

Instructions:

Evaluate the homework against the outlined criteria in both the assignment rubric in addition to the challenge rubric, assigning a rating to each criterion. Add points earned across all criteria and convert the total points to a letter grade, assigning a “+” or “-” letter grade designation at your discretion.

A (+/-)	160+	C (+/-)	70-114	F (+/-)	<25
B (+/-)	115-159	D (+/-)	25-69		

Notes:

The deployed assignment utilizes the **Pandas**, and **Matplotlib** libraries to analyze the Pymaceuticals challenge. The source code should also be deployed to **Github** or **Gitlab**.

Assignment Rubric for Pymaceuticals Inc and the Power of Plots:

	Mastery 20 points	Approaching Mastery 15 points	Progressing 10 points	Emerging 5-0 points	Incomplete
Summary Statistics	The notebook generates a summary data frame, that contains: ✓ All drug regimens ✓ All summary statistics (mean, median, variance, std. deviation or SEM)	The notebook generates a summary data frame, that contains at least one of the following: ✓ All drug regimens ✓ All summary statistics (mean, median, variance, std. deviation or SEM)	The notebook generates a summary data frame, that contains at least: ✓ One or more drug regimens ✓ One or more summary statistics (mean, median, variance, std. deviation or SEM)	✓ The notebook does not generate a summary data frame, but does create a data frame with calculated columns	No submission was received -OR- Submission was empty or blank -OR- Submission contains evidence of academic dishonesty
Bar Plots	✓ Two bar plots are successfully generated depicting the number of data points for each treatment regimen using both plotting methods: ✓ <code>pandas.DataFrame.plot()</code> ✓ <code>matplotlib.pyplot()</code>	✓ A bar plot is successfully generated depicting the number of data points for each treatment regimen using only one plotting method: ✓ <code>pandas.DataFrame.plot()</code> ✓ <code>matplotlib.pyplot()</code>	✓ A bar plot is successfully generated, but not for the number of data points for each treatment regimen	✓ The contains broken code that attempts to generate a bar plot	
Pie Plots	✓ Two bar plots are successfully generated depicting the distribution of male versus female mice using both plotting methods:	✓ A bar plot is successfully generated depicting the distribution of male versus female mice using only one plotting method: ✓ <code>pandas.DataFrame.plot()</code>	✓ A pie plot is successfully generated, but not for the distribution of male versus female mice	✓ The notebook contains broken code that attempts to generate a pie plot	

	<ul style="list-style-type: none"> ✓ <code>pandas.DataFrame.plot()</code> ✓ <code>matplotlib.pyplot()</code> 	<ul style="list-style-type: none"> ✓ <code>matplotlib.pyplot()</code> 			
Quartiles, IQR and Outliers	<ul style="list-style-type: none"> ✓ The notebook calculates all of the following for all four drug regimens: <ul style="list-style-type: none"> ✓ Quartiles ✓ IQR ✓ Outlier boundaries ✓ All potential outliers 	<ul style="list-style-type: none"> ✓ The notebook calculates all of the following for one drug regimen: <ul style="list-style-type: none"> ✓ Quartiles ✓ IQR ✓ Outlier boundaries ✓ All potential outliers 	<ul style="list-style-type: none"> ✓ The notebook calculates two of the following for one drug regimen: <ul style="list-style-type: none"> ✓ Quartiles ✓ IQR ✓ Outlier boundaries 	<ul style="list-style-type: none"> ✓ The notebook calculates one or none of the following: <ul style="list-style-type: none"> ✓ Quartiles ✓ IQR ✓ Outlier boundaries 	
Box Plots	<ul style="list-style-type: none"> ✓ A box and whisker plot is successfully generated for the final tumor volume, and meets all of the following criteria: <ul style="list-style-type: none"> ✓ All four treatment regimens are on the same plot ✓ Potential outlier data points have a custom style or color 	<ul style="list-style-type: none"> ✓ A box and whisker plot is successfully generated for the final tumor volume, but does not meet all of the following criteria: <ul style="list-style-type: none"> ✓ All four treatment regimens are on the same plot ✓ Potential outlier data points have a custom style or color 	<ul style="list-style-type: none"> ✓ A box and whisker plot is successfully generated, but not for the final tumor volume 	<ul style="list-style-type: none"> ✓ The notebook contains broken code that attempts to generate a box and whisker plot 	
Line Plots	<ul style="list-style-type: none"> ✓ A line plot is successfully generated for the time point versus tumor volume for a single mouse treated with Capomulin 	<ul style="list-style-type: none"> ✓ A line plot is successfully generated for the time point versus tumor volume but is not representative of a single mouse treated with Capomulin (i.e., some alternative drug regimen) 	<ul style="list-style-type: none"> ✓ A line plot is successfully generated, but not for the time point versus tumor volume for a single mouse treated with Capomulin 	<ul style="list-style-type: none"> ✓ The notebook contains broken code that attempts to generate a line plot 	
Scatter Plots	<ul style="list-style-type: none"> ✓ A scatter plot is successfully generated depicting mouse weight versus average tumor volume for the Capomulin regimen 	<ul style="list-style-type: none"> ✓ A scatter plot is successfully generated depicting mouse weight versus average tumor volume, but not for the Capomulin regimen 	<ul style="list-style-type: none"> ✓ A scatter plot is successfully generated, but not depicting mouse weight versus average tumor volume for the Capomulin regimen 	<ul style="list-style-type: none"> ✓ The notebook contains broken code that attempts to generate a scatter plot 	
Correlation and Regression	<ul style="list-style-type: none"> ✓ All conditions are met: <ul style="list-style-type: none"> ✓ The correlation coefficient is calculated for mouse weight versus average tumor volume ✓ The linear regression model is calculated for mouse weight versus average tumor volume ✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume 	<ul style="list-style-type: none"> ✓ Two of the three conditions are met: <ul style="list-style-type: none"> ✓ The correlation coefficient is calculated for mouse weight versus average tumor volume ✓ The linear regression model is calculated for mouse weight versus average tumor volume ✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume 	<ul style="list-style-type: none"> ✓ One of the following conditions are met: <ul style="list-style-type: none"> ✓ The correlation coefficient is calculated for mouse weight versus average tumor volume ✓ The linear regression model is calculated for mouse weight versus average tumor volume ✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume 	<ul style="list-style-type: none"> ✓ The notebook contains broken code that attempts to calculate the correlation coefficient or linear regression model. 	

Observations and Insights	✓ The notebook contains three observations or insights about the data	✓ The notebook contains two observations or insights about the data	✓ The notebook contains one observation or insight about the data	✓ The notebook contains no observations/insights, or observations/insights are inappropriate to the data set	
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