

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:
mean, median, variance, standard deviation, and SEM of the tumor volume.
Assemble the resulting series into a single summary dataframe.

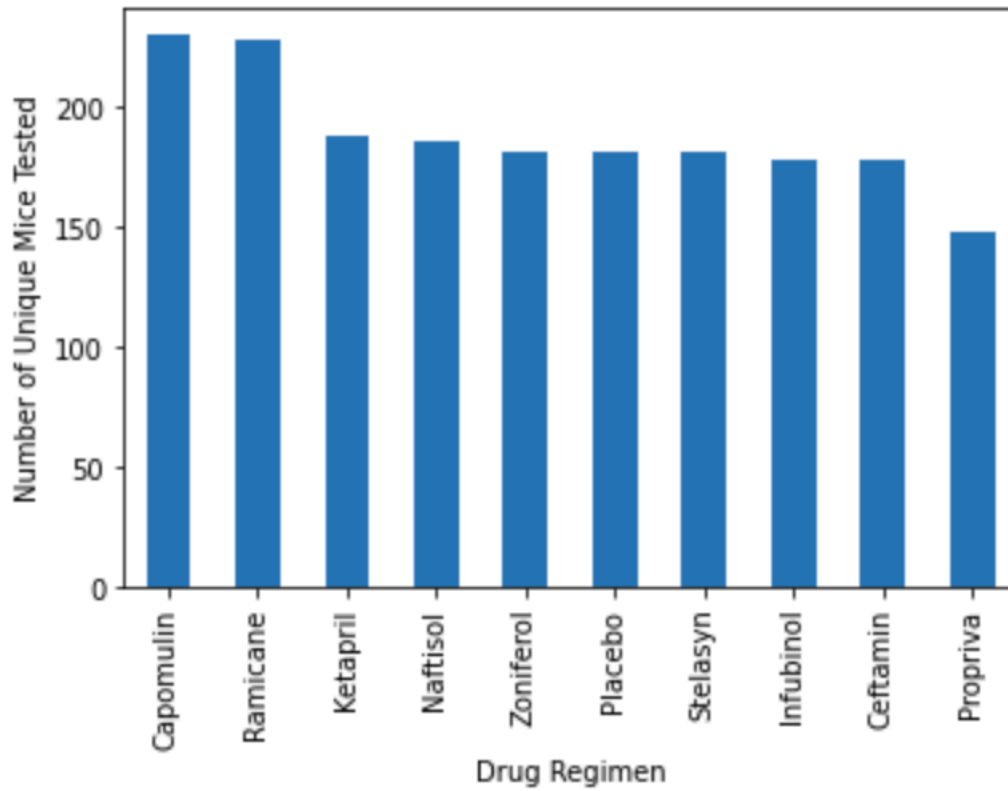
Drug Regimen	Mean Tumor Volume	Median Tumor Volume	Tumor Volume Variance	Tumor Volume Std. Dev.	Tumor Volume Std. Err.
Capomulin	40.675741	41.557809	24.947764	4.994774	0.329346
Ceftamin	52.591172	51.776157	39.290177	6.268188	0.469821
Infubinol	52.884795	51.820584	43.128684	6.567243	0.492236
Ketapril	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

Generate a summary statistics table of mean, median, variance, standard deviation, and SEM of the tumor volume for each regimen

