.469821
Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
Ketapril	55.235638	53.686743	68.553577	8.279709	0.603860
Nafitsol	54.331565	52.509285	66.173479	8.134708	0.596466

```
In [8]: # Generate a summary statistics table of mean, median, variance, standard deviation, and SEM of the tumor volume for each regimen
```

```
# Using the aggregation method, produce the same summary statistics in a single line
combined_df.groupby("Drug Regimen").agg(["Tumor Volume (mm3)":["mean","median","var","std","sem"]])
```

```
Out[8]:
```

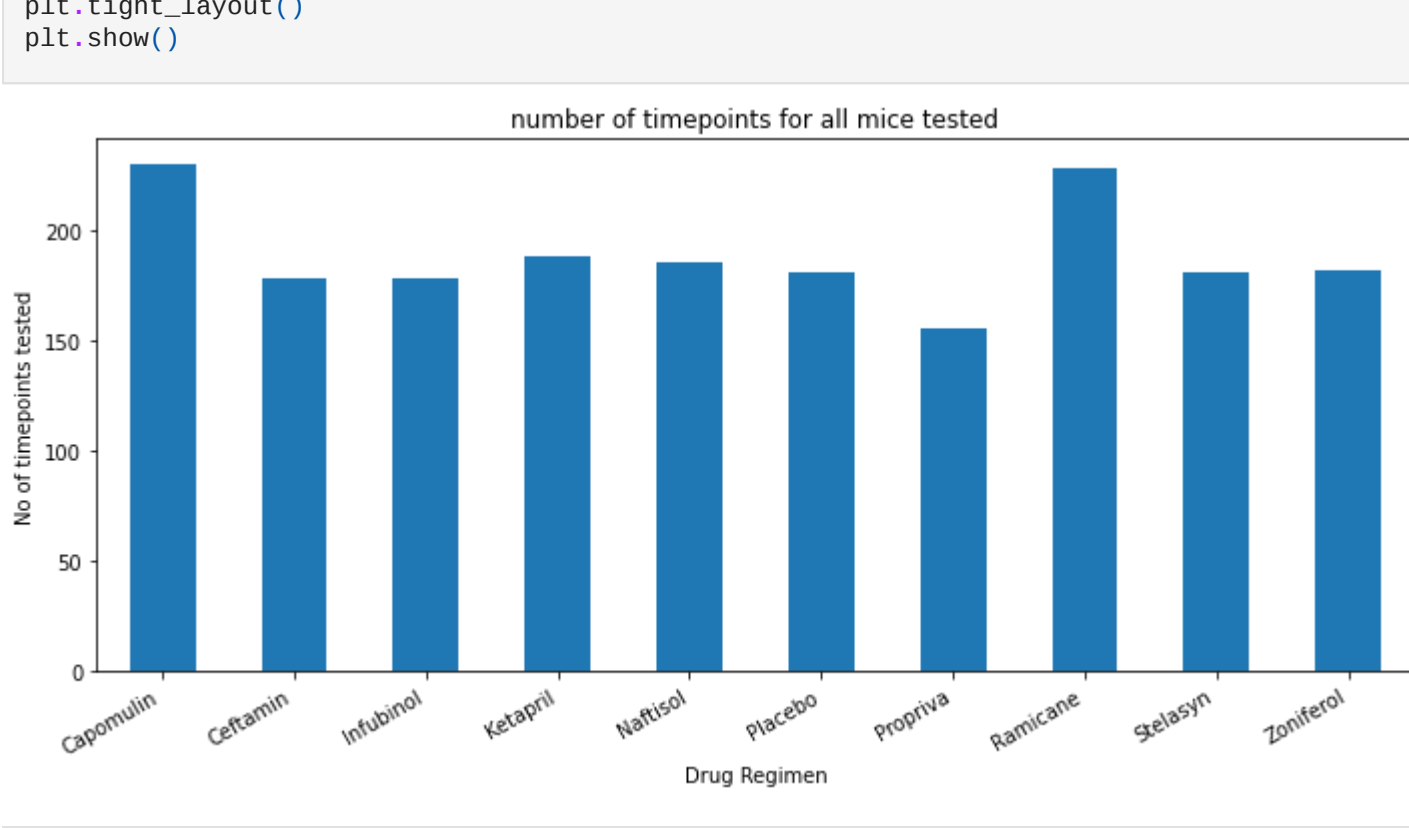
						Tumor Volume (mm3)					
						mean	median	var	std	sem	
						Drug Regimen					
						Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
						Ceffamin	52.591172	51.776157	39.290177	6.268188	0.469821
						Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
						Ketapril	55.235638	53.686743	68.553577	8.279709	0.603860
						Nafitsol	54.331565	52.509285	66.173479	8.134708	0.596466
						Placebo	54.033581	52.288934	61.368083	7.821003	0.581331
						Propriva	52.382993	50.783528	43.220205	6.574208	0.526358
						Ramincane	40.216745	40.673236	23.486704	4.846308	0.320955
						Stelasyln	54.233149	52.431737	59.455052	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 timepoints for all mice tested for each drug regimen using Pandas.
bar_data=regimen_group["Timepoint"].count()
bar_data
```

