

**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:**

	<b>Mastery 20 points</b>	<b>Approaching Mastery 15 points</b>	<b>Progressing 10 points</b>	<b>Emerging 5-0 points</b>	<b>Incomplete</b>
<b>Summary Statistics</b>	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
<b>Bar Plots</b>	✓ Two bar plots are successfully generated depicting the number of unique mice 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 unique mice 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 unique mice for each treatment regimen	✓ The contains broken code that attempts to generate a bar plot	
<b>Pie Plots</b>	✓ 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"> <li>✓ <code>pandas.DataFrame.plot()</code></li> <li>✓ <code>matplotlib.pyplot()</code></li> </ul>	<ul style="list-style-type: none"> <li>✓ <code>matplotlib.pyplot()</code></li> </ul>			
<b>Quartiles, IQR and Outliers</b>	<ul style="list-style-type: none"> <li>✓ The notebook calculates all of the following for all four drug regimens: <ul style="list-style-type: none"> <li>✓ Quartiles</li> <li>✓ IQR</li> <li>✓ Outlier boundaries</li> <li>✓ All potential outliers</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook calculates all of the following for one drug regimen: <ul style="list-style-type: none"> <li>✓ Quartiles</li> <li>✓ IQR</li> <li>✓ Outlier boundaries</li> <li>✓ All potential outliers</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook calculates two of the following for one drug regimen: <ul style="list-style-type: none"> <li>✓ Quartiles</li> <li>✓ IQR</li> <li>✓ Outlier boundaries</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook calculates one or none of the following: <ul style="list-style-type: none"> <li>✓ Quartiles</li> <li>✓ IQR</li> <li>✓ Outlier boundaries</li> </ul> </li> </ul>	
<b>Box Plots</b>	<ul style="list-style-type: none"> <li>✓ 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"> <li>✓ All four treatment regimens are on the same plot</li> <li>✓ Potential outlier data points have a custom style or color</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ 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"> <li>✓ All four treatment regimens are on the same plot</li> <li>✓ Potential outlier data points have a custom style or color</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ A box and whisker plot is successfully generated, but not for the final tumor volume</li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook contains broken code that attempts to generate a box and whisker plot</li> </ul>	
<b>Line Plots</b>	<ul style="list-style-type: none"> <li>✓ A line plot is successfully generated for the time point versus tumor volume for a single mouse treated with Capomulin</li> </ul>	<ul style="list-style-type: none"> <li>✓ 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)</li> </ul>	<ul style="list-style-type: none"> <li>✓ A line plot is successfully generated, but not for the time point versus tumor volume for a single mouse treated with Capomulin</li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook contains broken code that attempts to generate a line plot</li> </ul>	
<b>Scatter Plots</b>	<ul style="list-style-type: none"> <li>✓ A scatter plot is successfully generated depicting mouse weight versus average tumor volume for the Capomulin regimen</li> </ul>	<ul style="list-style-type: none"> <li>✓ A scatter plot is successfully generated depicting mouse weight versus average tumor volume, but not for the Capomulin regimen</li> </ul>	<ul style="list-style-type: none"> <li>✓ A scatter plot is successfully generated, but not depicting mouse weight versus average tumor volume for the Capomulin regimen</li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook contains broken code that attempts to generate a scatter plot</li> </ul>	
<b>Correlation and Regression</b>	<ul style="list-style-type: none"> <li>✓ All conditions are met: <ul style="list-style-type: none"> <li>✓ The correlation coefficient is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ Two of the three conditions are met: <ul style="list-style-type: none"> <li>✓ The correlation coefficient is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ One of the following conditions are met: <ul style="list-style-type: none"> <li>✓ The correlation coefficient is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model is calculated for mouse weight versus average tumor volume</li> <li>✓ The linear regression model has been plotted over the scatter plot depicting mouse weight versus average tumor volume</li> </ul> </li> </ul>	<ul style="list-style-type: none"> <li>✓ The notebook contains broken code that attempts to calculate the correlation coefficient or linear regression model.</li> </ul>	

<b>Observations and Insights</b>	✓ 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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