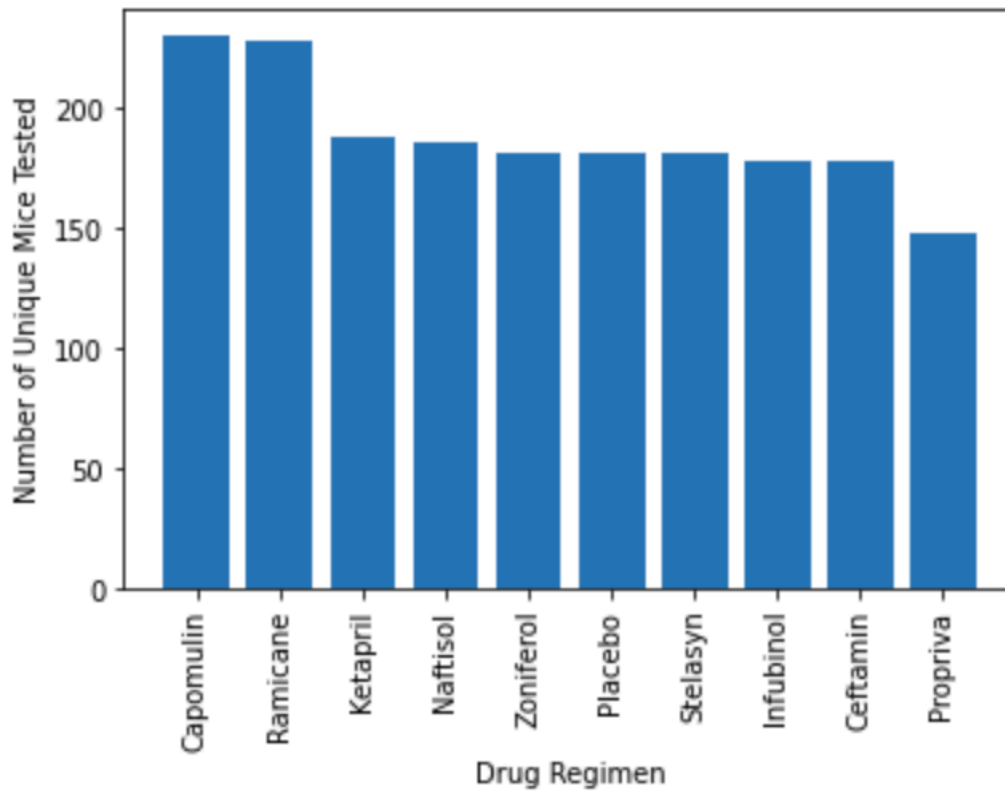
Using the aggregation method, produce the same summary statistics in a single line

Drug Regimen	Tumor Volume (mm3)				
	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	52.320930	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

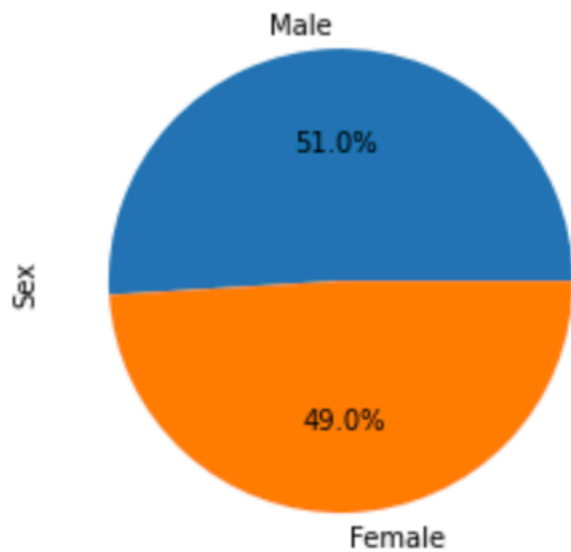
Generate a bar plot showing the total number of measurements taken on each drug regimen using pandas.



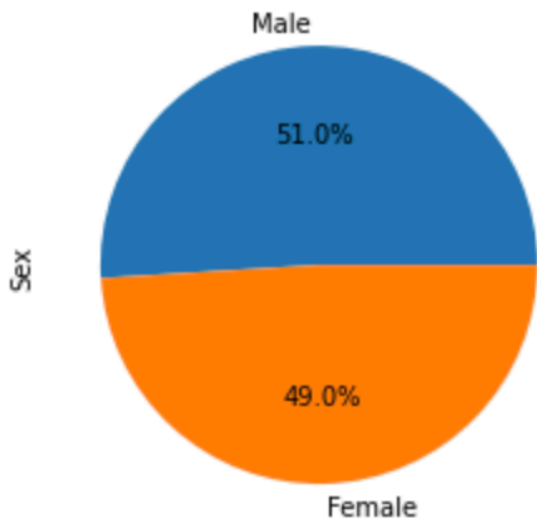
Generate a bar plot showing the total number of measurements taken on each drug regimen using using pyplot.



