When designing pathways to put into cells it is important to take into account the stoichiometry of the components of the pathway. If two of protein A are needed for every protein B, then when we design the pathway, we want to make protein A be produced twice as frequently as protein B. If we produce more A than that, then we are wasting resources since those protein As will not be used for anything. If we produce less than that amount, then we are still wasting resources because then protein B will be produced in excessive amounts. If we can determine what in the RNA makes the RNA produce more protein, then we can tailor the genes in the pathway more precisely.

Current methods for predicting the amount of protein produced based on Shine Delgarno sequences and Ribosome Binding Sequence (RBS) strength analysis are very inaccurate. The goal of this project is to create a more accurate method for predicting translational efficiency from the mRNA sequence by using ribosome profiling and analysis of mRNA secondary structures. It has been observed that ribosomes move slower around certain codons than around others. If this contributes to the translational efficiency, then current methods that predict protein production by determining the strength of an RBS may not capture the whole picture.

Ribosome profiling is like taking a snapshot of where the ribosomes are on mRNA on the cell. The slower the ribosome move through a section, the more ribosomes will be present on that section in various mRNA copies. Ribosome profiling starts by taking cells and cutting up everything in the cell including all the mRNA except for the ones protected by ribosomes. Then we remove those protected fragments and sequence them and map them to organism’s genome counting how often specific fragments were protected.

I still need to figure out what specifically I will be helping with, but I will begin by learning more about how ribosome profiling data is gathered and analyzed. I should be able to get from the raw data to the graphs presented in the research paper.