```
Out[9]: Drug Regimen
Capomulin    230
Ceffamin     178
Infubinol    178
Ketapril     188
Nafitsol     186
Placebo      181
Propriva     156
Ramincane    229
Stelasyln    181
Zoniferol    182
Name: Timepoint, dtype: int64
```

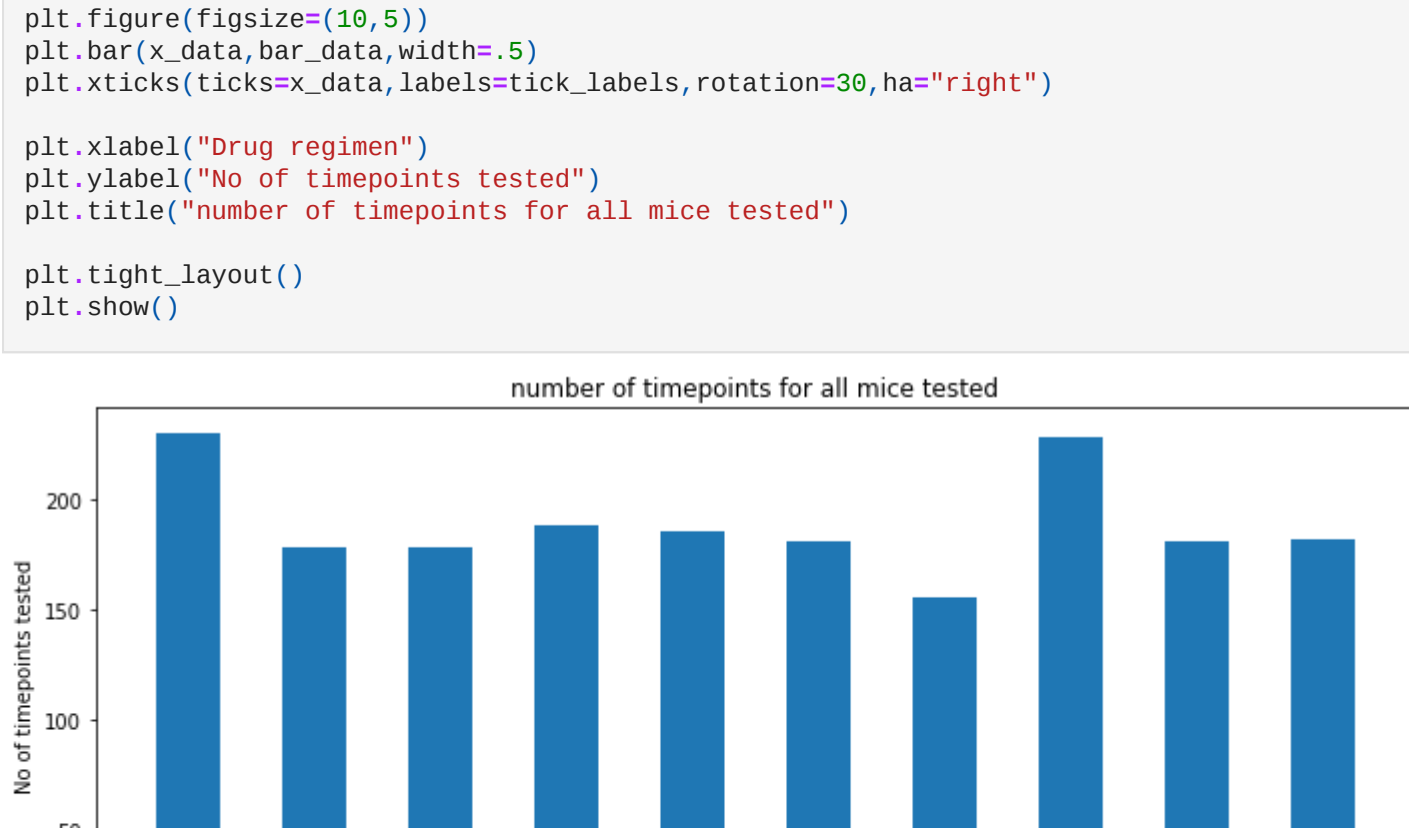
```
In [10]: bar=plt.bar_data.plot(kind="bar",figsize=(10,5),width=.5)
bar=plt.set_ylabel("No of timepoints tested")
bar=plt.set_title("number of timepoints for all mice tested")
plt.xticks(rotation=30,ha="right")
plt.tight_layout()
plt.show()
```



