| **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 (+/-) | 90+ | C (+/-) | 70-79 | F (+/-) | <60 | | --- | --- | --- | --- | --- | --- | | B (+/-) | 80-89 | D (+/-) | 60-69 |  |  | |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **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:**

|  | **Proficiency**  **100 to > 90 points** | **Approaching Proficiency**  **89 to > 80 points** | **Developing Proficiency**  **79 to > 60 points** | **Emerging**  **59 to > 0 points** | **Incomplete** |
| --- | --- | --- | --- | --- | --- |
| **Summary Statistics** | The notebook generates a summary DataFrame, that contains:  ✓ All drug regimens  ✓ All summary statistics (mean, median, variance, std. deviation or SEM) | The notebook generates a summary DataFrame, 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 DataFrame, 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 DataFrame, but does create a DataFrame 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 total number of measurements taken for each treatment regimen using both plotting methods:  ✓pandas.DataFrame.plot()  ✓ matplotlib.pyplot() | ✓ A bar plot is successfully generated depicting the total number of measurements taken for each treatment regimen using only one plotting method:  ✓ pandas.DataFrame.plot()  ✓ matplotlib.pyplot() | ✓A bar plot is successfully generated, but not for the total number of measurements taken for each treatment regimen | ✓The contains broken code that attempts to generate a bar plot |
| **Pie Plots** | ✓ Two pie plots are successfully generated depicting the distribution of male versus female mice using both plotting methods:  ✓ pandas.DataFrame.plot()  ✓ matplotlib.pyplot() | ✓ A pie plot is successfully generated depicting the distribution of male versus female mice using only one plotting method:  ✓ pandas.DataFrame.plot()  ✓ matplotlib.pyplot() | ✓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 |
| **Quartiles, IQR and Outliers** | ✓The notebook calculates all of the following for all four drug regimens:  ✓ Quartiles  ✓ IQR  ✓ Outlier boundaries  ✓ All potential outliers | ✓The notebook calculates all of the following for one drug regimen:  ✓ Quartiles  ✓ IQR  ✓ Outlier boundaries  ✓ All potential outliers | ✓The notebook calculates two of the following for one drug regimen:  ✓ Quartiles  ✓ IQR  ✓ Outlier boundaries | ✓The notebook calculates one or none of the following:  ✓ Quartiles  ✓ IQR  ✓ Outlier boundaries |
| **Box Plots** | ✓A box and whisker plot is successfully generated for the final tumor volume, and meets all of the following criteria:  ✓ All four treatment regimens are on the same plot  ✓ Potential outlier data points have a custom style or color | ✓A box and whisker plot is successfully generated for the final tumor volume, but does not meet all of the following criteria:  ✓ All four treatment regimens are on the same plot  ✓ Potential outlier data points have a custom style or color | ✓A box and whisker plot is successfully generated, but not for the final tumor volume | ✓The notebook contains broken code that attempts to generate a box and whisker plot |
| **Line Plots** | ✓A line plot is successfully generated for the time point versus tumor volume for a single mouse treated with Capomulin | ✓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) | ✓A line plot is successfully generated, but not for the time point versus tumor volume for a single mouse treated with Capomulin | ✓The notebook contains broken code that attempts to generate a line plot |
| **Scatter Plots** | ✓A scatter plot is successfully generated depicting mouse weight versus average tumor volume for the Capomulin regimen | ✓A scatter plot is successfully generated depicting mouse weight versus average tumor volume,but not for the Capomulin regimen | ✓A scatter plot is successfully generated, but not depicting mouse weight versus average tumor volume for the Capomulin regimen | ✓The notebook contains broken code that attempts to generate a scatter plot |
| **Correlation and Regression** | ✓All conditions are met:  ✓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 | ✓Two of the three conditions are met:  ✓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 | ✓One of the following conditions are met:  ✓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 | ✓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 |