The goal of my work for Dr. Mansfield was to develop a computational method of producing a phylogenetic tree with special characteristics for a group of species. The tree’s branches were to be proportional to the species’ divergence times, and carry a label indicating the number of changes within a given amino acid sequence, in this case the HOXA5 gene, in each branch. The number of changes in the amino acid sequence was determined using software in the PAML package.

The final product achieved over the summer was not completely successful due to some issues with the software that required some workarounds, but progress was made. To achieve the desired results the following programs were used: ClustalW2, PAML, and TreeView. First, the amino acid sequences of each species had to be aligned; to do this I used ClustalW2. Then the sequence alignments were input to PAML, specifically the aaml program, twice to deal with the alignment gaps. Using the results obtained from PAML I determined which sites changed in the alignment and on which branches on the tree the sites changed.

I was unable to achieve the desired results using TreeView. I had not been able to find out how to convert the existing data we had from millions of years of genetic divergence into some sort of decimal input or another format that TreeView would accept. Also, after using the default decimal input generated from PAML, I encountered another problem. I had not been able to find a way to label the branches without having TreeView remove the proportionality of the branches.

To achieve a well polished result, work remains to be done on this project. Some simpler and more accurate workarounds for the aaml program must be generated. The current method requires the sequence to be run through the program twice, each time with different options, and then the results are compared and manually analyzed a second time to determine ancestral sequences. This second analysis is not automatic, does not fully implement accurate methods such as maximum likelihood, and is time-consuming.

The goal of my work for Dr. Son was to produce a computer program in REALbasic that runs an experiment that logs user input and will be used to determine the meaning of a confidence judgment in regards to time allocation. The experiment assumes that if
there is a certain confidence judgment associated with an item, a certain amount of additional study time must be given to bring the item to a “learned state.”

The program contains two parts. The first part consists of displaying word pairs to subjects for a certain amount of time and asking them to judge how confident they are that the item is in a “learned state,” on a scale of 0, 25, 50, or 100 percent. The amount of time each word pair is shown and the confidence judgment the subject chose are logged by the program.

The second part of the program uses the judgments obtained from the first part to determine a certain amount of additional study time. After allowing subjects to use this additional study time they are tested and the results of the tests are recorded.

For this program I’ve had to work with REALbasic, an object-oriented variant of the BASIC programming language. The first part of the program is nearly complete. The framework of the second part of the program has just been put in place. I still need to learn how to properly deal with certain aspects of the language such as input streams to complete this program.