

ANDREW K. TENG

NLM Predoctoral Trainee | akteng@uw.edu | andrewteng.github.io

Personal Statement

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 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.

While pursuing the bioinformatics master's program at Georgia Tech, I was 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 project consisted 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.

Currently, I am a National Library of Medicine (NLM) predoctoral trainee in the Biomedical and Health Informatics program at the University of Washington (UW). I have broadened my research scope to also include both qualitative and quantitative research to gain a greater and more holistic understanding of the field. Working with Dr. Adam Wilcox, I gained further machine learning experience using Weka to predict readmissions at the UW Medical Center. I am currently writing a systematic review on predictive analytics tools for sepsis detection. Afterwards, I hope to create a transferable and generalizable model without configuration that will help standardize sepsis detection across institutions. On the other hand, I am working with Dr. Annie Chen and Dr. Oleg Zaslofsky to test the feasibility and usability of using an online discussion platform for frail elderly adults to learn, manage, and cope with their changing symptoms. I have interviewed a group of elderly individuals to understand how they interact with the computer and designed training materials that matched their learning styles. Furthermore, I performed one-on-one training sessions with the participants and was a moderator on the discussion forum to engage conversation amongst participants.

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 for consumers.