As mentioned in yesterday’s notes, the ribosome occupancy seemed to be centered on 1, and the codon usage seemed to range from 0 to 1. The units in the graph were arbitrary. I want to try manipulating the data a bit to see if I can make a graph in python that looks similar to what they have. My plan is to take the average of the ribosome occupancies and divide each by the average. Then for codon usage, I plan to find the maximum and then divide each codon usage by the maximum value. This will make a y axis centered on 1 and an x axis with a max value of 1. I will try this for the fp wig file and see how it looks. There may still be some missing normalization factor like dividing by the total number of transcripts as determined by the mrna-seq data, but I am not yet sure how to do this, so I will keep that idea on the side and just look for something that generally looks like what is in the paper.

First I need to refigure out how plotting in python works.

I figured out how plotting works and plotted the graphs. It didn’t look very similar to the graphs Jing had. I am not sure if the graphs Jing had were made using the exact same data or not. I will need to check this when she comes.

Bryan wanted me to compare the minimal media to the rich defined media in terms of codon usages and gene reads. I had to recode a lot of the previous codes to make it more adaptable to using different wig files. I am not exactly sure whether to just graph the scores from each codon and each gene for both cases or if I am supposed to divide it by something like the average or the minimal defined media or something. Currently the program just graphs the values. For the genes the graph just looks like a giant blot with no visible trends. For the codon usages it seems like the minimal media had slightly higher ribosome binding than rich media. I didn’t do any statistical tests or lines of best fits though.

Jing and I started to try and reproduce the graph that compares the first half of a gene to the second half minus the edge 5 codons at the beginning and end. We didn’t finish bet we started.