Dear Faculty Members,

My name is Brian and I am currently completing my M.S. in Bioinformatics at Johns Hopkins University. My programming studies so far have included computer algorithms and machine learning, while my biology studies have included molecular biology of the gene, epigenetics, and protein bioinformatics. While I have wet lab experience in DNA transformation and isolating genes in E. coli and Cell biology wet lab I favor performing analysis in the computer lab. I have 3 years programming experience in Python, R and Java in biological and non-biological topics. My studies this fall will continue with implementing databases, Next-gen sequencing including ChIP- and RNA-seq, RNA microarray analysis and Perl programming while next spring I will finish my degree with Cancer biology, more database modelling, as well as advanced genomics and genetic analyses of splice variants, mutation analysis and copy number variation. Additionally, I completed and continue to use in my studies the material learned in Organic chemistry and Biochemistry when studying biotherapeutics and protein bioinformatics.

I am interested in the field of high-throughput computing in proteomics, signal pathways, metabolic regulation, and gene networks to define therapeutic targets in hematological cancers. Not only do I enjoy researching the pathology and biological targets in these cancers but my goal during my PhD and career are to use computational tools and algorithms to model small molecules, protein drugs, and antibodies as therapies. I hope to narrow down a specific type of hematological cancer throughout your program. I completed a project on Leukemia stems cells in my Epigenetics course on the role of differentiation in ALL and AML which was really exciting however I am also interested in immunotherapies targeting receptors in aggressive B-cell lymphomas and B-cell acute lymphoblastic leukemia.

During the completion of your program I wish to obtain the skills to collaborate with bench scientists and other bioinformaticians to design creative workflows that increase efficiency of drug targeting in leukemia and lymphoma and personalized drug targeting of mutated genes and fusion proteins. I also want to collaborate with laboratories in pharmaceutical chemistry and biophysics to learn more about requirements for designing drug modelling software. I would also like to take classes in these two disciplines to better sort through databases and implement physical chemistry algorithms.

Brian Wiley