```
In [11]: # Generate a bar plot showing the total number of timepoints for all mice tested for each drug regimen using pyplot.
x_data=np.arange(len(bar_data))
tick_labels=bar_data.keys()

plt.figure(figsize=(10,5))
plt.bar(x_data,bar_data,width=.5)
plt.xticks(ticks=x_data,labels=tick_labels,rotation=30,ha="right")

plt.xlabel("Drug Regimen")
plt.ylabel("No of timepoints tested")
plt.title("number of timepoints for all mice tested")
plt.tight_layout()
plt.show()
```

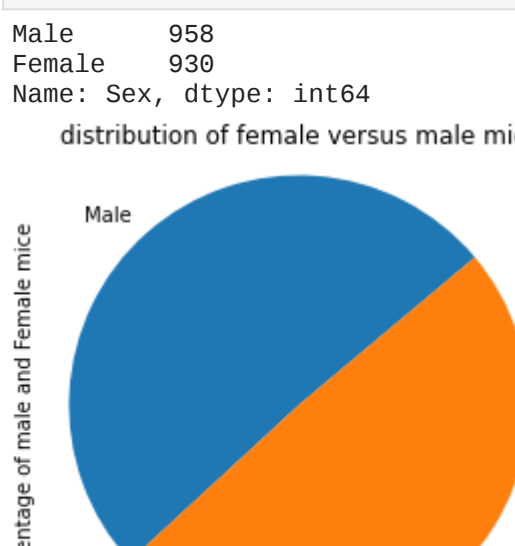


```
In [64]: # Generate a pie plot showing the distribution of female versus male mice using Pandas
gender_count=combined_df["Sex"].value_counts()
print(gender_count)
```

```
pie=plt.gender_count.plot(kind="pie",startangle=40,figsize=(4,4))
pie=plt.set_ylabel("Percentage of male and female mice")
pie=plt.set_title("distribution of female versus male mice")
```

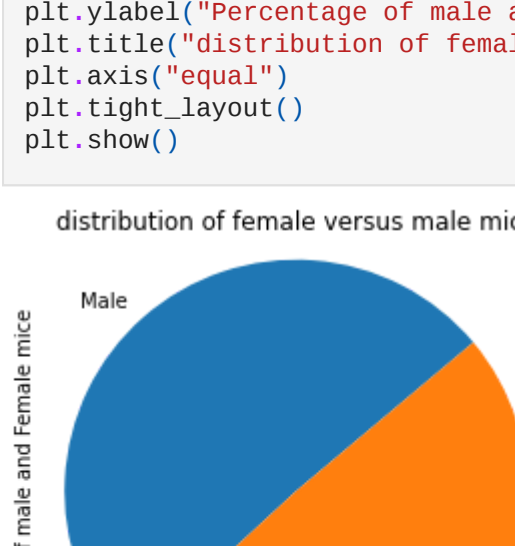
```
plt.tight_layout()
plt.axis("equal")
plt.show()
```

```
Male      958
Female    930
Name: Sex, dtype: int64
distribution of female versus male mice
```



