Andrew Teng

Within the medical field, recent advances and strides have been direct effects of the powers of modern technology. This backbone of human progress continues to pave the way for future success and development. Computing algorithms and logic derived from mathematics can be easily integrated in any field, especially medicine and clinical decision making. During my undergraduate career at Emory University, I studied mathematics and computer science and my primary focus was to explore and apply the logic and methods behind these two interlocking concepts. By following a pre-medical track while studying mathematics and computer science, I was able to delve into these unique spheres to explore problems from a holistic perspective.

In order to fully understand how to integrate these disciplines, I needed to see the medical field in action. I was fortunate to shadow anesthesiologists and nurses at Emory St. Joseph's Hospital. During my time there, I noticed the healthcare and clinical settings were not taking advantage of genomic data to provide more optimal personalized care. In a world where interoperability and usability are assumed, I was astounded to see such contrast. With the abundance of personal health data available provided from fitness trackers, such as smartphones, it was apparent that more personalized care could be and should be offered. In addition, I had a glimpse of the electronic health record systems currently in place and was able to see first hand how disconnected and convoluted patient records can be. Working with the eICU department at Emory Healthcare, I helped to develop a web application that would connect to the intensive care unit's database system and visualize all the data from a population perspective, rather than a traditional patient-centered view. This unique way of displaying the data would allow a clinician to spot abnormalities faster, easily analyze trends, and deliver precise personalized treatment.

Furthermore, the same data used to create more personalized care can also be applied to prediction and prevention. I had the opportunity to intern at the National Cancer Institute under Dr. Kai Yu. Focusing on the correlation between human papillomavirus 16 and cervical cancer, I built a supervised learning prediction model based on pap smear results to predict cervical cancer risk for any given individual. My primary focus was to identify the viral genetic basis of HPV carcinogenicity and to create a prediction model using random forests. Because the sample size for the testing and training sets were smaller than desired, the model proved to be slightly better than random chance. The idea of building a prediction and classification model could be applied to other diseases and eventually applied in a clinical setting for more personalized patient care.

Since joining the bioinformatics master's program at Georgia Tech, I have been a graduate research assistant in the Lachance Lab. My primary interests are in precision medicine as well as predictive health, which ideally would be applied in a clinical setting. Our current project consists of finding evidence of male-biased migration out of Africa as well as analyzing the increased risk of prostate cancer in men of African-descent. I took 147 genome-wide association study hits that were known to be associated with prostate cancer and narrowed the list down to 68 independent and unique single nucleotide polymorphisms from 64 global populations using odds ratios and risk allele frequencies. After simulating the chance of getting prostate cancer for one million virtual individuals using MATLAB, I was ready to ask the question, "how do genetic risk scores translate to one's chance of actually getting a disease?" and

to see if genetic risk scores accurately predict health disparities. Using prostate cancer mortality data from the CDC, I found that our results successfully captured ethnic differences in incidence and mortality and the robustness of the results were tested via bootstrapping. By creating an automatic pipeline, many types of cancers can be analyzed, allowing for an easy and streamlined analysis of genetic risk scores for various cancers of interest.

All of my experiences have enriched, educated, and shaped me over the years. Through group problem solving and teamwork, I have been able to communicate and present ideas with others and play an integral role in team projects. In the long run, I hope to take advantage of my research background to conduct research projects that would have practical applications in patient care. I am interested in learning all that I can within this field, so that I can utilize my knowledge, together with my existing skills, to further my understanding in bio and health informatics as well as precision medicine.