I forgot to start taking notes at the beginning of the day, so this may be shorter than usual.

Bryan wanted us (Alex and me) to produce a graph that can somehow show what the mRNA and protein level of each gate is at each truth value after stabilization and also tell whether the expected was high or low.

Alex and I worked on this together. Alex worked primarily on getting the values after each stabilization. I worked primarily on the truth values because I was more familiar with the Gate and Wire and DAG objects. We were successfully able to generate the graphs, however while showing it to Bryan we noticed that there was a problem. We were not able to produce efficient pathways no matter how we manipulated values.

As Bryan mentioned earlier, the inputs are supposed to be activating not repressing. We never fixed that problem. We also noticed that we were graphing the promoter levels rather than the protein levels of each gate. So I worked to fix this. Both of them were essentially fixed at the same time. I added several properties and functions to the Gate and DAG class. The Gate class now has a property that tells how close the gate is to its furthest input. This is done using recursion. The gates also have two properties that store the expected protein and mRNA levels. A 1 means it is expected to be high and 0 means it is expected to be low. This is also done using recursion to start at inputs and work to the output. The DAG has the functions to sort the gates by their closeness to the inputs which will allow for the netlist to be printed in order. The DAG also has a function to update the expected mRNA and promoter levels because we can only do these when the graph is complete. We will get an error if the graph is incomplete with a wire leading from None to a gate. The distance finder works for sequential circuits while the expected protein and promoter finders do not. I also updated General to graph the protein levels rather than the promoter levels. When I say promoter level I guess I am referring to the frequency of the promoter being on in a cell population.

In summary everything is working as expected now and it is possible to create efficient pathways. However, the randomly generated libraries do give some very unexpected behaviors. Perhaps it is because the values are too erratic. I will have to look into these tomorrow.

Note: mRNA values seemed a bit low especially compared to protein levels. It might be because of the log scale, but it seemed like there was no mRNA present but protiens were still being produced. Also the randomly generated libraries were producing weird values. These need to be looked into tomorrow.

Tomorrow I will also look into getting the score for each gate by comparing the highest low and the lowest high.