```
In [13]: # Generate a pie plot showing the distribution of female versus male mice using pyplot
label=gender_count.keys()
plt.figure(figsize=(4,4))
plt.pie(gender_count,labels=label,startangle=40)
plt.ylabel("Percentage of male and female mice")
plt.title("distribution of female versus male mice")
plt.axis("equal")
plt.tight_layout()
plt.show()
```

```
distribution of female versus male mice
```



Quartiles, Outliers and Boxplots

```
In [78]: # Calculate the final tumor volume of each mouse across four of the treatment regimens:
# Capomulin, Ramincane, Infubinol, and Ceffamin
# Start by getting the last (greatest) Timepoint for each mouse
```

```
tumor_vol_df=combined_df[["Mouse ID","Timepoint","Tumor Volume (mm3)"]]
tumor_vol_df.sort_values(by=["Mouse ID","Timepoint"],reset_index(drop=True))
final_tumor_vol_df=tumor_vol_df.drop_duplicates(subset=["Mouse ID"],keep="last")

# Merge this group df with the original dataframe to get the tumor volume at the last Timepoint
merged_df=pd.merge(combined_df,final_tumor_vol_df,ons=["Mouse ID","Timepoint"])
merged_df.drop(["Tumor Volume (mm3)","y",axis=1,inplace=True)
merged_df.rename(columns={"Tumor Volume (mm3)","x":"final tumor volume"},inplace=True)

treatments=["Capomulin", "Ramincane", "Infubinol","Ceffamin"]
tumor_data=merged_df.groupby("Drug Regimen").isin(treatments)]
tumor_data=tumor_data.sort_values(by="Drug Regimen")

tumor_data
```

```
Out[78]:
```

	Mouse ID	Drug Regimen	Sex	Age_months	Weight (g)	Timepoint	final tumor volume	Metastatic Sites
32	j246	Capomulin	Female	21	21	35	38.753265	1
36	v923	Capomulin	Female	19	21	45	40.658124	2
35	w150	Capomulin	Male	23	23	10	39.952347	0
34	j119	Capomulin	Female	7	23	45	38.125164	1
39	i509	Capomulin	Male	17	21	45	41.483008	3
...
46	r921	Ramincane	Female	5	25	30	43.419381	1
47	w678	Ramincane	Female	5	24	5	43.166373	0
48	y449	Ramincane	Male	19	24	15	44.183451	0
23	r811	Ramincane	Male	9	19	45	37.225650	1
0	k403	Ramincane	Male	21	16	45	22.050126	1

100 rows x 8 columns

```
In [79]: # 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
```

```
for treatment in treatments:
    filt=tumor_data["Drug Regimen"]==treatment
    final_tumor_vol_data=tumor_data.loc[filt,"final tumor volume"]

    quartiles=final_tumor_vol_data.quantile([.25,.5,.75])
    upper=quartiles[.75]
    lower=quartiles[.25]
    iqr=upper-lower
    upper_bound=upper+(1.5*iqr)
    lower_bound=lower-(1.5*iqr)

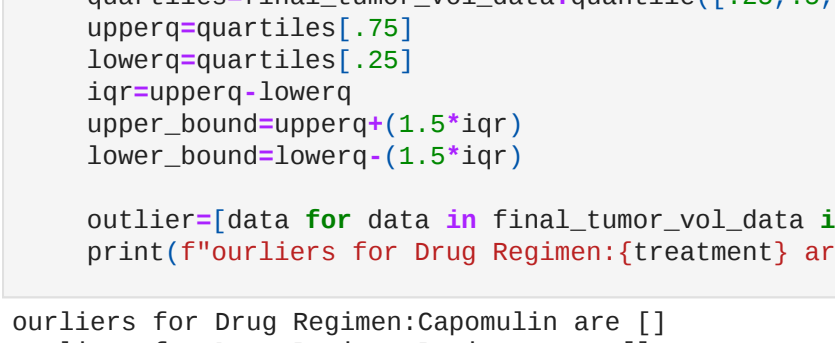
    outlier=[data for data in final_tumor_vol_data if (data>upper_bound)or(data<lower_bound)]
    print(f"outliers for Drug Regimen:{treatment} are {outlier}")

outliers for Drug Regimen:Capomulin are []
outliers for Drug Regimen:Ramincane are []
outliers for Drug Regimen:Infubinol are [36.321345799999996]
outliers for Drug Regimen:Ceffamin are []
```

