E0 259 - Assignment 3

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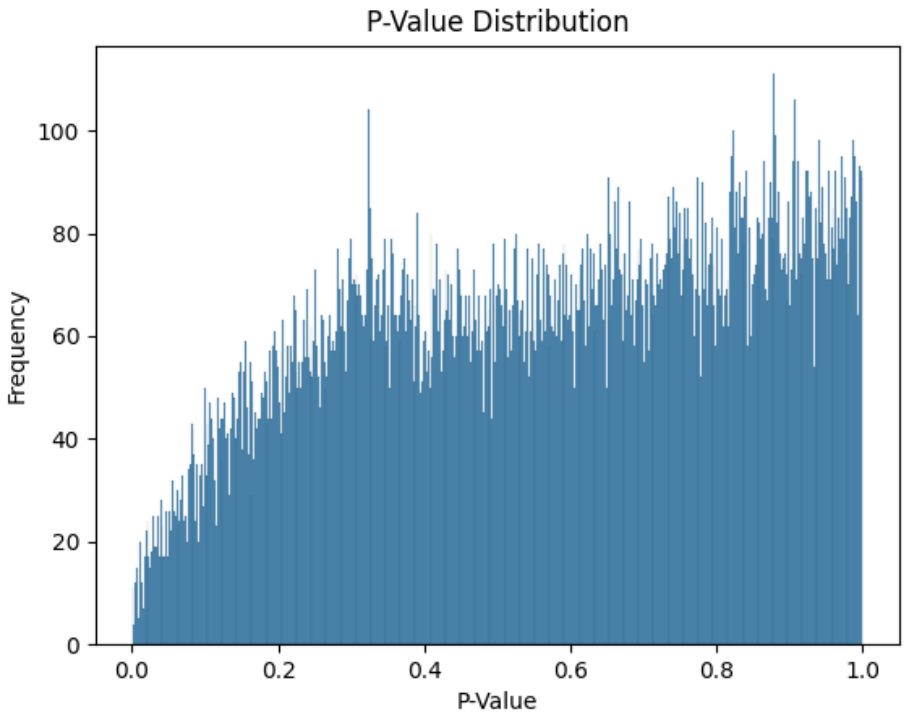
Output

After running the code, the output is as follows:



Implementation Summary:

I used a slew of libraries in Python to implement the code. The libraries used are:

- numpy
- matplotlib
- scipy
- pandas
- seaborn

- math

I used pandas to read the data from the text file, and drop all rows with NaN values in the GeneSymbol and EntrezGeneId columns.
I manually created the N and D arrays used for the formula of 2 way ANOVA. Afterwards I converted them to numpy arrays for fast computation.
To compute the p values, I go through each row, get the X vector and exponentiate the values as instructed in the slides. I then convert X vector to a numpy array and apply the formula for 2 way ANOVA which is:

$$\frac{1/(rank(D) - rank(N))}{1/(n - rank(D))} \times (\frac{X^T(1 - N(N^TN)^\dagger N^T)X}{X^T(1 - D(D^TD)^\dagger D^T)X} - 1)$$

Then I use the scipy.stats.f.cdf function to get the p value for each row.
After getting the p values, I plot the histogram of the p values using seaborn and matplotlib.