Generate a pie plot showing the distribution of female versus male mice using pandas



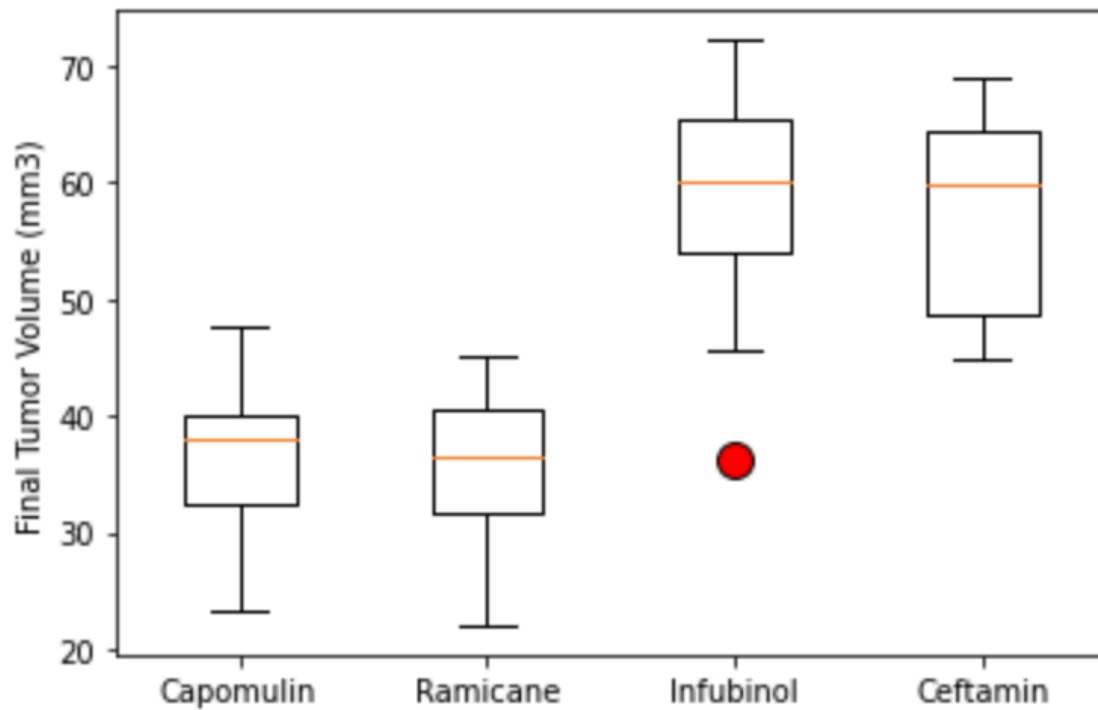
Generate a pie plot showing the distribution of female versus male mice using pyplot



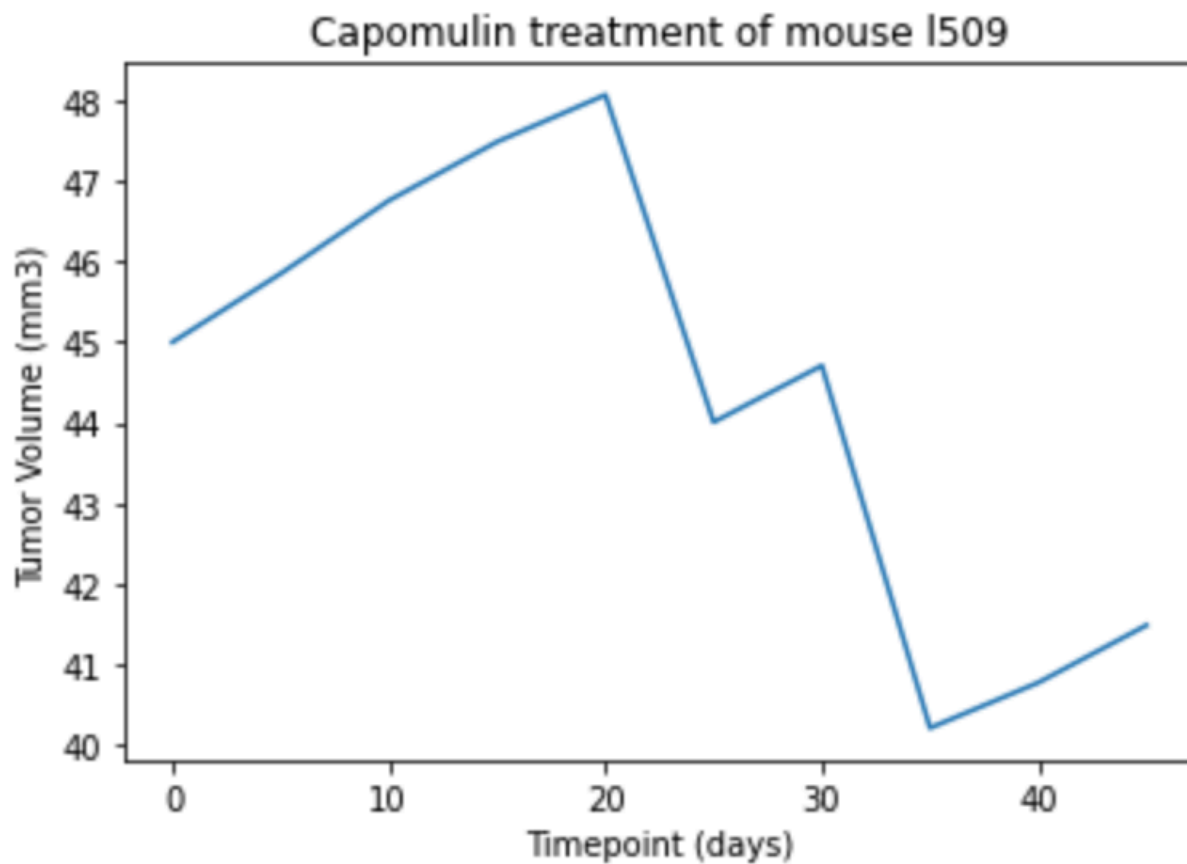
Quartiles, Outliers and Boxplots

```
Capomulin's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
Ramican's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
Infubinol's potential outliers: 31      36.321346
Name: Tumor Volume (mm3), dtype: float64
Ceftamin's potential outliers: Series([], Name: Tumor Volume (mm3), dtype: float64)
```

