**Overview: Analysis Tutorial – NMD-Mediated Regulation of Arsenic Detoxification Genes in *Saccharomyces cerevisiae.***

This tutorial expands on my research prospectus by showing how the nonsense-mediated mRNA decay (NMD) pathway post-transcriptionally regulates arsenic detoxification genes using RNA-Seq data and R-based data visualization. The central question driving this is whether NMD differentially influences the expression of important arsenic detoxification genes (ARR1, ARR2, and ARR3) under normal, low iron, and copper stress (both high and low levels) is the main question guiding our investigation.

To investigate this, with the help of chat GPT, I created an R script to handle RNA-Seq data from yeast strains that are wild-type and NMD mutants (upf1Δ, upf2Δ, and upf3Δ). Using ggplot2 to construct a bar plot that displays expression patterns among NMD mutants, organizing the gene expression data into a data frame with log2 fold changes, and loading necessary packages (including ggplot2, dplyr, and tidyr) are all part of the tutorial. The outcome is an easy to see comparison that shows how each ARR gene reacts to disruption of NMD.

I used RNA-Seq data from a work by Dr. Allan Jacobson that focused on high-resolution identification of NMD sites in yeast and was made available to the public in the supplementary data. Gene expression profiles for wild-type and NMD mutant strains (upf1Δ, upf2Δ, and upf3Δ) under typical circumstances were provided by this dataset. I will use the same yeast strains from ongoing investigations in my lab to generate RNA-Seq data for comparisons under low iron and high/low copper stress conditions in the future.

I developed a systematic workflow in R that imports the data, compares the behavior of the ARR gene in the three NMD mutants, and visualizes log2 fold changes in expression. Different regulatory patterns are displayed in the ensuing bar plot, with genes such as ARR3 displaying more noticeable upregulation, indicating that it might be a potent NMD target.

Finding out how NMD helps regulate metal detoxification pathways in response to stress is a major goal of my project, and this analysis supports that goal. I hope to identify condition-specific regulation and shed light on how RNA quality control systems adjust to environmental stressors by combining publicly accessible and lab-generated data. This is an area that has significant ramifications for both basic biology and environmental health.