New Tenure-Track Faculty Spotlight— Dr. Heather Wheeler

I began thinking about a career in science, specifically forensic science, when I was a teenager growing up in rural Minnesota. I loved reading gory crime novels centered on forensics by authors like Patricia Cornwell, Jeffery Deaver, and, of course, Sir Arthur Conan Doyle. As an undergraduate at Hamline University, I worked at the Minnesota state crime lab in the DNA unit. While it was amazing that you could use DNA as a fingerprint to identify someone, I realized I was more interested in how the DNA variation we were measuring led to differences among people. My undergraduate advisor encouraged me to go to graduate school and I went to Stanford University and got a PhD in genetics and did postdoctoral research in genomics at The University of Chicago. Along the way, I picked up programming and data analysis skills to further my research. I was often the first person to put all the data that had been collected in the clinic and DNA sequencing centers together, run the analysis pipeline that I built, and visualize the results. I found data analysis to be very exciting, especially when I discovered something new because I was the first to see the result!

Dr. Wheeler teaches her Computational Biology Class. Students L to R: Virginia Saulnier, Shyam Shah, Jeffrey Ng, Alexa Badalamenti . (photo by Natalie Battaglia)

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I became an assistant professor at Loyola in Fall 2015 and will now get to pass on the thrill of discovery to my students. Our lab develops systems approaches to complex trait prediction by building computational models that leverage and integrate similarity in genome-wide genotype, gene expression, and other omics-level data. We are a dry lab, which means our scientific tools are powerful computers, we leave the pipettes and test tubes to others. We want to better understand how genetic variation leads to phenotypic variation for complex traits like disease susceptibility and drug response. The human genome is composed of a vast array of 3 billion bases, yet less than 2% of these bases encode proteins. What is the rest of the genome doing? Some of the non-coding regions are involved in gene regulation, controlling whether a gene is on or off and how much of it is expressed. Differences in DNA sequence among individuals can lead to differences in gene expression levels, which in turn can lead to trait differences. We have developed a method that harnesses these DNA differences to predict gene expression levels, which are then tested for correlation with a disease or other trait of interest to identify potential underlying biological mechanisms. My group will continue to develop innovative models to optimize prediction of gene expression and other complex traits using statistical machine learning approaches. We plan to apply and extend methods we have developed using genome-wide datasets from both collaborators and publicly-accessible databases. Many funding sources require database deposition of genome-wide datasets and thus the amount of data available to mine will continue to grow and allow us to learn more about the genetic architecture of complex traits. More information about Dr. Wheeler and her lab can be found at: http://hewlab.org.