```
In [80]: # Generate a box plot of the final tumor volume of each mouse across four regimens of interest
treatment_data=tumor_data[["Drug Regimen","final tumor volume"]]

plt.figure(figsize=(10,10))
(treatment_data.boxplot(column="final tumor volume",by="Drug Regimen")
plt.title("Boxplot for final tumor volume for each drug regimen")
plt.ylabel("Final Tumor Volume")
plt.tight_layout()
plt.show())
```

<Figure size 720x720 with 0 Axes>



Line and Scatter Plots

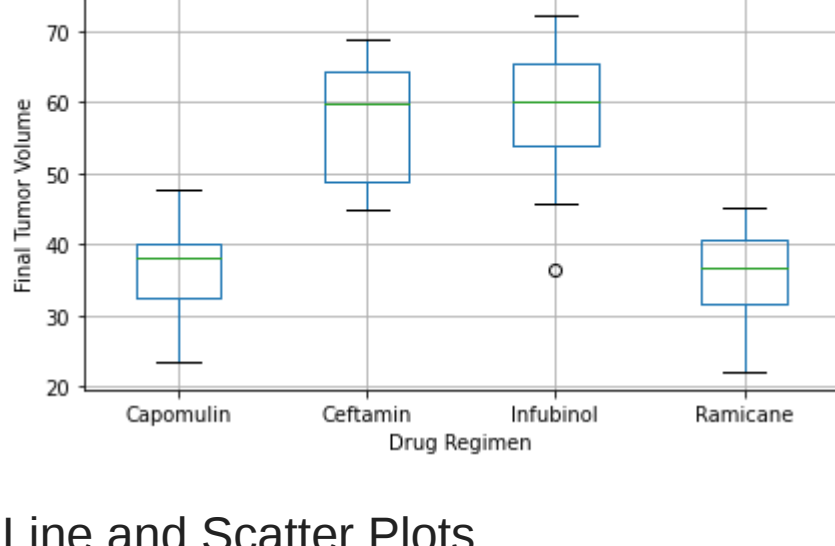
```
In [83]: # Generate a line plot of tumor volume vs. time point for a mouse treated with Capomulin
filt=merged_df["Drug Regimen"]=="Capomulin"
capomulin_mouseId=merged_df.loc[filt,"Mouse ID"]
print(capomulin_mouseId)
```

```
mouse_id="x401"

filt=combined_df["Mouse ID"]==mouse_id
mouse_data=combined_df.loc[filt,:]
```

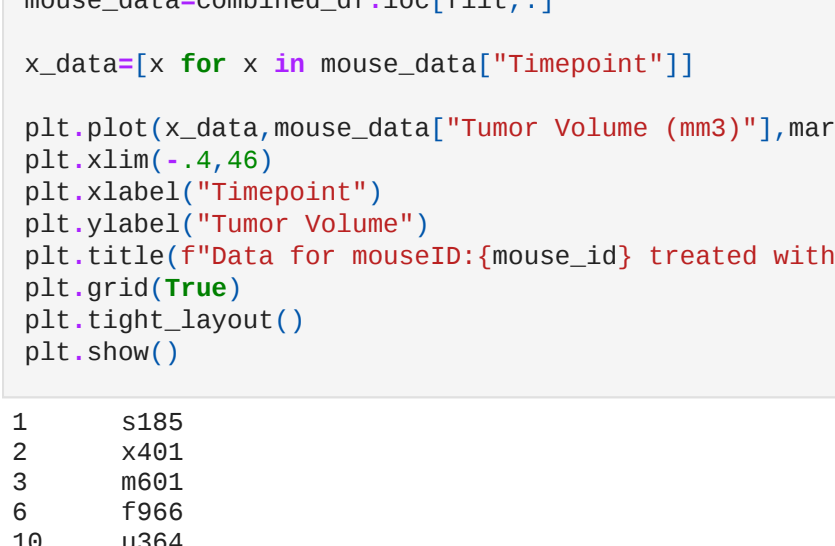
```
x_data=[x for x in mouse_data["Timepoint"]]

plt.plot(x_data,mouse_data["Tumor Volume (mm3)"],marker="o")
plt.xlim(-.4,46)
plt.xlabel("Timepoint")
plt.ylabel("Tumor Volume")
plt.title(f"Data for mouseID:{mouse_id} treated with Capomulin")
plt.grid(True)
plt.tight_layout()
plt.show()
```



