I am interested in the field of high-throughput computational proteomics and applying topological, statistical, and matrix theory models to large-scale data and clinical studies. I want to utilize my interest in computational biochemistry tools to study the effects and increase the success of personal drug treatments and gene therapy for individuals with cancer and neurodegenerative and neuromuscular diseases, to improve the probability of success rates. I want to combine my aptitude for mathematics, with my new-found interest in statistical computing and apply these two subjects to help people in the most impactful way -- to improve health and cure disease and malnutrition.

My coursework so far has included multivariate calculus, linear algebra and matrix theory, computer programming and scripting in Python, R, Linux and Java, as well as Biology for Healthcare, Organic and Biochemistry, and Differential Equations. My current experience has prepared me for a Master's in Bioinformatics along with my career goals to study protein topology, protein chemistry and 3-dimensional hotspots, fluid mechanics and thermodynamics, drug interaction with proteins for cancer and disease therapy, and developing computational programs to analyze, target and learn from this information. In addition to my coursework I have participated in a biotechnology wet laboratory which trained in preparing reagents, streak for isolation, preparing agar plates, growing E. coli cultures, preparation of chemically competent cells, transformation and plasmid DNA isolation, restriction digest, electrophoresis gel, cloning DNA with PCR, DNA extraction from GMO foods, and gene manipulation in the transformation of E. coli.

I have gained an increased interest in mathematics, physics and the application of stochastic models for studying biological processes and how drugs treat and affect disease. I believe currently we have the technology needed to create personalized medicine to better target and fight cancer. We are making breakthroughs in the quantitative analysis of therapeutic pathways using probabilistic graphing models, the study of proteins in 3-dimensional space with x-ray diffraction, illumination and cryogenic electron microscopy, and my latest interest includes using matrix theory to come up with machine learning solutions that can predict interactions of drugs. My coursework in the Bioinformatics program at Johns Hopkins will need to include overlaying classes with the programs of Applied and Computational Mathematics and Biostatistics. I have learned lots just from reviewing the information in the Data Science Specialization and Biostatistics Bootcamp classes on Courseera taught by Dr. Brian Caffo, Dr. Jeff Leek, and Dr. Roger Peng. I have also reviewed the information in the Genomic Data Science Specialization while performing bioinformatic tasks myself and will continue to study the courses in this specialization this summer along with case studies in Bioconductor and Biopython. I am excited to perform more work in proteomics and RNA analyses using the HITSAT2 application developed by Johns Hopkins. I am also excited to utilize the power of AWS needed to run these analyses.

I have been learning necessary Bioinformatics sequencing and greedy motif algorithms from the Courseera course in Bioinformatics at USC using Python to prepare for the classes in Introduction to Bioinformatics, Bioinformatics: Tools for Genome Analysis, and Advanced Practical Computer Concepts for Bioinformatics. I am very interested in the courses in Protein Bioinformatics and Methods in Proteomics along with the Recombinant DNA Laboratory; especially in the laboratory tools used in these applications. My wet lab experience and extensive research in biochemistry will prepare me for these courses.

My goals for my Master’s in Bioinformatics will be to continue to learn about quantitative proteomics and machine learning for prediction of protein interaction. This include protein annotation with biomarker workflows, molecular protein structure in three dimensions, analyzing liquid chromatography and mass spectrometry data in the chemical makeup of proteins, design computer algorithms and statistical methods for understanding protein-protein interaction, hotspot residues for drug targeting, vector analysis of x-ray crystallography and x-ray diffraction in proteins, and drug-protein interaction. I want to excel in program scripting in R and Python to run most of the functional analysis and machine learning that occurs in these processes and continue to write software and work with current software applications to visualize and present this information to and for pharmaceutical and bioengineering companies. I would also like to add that I am excited to perform research under Karen Wells, with her research experience in membrane transport proteins and neurotransmitter receptors. This will be integral to my study of cancer cell metabolism and target for cancer therapies.