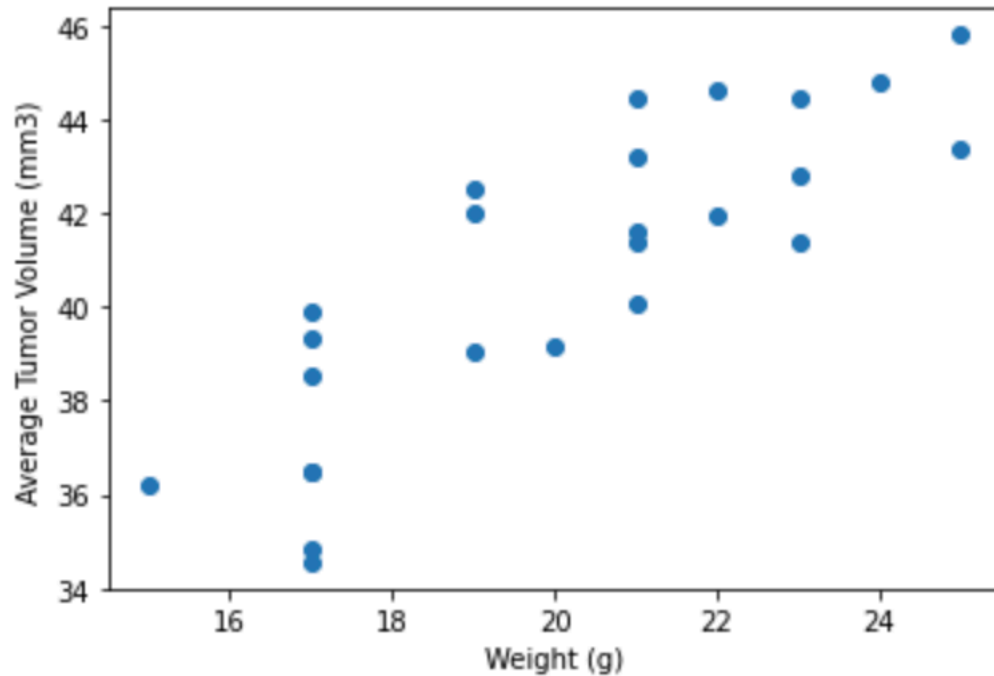
Generate a box plot of the final tumor volume of each mouse across four regimens of interest



Generate a line plot of tumor volume vs. time point for a mouse treated with Capomulin



Generate a scatter plot of average tumor volume vs. mouse weight for the Capomulin regimen



Calculate the correlation coefficient and linear regression model

for mouse weight and average tumor volume for the Capomulin regimen

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