```
In [18]: # Generate a scatter plot of average tumor volume vs. mouse weight for the Capomulin regimen
Capomulin_df=regimen_group.get_group("Capomulin")
plt.data=Capomulin_df.groupby("Mouse ID").agg(["Weight (g)":("first","Tumor Volume (mm3)":("mean"))])
```

```
vol_vs_weight_plot=plt.data.plot(kind="scatter",x="Weight (g)",y="Tumor Volume (mm3)",figsize=(6,5),grid=True)
vol_vs_weight_plot.set_title("average tumor volume vs. mouse weight for the Capomulin regimen")
plt.tight_layout()
plt.show()
```



Correlation and Regression

```
In [19]: # Calculate the correlation coefficient and linear regression model
# For mouse weight and average tumor volume for the Capomulin regimen
```

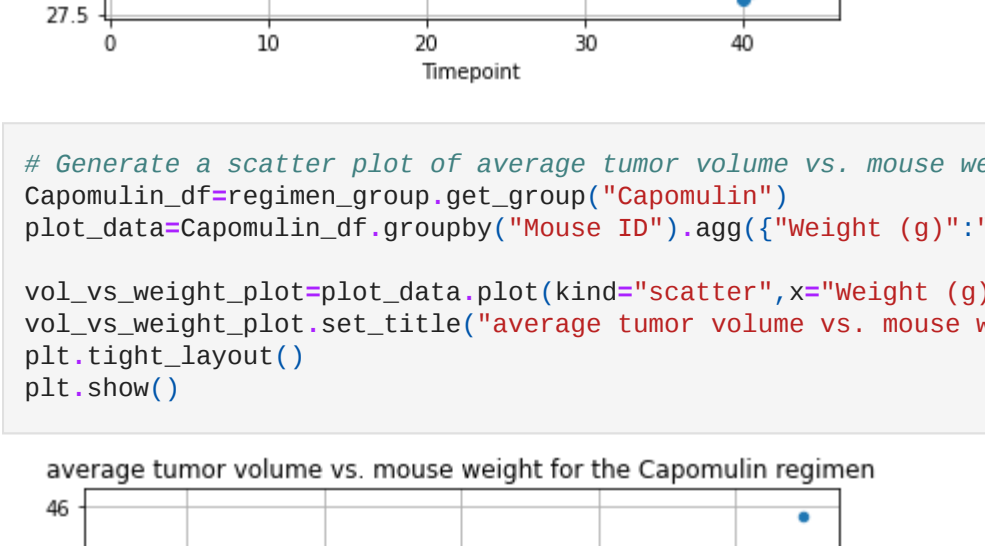
```
corr_coeff=sts.pearsonr(plot_data["Weight (g)"],plot_data["Tumor Volume (mm3)"])
print(f"Correlation coefficient for mouse weight and average tumor volume for the Capomulin regimen is {round(corr_coeff[0],2)}")
```

```
#regression line plot
x_value=plot_data["Weight (g)"]
y_value=plot_data["Tumor Volume (mm3)"]
(slope, intercept, r_value, pvalue, stdev)=sts.linregress(x_value,y_value)
regress_values = slope * x_value + intercept
line_eq="y="+str(round(slope,2))+ "x"+str(round(intercept,2))
```

```
plt.figure(figsize=(7,5))
plt.scatter(x_value,y_value)
plt.plot(x_value,regress_values,"r-")
plt.annotate(line_eq,(20,36),fontsize=20,color="red")
```

```
plt.title("average tumor volume vs. mouse weight for the Capomulin regimen")
plt.xlabel("mouse weight")
plt.ylabel("average tumor volume")
plt.grid(True)
plt.tight_layout()
plt.show()
```

correlation coefficient for mouse weight and average tumor volume for the Capomulin regimen is 0.84



```
In [ ]:
```