My research this summer at the Wenner-Gren Institute at Stockholm University offered me with a truly life-changing experience. The projects I worked on consisted primarily of analyzing how the uncoupling protein 1 (UCP1) gene evolved in eutherian mammals, as the gene plays an important role in nonshivering thermogenesis and can be used to help create medications to combat obesity. I spent the majority of my time there reconstructing a possible UCP1 sequence for the ancestral stem eutherian from a data set of approximately 240 species. After learning how to perform this from reading other publications from the lab, I used the Phylogenetic Analysis for Maximum Likelihood (PAML) software package to recreate this ancestral sequence as well as ancestral sequences for several subsets of species. This highlighted the key amino acids needed for thermogenesis and for UCP1 to function. For the last two weeks, I focused specifically on the branch of the tree ancestral to pigs and peccaries, as inactivations were found in both species pushing back estimates for the inactivation date up to 35 million years, while it had previously been thought to occur after their divergence 28.8 million years ago. Using PAML and following procedures outlined in other published works, I was able to estimate this inactivation as having occurred anywhere between 40.73 and 43.96 million years ago with a data set of 58 species. We are currently in the process of submitting a publication on these findings to the Proceedings of the Royal Society B: Biological Sciences journal.

I am really glad to have taken part in this research and worked with some of the best thinkers in this field. I felt that I got a firsthand experience of what research really is and definitely enjoyed my time working in the lab. In my research, I saw how mathematics and computer science intersected in the professional world and how to use both in conjunction with each other to produce meaningful advances in this field of research.