**Transcriptomic Analysis**

**Objective:**

This purpose of this task is for the applicant to perform differential expression analysis while controlling for age and gender with DESEQ2.

**Data:**

A matrix of gene counts generated by Salmon: mayo.path\_aging.con.salmon.gene.counts.txt

A csv file containing phenotype information: mayo.path\_aging.con.phenotype.csv

**Process:**

Using the count matrix and phenotype file, use DESEQ2 to determine the differential expression, controlling for gender and age.

**Output:**

1. Calculate the differentially expressed genes (Pathologic aging vs controls).
2. Present the results in an R Shiny application
   1. An ordered table with the results.
   2. A way to let the user pick any gene and have the system present a chart with the expression of cases and controls.

Please provide the documented R code, any intermediate files and instructions how to deploy.