In my younger years, growing up in the farmlands of China's rural Hubei province, I learned that if you liked a boy, you shared with him your food. But if you loved a boy, you shared with him your knowledge. Thanks to the intellectual dedication and hard work of my parents, I was blessed with the opportunity to come to America at the age of six. As a result of my own intellectual dedication and hard work, I was able to test into the MBHS Math, Science, and Computer Science Magnet program and now thrive at Johns Hopkins University. But even as I've traveled across the world to establish my new home in once alien lands, this lesson, this philosophy - that if you love your fellow Man, you will share with him your knowledge - has stayed with me and has lead me to share my knowledge through teaching as well as through discovering new knowledge.

Sharing Knowledge through Teaching

I came America with no knowledge of the English language. Cast into the public educational system, I was able to succeed thanks to language assistance provided by my English teachers. Despite the rigors of the MBHS Magnet program, I sought to pay forward this language assistance and volunteered to tutor non-native English-speaking students with math during my lunch period. However, most of my students simply didn't find math interesting so I drew them a picture illustrating the underlying mathematical concepts instead.

Driven to provide a more non-conventional and fun method of teaching STEM subjects, during my sophomore year at Hopkins, I became the head software engineer for Bioinfor.me: BioHazards, a freely available educational video game designed to teach students the fundamentals of protein evolution framed in the context of disease progression and prevention. Collaborating with a group of graduate and postdoctoral biomedical engineering and art students, I programmed a 3D gaming environment to submerge players into a virtual DNA world in which they take control of a cell's cancer-prevention machinery and race against the molecular clock to discover and repair deleterious mutations by recruiting the appropriate proteins and repair molecules. The game has been a hit with high school students at the Baltimore Polytechnic Institute. Collaborative efforts are currently being made with the Weizmann Institute of Science in Israel to translate the game into Hebrew. In my future career, I hope to continue collaborative outreach efforts to develop non-conventional methods of teaching STEM subjects at all educational levels and continue infusing learning with fun and interactivity.

Taking a more conventional approach to teaching STEM subjects, I am currently the teaching assistant for Introduction to Optimization. I lecture weekly in a small auditorium of students to review and reinforce concepts presented in class. To further assist my students, I started the website JEFtalks to share additional class material and study guides. In being a teaching assistant, I learned to accommodate a wide range of learning styles and personalities, a skill that may prove crucial in my future collaborative efforts. More importantly, I've learned that, at the end of the day, what I teach isn't necessarily just optimization; it's also attitude - an attitude that encourages peer collaboration and active discussion concerning class material, an attitude that views homework as puzzles rather than problems, an attitude that I hope will be paid forward. I plan to continue teaching STEM subjects as a professor in my future career.

Sharing Knowledge through Discovering New Knowledge

During my junior year in the MBHS Magnet program, I began applying myself towards research so that I may not only share knowledge through teaching but also contribute new knowledge to the greater community. I contacted numerous PIs in search of an opportunity and was eventually accepted into a program at the National Institutes of Health. There, I investigated the $8p_{11-12}$ amplicon, a region of genetic amplification associated with poor breast cancer

prognosis. Out of the handful of potential oncogenes within this amplicon, *BRF2* was arbitrarily chosen to be the focus of my investigation and subsequently the target in months of immunoblot analyses, gene knockdowns, and clonogenic assays.

Frustrated with the seeming arbitrariness of gene selection for empirical analysis, I sought bioinformatics as a more powerful means of rapidly identifying putative disease drivers. Starting my freshman year at Hopkins, I began interning at the Institute for Computational Medicine to develop and improve sophisticated computational models and bioinformatics methods to predict for the functional impact of genetic mutations, integrating data from molecular modeling and sequence conservation analysis with clinical patient data and in vitro functional studies. In my most recent work, I devised a supervised machine learning approach to detect the optimal orthologous sequences depth used in bioinformatics methods to improve their accuracy in predicting the functional impact of mutations. I am currently developing a free web application to allow others to easily implement my method for detecting the optimal orthologous sequence depth and integrate this feature into their own bioinformatics methods to improve prediction performance. In my future career, I expect to continue developing free web applications aimed at improving the accuracy, reproducibility, and reliability of bioinformatics methods in predicting the functional impact of mutations.

The Next Generation of Knowledge

Technology has the potential to drastically revolutionize the way we discover new knowledge, now, through genomic data. With the decreasing cost and increasing speed of DNA sequencing, we are currently at the forefront of the genomic revolution. The challenge in this revolution, however, no longer lies in acquiring genomic data, but in interpreting genomic data.

Having taken both empirical and computational approaches to interpreting genomic data, I recognize the need for collaboration among wet and dry labs. In my future career, I aim to establish collaborative efforts between wet and dry labs to fundamentally change the biomedical research approach from selecting genes based on arbitrary intuition to selecting genes based on probabilistic likelihood, using bioinformatics methods to prioritize genes based on their predicted functional impact and focus empirical analysis on genes most likely to be associated with disease.

For my proposed graduate work, I plan to develop a Bayesian network approach for assessing the effects of genetic and environmental factors in complex disease etiology to acquire a better understanding of the degree to which these factors, either independently or combinatorially, contribute to disease development and progression. I plan to apply my Bayesian network approach to rapidly analyze numerous genetic alterations to identity mutations, proteins, genes, pathways, or interactions likely to be involved in the expression of diseased phenotypes. Identification of these biomarkers may provide new leads into drug development or drug repurposing, resulting in more targeted and personalized treatments. I aim to consolidate these efforts into developing freely accessible, open-source bioinformatics software.

With the support from and opportunities provided by the National Science Foundation Graduate Research Fellowship Program, I aspire to be a leader of this genomic revolution in the emerging field of translational bioinformatics, using bioinformatics for rapid interpretation of genomic data to help better understand the development and progression of complex human diseases and ultimately bring better, more personalized treatments back into the clinic to, one day, allow for, not simply, the treatment of a disease, but your unique disease.

If to love means to share knowledge, then I hope to continue to learn in order to love, and I to love in order to learn.