My lab for this summer is Dr. Ali Akoglu's, in which our goals are to more efficiently and effectively use a DNA recombination algorithm to model the TCR$\beta$ strand. Analysis of TCR pool (repertoire) is crucial for understanding the functionality of a healthy immune system, determining the nature of successful and unsuccessful immune responses, and understanding the immune mechanism in the presence of different diseases such as type 1 diabetes, various cancers (blood, breast, colorectal, etc.), rheumatoid arthritis (an autoimmune disease), and multiple sclerosis. The response of the immune system to a specific antigen often leaves evidence in the form of repertoire sequence patterns (signatures) that are common across individuals. The ability to detect such patterns is critical for understanding the correlation between the immune receptors and different diseases, and identifying immune receptor clones that can be converted into precision vaccines. The earliest clinical contributions in the field have already saved countless lives while garnering a Nobel Prize, yet the field is in its infancy and progress is hampered by a lack of understanding of the nature of which immune receptors are 1) created by the immune system, 2) bind to which antigenic targets, 3) become recruited into an immune response, and 4) retained in a memory anamnestic response.

A diverse set of T-cell receptors, TCRs, is required for the adaptive immune system to detect a wide variety of antigens successfully. V(D)J recombination is the primary mechanism for generating a diverse repertoire of TCRs essential to the adaptive immune system for recognizing a wide variety of diseases. However, modeling the TCR repertoire is computationally challenging. The main hindrance is the enormous magnitude of the repertoire of TCR species that can be made by the immune system. Replicating the recombination process in a simulation environment allows immunologists to test different hypotheses on immune system response analysis. My research covers automating the process of launching experiments for various configurations of the simulation. My research will culminate in applying statistical methods and visualization approaches for understanding the significance of the increased number of unique recombination pathways that are found as a result of the simulated experiments.

My lab does not use any specific software and doesn't follow a certain template. I talked with Dr. Akoglu, my PI, and he told me that there is no certain way I need to create my poster.